Advances in Management of Animal Genetic Resources

Edited by

Raja K N
Sonika Ahlawat
Sagar Surendra Deshmukh
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B P Mishra

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ICAR-National Bureau of Animal Genetic Resources
Karnal (Haryana), 132001

National Institute of Agricultural Extension
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This e-book is a compilation of resource text obtained from various subject experts for Collaborative Online Training Programme of MANAGE, Hyderabad, Telangana and ICAR-NBAGR on "Capacity Building of Field Veterinary Officers on Management of Indigenous Domestic Animal Diversity" conducted from 14-18 November, 2022. This e-book is designed to educate the field functionaries of the state animal husbandry departments of the country, extension workers, students, and research scholars, academicians related to veterinary science and animal husbandry about strategies for characterization and conservation of indigenous animal genetic resources and appropriate policy interventions that are required to ensure their sustainable utilization. Neither the publisher nor the contributors, authors and editors assume any liability for any damage or injury to persons or property from any use of methods, instructions, or ideas contained in the e-book. No part of this publication may be reproduced or transmitted without prior permission of the publisher/editor/authors. Publisher and editor do not give warranty for any error or omissions regarding the materials in this e-book.

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PREFACE

ICAR-National Bureau of Animal Genetic Resources established in the year 1984 is the nodal organization for the identification, evaluation, characterization, conservation, and utilization of mega biodiversity of livestock and poultry genetic resources of the country. The farm animal genetic resources of India are represented by a broad spectrum of native breeds/populations of a large number of species like cattle, buffalo, sheep, goat, equine, camel, yak, mithun, pig, dog, and poultry. Adaptation to vivid climatic and traditional management conditions has endowed the indigenous breeds with better disease resistance, heat tolerance, and feed conversion efficiency.

Recently, the Bureau has initiated country-wide AnGR documentation after the launch of the "Mission towards Zero Non-descript AnGR of India". It has provided a perfect platform to spearhead our endeavour to describe the vast livestock and poultry diversity of the country. The book aims to put forth the current state of valuable AnGR diversity in our country and also discusses various strategies for their characterization and conservation. The approaches for phenotypic and genetic characterization of AnGR have been elaborated upon for field functionaries of state animal husbandry departments so that they contribute to our mission to document the AnGR diversity of the country. The importance of the National Gene Bank in cryopreserving semen, somatic cells, and DNA from different livestock/poultry breeds has been given special emphasis. National policies and programs for the genetic improvement of both small and large ruminants have been extensively discussed to ensure the sustainable utilization of livestock. Unique attributes present in AnGR which can promote their conservation have also been dealt with in this book.

Animal husbandry officials can serve as an important link to disseminate the knowledge and experience of scientists and subject matter specialists to the livestock keepers, which are the real stakeholders. In accordance, this book is the product of MANAGE sponsored online training program on "Capacity building of field veterinary officers on management of indigenous domestic animal diversity". We hope that this compilation will serve as a ready reference for students, researchers, animal husbandry officials, policymakers, and stakeholders interested in the facts and issues concerning the AnGR wealth of India. Contributions to this book have been solicited from esteemed scientists whose cooperation is thankfully acknowledged.

Editors

Contents

Role of ICAR-NBAGR in management of indigenous animal genetic resources (AnGR)

B P Mishra and S K Niranjan
ICAR-National Bureau of Animal Genetic Resources, Karnal-132001 (Haryana) India

Animal genetic resources (AnGR) history dates back about 12 to 14 thousand years old which was started with domestication of wild ancestors of about 40 present day livestock species which are exclusively utilized for food and agriculture. Cattle, sheep, goat, pig, horse and donkey are the domesticated livestock species distributed worldwide where as species like buffalo, dromedaries and bactrian camel, llama, alpaca, yak, mithun, are region specific. Among poultry, chicken, duck, geese, quail, guinea fowl, turkey are important species which are distributed in large part of the world. To meet the food demand in an imminent global scenario, with a challenge of maintaining the sustainability of the agricultural production system as well as biodiversity would be most challenging for AnGR in the near future.

The vast diversity of animal genetic resources has been developed in the form of "breeds" has been developed over hundreds of years through various evolutionary forces, including intensive selection, preferred mating for various utilization purposes etc. Migration of domesticated animals further disseminated the germplasm to various regions and continents, initiating the diversification of the farm animals across the globe and making them adapted to the native environment and human needs. The artificial selection for different needs and utilizations was the chief element for development of large-scale genetic diversity in form of distinct breeds among the farm animals. Natural adaptation of farm animals to different climates and habitats confounded with artificial selection has set to develop an array of breeds of livestock species. Today, the world possesses more than eight thousand livestock and poultry breeds, evolved from only few founder populations and catering various needs of human society around the world.

Management of AnGR

Global initiative on AnGR Management

In the year 2007 FAO laid the Global Plan of Action (GPA) for Animal Genetic Resources (also known as Interlaken declaration) was the first internationally accepted framework for the management of AnGR diversity in recent time. The necessity for the inventory of native germplasm as a prerequisite for long term preservation of germplasm, was realized by the courtiers only after adoption of global plan of action. As per Global data bank on Animal Genetic Resources of FAO, a total of 8774 breeds of 38 species were reported, worldwide (data from 182 countries) in 2014. Among these, 7718 are local breeds (in one country) and 510 are regional transboundary breeds (in one region) and 546 are international transboundary breeds (in more than one region).

Importance of the AnGR biodiversity preservation has also been emphasized by United Nations (UN), through their Sustainable Development Goals (SDGs) set in 2015, wherein it appealed for management of all genetic resources globally specifically to promote sustainable agriculture and achieving food security. SDG Goal 2 (Zero Hunger), Target 2.5 (Indicator 2.5.1: Number of plant and animal genetic resources for food and agriculture secured in either medium or long-term conservation facilities or Indicator 2.5.2: Proportion of local breeds classified as being at risk of extinction) are well related to the farm animal biodiversity.

Indian initiative on AnGR management

Animal genetic resource diversity in India

Cattle, buffalo, sheep, goat, pig, horse, donkey, camel, yak, mithun, dog and rabbit comprise the 12 farm animal species in India with few domesticated poultry species like chicken, geese, duck, Guianese fowl, Japanese quails etc. Indian subcontinent witnessed the earliest domestication of many farm species including Indicine cattle, buffalo, goat and poultry. In Indus valley civilization, cattle husbandry was main occupation playing important role, both in nutritional as well as economic, in their society. Selection of animals for specific work, based on specific traits, has laid foundation of breed formation in Ancient India.

A total of 212 registered indigenous breeds of livestock, poultry and dog, which include 53 of cattle, 20 of buffalo, 37 of goat, 44 of sheep, 7 of horses and ponies, 9 of camel, 13 of pig, 3 of donkey and one of yak in livestock and 19 of chicken, one of geese and two of duck in poultry has been registered till date, since 2008. Three indigenous breeds of dog have also been registered during 2020, for the first time in the country. During the last 10 years, more than 100 new populations were identified across the country and 83 breeds of different farm animal species were registered.

However, considering country's vast geographic and ecological regions, contrasting climatic conditions along with diverse necessity of the farmers, there is still a sizable undefined population of farm animals. There is one breed per 3 million livestock population in India, which is much lower than the world average (one breed per 0.9 million animals). At present, there are 353 population entries, including all of the registered breeds, in the Domestic Animal Diversity-Information System (DAD-IS) database of FAO.

Establishment of National Bureau

ICAR-National Bureau of Animal Genetic Resources was established on 21st September, 1984 by Indian Council of Agricultural Research at Bangalore in the form of twin institutes namely National Bureau of Animal Genetic Resources and National Institute of Animal Genetics and then shifted to Karnal in 1985, the two institutes were merged to function as a single entity in the form of National Bureau of Animal Genetic Resources (NBAGR) in 1995. The institute has been involved in characterization, documentation and conservation since its inception with the following objectives, mandate and mission:

Mandate

- Identification, evaluation, characterization, conservation and utilization of livestock and poultry genetic resources of the country.

- Co-ordination and capacity building in animal genetic resources management and policy issues.

Objectives

- To conduct systematic surveys to characterize, evaluate and catalogue farm livestock and poultry genetic resources and to establish their National Data Bank.
- To design methodologies for *ex-situ* conservation and *in-situ* management and optimal utilization of farm animal genetic resources.
- To undertake studies on genetic characterization using modern techniques of molecular biology.
- To conduct training programms as related to evaluation, characterization and utilization of animal genetic resources.

Mission

- To protect and conserve indigenous Farm Animal Genetic Resources for sustainable utilization and livelihood security.

Breed registration

Indian Council of Agricultural Research (ICAR) initiated "Registration of Animal Germplasm" specifically indigenous livestock and poultry breeds in the country. In the year, 2008, ICAR-National Bureau of Animal Genetic Resources (NBAGR), Karnal was given the temporary authority for the registration of germplasm related to livestock and poultry in the country. First time in the year 2008, all 129 extant breeds of livestock and poultry were registered by the NBAGR. Further 83 breeds were newly added and by 2022, the number reached 212. Registration of livestock and poultry genetic resources has been initiated to protect indigenous AnGR. Our country has a mechanism for recognizing the valuable sovereign animal genetic resource with known characteristics in form of an authentic national documentation system.

A total of 83 new breeds were added subsequently after initiation in 2008, which has put more than 20 million livestock and poultry into the descript category in the country. It enabled to conduct breed wise livestock census by the Govt. of India which could ensure the precise population of each of the breed in the country. This has become useful for suitable policy formulation for their conservation and development. In the 19th Livestock Census (2012), a total of 143 breeds were included in breed wise survey. National Kamdhenu Breeding Centre, an initiative by Govt. of India has covered all NBAGR registered breeds of cattle (41) and buffalo (13) for conservation, promotion, and development. After breed recognition, superior quality germplasm of the breed becomes available to the livestock owners. Various governmental facilities for animal-based farming, small to large /commercial scale become available to the farmers when the animal farming is based on the registered breeds. Breed societies have been initiated for some native livestock breeds in their native tract by the local livestock keepers, which ensured improvement of germplasm, strengthening of the production system and marketing of the products and benefit-sharing among the society.

Gazette notification for sovereignty over native germplasm

To provide legal safeguards for germplasm protection, notification of indigenous breeds being registered by ICAR has started in the year 2019 through publishing Official Gazette by the Government of India. The Government of India has notified 199 breeds of livestock and poultry for keeping and rearing for the purposes of animal husbandry, production, breeding, conservation, utilization, consumption, and trade through three Gazette Notifications [No. 3364 (S.O. 3699(E)) dated 14.10.2019; No. 1420 (S.O. 1583(E)) dated 22.05.2020; No. 3839 (S.O. 4174(E)) dated 08.10.2021 and No. 3839 (S.O. 4174(E))]. Three newly registered dog breeds were also notified by the Government [No. 3589 (S.O. 4086(E)) (13.11.2020)].

Establishment of National Gene Bank

Cryopreservation of germplasm in form of gamete (semen, ova), cell (somatic cells, stem cells) and embryo, DNA, in the cryobank is another important way for protecting germplasm, not only to avert the future extinction but also assessing temporal genomic changes in a breed. Preserving whole embryo, utilizing reproductive biotechniques like embryo cloning and splitting may give the advantage to produce a greater number of animals in case of impending threat. Germplasm of all kind of breeds/distinct populations may be preserved in gamete, cell and embryo form. The National Gene Bank at ICAR-NBAGR since inception until September, 2022 the cryopreserved germplasm of native breeds in National gene bank consists of Semen (2.88 Lakh doses of 61 breeds), Somatic cells (6050 vials of 30 breeds/populations) and DNA repository (169 breeds/populations). The genomic database of all breeds may be developed would be important for future use. Coded information of the DNA, Transcriptome, metablome etc. may also be preserved in form of Digital Gene Bank (eGene Bank).

Mission towards Zero non-descript population AnGR of India

AnGR documentation is the most crucial in management of AnGR biodiversity in country. Creating a breed inventory is started in about 12 years ago, and with all of the best efforts, around 50 percent of all AnGR has been documented, in form of types, breed, grades, so far. Completing the documentation, towards zero non-descript AnGR goal has already been initiated in Mission mode in collaboration of state and central agencies, which envisage the documentation/registration of >100 breeds in national inventory in next 5 to 10 years. Use of media and IT based public participation like crowd sourcing combined with Artificial Intelligence for recognising the breeds and their grades would be the most important tools for identifying new breeds and documenting all kinds of AnGR in any region. Developing mobile apps for characterizing AnGR, information about unique products, markets would help in creating mass awareness. Under this program ICAR-NBAGR has already started the documentation program in all the NEH states and other states and UTs in collaboration with State Veterinary/Agricultural Universities and State Animal Husbandry Department.

Network Program on AnGR characterization and conservation

A National Breed Watchlist-2022 has been prepared based on the 20th Livestock Census data of DAHD, GoI. As per National Breed Watchlist-2022 following is the risk status of indigenous livestock and poultry:

Species	**Critical**	**Endangered**	**Vulnerable**
Cattle	-	Belahi, Krishna Valley, Khariar, Pulikulam	Mewati, Punganaur, Siri, Ponwar, Vechur
Buffalo	-	-	Chilka, Toda
Sheep	Tibetan	Karnah, Katchaikatty Black, Nilgiri	Gurej, Jalauni, Kendrapada, Poonchi, Rampur Bushair
Goat	Teressa	Chegu, Sumi-Ne	Konkan Kanyal
Pig	-	Angoda Goan, Tenyoi Vo,	-
Horse	-	Bhutia, Kachchhi Sindhi, Manipuri, Spiti, Zanskari	-
Camel	Malvi, Mewati, Mewari	Jalori, Kharai, Marwari	-
Chicken	-	-	Kalasthi

The main objective of this program is to undertake characterization and conservation of indigenous livestock and poultry genetic resources in a collaborative mode with state AHD and Veterinary/Agriculture Universities and was started during early 1990s. During the long journey of three decades many indigenous livestock and poultry genetic resources were characterized and four core labs were also established during this period for the genetic characterization of these populations through species specific FAO recommended microsatellite markers. Breeds like Krishna Valley cattle, Katcahkatty sheep, Beetal sheep, Toda buffalo are few examples among those breeds which were revived through the implementation of *in-situ* and *ex-situ* conservation programs.

Breed societies

Breed societies have been developed for various native livestock breeds in their native tract by the local livestock keepers, which ensured improvement of germplasm, strengthening of the production system and marketing of the products and benefit-sharing among the society. Banni Breed Society (*Banni Pashu Uchherak Maldhari Sangathan*) in Bhuj working towards lifting the socio-economic status of the Maldharis, the Sangathan helped get the Banni buffalo recognized and also conserved the breed. Similarly, Chilika buffalo was recognized only when the Chilika Buffalo Promoters' Society had been established during 2004. Few successful breed societies are Malaimadu Cattle Herders' Association, Umblachery Cattle Herders' Association from Tamil Nadu; Vechur Conservation Trust (VCT), Kerala; Marwar Horse Society, Rajasthan; Sahiwal Breed Society, Punjab etc.,

Breed conservation award

Breed conservation award was initiated by the Bureau in the year 2017, was bestowed upon individuals and institutes/organisation/NGOs etc. for their remarkable contribution in conserving the animal genetic resources of the country. The award is conferred on the occasion of 'Farmers Day' on 23rd December every year. The award carries cash Prize and certificate/citation given under the two categories – individual and institutional. The award is highly acclaimed by the farmers/livestock keepers and organisation across the country, and receives coverage from the

National Media. Till date, 14 organizations and 16 farmers/livestock keepers have been felicitated with this award.

Human Resource Development

ICAR- National Bureau of Animal Genetic Resources organises regular training program to various stake holders of AnGR like Scientists/Professors, Research Scholar, field Veterinary Officers etc., on the area of effective management of AnGR. These training programs aims to sensitize the stake holders on characterization (phenotypic and genetic), documentation, registration, conservation and sustainable utilization.

Conclusion

It's becoming more imperative to approach with concentrated efforts for preserving AnGR biodiversity for social and food security as well as sustainable development. India is much privileged to possess a large and diverse indigenous AnGR, with specialized gene pool in form of livestock and poultry breeds, evolved in generations for various production systems. However, with the time AnGR diversity is facing threat due to various reasons, which needs an urgent attention to curb the trend of depletion. Preserving each and every unique germplasm is our utmost priority at National level, where different stakeholders are needed to join in hand in a collaborative approach to achieve the goal for the benefit of the present and future generation livelihood.

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Livestock census: Importance and its role in management of AnGR

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Livestock sector of India is one of the largest in the world and it contributes 4.11% of GDP and 34% of total agriculture GDP. (https://testbook.com/ias-preparation/gross-domesticproduct/). Livestock sector also provides livelihood to two-third of rural community and employment to about 8.8 % of the population in India. The implementation of plan and policies related to animal improvement and conservation largely depends on quality of information collected on livestock genetic resources. Thus, it is imperative to timely conduct the livestock census and collection of data should be done with utmost sincerity by those having skills and acquaintance with livestock.

Aim of livestock census

The main objective of the census is to find out the density of the population of the species and to collect information about all the livestock and poultry along with their age, sex composition, etc. The data also needs to be digitized and maintained in a proper data framework for its optimum utilization. The livestock census is also used to collect breeds information. For proper planning and formulation of any programme meant for bringing improvement in this sector and its effective implementation and monitoring their impact, livestock census data are required at every possible administrative and geographic level. Further the livestock census data can serve as an indicator to ascertain the risk status of any species or breeds.

Important facts about Livestock census

- First all India livestock census was carried out during 1919-20 by the erstwhile British Government. Main purpose of this census was to ascertain the production of livestock and introduce taxation policies on livestock. It was also aimed to have an idea on profitability of livestock rearing by the common people. The census generated results which helped then to take policy decisions on livestock sector. Since then, the census is repeated periodically after every 5 years, to access the dynamics and change in domestic farm animal populations across the country.
- In the post independence era, the first livestock census was carried in 1950-51 by the Govt. of India. So far, 20 such censuses have been conducted by the Ministry of Fisheries, Animal Husbandry and Dairying, in participation with State Governments and UT administrations. The census results were of the paramount importance for the Government to take policy decision in the sector but the census work was carried out by the State Govt.by mobilizing resources from the states under overall supervision of Directorate of Economics and Statistics, Ministry of Agriculture. From the 17th Livestock Census, Department of Animal Husbandry, Dairying and Fisheries, Ministry of Agriculture, Government of India has been given this responsibility to conduct livestock census.

- It covers the survey of all domestic livestock species including poultry and fishery, implements and machinery used for livestock rearing. The livestock species namely cattle, buffalo, sheep, goat, pig, camel, horses and ponies, mules, donkeys, mithun and yak are covered in the census. The other species covered in the census includes stray cattle, dog, rabbit and elephant. Likewise under poultry, the species of fowl, ducks, turkeys, quails and other poultry birds along with number of birds at farms/ hatcheries are included in the census.
- 20th Livestock Census - First time, household-level data through online transmission from the field has been used.
- The census covers the livestock species for policy planning, AnGR conservation and overall development of livestock sector. It becomes essential for the policy maker to ascertain the various breeds of livestock species, so that the livestock species can be genetically upgraded for optimum achievement for its product. It is also essential to ascertain breed population dynamics and positive or negative trends and above all, the assessment of breed status so as to prepare necessary conservation plans, if required.
- For the first time the breeds of livestock were introduced in 17th livestock census. The expansion of livestock breed for different species was considered in 18th livestock census. The identification of the breeds for any livestock species was not systematically and scientifically adopted in 18th livestock census. Even several breeds locally named also found place in the list of breeds and the livestock census continued to identify 218 breeds of livestock for the 15 species across the country. Breed survey 2013, an independent survey other than census, considered 143 breeds registered by NBAGR (except native chicken breeds) for the survey, under the ages of 19th Livestock census. In 20th Livestock Census 182 breeds were considered. The breed survey (2013) was done on 15% sample basis and latter survey results were multiplied by a factor to generate the breed-wise estimate of livestock breeds across the country.
- For the first time on the recommendation of ICAR-NBAGR, the graded animals of each breed of livestock were enumerated separately through breed survey activity. The livestock census is a routine and important activity required for livestock animal improvement programmes and for conservation of farm animal genetic resources.

Survey Schedule

- Information on number of livestock breed-wise is recorded by their age, sex, utility etc. separately for (i) households and household enterprises (ii) non-household enterprises and institutions. Household/ household enterprises schedules are only for recording data of those livestock farmers who are either individually or by group rearing the livestock, poultry and fishery.
- The enumeration has to be done by technical staff including veterinary practitioners/para veterinarians /veterinary graduates/ interns either in job or retired. The duty of the breed survey enumerator/supervisor is of great national importance. They play most crucial role in maintaining the timelines in collection as well as quality of data.

- Enumerator/supervisor should be well conversant with the local conditions and the work required. They must develop a cordial relation with the inhabitants of the area by meeting the imminent personalities such as gram pradhan, panchayat members, government officials, community leaders etc. The enumerators/supervisors should take them in confidence while carrying out the survey work.
- The enumerator shall fill up the breed-wise information only in respect of those breeds which are registered as per NBAGR guidelines. They should have a clear idea on breed identification as well as recognizing the graded breeds of a particular pure breed. The enumerator should carry the information regarding their local breeds registered as per NBAGR guidelines for filling up Schedule-3. All other unregistered local breeds should be considered under non-descript category.

The following schedules are canvassed in the livestock census:

Schedule-1: House list schedule

It is canvassed for re-cording the list of households, household enterprises and non household enterprises engaged both under livestock and poultry rearing as well as fishery related activities existing in the area under enumeration.

Schedule-2: Village profile

This schedule is filled up after completion of Schedule 1, Schedule 3 and Schedule 4. It provides general profile of the village/ward and contains the information on stray cattle and dog also. The information on stray cattle and dogs shall be collected mainly from the Panchayat Revenue Officials/Gram Pradhan and other known sources of the village/urban ward.

Schedule-3: Main schedule

This is the main schedule for collecting data on breeds of various livestock which has to be canvassed in every household having livestock and poultry. The schedule is divided into two parts:

- ***Schedule 3A*** (Household/Household enterprises)- Household/ Household enterprises schedules are only for recording data of those livestock farmers who are either individually or by group rearing the livestock, poultry and fishery.
- ***Schedule 3B*** (Non Household enterprises/Institution)- Non-household enterprises / institution schedules are only for recording data of those livestock, poultry and fishery in such farms including educational institutions, temples, mosque etc.

Schedule-4: Household Schedule

Schedule-4 is designed to capture data on fishery related information.

Concepts and definitions used in livestock Census

Geographical coverage

The census is conducted in all villages/wards of all the districts of the India. All species of domestic livestock species possessed by the households, enterprises and institutions is counted at their site. The identification of breed is done by the enumerators using the phenotypic characteristics of each breed. The migratory pastoral groups are surveyed at their original place of residence and locating them at the place of rearing the livestock.

Different entities and terms used in the survey

Household: A group of persons normally living together and taking food from a common kitchen will constitute a household. Head of household is that member of the household who is accepted generally as the head of the household by the members of the family. He/she may or may not be the major earning member. It should be left to the members of a household to decide upon whom they consider to the head of the household.

Rural and Urban Areas:

Urban areas: An urban area, according to the census definition, consists of:

1) Statutory towns: All places with a municipality, corporation, cantonment board or notified town area committee, etc. so declared by state law, and

2) Census towns: Places which satisfy following criteria are declared as town:-

- A minimum population of 5000
- At least 75 percent of male working population engaged in non-agricultural pursuits
- A density of population of at least 400 persons per sq. km.

In addition to it, some areas falling in the vicinity of city or town are also considered as urban area if they are treated as the out growths (OGs) of the main urban unit.

Rural Areas: All areas not covered under statutory towns and census towns are considered as rural areas for the survey.

Village/Ward: In the rural areas, the smallest area of habitation, viz., the village/ward generally follows the limits of a revenue village/ward that is recognized by the normal district administration. The revenue village/ward need not necessarily be a single agglomeration of the habitations. But the revenue village/ward has a definite surveyed boundary and each village/ward is a separate administrative unit with separate village/ward accounts. It may have one or more hamlets. The entire revenue village/ward is one unit. There may be un-surveyed village/wards within forests etc., where the locally recognized boundaries of each habitation area are followed within the larger unit of say the forest range officer's jurisdiction.

Enterprise: An enterprise is an under-taking which is engaged in production and or distribution of some goods and or services meant mainly for the purpose of sale.

Household enterprise: A household enterprises is the one which is run by one or more members of a household or run jointly by two or more households on partnership basis irrespective of whether the enterprise is located in the premises of the household or not.

Non-household enterprise: A non-household enterprises is one which is institutional i.e. owned and run by the public sector (Central or State Government, local bodies, government undertakings, etc.), private corporate sector (include public and private limited companies registered as joint stock companies under the Companies Act 1956), Co-operative societies, other type of societies, institutions, associations, trusts, etc.

Institution: For the purpose breed survey, Temple, Mosque, Church and Gurudwara, Agriculture Universities, Veterinary Colleges, Dharamsala, etc. are covered under Institution.

Indigenous animals: Animals which belongs to descript/ non-descript breeds of indigenous origin.

Exotic animals: Animals which belong in other countries/foreign origin.

Crossbred animals: Animals which are produced by crossing indigenous animals with exotic breeds or indigenous animals which have retained exotic inheritance are described as crossbred animals.

Other exotic crossbred animals: Animals which are crossed with crossbreds of two crossbred animals of two different pure exotic breeds

Graded breeds: Indigenous crossbred animals of two different pure breeds which have retained indigenous inheritance of any particular breed having more than 50% phenotypic characteristics for cattle, buffalo, sheep and goat to be characterized as graded breed of the same livestock.

Animals in milk: Animals in milk production are described as animals in milk.

Dry animals: Animals which have calved at least once but at present not in production, are described as dry animals. Animals that cannot be calved in future are not covered under this category.

Non-descript breeds: The Non-descript breeds are those Indigenous breeds which cannot be identified as or do not have more than 50% similarities of any recognized breed

'Desi' and 'improved' poultry birds: If a hen/duck lays more than 100 eggs in a year, then it is categorized as 'improved' hen/duck or else it is categorized as 'desi'. If a cock/ chicken/ drake/ duckling falls into the flock of an 'improved' hen/duck then it an 'improved' cock/ chicken/ drake/ duckling or else it is 'desi'.

Slaughter house: Wherein 10 or more than 10 animals are slaughtered per day and is duly licensed or recognized under a Central, State or Provincial Act or any rules or regulations made there under.

Meat/butcher shop: A butcher is a person who may slaughter animals, dress their flesh, sell their meat or any combination of these three tasks. Some butchers sell their goods in specialized stores, commonly termed a butcher shop.

Meat processing: Preparation of meat for human consumption.

Meat processing plant: A licensed manufacturer/processing industries/units used for preparation of meat (preserving and packaging) for human consumption. These entities should be within the revenue boundary of the village/urban ward.

Poultry farms: Farms having more than 1000 birds is considered as Poultry Farms. Farms having only Emu/Ostrich birds are considered as farm if having more than 20 birds. However, all government enterprises having poultry are considered as poultry farms irrespective of the number of birds in them.

Migratory pastoral groups: Migratory pastoral group are animals in a species reared by an individual or group that travel across the regions for their livelihood. The animals belong to these special category is to be counted or taken from either at the point of contact with the group or with the respective known household.

Census data – Quality

- All possible efforts are made by the state departments to collect livestock census information but the quality of data generated needs attention and strict supervision. Quality of data generation depends upon the skills and training of enumerators, who are employed to conduct the livestock census, often they are not trained enough and are unable to differentiate between the various livestock breeds within a species.

- The enumerators should be vigilant while collecting census information from each household and all records must be properly kept and arranged in sequence of house listing, so as to avoid confusion/wrong data entry.
- It is suggested to collect and digitize the data at the source through the use of Tabs and storing data on single server through internet. Such an effort can improve the data quality through continuous supervision and easy handling of large data.
- It must be kept in mind that the accurate breed wise data generated and information about its grades in a region shall help in choosing the improver breed of a species for that region and the decision on conservation of AnGR.
- ICAR-National Bureau of Animal Genetic Resources, Karnal has been actively involved in breed wise census and in order to improve the quality of breed wise data, the Bureau has provided the breed identification particulars based on prior known native breeding tract and visible distinguishing traits of each breed to Department of Animal Husbandry, Dairying and Fisheries, Ministry of Fisheries, Animal Husbandry and Dairying Government of India.

Livestock Census: Role in management of AnGR

The livestock census is beneficial not only for policymakers but also for Animal Husbandry, Dairying and Veterinary services Departments of Central Government and respective state governments, Department of Fisheries of state governments, agriculturists, dairying industry, researchers, traders, entrepreneurs, and masses in general. Conservation today is the only means that the species, sub-species or local breeds within the species are saved from further reduction or extinction. Conservation refers to all human activities including strategies, plans, policies and actions undertaken to ensure that the diversity of animal genetic resources being maintained to contribute to food and agricultural production and productivity, or to maintain other values of these resources (ecological, cultural) now and in the future. Through livestock surveys, assessment of population status of a species/breed can be ascertained by obtaining the following information:

- Population size and structure by sex, and age groups.
- Geographical distribution of a population.
- Status of the breed in terms of risk of erosion of genetic variability or extinction. This will be in terms of not total but effective population size (N_e) which is a function of breeding males used per unit time/generations.
- Production potential of the breed and its value in terms of genetic distinctiveness of production traits both quantitative and qualitative.
- Determining risk status, criteria for conservation and elements of action plan for conservation.

  Based on the above information a quick decision can to be made to whether conservation effort is immediately required for an animal livestock genetic resource. Thus, breed wise livestock census and quality data generated can hasten the livestock improvement programs and its conservation.

Importance of breed societies and NGOs in identification, documentation and conservation of livestock biodiversity

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Introduction

Conservation is often quoted as a complex process. However, several NGOs and breed societies in the country undertook 'people oriented' approach to achieving *in situ* conservation of breeds that also led to upliftment of socio-economic status of the livestock keepers. In all such cases, the major factor leading to success has been the locally adapted breed, and the community approach. The need for conservation of livestock breeds is well understood in terms of the role of the biodiversity for the present and future generations. As conservation is a multidisciplinary process also involving social, cultural, economic aspects besides breeding and management, it is imperative that the differing approach taken by breed societies and by NGOs is fully appreciated, up-scaled and utilized for conservation of livestock biodiversity. Planned conservation of a newly noted population initiates with its 'identification' as a distinct population, its documentation for comparative analysis before undertaking its conservation. Once a breed has been identified and documented, 'Breed Societies' come up to undertake a community based approach to promote and conserve the breed.

What is a Breed Society?

A Breed Society is an officially recognized group of stakeholders joined together for upliftment of the livestock breed. There are a large number of Breed Societies in the western world and there are only a few in India. One of the early breed societies was formed for the Ongole cattle in erstwhile Andhra Pradesh while several horse societies have also been recognized in the country. In the last decade, a society formed for Chilika buffalo development in Odisha (in 2004) achieved recognition and registration of the Chilika buffalo breed. The methodology developed further led to the formation of Banni buffalo breeder's society in Kachchh during 2007, as well as a Berari Goat Society in Madhya Pradesh during 2015. Breed societies play an important role in involving several stakeholders and highlight the importance of local breeds, documenting their features and undertaking value addition leading to conservation of the breed.

What is an NGO?

An NGO or 'Non-Government Organization' is a registered group of persons joined together to work for a common cause. There are several NGOs in the country working on livelihood issues based on local livestock or the local breed. NGOs like Sahjeevan in Bhuj and 'SEVA' in Madurai have made significant contributions to saving the local breeds from further dilution. NGOs play a vital role in highlighting the role of the local breed in improving the local livelihoods.

What is Livestock Biodiversity?

Livestock are classified not only in terms of species viz. cattle, buffalo, sheep, goat etc. but also in terms of breeds within a species. For instance, cattle has 50 breeds like Gir, Ongole, Sahiwal and Vechur. In some cases, sub-groups within a breed may also be recognized. The entire assemblage of livestock species, the breeds in each species and the sub-types together is termed as 'Livestock Biodiversity'. Livestock Biodiversity is important not only for each breed being of a different type but, more importantly, for the reason that each breed also represents or belongs to a region or ecosystem, and is more a part of this ecosystem. It is the combination of the breed and it's ecosystem that makes each breed an efficient production type in its own eco-system. In reality, a breed has developed its characters in its ecosystem over hundreds and thousands of years - thereby fixing several genes which are suitable for the given breed and ecosystem combination. It is not appropriate to let the breed be diluted due to crossbreeding or other means – as; the loss of the breed is permanent. Once lost, there is no way to recreate the breed of the particular assemblage of genes that were suitable for the given ecosystem. Livestock Biodiversity is hence extremely important to be recognized and to be maintained.

Steps necessary to manage livestock biodiversity

Identification: The first step to understanding livestock biodiversity in any region is to look for or identify the presence of a unique population, if present, in the large mass of animals that often look mixed or non-uniform. This is largely a visual exercise and often carried out based on prior knowledge of other known breeds and populations (within same species). If based on phenotype alone, the population at hand appears to be different from the 'thus far known' and defined breeds, and, at the same time, it happens to be largely a uniform population, it qualifies to be considered further and is termed as 'a potential population' (low level of uniformity often disqualifies the population at hand). The next step is to gather more information on this population and assess its being a unique population. This second step is termed as documentation.

Documentation: It means recording all the qualities / parameters of the population that will help is accepting the population as unique or different from all the existing breeds. Parameters include body measurements, performance (production/reproduction), spread of the population, community involved, area/region where distributed, population numbers and observable distinctions from (geographically) nearby defined breeds. In addition to phenotypic parameters, population is documented for molecular parameters as well. Once documentation is sufficient, the new population needs to be critically examined by a team of experts (those already engaged in the process having access to wider details) often in institutional system to qualify the population at hand as a new breed.

Conservation: It means saving the breeds from possible extinction by raising the animal numbers and strengthening the environment around them. Need for conservation has been necessitated by man's own actions viz. overexploitation of natural resources and local populations, lookout for quick gains at the cost of long term sustainability, destruction of natural habitats for the sake of urbanization and ignoring the potentials of the genetic resources against the backdrop of one or two products in higher volumes. Represented by defined as well as lesser-known breeds, the animal genetic resources have largely been undervalued marking them as low producers without mentioning other valuable qualities and benefits. Almost always, the special survival qualities have not been included in evaluation of the local breeds. This has led to general ignorance of the special importance of local defined (and undefined) populations. In this scenario, crossbreeding has been 'widely' introduced – well beyond the experimentation necessity, without ever checking its feasibility and worthiness in the local input system that is constrained in terms of feed/fodder, climatic stress and health management. Crossbreeding could not succeed in the resource-poor areas of the country and whenever harsh conditions came back like shortage of feed or of water, only the local breeds could survive. Even though the production was low, it was acceptable under the prevailing input conditions. As large areas in the country are merely rainfed, local breeds are a better option to successfully face the vagaries of climate. The imminent climate change further accentuated the need for the local hardy breeds to meet man's demands. In addition to the ability to face the climatic stresses, the local breeds have other valuable features being disease-resistant, there is least demand of veterinary medicines and far less demand of elaborate management. In general, local breeds, local input systems and the local technical knowledge makes an efficient system combination par excellence. In addition to the above, indigenous breeds are a source of several specialized products e.g. therapeutics and pharmaceuticals. Conservation today is the only means that the local breeds are saved from further reduction or extinction.

How conservation is to be achieved also needs a consideration. It has been noted that conservation is breed-specific, area-specific and even agency-specific. Hence, there are several different ways in which conservation can be undertaken under field conditions, and, often, any singular approach is insufficient to make an impact. As a practice, different agencies have followed different ways and means to achieve conservation – hence conservation has been noted to be agency-specific. It is breed specific as well – different breeds follow different patterns for successful conservation. Moreover, conservation is also area-specific – different countries as well as different regions have followed different means and methods for conservation and shown success in the variegated ways. There are two major methods for conservation: *in situ* and *ex situ*. Former is conservation at the farmers' level i.e. at the site (or the habitat) where the animals are normally surviving. Conservation in the form of semen, embryos, cells etc. is termed as *ex situ* conservation and is achieved under laboratory conditions, hence termed as *ex situ in vitro* conservation. In contrast *ex situ in vivo* conservation is achieved on live animals (not semen or embryo) kept away from the natural habitat of the breed.

In addition to the default manner of conservation happening in the country, there are at least four different agents engaged in conservation in the country:

1. Government agencies.
2. Gaushalas.
3. Breed Societies.
4. NGOs.

Government agencies like animal husbandry department undertook conservation of "Threatened breeds" with a little success; ICAR (NBAGR) and state agencies (AH Dept., KVK and Universities) undertook conservation under the NATP, Network Project and other modes with significant success for some breeds e.g. Beetal goat in Punjab state.

Gaushalas have been on the forefront in saving indigenous breeds. In addition to Gangatiri which has been saved in the country only by the support of a Gaushala, other breeds are taken care of by the exemplary Gaushalas for instance Sahiwal is conserved at Gajipur, Uplana, Kurukshetra, Bhaini Sahib, Noor Mahal and Sri Jeevan Nagar Gaushalas; Hariana is conserved at Dharauli, Mastangarh and Uplana Gaushalas etc.

How Breed Societies and NGOs can play a role?

Several case studies in different parts of the country clearly showed that a planned support given to the local breeds under community approach system has led to improving the economic status of the rural communities. Some NGOs in the country are directly involved in breed conservation whereas others are engaged through improving the livelihoods by the use of the local breeds and/or by forming a breed society and thereby conserving the breed. Banni Breed Society (*Banni Pashu Uchherak Maldhari Sangathan*) in Bhuj raised the profit from sale of Banni buffaloes by as much as 27% in the first year of establishment. While lifting the socio-economic status of the Maldharis, the *Sangathan* helped get the Banni buffalo recognized and also conserved the breed just because increased income was now feasible from these buffaloes. Similarly, Chilika buffalo was recognized only when the Chilika Buffalo Promoters' Society had been established during 2004 and the breed was officially registered during 2010.

Names of breed societies in India are:

1. Banni Pashu Uchherak Maldhari Sangathan, Bhuj (Gujarat)
2. Kharai Camel Association, Bhuj (Gujarat)
3. Chilika Buffalo Promoters Society, Bhubaneswar (Odisha)
4. Malaimadu Cattle Herders' Association, Tamil Nadu
5. Umblachery Cattle Herders' Association, Tamil Nadu
6. Katchakatti Sheep Herders' Association, Tamil Nadu
7. Vembur Sheep Herders' Association, Tamil Nadu
8. Toda Buffalo Pastoralists' Association, Tamil Nadu
9. Pullikulam Cattle Herders' Association, Tamil Nadu
10. Indigenous Horse Society for Kathiawari, Manipuri, Zanskari and Spiti, (Raj.)
11. Marwar Horse Society, Rajasthan
12. The Chetak Horse Society of India, Rajasthan
13. Senaapathy Kangayam Cattle Research Foundation, Tamil Nadu
14. Gaolao Cattle Breed Society, Maharashtra
15. Vechur Conservation Trust (VCT), Kerala
16. Kerala Local Cattle Breeder's Society (KELOBS), Kerala
17. Kasaragod Dwarf Conservation Society (KDCS), Kerala
18. Vadakara Cow Conservation Trust (VCCT), Kerala
19. Mehsana Buffalo Breeder Association, Gujarat

20. Jaffarabadi Bhains Uchherak Sangathan, Gujarat
21. Marvadi Sheep Breeders' Association, Rajasthan
22. Sahiwal Breed Society, Punjab

A group like a breed society or an NGO with clear-cut motives or objectives of developing the breed and its surrounding system has the capacity to manage the complexity of conservation. A society formed by a majority of members from the breed community along with few facilitating expert stakeholders makes the combination that has shown favorable results in conserving the local breed.

There are several examples of NGOs in India that have successfully improved the livelihood status in cases e.g. Sahjeevan in Bhuj who attended to Banni Buffalo, Kharai camel and more recently six new lesser known breeds viz. Duma sheep, Kachhi Sindhi horse (registered in 2017), Halari donkey and Kahami goat (registered in 2018), Kutchi donkey and Nari cattle. Besides, there are more NGOs engaged in the act of improving livelihoods viz. SURE NGO in Barmer, Rajasthan (Sustainable Upliftment of Rural Economy) tending to Tharparkar breed, ANTHRA NGO (Telangana) attending to Deccani sheep, Kamdhenu Gaushala in Nurmahal near Jalandhar now conserving Sahiwal and Gir cattle; Timbaktu Collective (Anantpur, AP) have conserved Hallikar cattle; SPS (Samaj Pragati Sahayog) NGO (Bagli, MP) are now saving local desi birds and the Kadaknath poultry, SEVA NGO (Madurai) are attending to Malaimadu Cattle, Umblachery Cattle, Katchakatti Sheep, Vembur Sheep, Toda Buffalo and Pullikulam Cattle.

In general, NGOs worked closely with the farmers, assessed their requirements and utilized the traditional knowledge in management and selection of the breed animals. This resulted in greater success in raising the number of purebred animals in the areas undertaken. For example, ANTHRA undertook *in situ* conservation for Deccani sheep using traditional knowledge of the farmers. The rams for breeding were selected by a joint team of shepherds and researchers. In addition, ANTHRA established farmers' meeting points (named as '*Sangam*'). A *Sangam* was a housing place where the sheep keepers (shepherds) would meet periodically, discuss their problems and take joint solutions. Animal scientists also joined such informal meetings to provide on the spot solutions. The scheme was very popular with the shepherds. ANTHRA also made marketing interventions and provided support for the sale of wool products. Over the period, it was recorded that there was an increase in the average number of Deccani sheep kept by individual family as well as total number of families maintaining the breed, in the project area.

Sahjeevan NGO established a Banni Breed Association ('*Banni Pashu Uchherak Maldhari Sanghatan*') by involving the Banni buffalo keepers (i.e. Maldharis) in the Banni tract (Gujarat). The Maldharis participated in the society activities and arranged Banni Pashu Melas, an annual feature. By marketing through the Breed Association, the Banni keepers obtained higher price for their buffaloes. As the awareness increased through the fairs, demand for Banni buffalo also increased. This has helped in conservation of the breed. Under the banner of the society, the Maldharis arrange periodic meetings to discuss common problems on water availability, grazing, feed-fodder, veterinary, health, migration routes and marketing issues. For any conservation scheme to succeed, it is necessary to attend to all these interventions as the 'supporting environment' of the breed.

SEVA NGO in Tamil Nadu is engaged in community-based approach to conservation of indigenous livestock breeds. In order to promote local breeds, they have undertaken supporting activities in regard with pastoralists and traditional grasslands ('*Korangadu*'). They also facilitate community loan system based on collections made within community just because the banks are not coming forward to provide loans for fodder cultivation. The NGO arranges procurement and distribution of purebred bulls and pure-breed animals. In order to improve the availability of water, the NGO has de-silted the water ponds to strengthen water-recharging mechanisms. With the involvement of the community, the needed environment to support the breed animals has been strengthened. In Rajasthan, SURE NGO has undertaken the activities to select young purebred males of Tharparkar cattle and established "breeders' associations" in the villages and provided purebred bulls for natural service. They have developed arrangements with the community members to record calvings and milk yield from the progeny as an incentive to pure-breeding and selection. They also arrange regular meetings of the Breeders' associations in the undertaken villages. A significant increase in the number of Tharparkar cattle in the undertaken villages was recorded, with increase in per family income.

In an interesting case, the farmers of the Anantpur (AP) area were to decide on the type of cattle that would suit their agricultural requirements. During 2007, Timbaktu NGO took the initiative and the farmers were shown the production system of crossbred HF cattle in the vicinity, but they selected Hallikar cattle which the community people said would provide some milk but more valuable draught power without the need for elaborate feed/fodder or veterinary care requirements. Number of Hallikar cattle has subsequently increased in the area.

In order to achieve conservation, it is important to follow all the feasible means together in a coordinated manner. There is a need also to look for any specialized product or by-product in the breed that can be promoted or marketed.

Epilogue

As a means to managing the AnGR starting with identification of a new breed, documenting it and planning its conservation, NGOs and breed societies have amply expressed success stories with glaring examples like Poda Thurpu and Himachali Pahari cattle. NGOs and breed societies in the country have successfully achieved identification, documentation and conservation of breed animals in field areas by involving the community and taking a wholesome approach to improving the livelihoods of livestock keepers. Conservation is necessary as well as achievable; only the approach to conservation has to be multidimensional involving different stakeholders and, more importantly, some breed societies and NGOs to attend to it.

Indigenous AnGR in India: An approach to setting conservation priorities

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India is home to 535.8 million livestock. The country's livestock and poultry population currently consists of 212 recognised breeds, which together make up about 45% of the total population, with the remainder being non-descript. The importance of the livestock sector in India can be gauzed by the fact that it is one of the fastest growing components of country's rural economy, accounting for 5% of the national income and 28% of the agricultural GDP in 2018-2019. In the previous six years, crop farming rose by 2% while the livestock sector grew by 7.9% (at constant prices). Therefore, it is important to adequately characterize non-descript populations, create state-specific breeding plans for launching suitable genetic improvement programs, and establish state-wise and national conservation priorities for livestock and poultry breeds.

Genetic and phenotypic characterization are the most powerful tools to define breed criteria for livestock germplasm. Indigenous Animal Genetic Resources (AnGR) diversity has been described using morphological measurements, the analysis of which distinguishes breeds/local populations. Furthermore, DNA-based microsatellite studies have been successfully used to characterize the genetic diversity of AnGR. Once a breed has been defined and registered, it is desirable to manage and preserve it for sustainable use. The most obvious reasons to conserve AnGR are to protect and promote livestock biodiversity, maintain healthy and functional ecosystems, and meet the growing demand for food security and sustainable rural development. Conservation of indigenous AnGR encompasses all human activities, including policies and plans to conserve their diversity, their contribution to food and agricultural production, and their sustainable use. Traditional techniques for implementing AnGR conservation actions/plans include *in situ* and *ex situ* conservation. *In situ* is the maintenance of the breeds within their production systems, whereas *ex situ* techniques are outside the production system and preserve genetic material including semen, oocytes, in vivo and in vitro embryos, somatic cells and DNA . When a breed is at risk or is threatened by extinction, *in situ* conservation is to be preferred. *Ex situ,* however, continues to provide powerful and safe tools for conservation of AnGR. Therefore, it appears appropriate to make efforts to build a framework for the effective integration of *in situ* and *ex situ* approaches, where *ex situ* conservation is complementary to *in situ.* However, it is important to prioritize conservation activities in order to make the most of the limited funds and resources available to prevent the long-term loss and degradation of AnGR biodiversity.

Conservation decisions can be made based on multiple considerations, the most important being the level of endangerment. Limited resources force efforts to concentrate on a few endangered breeds. Insights into a breed's genetic variation and its merits are important indicators for its conservation. Genetic diversity can be quantified in a set of breeds/ populations and breed merits can also be assessed. A framework, taking into account both genetic diversity and breed merits, can be implemented to prioritize breeds for conservation at regional / national level. Generally, conservation priorities have been set based solely on genetic diversity indicators. Conservation priorities in India have been determined primarily by degree of endangerment based solely on population size. However, the integration of genetic and non-genetic factors in the conservation strategy can efficiently set conservation priorities. Threats and current utilities of the breed are a couple of the significant non-genetic factors. Threats include low population size and low preferences by farmers; current breed merits include economic, ecological, and cultural benefits. The relative conservation priorities are changed when ranked based on their contribution to genetic diversity and on their total utility.

Based on genetic and non-genetic indicators, Yadav et al. (2017) ranked five indigenous sheep populations of Maharashtra (Lonand, Kolhapuri, Sangamneri, Solapuri and Madgyal) for conservation by combining threat indicators (population size, average number of rams per flock, level of cross breeding, maintenance of pure stock, farmers opinion towards the breed), current breed merits (economic, ecological and cultural) and contribution to genetic diversity. Contributions to between-breed diversity were based on Weitzman scores estimated from Nei's genetic distances, leading to estimates of marginal loss of diversity associated with each breed. Assessment of breed threat score and estimates of extinction probabilities were based on a set of FAO recommended indicators. The breeds were prioritized for conservation based on the maximum-utility index, $U_i=2(z_i+D_i)+W_i$, where z_i is the probability of extinction, D_i is Weitzman marginal diversity, and W_i is the current merit of the i^{th} breed.

The measure of the marginal loss of diversity for each breed using the Weitzman approach enables the ranking of breeds for conservation purposes. The contribution of each population to overall diversity was between 16.8% and 26.6%. In the investigated set of breeds/ populations, the highest loss of diversity would be incurred with removal of Sangamneri (26.6%) and the lowest from the removal of Solapuri (16.8%) sheep. Sangamneri sheep depicting a higher marginal diversity (>26%) were potential contenders for conservation precedence over other investigated populations. The probability of extinction was highest for Lonand sheep (0.9) and lowest for Madgyal sheep (0.3). Socio-cultural scores ranged from 0.33 to 0.35. Economic merit scores range from 0.1 (Lonand) to 0.4 (Madgyal), representing the highest economic value of Madgyal sheep. The economic benefits of Sangamneri and Kolhapuri sheep were similar. Based on total utility score, the findings gave highest conservation priority to Lonand and least to Solapuri sheep. The results showed that the conservation priorities differed when breeds were ranked using only genetic diversity indicators. Weitzman's diversity approach prioritized conservation of Sangamneri sheep, while maximum-utility approach prioritized conservation of Lonand sheep. The study could be used as a model to define conservation priorities of AnGR and could contribute to a National Conservation Plan (NCPAnGR) of Indian livestock breeds.

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Extension interventions for animal genetic conservation: Socio-economic perspective

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Introduction

The World Wide Fund for Nature's (WWF) Living Planet Report-2022 has depicted a massive 69% decline in wildlife populations across the globe during the 1970-2018 period, indicating that the planet earth is in the throes of a biodiversity crisis. This acute disruption in the ecosystem should serve as a wake-up call to the world for taking a renewed pledge to redouble efforts for arresting the downward spiral and preventing the endangered species from going extinct. It is crucial for the survival of all forms of life on Earth. Undoubtedly, rampant overexploitation of the limited natural resources over the past 50 years by humans in the name of development indicates the biological annihilation and assault on the foundations of human civilisations.

In animal husbandry, several breeds of indigenous origin have tremendously contributed to the biological diversity. The interdependence of animal based enterprises with crop and other farm enterprises ensured the sustainability of rural life in general and agriculture in particular. However, owing to commercialisation, urbanisation and modernisation in tune with the advances in science and technology, number of indigenous breeds and species could not sustain their existence in the ongoing techno-socio-economic transformation. This deprived the opportunities to harness inherent benefits from these indigenous species. But, of late, the emphasis is shifting towards the vital role of animal genetic resources conservation and its accruing benefits for furthering the scientific development and sustaining the livelihood of future generation which can have multiplier effect through extension interventions. Moreover, the future of animal husbandry farming largely depends on the level of awareness, knowledge and adoption of relevant conservation strategies by various stakeholders. Therefore, it is pertinent to understand the socio-economic perspective of animal genetic resources conservation for deploying the appropriate extension strategies.

Animal husbandry: Journey towards decline of interdependence between farm enterprises

Indian agriculture once practised with multiple farm enterprises by every farmer ensured food, nutritional, environmental, income and employment security. But this interdependence got disturbed as a result of new developments in natural resource supply and demand, emerging opportunities and response to meet the challenges of persistence of socio-economic problems (Ponnusamy, 2006). In fact, different farming systems have been developed independently and are being practised by farmers indigenously. Livestock farming being a dependable "bank on hooves" in times of need acted as a supplementary and complementary enterprise. New profit making opportunities have prompted considerable number of the farmers to discontinue certain ecologically significant farming systems and shifted to few enterprises or even single enterprise. This leads to the economic imbalance by virtue of improper tapping of the potential of each component in the system and creating an impression among the farmers that the system is not viable between and within the farm holdings (Jayanthi *et al.*, 2002).

Due to several factors like unavailability of farm labour, rising labour costs, fast declining grazing lands, fluctuations in rainfall pattern, partial mechanisations of several farm operations, government policies such as minimum support price, input subsidies, declining family size, and preference of youth towards white collar jobs prompted the fast decline of average livestock holding of individual farm families in the villages. The typical farming system which was seen during 1950s and 1960s had declined owing to above mentioned factors. Solo enterprise farming has emerged severely affecting the food and nutritional security of farm families. The prospect of commercial dairy farming is witnessed in the north-western region especially in Punjab and Haryana. However, animal holding is increasing among the landless families in the villages, almost again as solo enterprise as they have to depend for the requirements of green fodder either from landlords or open market. Therefore, extension functionaries need to be prepared to deal these emerging challenges and opportunities in order to promote the sustainable livestock farming systems in the country.

Animal husbandry: Current status

In India, 137 km of the Sundarbans mangrove forest have been eroded since 1985, which has resulted in a reduction in the benefits provided by the ecosystem to 10 million residents of the area. Also, the country's rivers have been counted among 73 per cent of the over 1,000-km-long rivers of the globe that are no longer free-flowing and, thus, raise the risk of migration of fish. Equally worrisome is the decreasing population of honeybees and 17 species of freshwater turtles in India. Climate emergency and biodiversity destruction exacerbates the global food system crisis. Animal husbandry has played a prominent socio-economic role in India owing to favourable agro-ecological conditions. Traditional, cultural and religious beliefs have also significantly contributed in its growth and development. Visible benefits could be observed in generating gainful employment, particularly among the landless, small and marginal farmers and women, besides providing cheap and nutritious food to millions of people. As per estimate of NSS 68th Round (July 2011-June 2012) survey on Employment and Unemployment, 16.44 million workers as per usual status (Principal status plus subsidiaries status) were engaged in the activities of farming of animals, mixed farming, fishing and aquaculture. There are about 300 million bovines, 65.07 million sheep, 135.2 million goats and about 10.3 million pigs as per 19th Livestock Census in India. Past efforts helped in raising production and productivity in most animal products with 209.96 MT of milk production, 8.80 MT of meat production, 14.50 of MT fish production, 36.93 million Kgs (declined from 48.14 million kgs in 2014-15) of wool production and 122.05 billion numbers of egg production of during the year 2020-21 (DAHD, 2021-2022). Livestock sector contributed to 4.90 per cent (at constant prices) of total Gross Value Added (GVA) in 2020-21 showing a continuous growth in Compound Annual Growth Rate (CAGR) of 7.93 per cent (at constant prices) from 2014-15 to 2020-21.

Implications of scientific interventions

Significant technical, policy and institutional support over years contributed to incremental growth in milk production in the country. The state animal husbandry departments and private players continue to provide veterinary inputs and services. The cooperative dairy sector also provides animal health services only to its cooperative members. Despite poor satisfactory performance of private service providers at field level, they enjoy the advantage of their mobility and availability. However, commercial dairy farmers are willing to pay for immediate response and service delivery at doorstep.

While artificial insemination is well introduced and accepted, quality of frozen semen continues to be a concern in implementation of the breeding policy. Last two decades of work by state livestock development agencies also contributed to the strengthening of various breeding activities, in particular the promotion of AI services by private inseminators. Commercial dairy producers with crossbred cattle or high yielding buffaloes rather focus more on the procurement of concentrate feed than on the cultivation of fodder, typically reflecting "high input – high output" milk production systems. On the other hand, farmers who practise a less intensive dairying, are often neither prepared to spend the required amount on costly concentrate nor to use (part of) their land to cultivate fodder. Resorting to the feeding of large quantities of low quality paddy straw leaves the output from many dairy farms below its potential. Extensive grazing of specialised dairy animals is hardly practised anymore, as the availability of pasture land has reduced and the remaining areas are heavily overgrazed. Government of India has for long promoted dairying as a "landless" activity, with the result that many dairy farms heavily rely on concentrate, while hardly any fodder is cultivated.

Villages closer to government dispensaries have access to preventive health care services like vaccination and de-worming, regularly conducted as health camps. Sheltering the animals with proper space and ventilation in rural and peri-urban areas remain as major constraints.

Social status vis-a-vis animal husbandry farming

In the absence of fertile lands and assured irrigation which are controlled by a small population of rich farmers and lack of gainful employment opportunities in other sectors, most of these farmers maintain different species of livestock to supplement their income. The landless usually prefer to own sheep, goat and poultry as compared to the land owners who prefer cattle and buffaloes. About 80 million rural households are engaged in the milk production, with high proportion being landless, marginal and small farmers. Among various species of livestock, cattle and buffaloes are the major contributors from this sector to the National GDP.

There is an increasing exodus of the landless households out of livestock production mainly due to reduced access to grazing resources, lack of access to non-exploitable market and credit and other services. Over the period of time, grain production and livestock production have become increasingly specialised and separated from each other. As a result of this, complimentary / supplementary role of livestock enterprise has undergone drastic change to become a competitor for grain which could otherwise be consumed by humans.

Economic contribution of livestock husbandry

Milk is the main output of the livestock sector accounting for 66.7 per cent of the sector's total value. Meat and egg share 17.5 per cent and 3.6 per cent respectively of the value of the livestock output. The share of wool and hairs is negligible (0.2%). The share of dung, which is used as domestic fuel and farm yard manure, is about 9 per cent of the livestock sector's total output. Buffaloes, cows and goats contributed 53.4 per cent, 43.2 per cent and 3.5 per cent respectively to the total milk output in 2009-10. Women constitute 71 per cent of the labour force in the dairy sector. The rising demand for fresh and packaged livestock products and ethnic dairy specialities is broadening the base of Indian dairy sector. About 60 per cent of consumption is fluid milk in India. The dairy industry market in India is expected to be US$ 22.5 billion in 2020 from US$ 11.8 billion in 2015. Western India contributes 34.7 per cent of total dairy market followed by North India (28.6%), South India (23.7%) and East and North-East India (13%). At a juncture larger share of livestock feeding coming from crop residues, the declining trends in crop production system will challenge the livestock feeding situation and sustainable milk production in the hands of 70 million small holders that are into milk production now.

Farmers spend more than 60 per cent of their expenditure on feed in dairy farming. The Table 1 clearly indicates the perspectives on ways and means of motivating the resource poor farmers to enhance the current milk productivity and profitability to the potential level as farmers view any farm enterprise from economic angle. This calls for concerted efforts to promote scientific interventions for sustainable indigenous livestock farming.

Table 1. Average milk productivity of different species

Exotic Cows	Crossbred Cows	Indigenous Cows	Non-Descript Cows	Indigenous Buffalo	Non-Descript Buffalo	Goat
9.15 (kg/ day)	7.22 (kg/ day)	3.34 (kg/ day)	2.71 (kg/ day)	6.41 (kg/ day)	4.13 (kg/ day)	0.47 (kg/ day)

Source: Annual report of DAHD (2021-22), Government of India

Dairy farming: Political context

'Operation Flood' programme which was implemented between 1970 and 1996, enforced a shift from low prices for urban consumers towards fair prices for dairy producers. Tension will normally arise between the interests of consumers who benefit from low food prices and the interests of milk producers to receive a fair price for their produce. India is witnessing the emergence of larger dairy farms in India stimulated by the growth of private dairies. The overall milk processing capacity of the private sector has been developing at twice the rate of the cooperative sector in recent years, indicating the future dominant role of the private sector in the industry. Therefore, adequate space should be created for the role of differentiated producers without squeezing the small producers by larger farms.

Farmers often raise their voice for their right to trade in cattle especially withdrawal of restrictions on sales of bovines in animal markets, reduction in the age of sales of calves and cows and total protection for all players who are involved in the trade and transportation of animals. This is with regard to the Prevention of Cruelty to Animals (Regulation of Livestock Markets) Rule, 2017 (Gazette 396) and banning the trade of animals for slaughter in animal markets. The role played by cow vigilante groups, has impact on animal markets, fairs, jatras and animal transportation across the state, forcing section of farmers to abandon their non-productive cattle, resulting significant rise in 'stray cattle' which roams on the roads, leading to consequent traffic jams and accidents. Indian farmers do not rear cows and buffaloes for beef. However, they dispose of their unproductive animals, non-milking, non-reproducing and non-draught worthy cattle, as they will not be purchased by another farmer, but would be bought for slaughter alone. The animal continues to have a resale value, due to the post slaughter products like beef, leather and offals. With cows contributing 47 per cent of the total volume of milk produced in India (21% from indigenous cows and 26% from cross-bred animals), a positive environment needs to be created to motivate farmers to rear indigenous cattle in the context of recent happenings relating to cow slaughter.

Need for interventions

Training and extension enjoyed good attention over the past years, although the impact from it is difficult to assess. Livestock and dairy extension have to be seen with regard to its technical components like animal breeding, feeding, health and management. The emergence of private service providers in the livestock production sectors has given a new face to extension. While the specialised "extensionist" has disappeared, various public, cooperative and private service providers like veterinarians, para-veterinarians, AI workers, feed companies, dairy cooperative managers, milk vendors, etc. have taken over extension tasks and roles. The institutions of the Indian government, including veterinary colleges and agricultural universities, which provided training and extension in the past continue to be there, but many of them have yet to find their new role, either as coordinator and facilitator of special training or as a provider of specific technical expertise.

The challenges of the Indian dairy sector are indirectly shown by the reluctance of banks and credit institutes to provide loans to dairy farmers. It looks as if the formal banking sector does not believe in the potential of dairying. On the other hand, there have been bitter experiences in the past with low repayment rates for loans given out in the dairy sector. The situation will not improve in near future, unless credit for dairy animals can be linked with a functional livestock insurance system. Awareness on food safety increased in India with direct implications for the dairy sector. Especially consumers in urban areas are increasingly conscious about the quality of food. But despite the fact that a number of acts and regulations are in place and that controls of fresh milk and dairy products have increased, the proper implementation of food safety standards is yet to take place. Main hindrance is that the concerned authorities lack the required instruments and power to take effective measures against offenders. Climate change is a global issue, but it concerns every country and every sector. As a result of the changing climate, India's dairy sector expects that water and fodder will become critical factors in the future. Furthermore, rising temperature may affect the reproductive and productive performance of the dairy animals, especially of crossbreds with high levels of exotic blood.

Overall, the Indian dairy sector performed well over the past years as it was able to grow steadily and significantly. While government institutions did not really move, the improvements in the cooperative sector and the emergence of the private sector in livestock production and dairying contributed to this growth. Government policies and guidelines, however, created the conducive environment for this further development of the sector. On the other hand, livestock production and dairying as a socio-economic instrument to promote pro-poor growth in rural areas to a large extent has disappeared from the government's policies. This in the end is an interesting aspect given the fact that 90 per cent of India's milk is produced in the rural areas and smallholders account for 80 per cent of the total milk produced.

Extension interventions

The conservation of domestic animal diversity would help to meet the future needs of the animal husbandry sector in the country. Interventions are required to readily respond to directional forces imposed by a broad spectrum of forces and maintain genetic diversity as an insurance against future adverse conditions.

1. Involving panchayat raj institutions in conservation of indigenous animals and formation of indigenous breeders association should be encouraged. Farmers rearing pure breeds need to be encouraged to rear such animals in the breeding tract by involving them in breed improvement programmes with attractive incentives.
2. The drinking water needs of farm animals should be facilitated by desilting/renovation of village ponds.
3. Regulating grazing permits to pastoralists should be done as per the Forests Rights Act 2006.
4. Issuing permanent identity cards to keepers of indigenous animal breeds to protect them from police or forest officials while crossing highways.
5. Encroached areas in revenue sites which are originally grazing places for cattle herders need to be retrieved by the district administration.
6. Surveying of common grazing lands in the breeding tract need to be undertaken along with herders.
7. Demarking pasture lands or temple lands with boundaries for regeneration of vegetation.
8. Migratory routes for the migratory animal breeds especially sheep and goat are to be recognised and legitimised.
9. State Animal Husbandry Departments should organise at least two veterinary camps, one in beginning of rainy season and another in summer months especially for migratory animals.
10. Organising periodic animal fairs, cattle shows/camps, milk yield competition to identify best cows for breed improvement and suggesting remedial measures to the farmers 'problems.
11. Establishing herds of indigenous animals in the government and research farms.
12. Making available the semen of indigenous breeds to rearers in the respective regions.

13. Breed society and breeders association should be financially supported and entrusted with the responsibility of enrolment of pure bred cows and performance recording and taking up development activities.
14. Locating superior bulls of indigenous breeds of the breeding tract concern and using them for improving the quality of animals and farmers in the main breeding tract should be advised to avoid indiscriminate cross breeding.
15. Providing remuneration to herders for conserving the indigenous animals and their efforts in helping restoration of organic farming.
16. Making arrangement for regular sale of manure and other products from the indigenous animals although there is a challenge of upscaling the production due to local nature of production.
17. Promoting dairy cooperatives and contract dairy farming (Ponnusamy and Walli, 2007) for fetching better milk price to farmers as concept of A2 milk is gaining.
18. The officials of wildlife department should undertake participatory conservation of all components of biodiversity and prevent the heavy mortality due to prey of wild animals on indigenous animals.
19. Since dumping of plastics and garbage waste is a big nuisance to both humans and animals, it must be stopped.
20. Agro-forestry model with fodder grasses, legumes, trees in hedges need to be encouraged.
21. Fodder development, animal welfare and insurance for the benefit of rearers of indigenous animals should be given adequate focus in the planning and execution.
22. Nucleus breeding units should be promoted at farmer's level for small ruminants and there should be exchange of bucks or rams to avoid inbreeding.
23. Preparation of herbal recipes for treating number of ailments in the indigenous animals would require popularisation (Ponnusamy *et al*, 2009).
24. Decentralised extension models such as pashu sakhi (Ponnusamy *et al.,* 2017) and public private partnership models for maintaining gaushalas, fodder supply and other extension delivery services (Ponnusamy, 2013) should be considered to promote the indigenous livestock breeds.
25. Periodical publication of success stories and indigenous animals in newspapers to create more awareness among the public.

Assessment of sustainability of rearing indigenous breeds

Following three indicators need to be considered for measuring the sustainability of rearing indigenous animal species.

1. Economic Indicators
2. Social Indicators
3. Environmental Indicators

Six sub indicators under economic indicators

A. Production efficiency
B. Net profit
C. Market

D. Lactation length
E. Dry period
F. Calving Interval

Social indicators: Basic social requirements of sustainable cattle rearing are that there should be farmer's participation in group action and promotion in local institution and access to resources.

A. Community relations
B. Access to resource and support services

It refers to access to resource such as water, and support services such as extension and credit services among farmers.

Environmental indicators

A. Animal welfare
B. Use of dung as manure over fuel
C. Waste Management
D. Preparedness for flood

Conclusion

It is clear that the nations have failed to make sufficient progress in switching over to a sustainable mode of living designed to halt the catastrophic slide. The relentless strain on the flora and fauna and their habitats in pursuit of short-term goals and polluting industrialisation have pushed the people dependent on agriculture, fishing and forestry to the brink. This has jeopardised the other aim which is crucial to protecting biodiversity: that of reducing carbon emissions so as to limit global warming to 1.5°C. The rising temperature spells doom, with the climate change-induced extreme weather events likely to becoming the dominant cause of biodiversity loss in the coming decades. Policy-makers must step up conservation and restoration efforts to mitigate the crisis before it is too late.

The predominant position of indigenous animals in the Indian animal husbandry sector provides ample avenues for harnessing their inherent potential and promote them vigorously among farmers especially resource poor farm families as profitable enterprises with attractive incentives and extension programmes. This becomes very essential in the context of health consciousness of consumers, growing concerns of climate change, high cost of rearing pure and crossbreds, prevailing socio-cultural beliefs and changing priorities of planners and policy makers. The niche extension models that are documented across the country can be effectively harnessed to undertake the technology transfer. Collaborative efforts of farmer organisations, social media, mass media, consumer forums, SHGs, NGOs, PRIs and government extension machinery would bring more social and economic benefits for promoting eco-friendly and farmer centric indigenous livestock farming.

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Adaptive mechanisms of indigenous livestock for changing environmental scenario: An overview

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Introduction

The inhabitation across diverse climate conditions required adaptation as per the climate, available vegetation and animal husbandry practices. This resulted in phenotypic as well as genotypic diversity in different livestock species. These variations have been shaped through the processes of mutation, genetic drift, recombination, natural and artificial selection. Unique genetic makeup of different livestock species evolved through these processes define their production and adaptive capabilities. Adaption of individuals to different climatic regions is imperative as only those well-adapted to their environmental conditions are more likely to survive, grow and reproduce. As per one estimate of FAO (2009), about a billion people rely directly on livestock for their livelihoods. However, in today's era of climate change, livestock production is under immense pressure. The physiological changes like increase respiration/heart rate, rectal temperature, panting etc. indicate that there is major strain to the animals. These impacts can result in significant loss of income and increase in management costs. The reduction in productive performance in dairy animals due to heat stress is primarily due to certain homeokinetic changes that animals undergo in an attempt to regulate body temperature (Hansen, 2004). For example, heat stress related reduction in growth and milk production ability is mainly related to reduction in feed intake by the animal in order to minimize the metabolic heat production. The extent of reduction in feed intake is largely dependent upon the degree or severity of heat stress.

There is a need to identify breeds that are climate resilient that are well adapted to the specific region. The climate change is projected to have greatest impact in developing countries where demand is likely to be increased manifold *vis* a *vis* increase in production and could threaten the sustainability of many livestock production systems. There are several anatomical and physiological factors that control the ability of animals to thermoregulate. Properties of skin and hair, respiration capacity, relationship between surface area per unit body weight, relative lung size, endocrinological profiles and metabolic heat production are some of the well-known factors that influence heat stress response. The differential response of species/breed to heat stress have been documented on the basis of anatomical differences and physiological parameters; however, genetic components, alterations in gene expression and molecular mechanisms underlying changes in heat stress response are not well established in livestock. In general, the high performer and commercialized breeds from temperate regions are considered to suffer more as they are poorly adapted to high temperature. The animals coming from temperate climates fail to adapt to higher environmental temperature and become unproductive. On the contrary, many local breeds in the tropics and subtropics outperform commercial breeds in terms of superior thermotolerance ability as they are relatively well adapted to high temperatures.

Differences in heat tolerance ability

It is believed that *Bos taurus* and *Bos indicus* cattle have undergone separate evolution from a common ancestor (Bradley et al., 1996). During the course of evolution, zebu cattle have acquired set of genes/alleles which possibly help them to regulate body temperature more efficiently in response to heat stress. Consequentially, the effect of heat stress is less in tropically adapted *Bos indicus* than temperate zone *Bos taurus* breeds. Genetic differences in thermotolerance at the physiological and cellular levels are documented by a series of studies in *Bos indicus* and *Bos taurus* (Hansen 2004; Kishore et al., 2013). In the past, several studies have tried to characterize the physiological response of animals to heat stress. *Bos indicus* cattle are reported to have large sized and higher density of sweat glands attributing towards greater sweating rates. Further, transfer of metabolic heat to the skin occurs at a higher rate when body temperature increases in *Bos indicus* compared to *Bos taurus*. Hammond et al. (1996) investigated rectal temperature as an index of heat tolerance and found that cattle with heavier, thicker coats exhibited higher rectal temperature than those with slicker hair coats. Carvalho et al. (1995) compared the physiological and histological responses of heat stress in imported *Bos taurus* (Simmental cattle), native *Bos taurus* and native *Bos indicus* cattle of Brazil. Their study concluded that *Bos taurus* in tropical environments fail to fully adapt and was most sensitive to heat stress. Beatty et al. (2006) reported that *Bos taurus* (Angus cross) cattle showed significant physiological changes in cattle in terms of respiratory rate, core body temperature, feed intake, and blood electrolytes when exposed to prolonged heat and humidity in comparison to *Bos indicus* (Brahman) cattle. Simth et al. (2013), compared the effects of heat stress on milk and component for Holstein and Jersey cows and concluded that Jersey cows appeared to be more heat tolerant than Holstein cows. Recently, Scharf et al. (2014) evaluated the thermotolerance ability of Angus and Romosinuano steers by comparing the rectal temperature, respiration rate, sweating rate and level of endocrine markers. Their study re-establishes the superior thermotolerant ability of Romosinuano cattle over heat sensitive Angus cattle.

The heat tolerant breeds are considered to have acquired mechanisms to protect cells against damage from high temperature. The cellular resistance to elevated temperature has been reported for several *Bos indicus* breeds. For example, the embryos from heat tolerant Brahamn and Romosinuano breeds have found to be more resistant to elevated temperature than embryos from Angus or Holstein breed (Hansen et al., 2004, Hernandez-Ceronetal., 2004). Similarly, lymphocyte viability of European Angus cattle showed greater reduction due to heat stress than tropically adapted Brahamn and Seneopl cows (Kamwanja et al., 1994). Later on, Paula-Lopes et al. (2003) showed that lymphocytes from Brahamn and Seneopl are less sensitive to heat-induced apoptosis than lymphocytes from Angus and Hereford. While comparing the breed differences, Lacetera et al. (2006) also highlighted differential response of PBMCs from Brown Swiss and Holstein cows to heat stress. Kishore et al. (2013), have shown that at higher temperature PBMCs from Indian native cattle has higher cellular tolerance in comparison to PBMCs from *Bos taurus* cattle. These difference in susceptibility to elevated temperature at the cellular level may be an important evolutionary mechanism that confer superior cellular thermotolerance to tropically adapted breeds.

Molecular basis of heat stress response

Heat shock proteins have been identified as major proteins induced during cellular responses to various stresses such as heat shock and oxidative stress. These proteins act as molecular chaperons in regulating cellular homeostasis and folding-unfolding of damaged proteins during thermal or any other physiological stresses. HSPs expression is regulated by heat shock transcription factors (HSFs) through interaction with heat shock elements (HSEs) in the promoter. Several studies have indicated that constitutive elevation of the inducible HSP level provides cyto-protection upon thermal stress (Collier et al., 2008; Horowitz 2001; Sonna et al., 2002). Several efforts have been made to determine the HSP gene expression under stress state in different breeds (Collier et al., 2006; Gade et al., 2010; Kapila et al., 2013; Kishore et al., 2013). Studies have been carried out to look into the response of peripheral blood mononuclear cells to hyperthermia (Kishore et al., 2013; Lacetera et al., 2006) and identification and characterization of heat stress response-related genes in cattle (Adamowicz et al., 2005; Starkey et al., 2007, Sodhi et al., 2012) *etc.*

In recent past, several studies have shown that the individual animals differ in their capacity to manage heat stress. Several polymorphisms/SNPs identified in heat shock protein genes are shown to be associated with thermotolerance ability of the animals. In cattle several variants in promoter, 5'-UTR, 3'-UTR and coding region have been identified in HSP70A1A gene (Basirico et al., 2011; Brown et al., 2010; Rosenkrans et al., 2010; Sodhi et al., 2012). Similarly studies by Li et al. (2011) found 2 novel SNPs in the HSF gene T909C and G4693T respectively where they reported that such genotypes were associated with thermal tolerance in Chinese Holstein cattle. Baena et al. (2018) evaluated HSF1 and HSPA6 candidate genes for adaptability in Angus breed raised in subtropical climate. They identified 12 SNPs in the HSF1 gene and 6 SNPs in HSPA6 gene. Suck kind of variants may affect inducibility, degree of expression, stability of HSP70 mRNA and may contribute to difference in individual stress tolerance. Association of SNPs in HSP genes with higher thermotolerant ability were also found in other species such as pigs, chickens; ovine (Chen et al., 2013; Salces-Ortiz et al., 2013).

Efforts were also made to identify the heat responsive genes and pathways associated with heat stress response in cattle. Transcriptome analysis of 10 Holstein bull calves, identified 8567 genes to be differentially regulated (DEGs), out of which 465 genes were significantly upregulated (≥2-fold, $P < 0.05$) and 49 genes were significantly downregulated (≤2-fold, $P < 0.05$) in response to heat stress (Krishnamoorthy et al., 2017). Significant pathways enriched in response to heat stress included chaperones, co-chaperones, cellular response to heat stress, immune response, apoptosis, Toll-like receptor signaling pathway, PI3K/AKT activation, protein processing in endoplasmic reticulum, interferon signaling, estrogen signaling pathway and MAPK signaling pathway. They identified top ten upregulated genes after heat stress. Upregulated genes were heat shock 70 kDa protein 1A (HSPA1A), heat shock 105 kDa/110 kDa protein 1 (HSPH1), heat shock 70 kDa protein 8 (HSPA8), DnaJ (Hsp40) homolog, subfamily A, member 1 (DNAJA1), and CDC-like kinase 1 (CDK1). Most of the genes were seen to be participated in metabolic process, catalytic activity, transcription factor activity, enzyme regulatory activity, protein binding, apoptotic process, response to stimulus, cellular process and immune system process. Similarly, studies by Kapila et al. (2013) identified the heat responsive genes and biological pathways in heat stressed buffalo mammary epithelial cells (MECs). They found upregulated genes in heat stressed MECs belonged to heat shock family *viz.*, HSPA6, HSPB8, DNAJB2, HSPA1A. Along with HSPs, genes like BOLA, MRPL55, PFKFB3, PSMC2, ENDODD1, ARID5A, and SENP3 were also upregulated. The transcriptome data revealed that the heat responsive genes belonged to different functional classes *viz.*, chaperons; immune responsive; cell proliferation and metabolism related. Several pathways such as, the Electron transport chain, Cytochrome P450 pathway, Apoptosis, IL2 signaling, MAPK, FAS and stress induction of HSP regulation, Delta Notch signaling pathway, Apoptosis modulation by HSP70, EGFR1 signaling, Cytokines and Inflammatory response, Nuclear receptors, Oxidative stress, TNF-alpha/ NF-kB signaling pathway and GPCRs pathway were identified in the data set. Additionally, Skin fibroblast revealed the differential response of cellular parameters, HSP genes, and miRNA expression during heat stress to understand the adaptive capacity of the *Bos Indicus* (Shandilya et al. 2020). Such type of studies is helping to better understand the molecular basis associated with thermal stress response in cattle and buffaloes. Recently, it would be interesting to study genetic variations in miRNA target sites in heat responsive genes and miRNAs profiling under heat stressed state in order to understand the post-transcriptional regulation of heat stress response in different cattle types. Sharma et al. (2019) identified the different cellular response and expression pattern of miRNA across the cattle types and buffaloes might be associated with their PBMCs tolerance level to heat stress. Several miRNAs that are involved in the thermal stress response and provide the viable strategies to combat the cattle response to heat stress. Zheng et al. (2014) was identified miRNA-19a/b associated with innate immunity and targeting the *TLR2* gene during thermal stress. Another miRNA-26a has been associated with the regulation of the inflammatory response and increased cell apoptosis (Lee et al., 2019). Additionally, miRNA-26a directly associated with the synthesis of HSPs, cell viability and survivability under adverse climatic conditions (Raza et al. 2021). Prediction of network analysis and target genes of these miRNAs to be useful for future research to understand the mechanism associated with the heat stress.

Physiological basis of adaptation to high altitude

Life at high altitude is physiologically challenging because of multiple risk factors *e.g.* UV exposure, cold desert and hypobaric hypoxia. Body requires constant supply of oxygen to generate energy. Hypoxic stress at high altitude is due to low barometric pressure and lower oxygen content in the inspired air compared to sea level. Hypoxia (0.1–1%), physioxia or physoxia (~1–13%), and normoxia (~20%) of O_2 are terms used to define oxygen concentration in the cellular environment. Less Oxygen (hypoxia) or hyperoxia (excess oxygen) could be lethal for cell survival and adaptation. High-altitude populations have developed genetic adaptations that allow their survival in extremely hypoxic environments (Simonson *et al.,* 2012). Till date, many studies have been carried out to gain understanding of high altitude adaptation across different animal species *e.g.*, Ladakhi cattle (Verma *et al.*, 2018), yak (Qiu *et al.,* 2012), sheep (Wei *et al.,* 2016), domestic goat (Song *et al.,* 2016), snow leopards (Cho *et al.,* 2013), Tibetan antelop (Ge *et al.,* 2013), pigs (Wang *et al.,* 2015), horses (Xu *et al.,* 2007), snub nosed monkeys (Yu *et al.,* 2016), as well as humans (Bigham *et al.,* 2016). These native animals have developed certain physical changes like small stature, large hair fur, and thick skin so as to combat with tough environment. Most of these animals defend hypoxia by having unique circulatory adaptability with enlarged lungs, heart and and greater heart pumping to supply more O_2 to the cells resulting in higher pulse rate and blood pressure.The yak (*Bos grunniens*), a large ruminant of the bovine family is the best example of high altitude adaptation, that is physiologically and genetically adapted through natural selection over millennia. Yak has compact body structure, thick outer long hairs and a fine down undercoat in winter, generating the heat to protect themselves from cold. Because of more accumulated fat in subcutaneous layer and presence of less sweat glands, internal heat does not dissipate from the body and therefore protect the animal from relentless cold. Besides, they have highly efficient energy metabolism (Wang *et al*., 2011) that enables them to survive easily at high altitude hypoxic condition. Yaks also have higher haemoglobin content and a higher affinity between hemoglobin and oxygen (Wiener *et al.* 2003). Other species like pigs, sheep and goat are also well known for their strong adaptability and robustness at high altitude (Zhu *et al.,* 2009). The Tibetan Cashmere goat (*Capra hircus*), one of the most ancient breed, is an important source of meat for local farmers. This goat has developed distinct phenotypic traits compared to lowland breeds for adaptation to high altitude (Song *et al.,* 2016). Tibetan goat also exhibits higher adult haemoglobin (Hb) concentrations, large heart and lung as a physiological adaptation to hypoxic condition (Renzheng *et al.,* 1992). Similarly, Tibetan pigs have developed a number of key adaptive physiological features to survive in the harsh environment at high altitude (Chang *et al.,* 2005). They have long hair with black skin and dense bristle that shield them from solar radiation and low temperature. They have well-developed heart and lung for the increase blood flow and oxygen transportation to tissues in response to low O_2 concentration (Ai *et al.,* 2014; Ruan *et al.,* 2004). High-altitude hypoxia results in increase in number of erythrocytes as an adaptive mechanism. Several studies have reported increased red blood cells (RBCs), hematocrit/packed cell volume (HCT/PCV), Hb and decreased mean corpuscle volume (MCV) in animals such as yak (Ding *et al*., 2014). Increase in RBCs was attributed to the increased secretion of erythropoietin which stimulates RBC production. Increase in RBC and Hb level was also observed in high altitude cattle (Wuletaw, 2011; Kumar and Pachauri, 2000).

Molecular basis of adaptation at high altitude

At molecular level, animals offset their oxygen transport system in order to maintain the tissue oxygen level for their growth, development and reproduction. Further, animals initiate several oxygen sensing and signal transduction pathways by stimulation of *HIF-1a* which further regulates the transcription of several hypoxia inducing genes that regulates erythropoesis, angiogenesis and glycolysis to overcome the oxygen demand (Scheinfeldt *et al.,* 2012). Hypoxia inducible factor (*HIF*) works as oxygen sensors that give the capacity to the cell to handle with decreased oxygen tension. *HIF* also act as a transcription factors to regulate cellular adaptation in response to hypoxia and inducing production of endogenous metabolites and proteins to promptly regulate metabolic pathways. Genomic studies have revealed several potential candidate genes having roles in high altitude adaptation. Genes like disintegrin and metallopeptidase domain17 *(ADAM17),* arginase 2 (*ARG2),* matrix metallopeptidase 3 (*MMP3)* have been linked to high altitude adaptation in yak and Tibetan pigs (Qiu*et al.,* 2012; Zhang *et al.,* 2015). *ADAM17* and *ARG2* affect the HIF stability and activity, whereas *MMP3* is involved in numerous physiological processes such as angiogenesis, immunity and wound healing (Rosenberg, 2009*;* Loffek*et al.,* 2011). *VEGFA*, another important candidate gene plays an important role in angiogenesis and is associated with high altitude adaptation (Wu *et al.,* 2013). Several studies reported genetic polymorphism in VEGF-A in different species including yak (Wu *et al.,* 2013), bovine (Pang *et al.,* 2011) and humans (Ding *et al.,* 2012; Espinoza *et al.,* 2014) indicating its potential role in high altitude adaptation. Additionally, in Tibetan sheep, seven following genes were found to be associated with high altitude adaptation; namely endothelial pas domain 1 (*EPAS1),* crystalline alpha A *(CRYAA),* lon peptidase 1*(LONP1),* neurofibromin1 *(NF1),* dipeptidyl petidase4 *(DPP4),* peroxisome proliferator activated receptor gamma *(PPARG),* and suppressor of cytokine signaling 2 *(SOCS2*) (Wei *et al.,* 2016). Using ovine 50K SNP chip, they could identify regions with positive selection between highland and lowland sheep breeds of China. The regions detected under selection were mostly linked to have important roles hypoxia, angiogenesis, energy production and erythropoiesis.

Genome wide scan in high altitude Tibetans population revealed *EPAS1, EGLN1*, and *PPARA* as candidate genes to be associated with low hemoglobin levels. Both *EPAS-1* and *EGLN1* are involved in the hypoxic pathway as key regulator during chronic hypoxia while *PPARA*, is a master regulator of fatty acid oxidation. In Andeans, *EGLN1* (Egl-9 family hypoxia inducible factor1), *PRKAA1* (protein kinase, AMP activated α 1 catalytic subunit), and *NOS2A* (nitric oxide synthase 2A) involved in HIF pathway were marked as candidate genes for high-altitude adaptation. *NOS2A* contributes to nitric oxide synthase that plays an important role in smooth muscle relaxation, vasodilation and increased uteroplacental blood flow while *PRKAA1* is a cellular ATP stressor that effects *HIF-1* transcriptional activity.

Genetic polymorphism in *HIF* and its regulatory genes are found to be associated with high altitude adaptation in animals and humans. Studies have reported genetic polymorphism in *EPAS-1* associated with high-altitude adaptation in animals such as yak (Wu *et al.,* 2015), dogs (Wang *et al.,* 2014), sheep (Ai *et al.,* 2014), cattle (Newman *et al.,* 2015). Song *et al.* (2016) identified a missense mutation in *EPAS1* at Q579L in Tibetan goats associated with higher Hb concentration relative to their lowland counterparts suggesting this as a crucial adaptation mechanism for high-altitude adaptation. In yak genetic polymorphism at G83065A in *EPAS-1* was associated with increased Hb level (Wu *et al.,* 2015). Dong *et al.* (2014) also reported SNPs (G963A), (C1632T), (G1929A) and (G1947A) in *EPAS-1* associated with high-altitude adaptation in Tibetan pigs. Genetic variation in other hypoxia related genes has also been identified. *VEGF-A*, essential for the growth of new blood vessels promoting angiogenesis plays an important role in high altitude adaptation. Wu *et al.* (2013) reported two SNPs g.8430T>C in intron 4 and g.14853G>A in 3' untranslated region of *VEGF-A* and suggested their possible association with high altitude adaptability in yak. SNP rs3025033 in *VEGF-A* gene in humans has been found to be associated with chronic mountain sickness in Andeans (Espinoza *et al.,* 2014). Pang *et al.* (2011) reported genetic polymorphism in *VEGF-A* associated with growth and development of Chinese cattle.

Some other studies were carried out to identify genes involved in high altitude adaptation in different species. Zhang *et al.*, (2015) determined the expression level of four hypoxia-related genes (*ADAM17, ARG2, MMP*, and *HIF1A*) in two distinct skeletal muscle tissues from Tibetan pigs from different altitudes (500 and 3650 m). The pigs from high altitude had higher mRNA abundances of the four genes, indicating their critical roles in skeletal muscle response to hypoxic condition. Wang *et al.* (2015) examined the differences in the RNA-seq based transcriptomes of heart, kidney, liver and lung between yak and cattle, distributed at high and low altitudes, respectively. Of the four organs, heart shows the greatest differentiation between the two species in terms of gene expression profiles. They identified 3788 genes that were differentially expressed between cattle and yak for one or more of the four organs. Detailed analyses demonstrated that some genes associated with the oxygen supply system and the defense systems that respond to threats of hypoxia were differentially expressed. They reported that *EPAS-1, CRYAA1, LONP1, NF1, DPP4, PPARG,* and *SOCS* genes are involved in angiogenesis, erythropoiesis and energy production. Ghoreishifar et al. (2020) identified several candidate gene related to high altitude hypoxia (*DCAF8*, *PPP1R12A*, *SLC16A3*, *UCP2*, *UCP3*, *TIGAR*) and cold acclimation (*AQP3*, *AQP7*, *HSPB8*) condition in the Swedish breed. Additionally, *LETM1*, *TXNRD2*, *STUB1*, *NOXA1*, *RUVBL1* and *SLC4A3* genes, were identified in the Chinese indigenous cattle breed, involved in the adaptation to hypoxia (Zhang et al., 2020). Recently, our group has generated the transcriptome data in PBMCs of Ladakhi cattle adapted to high altitude region *viz a viz* Sahiwal cows from tropical region Verma *et al.,* (2018). Our studies revealed a total of 8417 differentially genes between Ladakhi and Sahiwal PBMCs with multiple testing (FDR<0.05). The top up-regulated genes in Ladakhi cows observed were *INHBC, ITPRI, HECA, ABI3*, *GPR171*, and *HIF-1a* involved in hypoxia and stress response whereas in Sahiwal cows, the top up-regulated genes *eEF1A1, GRO1, CXCL2, DEFB3* and *BOLA-DQA3* were associated with immune function and inflammatory response indicating their strong immune potential to combat the pathogens prevalent in the tropical conditions. The molecular pathways that were highly impacted included MAPK signaling, ETC, apoptosis, TLR signaling and NF- kB signaling pathway indicating signatures of adaptive evolution of these two cattle types in response to diverse environments. Overall, this study revealed that high altitude adapted Ladakhi cattle is highly distinct from that of low altitude adapted Sahiwal cows.

Conclusion

The distinct gene pool of indigenous livestock breeds/populations with superior adaptive traits presents an opportunity for mining specific allele(s). Unraveling the distinctive gene(s) would help to check depletion of native resources due to emergence of crossbred populations resulting in loss of important gene(s)/gene combinations responsible for adaptive traits. The present scenario calls for mining of these genetic resources for identifying the genes/genomic regions associated with thermoregulation and adaptive biology and further develop functional gene resource for native livestock as a model for better understanding of thermoregulation pathways/molecular mechanism of heat stress. Our understanding on the adaptation in animals and humans to high altitude environment has increased several folds in recent years. More research on high altitude adaptation mechanism in livestock will further increase our understanding of genetic adaptation to high-altitude environments.

The systematic assessment and recording of phenotypes (phenomics) related to adaptive traits in response to heat load/cold/oxidative stress in breeds of livestock will be key to undertake accurate phenotype-genotype association studies. Such an effort will provide the possibility to introgress desirable genes/alleles and drift herds toward superior thermo-tolerant ability. It is expected that multifunctional local breeds that are well adapted to thermal stress and high altitude will continue to play a role in the livelihoods of poor people and in marginal areas.

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Important biomolecules and uniqueness in native breeds with special reference to A1A2 milk

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Cow milk with perfect balance of all nutrients has been part of human diet since long providing nutritional support for growth and development (Weinberg et al. 2004). It has innumerable benefits and also exhibit medicinal properties (Zemel et al. 2004; Phelan et al. 2003; Heaney et al. 1999). Unique nutritional balance makes the nutritional value of milk as a whole greater than the value of its individual nutrients. It is a good resource of fat, proteins/amino acids, hormones, immunoglobulins, growth factors, cytokines, nucleotides, peptides, polyamines, enzymes and other bioactive peptides. It provides high quality source of energy and fulfils our needs for selenium, the B-group vitamins (thiamin, riboflavin, niacin, vitamin B6, and folate), calcium, phosphorus and vitamin A, vitamin C, magnesium, zinc as well (Jelen 2005). Different livestock species contribute to the global milk pool and can be categorised as cattle (Bos taurus and Bos indicus, cow) and non-cattle (such as buffalo, goat sheep, camel and donkey). Among these cows with a total herd capacity of 264 million producing 600 million tonnes of milk contribute highest to the total milk production (83%). Cow milk is the most consumed milk not only because of its widespread availability and large production volumes but also in terms of nutritive values as amongst different milk resources, cow milk resembles the human milk the most (Table 1).

Table 1. General composition (g /100 mL) of milk from different mammalian species

Properties	Ruminants					Non ruminants		Human
	Cattle	Buffalo	Goat	Sheep	Camel	Horse	Donkey	
Total solids	11.8–13.0	15.7–17.2	11.9–16.3	18.1–20.0	11.9–15.0	9.3–11.6	8.8–11.7	10.7–12.9
Protein	3.0–3.9	2.7–4.7	3.0–5.2	4.5–7.0	2.4–4.2	1.4–3.2	1.4–2.0	0.9–1.9
Fat	3.3–5.4	5.3–9.0	3.0–7.2	5.0–9.0	2.0–6.0	0.3–4.2	0.3–1.8	2.1–4.0
Lactose	4.4–5.6	3.2–4.9	3.2–5.0	4.1–5.9	3.5–5.1	5.6–7.2	5.8–7.4	6.3–7.0
Ash	0.7–0.8	0.8–0.9	0.7–0.9	0.8–1.0	0.69–0.9	0.3–0.5	0.3–0.5	0.2–0.3
Oligosaccharides	0.003–0.006	No data	0.025–0.030	0.002–0.004	No data	No data	No data	0.500–0.800
Total casein	24.6–28	32–40	23.3–46.3	41.8–52.6∞	22.1–26.0	9.4–13.6	6.4–10.3	2.4–4.2
Total whey proteins	5.5–7.0	6	3.7–7.0	10.2–16.1∞	5.9–8.1	7.4–9.1	4.9–8.0	6.2–8.3
Casein-to-whey protein ratio	82:18	82:18	78:22	76:24	73:27–76:24	52:48	56:44	29:71–33:67

In the past few decades, it has been realized that along with nutritional aspects, milk is a highly valuable source of biomolecules that extend the value of milk in human nutrition. These biologically active molecules in milk can have a direct and significant effect on health including digestive functions, metabolic responses to absorbed nutrients, growth and development of organs ((Tailford et al. 2003; Marshall 2004; Sodhi et al. 2012, 2022; Kuellenberg et al 2022) and thus milk and milk products are considered as functional foods. Most often milk and milk products includes, caseins, and whey proteins based bioactive peptides (Nielsen et al. 2017).

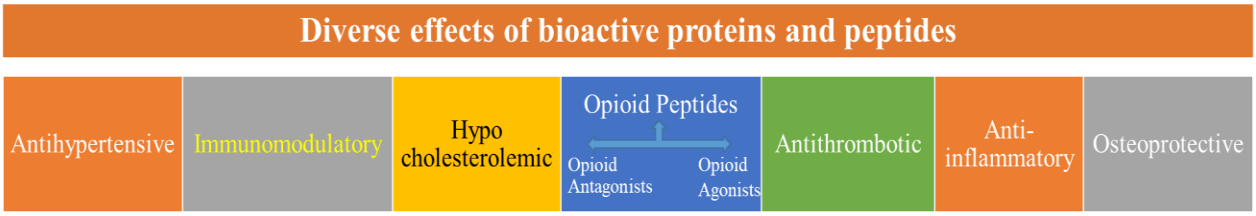
Milk proteins derived biomolecules

Milk proteins are known for their high nutritive value and diverse functional properties. The potential health effects of milk proteins are recognized by the recent discovery of many biologically active peptides exerting different bioactivities depending on their amino acid composition and sequence. These biologically active peptides can be released during digestion by gastrointestinal digestive enzymes (pepsin, trypsin, and chymotrypsin), fermentation with proteolytic starter culture or hydrolysis with commercial protease derived from microorganisms or plants (Korhonen and Pihlanto, 2003). Protein-derived biomolecules are found in colostrum as well as mature milk; both casein and whey protein fractions of milk of all domesticated mammals but their concentrations differ remarkably between species. The focus in this lecture will be on cow milk that has been regarded as nature's perfect food.

Bioactive peptides and cow milk proteins

Cow milk has 3.0–3.9 percent proteins and more than 95% of these are constituted by caseins (80%), whey proteins (20%) and remaining 5% include peptones/low molecular weight peptides milk fat globule membrane proteins. Caseins, the major group of bovine milk proteins has four main proteins: αs1 (39-46% of total caseins), αs2 (8-11%), β (25-35%), and ϰ (8-15%) casein (Eigel et al. 1984). The major whey proteins in are β-lactoglobulin (50%), α-lactalbumin (12%), immunoglobulins (10%) and bovine serum albumin (5%). The proteins in cow milk are of excellent quality containing all the essential amino acids, and elements that our bodies cannot produce. However, it's not only the overall content of amino acids that decide the nutritive value of proteins but it is also determined by the bioactive peptides released from these proteins.

Most of the bioactive peptides are released during digestion of proteins (Korhonen and Pihlanto, 2006; Park 2009) but there are some naturally contained intact bioactive molecules in milk like lactoferrin, immunoglobulins, growth factors and hormones 1, that can directly exert the *in vivo* effect by binding to the receptors in the intestine. These bioactive proteins are generally resistant to digestive enzymes. Milk-derived bioactive peptides are usually encrypted and kept inactive within the primary structure of milk protein and they are generated by proteolysis of casein (α-, β- and ϰ-casein) and whey proteins (β-lactoglobulin, α-lactalbumin, serum albumin, immunoglobulins, lactoferrin and protease-peptone fractions). The probable health benefits of milk proteins are expanded with the discovery of peptides released upon gastrointestinal digestion, enzymatic hydrolysis or microbial fermentation (Korhonen and Pihlanto, 2003; Danquah and Agyei, 2012; Dziuba and Dziuba, 2014) and these positive attributes have made the bioactive peptides as potential ingredients of functional food. These positive attributes of bioactive molecules include immune-stimulating, antithrombotic, anti-hypertensive and opioid-like activities; enhancement of calcium absorption; antibacterial and antiviral impacts (Demers et al. 2013; Clare and Swaisgood 2000). Whey proteins have mainly been associated with reduction of the risk of chronic human diseases reflected by the metabolic syndrome, e.g. obesity, hypertension and type 2 diabetes.



Because of the physiological versatility, milk-derived bioactive peptides are used in formulation of pharmaceutical and nutraceutical products with health promoting functions (FitzGerald and Meisel, 2003). In order to elicit their action bioactive peptides are either absorbed from the intestine to the blood stream, act directly on the intestinal tract or via receptors and cell signalling.

Beta casein and bioactive peptides

Bovine β-casein is located on the 6th bovine chromosome among the cluster containing other casein genes i.e. α-casein and ϰ-casein and spans a region of 8.5 kb. Generation of large number of peptides have been reported from β-casein with different activities. Fragment position, amino acid sequence and activity of some of major bioactive peptides released from bovine β-casein are mentioned in table 2.

Table 2. Fragment position, amino acid sequence and activity of different bioactive peptides released from bovine β-casein

Activity	**Fragment**	**Sequence**
Angiotensin converting-enzyme inhibitor		
	59-64	-Val-Thr-Tyr-Arg-Pro-Phe-Pro-Gly-
	59-61	-Val-Thr-Tyr-Arg-Pro-
	60-66	-Thr-Tyr-Arg-Pro-Phe-Pro-Gly-Pro-Ile-Pro-
	60-66	-Thr-Tyr-Arg-Pro-Phe-Pro-Gly-Pro-Ile-
	60-68	-Thr-Tyr-Arg-Pro-Phe-Pro-Gly-Pro-Ile-Pro-Asn-
	63-67	-Pro-Gly-Pro-Ile-Pro-
	80-90	-Thr-Pro-Val-Val-Val-Pro-Pro-Phe-Leu-Gln-Pro-
	104-120	-Pro-Lys-His-Lys-Glu-Met-Pro-Phe-Pro-Pro-Lys-Thr-Tyr-Arg-Pro-Val-Glu-Pro-Phe-Thr-
	108-113	-Glu-Met-Pro-Phe-Pro-Lys-
	120-126	-Thr-Glu-Ser-Gln-Ser-Leu-Thr-
	125-131	-Leu-Thr-Leu-Thr-Asp-Val-Glu-
	140-143	-Leu-Gln-Ser-Trp-
	169-174	-Lys-Val-Leu-Pro-Val-Pro-

	169-175	-Lys-Val-Leu-Pro-Val-Pro-Gln-
	177-183	-Ala-Val-Pro-Thr-Tyr-Arg-Pro-Gln-Arg-
	177-179	-Ala-Val-Pro-
	179-181	-Pro-Thr-Tyr-Arg-Pro-
	180-197	-Thr-Tyr-Arg-Pro-Gln-Arg-Asp-Met-Pro-Ile-Gln-
	189-192	-Ala-Phe-Leu-Leu-
	191-197	-Leu-Leu-Thr-Tyr-Arg-Gln-Gln-Pro-Val-
	193-198	-Thr-Tyr-Arg-Gln-Glu-Pro-Val-Leu-
	193-198	-Thr-Tyr-Arg-Gln-Gln-Pro-Val-Leu-
	193-202	-Thr-Tyr-Arg-Gln-Glu-Pro-Val-Leu-Gln-Pro-Val-Arg-
	202-209	-Arg-Gly-Pro-Phe-Pro-Ile-Ile-Val-
	203-209	-Gly-Pro-Phe-Pro-Ile-Ile-Val-
	205-209	-Phe-Pro-Ile-Ile-Val-
Antibacterial		
	184-210	-Gln-Glu-Leu-Leu-Leu-Asn-Pro-Thr-His-Gln-Thr-Tyr-Arg-Pro-Val-Thr-Gln-Pro-Leu-Ala-Pro-Val-His-Asn-Pro-Ile-Ser-Val-
	169-176	-Lys-Val-Leu-Pro-Val-Pro-Gln-Lys-
	170-176	-Val-Leu-Pro-Val-Pro-Gln-Lys-
	177-183	-Ala-Val-Pro-Thr-Tyr-Arg-Pro-Gln-Arg-
	183-188	-Arg-Asp-Met-Pro-Ile-Gln-
Immunomodulatory		
	1-28	-Arg-Glu-Leu-Glu-Glu-Leu-Asn-Val-Pro-Gly-Glu-Ile-Val-Glu-Ser-Leu-Ser-Ser-Ser-Glu-Glu-Ser-Ile-Thr-Arg-Ile-Asn-Lys-
	1-28	-Leu-Leu-Thr-Tyr-Arg-Gln-Glu-Pro-Val-Leu-Gly-Pro-Val-Arg-Gly-Pro-Phe-Pro-Ile-Ile-Val-
	63-68	-Pro-Gly-Pro-Ile-Pro-Asn-
	91-93	-Gly-Val-Met-
	191-193	-Leu-Leu-Thr-Tyr-Arg-

Data from BIOPEP (2018)

The peptides of main concern from β-casein are opioid peptides which are released after digestion of beta casein. The opioid peptides fragments of beta-casein are called beta-casomorphins (BCMs). These opioid peptides are opioid receptor ligands with pharmacological similarities to morphine, can pass the gut-blood barrier and get access to their target sites. Structurally, these have a tyrosine (Tyr; Y) residue at the amino terminal end coupled with aromatic residues, such as phenylalanine or tyrosine in the second, third, or fourth positions. Like other casein, β-casein is highly polymorphic and this abundance of polymorphism is responsible for generation of diverse opioid peptides with different activities.

Opioid peptides from A1 and A2 alleles

During the course of evolution, different mutations have led to generation of different genetic variants of beta casein: A1, A2, A3, B, C, D, E, F, H1, H2, I and G. Amongst these, A1 and

A2 are the most common, with A2 considered as ancestral allele. These variants are the result of a point mutation on exon VII of bovine beta-casein gene involving the conversion from cytosine to adenine base (C8101A) that leads to replacement of proline (A2 allele, codon; C<u>C</u>T) by histidine (A1 allele, codon; C<u>A</u>T) amino acid at position 67 (Groves, 1969). Based on this specific variation, milk can be divided into A1 and A2 "like" groups. A1 or "A1 like" milk has β-casein gene with A1, B, C, F or G alleles, all having a common amino acid histidine (His) at position 67 (–Tyr60– Pro61–Phe62–Pro63–Gly64–Pro65–Ile66–**His67–**), but variations at other positions of amino acids. Conversely, in A2 or "A2 like" milk beta-casein alleles are A2, A3, D, H1, H2 and I, which irrespective of variations at other positions of amino acids, have a common amino acid proline (Pro) at position 67 (–Tyr60–Pro61– Phe62–Pro63–Gly64–Pro65–Ile66–**Pro67**).

The specific codon conversion of proline to histidine leads to key conformational changes in the secondary structure of expressed β-casein protein. The presence of proline confers high proteolytic resistance to these bioactive peptides, so they can bypass the stomach without degradation. The gastrointestinal proteolytic digestion of A1 milk (raw/processed milk) with leucine aminopeptidase, elastase and carboxypeptidase Y, releases a 7 amino acid bioactive peptide 'opioid' called beta-casomorphin 7 (BCM7) in small intestine, while proline in A2 milk at 67 position prevents the split at this particular site and generates nine amino acid peptide BCM9 (Roginski, 2003; Kostyra et al. 2004). BCM7 has been observed in hydrolyzed milk with A1A1 genotype, however, it has not been detected in fermented dairy products like cheese, and yoghurt. It may be postulated that BCMs might be formed from the fermented products, cheese and yoghurt but are degraded during processing (Nguyen et al. 2015). BCM7/9 may further be broken down to BCM5 by dipeptidyl peptidase IV (DPP IV) enzyme present on surface of enterocytes or in blood. The opioid peptides generated from by enzymatic digestion of cow milk thus include BCM7/9 or BCM5. Beta-casomorphins are found in the analoguous position of the natural proteins in cow, sheep, water buffalo, and human β-casein (Meisel and Schlimme, 1996).

Absorption of opioid peptides

Independent of the origin, the action of opioids (neuroactive substances), is mediated by the μ-, ϰ- and δ-opioid receptors, which are widely distributed over the intestinal lining. Majority of bioactive peptides cause systemic effects and therefore must either be absorbed from the intestine, act directly on the intestinal tract or via receptors and cell signalling. In the human gut, mu-opioid receptors having the maximum affinity for opioids are present on myenteric and submucosal neurons; and on immune cells in the lamina propria. In general, peptides must be absorbed in sufficient amounts to elicit a quantifiable and sustained response, however, opioid peptides are thought to be biologically very potent and even micro molar amounts may be enough to exert physiological effects (Meisel and FitzGerald, 2000).

Beta casomorphins have good affinity for opioid receptors, especially the μ-opioid receptor, which are widely distributed over cell surfaces of gastrointestinal tract, immune cells, pancreatic cells and various cells and tissue types in central nervous system; and are thus able to exert opiate-like effects by affecting the nerve system and gastrointestinal functions. BCM7 is reported to have more affinity for μ opioid receptor compared to BCM9. The BCM5, primarily released from further proteolytic digestion of BCM7 and BCM9 by brush border peptidases is even more potent. Presence of tyrosine at the N-terminal and aromatic residues, such as phenylalanine or tyrosine in the second, third, or fourth positions allows the peptides to fit into the binding pocket of the opioid receptors. The proline present at the 2nd position is crucial for the formation of bioactive conformation of the peptide.

These peptides can cross the epithelial layer and are then free to exert their physiological effect(s) on various tissue types and cells by participating in cellular pathway by virtue of being "atypical" opioid peptides or in intact form as immunomodulatory peptides. The suggested modes of transport across intestinal epithelial barrier are transcellular, transporter mediated and paracellular. The transport is more common in neonates due to high permeability of intestine or improper function of DPP (IV) enzymes. Adults with compromised digestive health such as celiac disease, stomach ulcers or autism have increased intestinal permeability and therefore the probability of BCM7 entering the bloodstream is more in such cases. The mu opioid receptors have seven trans membrane spanning domain coupled to G inhibitory protein and after binding of exogenous ligand such as BCM7, the GβϒY subunit dissociates from Gα and various intracellular pathways are initiated that may lead to different health disorder (Parasher et al. 2015). Through this postulated mode of action, role of BCM7 have implicated in many illnesses, including heart disease, type I diabetes, and sudden infant death syndrome. Both *in vitro* and *in vivo* studies have suggested the absorption and transport of beta-casomorphine-7 across epithelial barrier of small intestine. But in the case of BCM9, there are no studies suggesting the trans-epithelial movement. The difficultly to pass the epithelial membrane may attributed to the comparatively bigger size and high hydrophobicity value of the peptide.

Milk with A1/A2 allelic variant of β-casein and human health

Cow milk has always been considered as a safe source of high-quality protein and micronutrients and has been an essential part of the human diet since long. However, recently, disease risk with consumption of a specific bovine β-casein fraction has been suggested (Bekuma et al. 2019; McLachlan 2001; Birgisdottir et al. 2006; Laugesen et al. 2003). All livestock as well as well human have proline at amino acid position 67, which is referred as A2 variant, but in cattle, specially the taurine breeds, another genetic variant called A1 with histidine at amino acid position 67 is present. This A1 type variant of β-casein or A1 type milk is suggested to be associated as a risk factor for human diseases like type 1 diabetes and CVD (Laugesen and Elliott, 2003; Virtanen et al. 2000; Birgisdottir et al. 2002), schizophrenia and autism (Woodford, 2006), arteriosclerosis (Tailford et al. 2003), and sudden infant death syndrome (Sun et al. 2003).

Probable association of A1 with diseases was reported first time by Dr. Elliott's group in Australia. In one of their study data on type of food consumed and incidence of mortality rates due to chronic heart diseases, juvenile insulin-dependent type I diabetes mellitus (DM-I) and other diseases was collected across 20 developed countries. They observed strong association between consumption of high A1 type β-casein and chronic heart diseases/DM-I particularly in the populations from high altitude countries, such as North America and North Europe. There are some contradictory results as well e.g., even though the average consumption of A1 type β-casein in France and Australia was similar (0.3 g/day), but percent mortality rates due to chronic heart diseases were much higher in France (0.088) compared to Australia (0.033). On the other hand, consumption of A1 type β-casein varied across population of Sweden, Austria, Iceland, Canada, Germany (0.3 to 2.8 g per day), but mortality rate was similar (0.070-0.080). Though, this was purely an epidemiological study, assumed that all the individuals are exposed equal level of risk factor and had some lacunas also but started the concerns about A1 type β-casein or A1 milk.

In another study on Samoan children, it was observed that incidence of Type 1 diabetes in Samoan children living in New Zealand was much compared to those living in Samoa. The reason proposed was the higher milk consumption by Samoan children living in New Zealand. Contrary to this study, reports indicate that Masai people in Kenya drink large amounts of milk but the incidence of childhood diabetes is extremely rare. Explanation lies in the fact that it is not only the milk but the type of milk or milk constituents, caseins in particular. The milk, the consumed by Masai people has A2 type variant of beta casein/ A2 milk whereas the people in New Zealand drink A1 milk. This supported the hypothesis that type of beta casein variant in milk -A1 variant might be the casual factor for Type 1 diabetes. The studies were further extended to assess the effect of BCM 7, specific bioactive peptide released from digestion of milk with A1 variant beta casein. Reports from University of Florida indicated that removal of BCM7 sources (milk and gluten) from the diet of patients suffering from childhood autism resulted in considerable improvement of their health conditions. This pointed towards association of BCM7 with autism and schizophrenia. Similarly, Tonstad et al (2002) also indicated comparative advantage of soy-based diet over the caseins in reducing the risk for heart diseases. Following these epidemiological studies, large number of *in vivo* and *in vitro* investigations are being conducted to establish the hypothesis of association of A1/A2 milk/BCM7 with health disorders.

A number of studies have indicated systemic inflammation and gastrointestinal discomforts; impairment of gut barrier integrity and bile acid metabolism; altered gut microbial composition on intake of milk containing A1variant of β-casein through the release of BCM7. Study by Haq et al. (2014) indicated significantly increase in the levels of inflammation-associated molecules, humoral immune response, leukocyte infiltration in intestine and up-regulated expression TLR2 and TL-4 on consumption of A1 type milk. The authors suggested the induction of inflammatory response in gut through activation of Th2 pathway on intake of A1 type milk. Many other studies have also demonstrated impairment of gastrointestinal motility and inflammation on digestion of A1 but not A2 milk. In a clinical trial by Ho et.al. (2014) significant correlation was observed for fecal calprotectin and abdominal pain (A1, 0.46 vs. A2, 0.03; $p = 0.02$) as well as bloating and gut inflammation (A1, 0.36 vs. A2, −0.02; $p = 0.05$). Significant positive association ($P<0.001$) between abdominal pain and stool consistency on intake of A1milk (r=0.52) unlike A2-milk diet (r=-0.13) clearly pointed towards the ill effect of A1 milk on gastrointestinal measures. Similarly, Jianquin et al. (2016) also observed A1 milk to be a causative factor for the gastrointestinal discomforts in Han Chinese. Feeding of A1 type and mixed type of milk caused digestive discomfort, increased gastrointestinal transit time, inflammation and cognitive behavior. The group which received A2 type and mixed milk (3:2 ratio) showed symptoms of gastrointestinal discomfort with increased gastrointestinal transit time; increased inflammatory serum marker level as well as retarded cognitive processing speed while none of these adverse effects were observed in group fed with A2 (A2A2) type milk. He et al. (2017) clearly revealed positive effects of A2 milk diet like attenuation of acute gastrointestinal symptoms of milk intolerance while A1 milk was reported to reduce lactase activity and increased gastrointestinal discomfort. Milan et al (2020) also showed improvement in digestive discomfort in individual having lactose intolerance or lactose malabsorption Impairment of functions including reduction in the frequency and amplitude of intestinal contractions by BCM7 is also well reported (Daniel et al. 1990; Mihatsch et al. 2005).

A number of studies have also been published correlating the specific milk-based diet and induction or aggravation of neurological disorders. The preliminary findings of study at University of Florida observed higher levels (100 times than normal) of milk protein in the blood and urine of autistic children. Removal of milk from the diet of these autistic children improved the conditions and more than 80% of children no longer had symptoms of autism or schizophrenia. Confirmation of the fact that bioactive peptides released from digestion of casein can leak through the gut wall into the blood, and from there into the brain causing significant behavioral problems supports the results of such studies. Neural disorders/ erratic behaviors have also been observed in rats dosed with varying levels of BCM7. Furthermore, these changes did not occur when the rats were pre-treated with naloxone, an opioid antagonist, suggesting the role of BCM7 in behavioral disorders such as schizophrenia and autism. Other health issues associated with A1milk or BCM7 are sudden infant death syndrome and apnea.

At large, epidemiological studies pointed towards increased risk of type-1-diabetes on consumption of A1-milk in childhood (Bekuma et al. 2019; Laugesen et al. 2003). Still, potential role of A1 milk in induction of diabetes is still debated and there is no consensus on the diabetogenicity of individual milk proteins. Study by Chia et al (2018) supported the increased incidence of type-1-diabetes with consumption of A1-milk in genetically susceptible mice, which further became evident in later generations. There are clear evidences that BCM7 released by digestion of A1 milk activate receptor that compress our immune system and also produce autoantibodies against pancreatic beta cells that might lead to the progression towards diabetes. Suppression of body's immune system by BCM7 may also enhance the survival of pathogens such as enteroviruses or bacteria involved in triggering of type1 diabetes like symptoms. Also, sequence of some of the bioactive peptide generated from β-casein mimic the GLUT-2 transporter sequence are recognized as an antigen by the T cells leading to activation of B cells for the production of antibodies which target the peptides of beta casein as well as insulin producing beta cells, causing type 1 diabetes. On the contrary, many studies revealed no difference with intake of A1 or A2 milk with respect to type-1-diabetes (Beales et al. 2002; Yin et al. 2012).

Atherogenic property of A1 based diet over A2 diet has been demonstrated by Tailford et al. (2003) during *in vivo* study in rabbit. Allison et al. (2006) has also suggested linkage of cardiovascular diseases with the consumption of milk and dairy products with the A1 variant. The postulated ways through which BCM7 act to contribute for cardiovascular diseases encompasses i) angiotensin converting enzymes inhibitory action ii) low density lipid oxidation property and iii) associated complication with diabetes and obesity such as hypercholesterolemia. However, in some of the studies, no association of A1 casein with any cardiovascular health disease was observed. The experimental trials conducted at ICAR-NBAGR, clearly demonstrated that feeding of milk with A1A1 or A1A2 genotype induces progressive inflammation in C57BL/6 mice. Histopathological examination of liver revealed congestion fatty changes, cellular swelling, pyknotic nuclei and amyloids in A1A1milk diet group at all-time points. Similar changes though observed in A1A2 group but had lower alteration prevalence. Liver amyloids were observed in mice group fed with A1A1 and A1A2 diets at the stage of 9 months while karyomegaly was observed only in A1A2 MD group both at 6 and 9 months of trial. Overall, the results indicated time dependent change in the histopathological profiles of C57BL/6 mice after intake of A1A1 and A1A2 milk-based diet.

Indian livestock breeds: A resource for A2 allele

On one hand, β-casomorphins originating from milk have been associated with various health issues, while on the other hand, these peptides are potential modulators of various regulatory processes as well. At this juncture, to be on the safer side, it is essential to genotype the animals to ascertain the frequency of A1/A2 allele of beta casein in cows and breeding bulls and then efforts should be put in to drift the herds towards A2. The distinguishing amino-acid sequence that characterizes A1 beta–casein is essentially unique to some European cattle breeds (taurine breeds). All Asian and African cattle (Bos indicus breeds); Goats, sheep, yaks and camels produce A2 milk. Human beta-casein is also of the A2 type as defined by the relevant amino-acid sequence. Even all animals belonging to genus *Bos taurus* (Exotic) were initially of A2A2 type. Due to mutation (A2-proline: CCT to A1-histidine: CAT) some animals possessed A1 allele of beta casein. With the advent of selective breeding for high production, better fertility and protein quality, unconsciously the genetically superior bulls used in breeding programs were carrying A1 allele of beta casein. This led to the perpetuation and predominance of A1 allele in in European cattle (taurine breeds). It is a major variant in the milk of Friesian, Ayrshire, British Shorthorn, and Holstein-the common dairy cows of north European origin. Frequency of A1 type beta casein has increased over the last century as *Holstein Friesian* (*HF*), known for its high milk production character has become breed of choice for crossbreeding in many countries. Artificial insemination of large number of cows with *HF* bulls' semen has multiplied frequency of A1 beta casein over time. On the contrary, zebu/Indicine breeds have been reported to possess all frequency of A2 type beta casein.

Status of β- casein variants in Indian cattle breeds

The status of A1/A2 alleles of β-casein gene was delineated systematically at NBAGR, Karnal. PCR-RFLP genotyping protocol was followed to ascertain the genotype/allelic status. In a comprehensive analysis, animals representing 27 breeds of Indian cattle were genotyped to understand the distribution of A1/A2 variants. Majority of the Indian native cattle (90.4%) showed A2A2, the desirable genotype, followed by heterozygous A1A2 (0.091) genotype. A1A1 genotype was not observed in any of the Indian breed, only few animals of Malnad Gidha and Kherigarh cattle showed heterozygous A1A2 genotype with frequency of 0.191 and 0.218, respectively. The overall frequency of favourable A2 allele across all the analysed animals was 0.95. Distribution of A1 type allele across the different utility types (milch, dual and draft purpose breeds) revealed complete fixation of A2 allele in milch breeds, whereas the frequency across dual and draft purpose breeds was 0.95 and 0.92, respectively. The allelic profile clearly pointed towards preponderance of A2 type β-casein variant in cattle breeds of India and also indicated the indicine origin of A2 allele (Mishra et al. 2009; Mukesh et al. 2022).

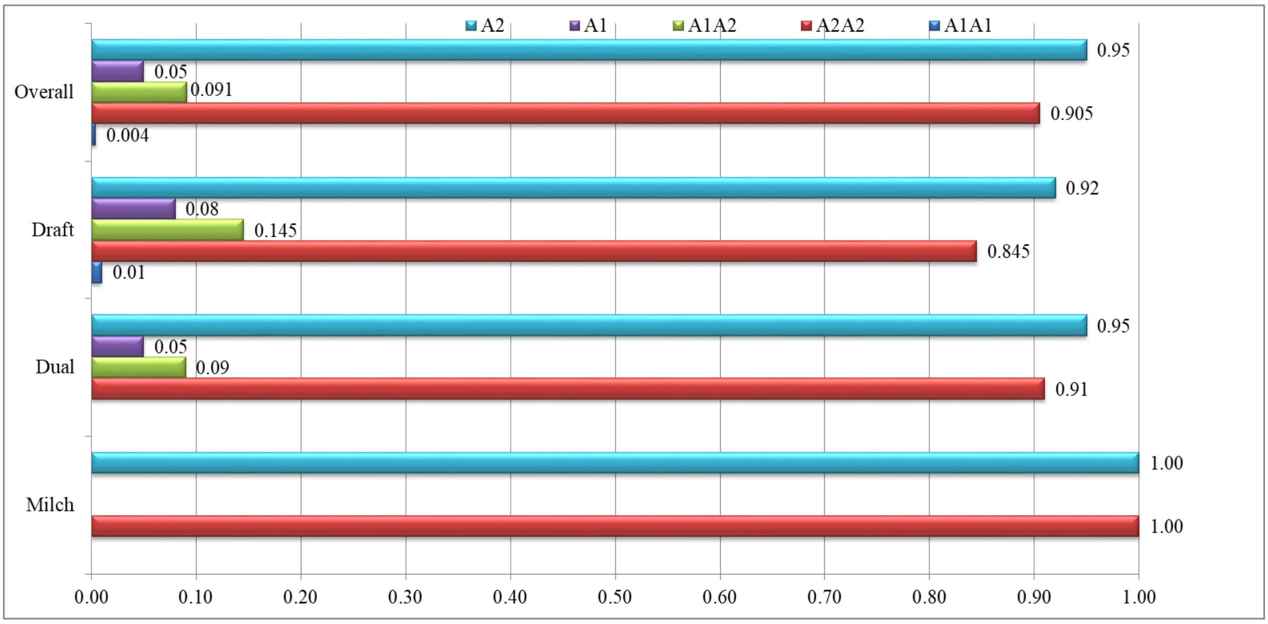


Figure 1. Genotypic and allelic status of β-casein A1/A2 variant across all analysed and different utility group Indian cattle

Conversely, much higher frequency of A1 allele (0.435) has been reported in *Bos taurus* breeds from different countries. Considering the high frequency of A1 in taurine breeds and widespread use of taurine germplasm in our country's cross-breeding program status of A1/A2 alleles was assessed in all breeding bulls (Sodhi et al. 2012). Across the genotyped taurine and crossbred bulls, frequency of heterogygous genotype (A1A2) was highest (0.481) followed by homozygous A2A2 (0.405) and homozygous A1A1 genotype (0.114). The mean frequency of A1 and A2 alleles was 0.355 and 0.645 respectively. Frequency of preferable A2 allele in cross-bred bulls was 0.702 whereas in Jersey and Holstein Frisian bulls, it was 0.675 and 0.559, respectively. Apparently, it seems a happy scenario with high frequency of A2 allele (0.645), nut high frequency ((0.481) of A1A2, the heterogygous genotype is matter of concern. Still, to minimize the risk of disseminating the A1 allele in Indian cattle and to drift herds towards A2, careful screening of sire lines being used in the breeding programmes is required for status of genotype (A1A1/A1A2/A2A2). Cow milk is the most exploited sources of bioactive proteins. The recognized biodiversity of milk biomolecules offers great potential for its better utilization and conservation. There is need to develop suitable breeding strategies to check the flow of undesirable alleles in our native breeds. In context of A1/A2 variants of beta casein and biomolecules generated therefrom, our native Indian cattle breeds are natural source of A2 beta casein allele and have an edge over taurine breeds having comparatively higher proportion of A1 type variant. If global demands for A2 milk increases, our native cattle breeds would be the best resource to meet the demands in the international dairy sector. This would further help in enhancing their value, better utilization and conservation.

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Need for conservation of indigenous AnGR: Strategies and success stories

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Global demand for livestock products is expected to double by 2050, mainly due to improvement in the worldwide standard of living. Meanwhile, extensive livestock production systems are being fast replaced with intensive and industrial production system due to change in land use, higher demand of livestock product and more and more keepers shifting to high producing improved breeds. Genetic diversity defines not only animal breeds' production and functional traits, but also the ability to adapt to different environments, including food and water availability, climate, pests and diseases. Diverse animal genetic resources are a key to economic development. Many local livestock breeds continue to represent the lifeline of rural populations. The diversity of these resources makes possible human livelihoods in some of the most inhospitable areas where crop production cannot be exclusively depended upon. While they may not be able to compete with "improved breeds" in milk and meat yields, they fulfill a much wider range of functions and provide a larger range of products. Being able to thrive even with low fodder inputs, their maintenance is ecologically more sustainable, especially in marginal environments. Requiring lower levels of health care and management, they commonly entail a lower workload in comparison with improved breeds. As is becoming increasingly clear, they often have scope for specialty products and can be essential to preserve habitats and cultures. At the local level, the loss of a breed means the loss of a livelihood strategy and loss of indigenous knowledge. It also emphasizes the need for the active involvement of indigenous communities and the role of local knowledge and institutions in conservation. India has vast Animal Genetic Resources (AnGR), which play a vital role in improving the socio-economic conditions of rural masses. AnGR is also of significant social and cultural importance, supplementing family incomes and generating gainful employment in the rural sector, particularly among the landless, small, marginal farmers and women. There are about 302.79 million bovines, 74.26 million sheep, 148.88 million goats and about 9.06 million pigs as per 20th Livestock Census in the country. Horses and Ponies, Mules, Donkeys and Camel population decreased by 45.6, 57.1, 61.23 and 37.1 percent, respectively, over previous Census. AnGR provide a range of products and services to their keepers and to the wider society – including food, fibre, transport and fuel.

Most of AnGR are reared in extensive production system which contributes directly to food and livelihood security because they produce more valuable nutrients for humans, such as proteins, than they consume. AnGR rearing can contribute to farmer's risk management of natural calamities in many ways. They are mobile, which increases survivability and may also be relatively omnivorous, and thereby able to survive dramatic effects on specific feed resources. Indigenous AnGR keepers require very little resources as they are mostly very well adapted to the local environments and can survive on meager feed resources without any housing needs, Indigenous AnGR keepers are able to earn their livelihood by selling animal products like milk, egg, wool, etc. and also by selling the animals for meat purposes. There are 212 registered breeds comprising 53 cattle, 20 buffalo, 44 sheep, 37 goat, 7 horse, 9 camel, 3 donkey, 13 pig, 19 chicken, 2 duck, 3 dog and one each of Yak, and Geese. All these breeds have been developed over centuries by natural and manmade selection to meet the specific needs as per production systems and native environments. The defined breeds have become prominent during last two decades with various activities and effective awareness generation by ICAR-NBAGR. More and more populations in the country are now being characterized and registered as breeds. Proportion of non-descript animals in each species has declined significantly and purity within breeds is also increasing. Various State AHD which are custodian of AnGR, are making effective strategies for conservation and improvement of their resources.

Conservation aims to maintain the option value of genetic diversity, it is therefore a priority of the Global Plan of Action for Animal Genetic Resources. Conservation measures for threatened breeds have already been established in some countries. Most current conservation programmes are based in developed countries with strong collaboration between gene banks and animal breeding organizations. In developing countries, the focus is typically on *in vivo* conservation. Conservation usually involves the characterization of animal genetic resources and the subsequent development of inventories, including information on the spatial distribution of breeds and valuable breeding stocks, and priority setting. Realization that AnGR are at risk of being lost has alarmed the researchers and planners which stimulated National livestock conservation efforts. The need for conservation is based on economic, cultural, and ecological values; unique biological characteristics; shifts in market demand; and research needs. A first step in assessing genetic conservation needs is development of baseline information on population and genetic relationships. Livestock breeds are not biological taxa but rather represent the outcome of social processes and are therefore unlikely to survive outside the social contexts and production systems that formed them. Conservation of ecosystem/production system guarantees breed survival. Traditional pastoralists have often tended to foster biodiversity, in both plants and animals. Many pastoral societies have developed elaborate systems that result in the preservation of genetic resources. Pastoralists have deliberately developed livestock to meet different needs and conditions.

In the changing socio-economic scenario, it is becoming increasingly difficult to save local breeds specially those which are low producing. Major reasons are increased pressure on land to meet food requirement, the need for higher income per unit land/input to sustain better quality of life, shift of livestock activity from subsistence occupation to commercial entrepreneurship etc. The changing scenario calls for breeds with high performance to have higher profits. Sustaining low producing local breeds with poor economic viability is therefore really a challenge. Use of few specialized breeds with optimized specific production traits has lead to narrowing of the genetic base, as native breeds and species are neglected in response to market forces. Declining livestock diversity may have adverse affect on our capacity to mitigate the enormous challenges posed by climate change and emerging diseases. We may need to rely back on the adaptability and potential of indigenous animal genetic resources to face an uncertain future.

Commercial breeds of livestock possess greater genetic variability than most crop varieties do. This diversity allows intensification of selection within breeds to be a fruitful approach for improving livestock productivity. However, if continued emphasis on breed replacement and increasing selection intensity (e.g. for greater productivity) take place at the expense of maintenance of genetic diversity, including the advantages of disease resistance and environmental adaptation, there may be significant long-term costs. As an example, Holstein cattle have become the pre-eminent dairy breed world-wide and have enjoyed sustained improvements in milk production potential, but only at the cost of declining genetic diversity within the breed. These losses weaken the potential of breeding programs that could improve hardiness of livestock. Indigenous breeds are considered hardy and well adapted to the environment. The hardiness of the indigenous breeds is believed to have resulted from natural selection under the management practices of the native breeders/herders and from the adverse feed conditions. Indigenous breeds show a high level of fertility and reproduction. *In situ* management of animal genetic resources can only be successfully accomplished through breeder actions.

Risk status of different Breeds

As per National Breed Watchlist (2022), following is the risk status:

Species	**Critical**	**Endangered**	**Vulnerable**
Cattle	-	Belahi, Krishna Valley, Khariar, Pulikulam	Mewati, Punganaur, Siri, Ponwar, Vechur
Buffalo	-	-	Chilka, Toda
Sheep	Tibetan	Karnah, Katchaikatty Black, Nilgiri	Gurej, Jalauni, Kendrapada, Poonchi, Rampur Bushair
Goat	Teressa	Chegu, Sumi-Ne	Konkan Kanyal
Pig	-	Angoda Goan, Tenyoi Vo,	-
Horse	-	Bhutia, Kachchhi Sindhi, Manipuri, Spiti, Zanskari	-
Camel	Malvi, Mewati, Mewari	Jalori, Kharai, Marwari	-
Chicken	-	-	Kalasthi

Conservation models

The most important factor of all conservation cum genetic improvement projects is that selection should be carried out for its traditionally valued characteristics and in the environment to which it is adapted. The herds must be managed within the natural environment for that breed and need to be exposed to conditions prevalent in the field.

***In-vivo* conservation**

- Establishment of nucleus herd in the tract with field agency (ONBS mode)
- Raising of breeding males from elite females.

- Production, processing and cryopreservation of semen from breeding males
- Registration of farmers' animals and recording for desirable traits by animal keepers
- Incentive for retaining the animals in shape of feed/mineral mixture/ de-worming/ vaccination etc.
- Health care and management help
- Use of elite breeding males in farmers herds/flocks either by AI or NS
- Improvement and conservation of various breeds in the field
- Creation of breed societies to take care of the conservation and improvement of breed/population after the project period.
- Value addition, creation of niche marketing and branding of animal products having specialty of a breed

Successful ventures

Murrah Buffalo by Haryana State Animal Husbandry Department
Gir, Sahiwal and Kankrej cattle by CIRC, Meerut
Mehsana Buffalo by Mehsana Dugdhsagar Dairy

With Organized Farm

Existing farms of indigenous breeds should be declared as germplasm repositories and used for production of quality breeding males and semen. Efforts should be made to establish one such farm for each breed in the native breed tract. Only pure breeding of the indigenous breeds should be practiced at these farms.

Cattle and Buffalo

- Twenty (20) unrelated young male progeny of elite animals from the breeding tract to be procured and maintained at the organized farm
- A total of 2000 semen doses per male to be produced from 15 males making the total number of doses as 30,000.
- Handing over 1000 semen doses from each bull to ICAR-NBAGR Gene bank
- Supply and utilization of frozen semen doses in the field through state agencies for breed improvement in the tract
- Producing 5000 progenies under field condition in breeding tract

Successful ventures

Krishna Valley cattle in Karnataka by NBAGR with BAIF

Sheep and Goat

- Twenty five (25) unrelated young male progeny of elite animals from the breeding tract to be procured and maintained at the organized farm for six months.
- These males would be trained to donate semen.
- A total of 1000 semen doses per male would be produced from 15 males making the total number of doses as 15,000.

- The semen doses would be cryopreserved.
- The males to be extensively used for breed improvement in the tract.

With livestock keepers

Owners of animals of the breed may be given suitable incentives to save the breed. The objective is to compensate the animal keepers for the difference in levels of production between the breed under consideration and the replacement breed under the same animal management system and agro-ecosystem. This will attract the farmers and will ensure the conservation of the breed *in-situ.* Incentives in form of husbandry inputs are always better than cash.

Cattle and Buffalo

- A total of 100 unrelated elite females in the farmer's herds, spread over the breeding tract would be identified and registered.
- Part of the maintenance cost of these elite females i.e. Rs. 1500/- per female per year will be given to the farmer/stakeholder.
- A minimum of 50 unrelated males would be produced from these elite females.
- A fixed amount of Rs.5000/- per male would be given to the farmer for raising the male progeny till maturity.
- These male progeny will be used for further breeding in the tract.

Sheep and Goat

- A total of 100 unrelated elite females spread over the breeding tract to be identified and registered.
- Part of the maintenance cost of these elite females i.e. Rs. 500 per female per year will be given to the farmer.
- A minimum of 50 unrelated males would be produced from these elite females.
- A fixed amount of Rs. 1500 per male would be given to the farmer for raising the male progeny till maturity.
- These male progeny will be used for further breeding in the tract.

Successful ventures

Beetal goat by NBAGR with KVK, Ambala

Horse and Camel

- A total of 100 unrelated elite females spread over the breeding tract to be identified and registered.
- Part of the maintenance cost of these elite females i.e. Rs. 3000 per female per year will be given to the farmer.
- A minimum of 50 unrelated males would be produced from these elite females.
- A fixed amount of Rs. 10,000 per male would be given to the farmers for raising the male progeny.
- These male progeny will be used for further breeding.

Successful ventures

Spiti horse by NBAGR with HPKV, Palampur

Chicken

- Clusters of progressive Chicken Keepers to be identified.
- Cluster should consist of only identified breed and none to be allowed to keep chicken of other breed/ strain.
- 50 keepers to be brought under the programme by identifying other cluster(s) as required.
- Each participating keeper has to raise minimum 300 chicks of 4 weeks age per year.
- While higher performer(s) will be facilitated suitably, the low performer(s) may be excluded after warning.
- Each keeper will be allowed to dispose the surplus birds after meeting their replacement requirement.
- The sale proceeds will be the income of keepers.
- At the end of project period, all units will be sustainable out of own income.

Successful ventures

Harringhatta Black by NBAGR with WBUAandFS, Kolkata

State-wise breeding policy for improvement and conservation of AnGR

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The breeding policy is an important document for genetic improvement of livestock resources of the area. It mainly depends on the livestock wealth, their production level and utility, infrastructure and available resources. The policy should focus on judicious use of input per unit of output to attain sustainable animal production and management. The genetic improvement programmes should be based on perception, wishes and needs of livestock keepers, which would enhance acceptability and facilitate easy implementation of the policies. In the normal course, a breeding policy shall be part of the overall developmental objectives and livestock production system. The breeding policies should be different for the different species of livestock. In India, Livestock is a state sector activity. Thus states evolved their own breeding policies; of course in tune with the overall guidelines prescribed by Government of India. States who made programme according to the availability of resources witnessed a good progress. For many states the breeding policy document has been prepared with lots of fine details but with little planning on its operational feasibility. Therefore, the success in implementing these policies varied from state to state.

Major objectives of breeding policy:

1. To define mating system to be undertaken in different categories of livestock populations i.e. exotic/crossbreds/indigenous breeds and its grades/nondescripts under different production systems and varying agro-climatic conditions (regions/zones) of a state.
2. To ensure fast genetic improvement of livestock for the economic traits taken as breeding goals.
3. To identify animals of high genetic merit and ensure their maximum propagation.
4. To encourage breeding of high yielding purebred animals available with the livestock keepers.
5. To workout production parameters and standards of breeding bulls/males.
6. To control the level of exotic blood in crossbreeding programmes.
7. To regulate the use of bull/semen to improve productivity and to check transmission of diseases.
8. To conserve the indigenous breeds of livestock.
9. To undertake systematic bull production and evaluation programmes so as to improve the productivity of animals by using latest technologies.
10. To phase out nondescript populations of livestock.
11. To identify the bulls of low/unknown genetic merit and keep them away from breeding programmes either through castration or other means to avoid indiscriminate breeding.

Assessment of livestock wealth and formulation of breeding policy:

1. Classify the livestock population of different species in to various categories (exotic/crossbreds/indigenous breeds/grades of indigenous breeds/nondescripts).
2. Work out the productivity status of all the categories, for which breeding plans is to be formulated.
3. Define the breeding goals for all the species in terms of economic traits.
4. Evaluate the socio-economic status of livestock keepers/farmers and their capacity to rear the genetically improved livestock.
5. Evaluate infrastructure facilities in a particular area in terms of feeds and fodder and other management inputs.
6. Divide the state into different zones and make the mating plan in each zone and each category of livestock within the zone.
7. Fix the breeding targets for particular period based on generation interval of the species/breed and review it to work out genetic gain and revise the policy, if required.

Develop breeding goals and breeding plans:

The breeding goals are defined as economic trait to be improved in the livestock population, which may be milk, egg, body weight, reproductive traits, health traits, quality of livestock products. More the traits considered as breeding goal, less genetic improvement is expected in each trait. Based on the breeding goals, selection may be planned for identification of animals of high genetic merit for the breeding goal. Selection of one sex or both the sexes may be planned in genetic improvement programmes. Each state may define the “animals of high genetic merit”, which may be in terms of superiority of animals to the average of the population for the trait(s) under consideration. It may be percent above or below the population mean or in terms of plus/minus 1-2 standard deviation of the population mean.

National Livestock Policy- 2013

The National Livestock Policy- 2013 has been developed by the Government of India, which also covers the breeding policy. As per this document the breeding policy for livestock should be as follows:

States would be encouraged to review their respective breeding policies for different livestock species. Species-wise breeding programmes will be fine-tuned and implemented for faster growth in production.

Breeding policy for cattle and buffalo

For increasing milk production in cattle and buffaloes and to increase their life time productivity, a broad framework of policy would include the following:-

- Selective breeding of defined indigenous breeds of cattle have high milk yield, and those with excellent draft abilities will be promoted to improve their production and reproduction potential. This will help their proliferation, conservation and genetic up-gradation. Efforts will be made to import semen of these breeds if necessary, to avoid/reduce inbreeding. Intrusions of crossbreeding in their defined breeding tracts will be avoided.

- Cross-breeding of non-descript and low producing cattle with high yielding exotic breeds suitable for respective agro-climatic conditions will be encouraged in selected areas having adequate facility for feed and fodder and marketing facilities etc. Up-gradation of non-descript and low producing cattle with defined indigenous breeds in resource deficient areas and the breeding tracts of defined indigenous breeds would be encouraged.
- Buffalo development will aim at improving milk production and to hasten growth, maturity and proliferation. Selective breeding of established native breeds, and upgrading low producers through breeding with defined high milk yielding breeds will be undertaken. If required, semen may also be imported to reduce inbreeding. Cross-breeding of non-descript buffalo breeds with improved indigenous breeds will be considered, where appropriate.
- Production of breeding males having high genetic potential will be an essential element of the breeding policy for each species and breed. Formation of breed associations involving farmers for improvement of indigenous breeds of various species and identification/registration of animals having good genetic potential would be promoted by providing financial, technical and organizational assistance.
- There is a need to focus on the hitherto neglected natural mating system and to produce quality disease free high genetic merit bulls for natural service through implementation of massive pedigree selection programme and progeny testing programme.
- For the purpose of cross-breeding, semen of progeny tested bulls would be used as far as possible.

Breeding policy for sheep and goat

This will aim to improve growth, body weight, reproductive efficiency, meat and wool quality and quantity, and to reduce mortality. An area specific approach would be adopted to improve quality and quantity of coarse wool and fine wool. Main focus will be to produce and distribute good quality rams/bucks of quality indigenous breeds which can thrive in different agro-climatic conditions. Artificial insemination would also be encouraged. Cross-breeding with high yielding exotic and other native breeds of goats will also be considered.

Breeding policy for pig

This will focus on improving growth, prolificacy, quality and quantity of meat produced, survivability and utilization of low cost locally available feed and managemental conditions. While efforts will continue to conserve some of the meritorious indigenous breeds of pigs in their defined local tracts, crossbreeding with high yielding, disease resistant exotic breeds will be encouraged, with maximum 50% level of exotic germplasm in crossbreeding.

Breeding of yak and mithun

This would be supported in high altitude agro climatic regions for preservation and further development through selection, and where possible, through crossbreeding with exotic germplasm.

Breeding of equine

Breeding of horses, mules, and donkeys would be promoted to produce high quality stock for draft power and sports purposes. Selective breeding of indigenous breeds and cross breeding, where necessary, will be considered.

Breeding of camels

It will aim at improving their desert specific draft power, milk production and disease resistance and sports traits. Breeding of Double hump camel in high altitude areas would be supported with import of semen to minimize otherwise high chances of inbreeding.

Breeding policy for any other useful livestock can also be developed as per local need.

New technologies for livestock breeding

Newer breeding and reproductive technologies, including those involving biotechnology and genetic engineering/genetic marker technology developed from time to time, will be adopted for faster implementation of various breed improvement programmes and for increasing production. Efforts will be made to develop semen sexing technology for sex pre-selection. The delivery of breeding services would be regulated by fixing standards with periodic evaluation of service providers.

Conservation of animal biodiversity

- The country has rich and diverse genetic resources of livestock in the form of a large number of species, breeds, and strains within a species. India has some of the best breeds of cattle and buffaloes with traits for dairy, draught power and dual purposes, several carpet wool breeds of sheep, highly prolific breeds of goats and adaptive breeds of poultry. These breeds of livestock and poultry are essentially the products of long term natural selection and are better adapted to tropical fodder, environment and diseases, and perform under low and medium inputs. Some of these breeds are suited to particular agro-climatic conditions in the country. Some of these breeds have useful genes for fast growth and prolificacy. Such utility genes and breeds would be identified, conserved and utilized for breeding and research. The focus would be on conservation of indigenous breeds of livestock and poultry.
- Pastoral communities, particularly those managing migratory animals like buffaloes, sheep, goats, yaks etc. shall be supported through creation of facilities along their migratory routes for feeding, breeding, healthcare, housing, and market channels for their produce and animals. Indigenous knowledge of pastoral communities about animal maintenance and breeding would be documented with active involvement of communities, breeders' associations, Gaushalas and NGOs.

Since agriculture and livestock are the state subjects under Indian constitution, each state Animal Husbandry Department develops its livestock breeding policy, which are reviewed and revised periodically. The essences of breeding policies developed by some of the states of India are given below:

1. Arunachal Pradesh

For improvement of milk in local cattle, Jersey/ Holstein Friesian exotic breeds will be used to produce half bred and subsequent inter-se-mating of half-bred with concomitant selection. The indigenous breed Tharparkar will be used for grading up of the indigenous local. At higher altitude selective breeding of local cows will be done so as to conserve and improve them.

The indigenous/ swamp buffaloes will be improved by selective breeding for draught, milk and conservation purposes. Pure breeding of Murrah under intensive system of management and crossbreeding of swamp and Murrah buffalo on experimental basis is also proposed. Pure breeding of yak and mithun for conservation and to increase population, improve milk and meat production and to improve draught power will be adopted. However, some experiments on hybridization with cattle can also be made under controlled conditions. For commercial farming of improved exotic pure bred/ crossbred pigs of proven potential, elite populations of breeds like Hampshire, Large White Yorkshire and large black may be maintained for providing quality germ-plasm. Cross breeding of indigenous pigs may be carried out using Hampshire Boars. The level of inheritance may be fixed at 50% for both exotic and indigenous pigs with inter-se-mating of the half bred. In elite herds of organized farms under intensive production system, the inheritance level of exotic breed can be raised to 75%.

Selective straight/ pure breeding of Arunachal Pradesh indigenous goats and cross breeding of A.P. indigenous with Beetal breed is recommended for augmenting meat production. Selective breeding of indigenous sheep (Bonpala) and cross breeding of indigenous sheep with Merino rams for improving body weight, weight gain and wool characteristics will be adopted. Inheritance level of exotic breed may be restricted to 50-75%. Pure lines of Merino and Indigenous sheep may be developed with selection.

Pure breeding of local ponies will be undertaken in the areas where they are largely used as pack animals. However, a pony-donkey crossbreeding pilot project may be carried out with reciprocal mating in farm conditions to evaluate pack qualities of different grades of crossbreds/ hybrids before making any recommendation as a policy in future.

For backyard poultry production, the strains like Giriraja, Vanaraja, Kroiler, Krishna J., and CARI Shyma which have colorful plumage, good egg production and small body size may be promoted. Hatcheries and grower units may be established in the district HQs/ Govt. farms for breeding and rearing of parent stocks. In order to have large-scale commercial egg production, the breeds and strains which are already tested in the state viz. WLH, RIR, BV-300, BV-800 etc. may be continued for breeding and rearing. For broiler production, introduction of already available hybrid broiler birds namely Hybrocross, Vencobb, Vencobb-100, Vencobb-400, may be continued as broiler parent stock. The state may also introduce Turkey and popularize its use for meat purpose. The local ducks may be bred following selective breeding for meat as well as egg production. Selection of sire and dams may be made on the basis of production performance and body weight gain. For gaining quick improvement in egg production of indigenous ducks, a cross breeding programme be carried out in farm conditions using Khaki Campbell males.

2. **Assam** (https://livestock.assam.gov.in/portlets/state-cattle-breeding-policy)

The State Cattle Breeding Policy formulated in 2002 continues to place emphasis on cross breeding with Jersey bulls in most areas of the State and use of Holstein bulls restricted to certain specified areas. Selective breeding is used for local cattle and swamp buffaloes.

Cattle Breeding Policy

Breeding policy using Jersey

Exotic Inheritance of 50% will be applied to entire state for large scale half-bred production whereas 62.5% will be in a limited scale on demand from farmers in some areas where there is plentiful fodder availability, good market channel, educated entrepreneur with knowledge and capacity for providing better management.

Breeding Policy using Holstein Friesian

Holstein Friesian (HF) inheritance will be infused only in limited scale. In some defined geographic areas / herds where fodder production and its availability is more, a well developed milk market and in areas of high elevation with congenial climate, desired by the farmer. The level of inheritance of H.F. in the crossbred will be fixed at 50 per cent by intense mating of the crossbred coupled with selection of superior F1 animals.

Policy for draft ability There are three policy options for improvement of draft power in the state. Policy for using Jersey halfbred(and graded) male :The Jersey half bred bullocks (Jersey x Indigenous) have higher draft capacity for shorter working hours than the local ones. Policy for using indigenous bullock:The policy aimed at improving the draft ability of indigenous cattle by selection and animal production and indigenous germplasm conservation to support this traditional system of draft animals utilization.Upgradation of local cattle by pure India breed(s):This upgradation programme aims at increasing both draft and milk production ability.

Buffalo Breeding Policy

The buffalo population of the state is primarily of swamp type distinctly different from the riverine breeds not only in behaviour but also in respect of chromosome numbers. . Though, in regard to milk yield, these buffaloes are not at par with those of improved riverine breeds, the milk of the swamp buffaloes is very rich in fat and protein content.

Straight breeding of swamp buffalo with selections

Improvement in the genetic potential of indigenous swamp type buffalo of Assam is done by selection and straight / pure breeding. This breeding policy of indigenous swamp buffalo of Assam will fulfill three basis requirement. These are :

1. Conservation of germplasm
2. Meeting a major part of the draft animal requirement for agricultural activities

3. Augment production of quality milk

Pure breeding of Murrah

Murrah and Surti were found to have performed satisfactorily under organized farm environment in the agro-climatic conditions of Assam. Educated entrepreneurs and well to do farmers may be encouraged to rear these two riverine breeds in scientific manner under intensive system of management. The sate Govt. will maintain at least one elite herd of each of Murrah and Surti as a source of germplasm.

Cross breeding of swamp with Murrah

The possibility of crossing Murrah bulls with swamp female to enhance milk production is kept open due to its chromosomal differences. In absence of sufficient data on the performance and fertility status of swamp x riverine crossbreds, the approach of such a crossbreeding programme has to be cautious. Therefore, initially such a crossbreeding programme will be taken up experimentally in limited scale using the bulls of organized elite herds of Murrah and crossing them to swamp females.

3. Bihar

For implementation of the bovine breeding policy in Bihar, the state has been divided into 9 clusters. Improver indigenous cattle breeds like Bachaur, Red Sindhi, Gir, Hariana, Tharparkar, Sahiwal have been recommended (one or two breeds in each cluster). In most of the clusters cross breeding have been kept under low or very low priorities, however, crossbreeding of local cattle with Jersey breed with exotic inheritance level of 50 to 62.5% has been recommended for progressive farmers with good resources. For the improvement of buffaloes, Mehsana and Murrah will be used as improver breeds either one or both in different clusters.

4. Chhattisgarh

The state has developed area-wise and species-wise breeding policy for the genetic improvement livestock and poultry. Up-grading of local cattle using Sahiwal, Red Sindhi, Tharparkar, Gir, Kankrej and Ongole breeds will be taken up. Crossbreeding of local cattle with Jersey and HF breeds while maintaining the exotic blood level between 50 to 62.5% is to be followed on demand in the areas adjoining the cities where assured irrigation facilities available for green fodder production. Up-grading of local buffaloes using Murrah and Surti breeds is also envisaged. Minimum standards (Dam's 305 days milk yield) for bulls/ buffalo bulls to be used for AI or natural service have been also defined. Up-grading of local sheep with Pashmina breed in hilly areas and with Ramboullet in other areas is proposed. Up-gradation of local goat with Jamunapari/ Barbari/ Black Bengal/ Sirohi breeds and up-grading of local pigs with Middle White Yorkshire/ Russian Charmukha/ Krishnashire breeds is also envisaged. In the breeding tract of Aseel fowl, the breed will be propagated and in other districts white leg horn for egg production, crosses of white leg horn, Rhode Island Red and Australorp and breeds like Vanraja, Giriraja for dual purpose, Japenese Quail, Turkey and Guniea fowl are to be promoted. For the improvement of local ducks, Khaki Campbell is recommended. Use of Chinchilla/ Angora/ Grey giant is recommended for rabbit improvement.

5. **Gujarat**

(Notification No. GHKH/107/2012/CDS/2002/2691/p.1 dated 4.1.2013 of Agriculture and Cooperation Department, government of Gujarat)

Gir and Kankrej are important indigenous cattle breeds of the state and these breeds will be further upgraded by selective breeding for milk production and fat percent. Crossbreeding of non-descript cattle using 100% high genetic merit of Holstein Friesian or Jersey semen with a restriction of 62.5% of exotic inheritance level will be carried out. The productivity of the crossbred cattle needs to be further increased by extensive use of genetically superior relevant crossbred bulls. In view of different geographical factors and local preferences, pure breeding or up-gradation with local established breeds is to be preferred. The important breeds of indigenous buffalo in the state include Jaffarabadi, Mehsana, Surti and Banni. Pure breeding of indigenous buffalo using semen of pedigreed selected and /or proven bull should be practiced. Non-descript buffaloes should be upgraded by using relevant pure indigenous high genetic merit buffalo for breeding.

6. **Haryana** (Haryana Government gazette notification No. 5125.AH-4.2009/917 dated 28.01.2010)

Selective breeding of indigenous cattle such as Hariana, Sahiwal and others will be carried out; however in the urban area if demanded by the owner, the crossbreeding with Holstein Friesian may be adopted. Non-descript, indigenous cattle will be upgraded by crossing with Holstein Friesian maintaining the exotic inheritance at 50%. Crossbreeding with the Jersey will be stopped. The state is the home of Murrah which is the best breed of buffalo in the world. Selective breeding of Murrah and upgrading of non-descript as well as buffaloes of other breeds with Murrah would be taken up. The minimum production standards for cattle and buffalo breeding bulls to be used for AI/ natural service has also been define in terms of dams best lactation milk yield (305 days milk yield).

7. **Himachal Pradesh** (http://www.hpagrisnet.gov.in/animal-husbandry/New_Folder/breeding.html)

According to breeding policy of the State inheritance of exotic blood i.e. Jersey/Holstein Friesean is to be kept at 50% and remaining 50% inheritance will be contributed by Pahari /Hilly cattle. This policy will ensure the benefit of higher milk production potential of exotic breeds and disease resistance and hardiness traits of Hilly /Pahari Cattle. Genetic makeup of the non-descript buffaloes of the State is to be improved by grading up process using Murrah Breed. Indigenous Gaddi and Rampur Bushair ewes are to be crossed with pure bred exotic rams of Rambouillet or Russian Merino breed so that in F-1 generation exotic and indigenous inheritance comes at 50:50 level. In F-2 generation, the progeny of F-1 generation (50% crossed bred ewe) is to be again crossed with purebred exotic ram of Rambouillet or Russian Merino breed so that the progeny thus produced has exotic and indigenous inheritance at 75:25 level.

Thereafter, in subsequent generation Rams with 75% exotic inheritance are to be used for cross breeding to maintain exotic and indigenous inheritance at 75:25 levels.

8. **Jammu and Kashmir** (http://www.jkanimalhusbandry.net/breeding_policy.htm)

Crossbreeding of local cattle with Holstein Friesian and Jersey for increasing the milk production is to be undertaken. The Exotic inheritance of Jersey and Holstein Friesian shall be maintained between 50 and 62.5 percent level in graded cattle. Selective breeding of buffaloes using superior sires available locally or frozen semen of Murrah/Nili Ravi bulls maintained at CIRB, Hisar/ Nabha will be practiced. Pure Breeding with selection is the only choice for Yak improvement. Pure Breeding coupled with selection should be adopted especially in Zanskari Breed of horses. In the high land areas where horses are still utilized for transport, improvement of non-descript Horses can be taken up with Zanskari horses. However, in the areas where horses are used for draft purpose, along with pure breeding, inter-species breeding with Ass will form the important aspect of Equine breeding policy. Since the total number of Double Humped Camel is very less, *in situ* conservation of this stock is inevitable. For successful *in situ* conservation, the Department of Animal Husbandry must register all the animals available in Nubra Valley. The registration should be followed by the pure breeding programme in such a way that the in-breeding of the stock is avoided.

9. **Jharkhand** (Memo No. Gavvya (y0-1) 303/09/525/Ranchi 2/6/2011 from Secretary Dept. of AH and Fisheries. Govt of Jharkhand)

In urban and semi urban areas, cross breeding of available cattle with Holstein Friesian and Jersey with restriction that the level of exotic inheritance shall not exceed more than 50%. In less remote areas, upgrading of local cattle through semen of proven Sahiwal, Red Sindhi and Gir bulls is proposed. In more remote areas, upgrading of local cattle through semen of Tharparkar and Hariana shall be practiced. In urban and semi urban area, local/ improved buffaloes shall be inseminated with Surti/ Murrah/ Mehsana semen. In the rural areas the policy remains the same. In Palamu division, local goats shall be improved by crossbreeding/ upgrading with Beetal, Barbari, Sirohi and Jhakrana bucks. In other divisions selective breeding of Black Bengal shall be practiced. In Palamu region local sheep shall be improved through crossbreeding/ upgrading with Muzaffarnagri rams whereas, in other divisions selective breeding of Chhotanagpuri sheep shall be practiced. Local pigs shall be crossed/ upgraded with Tamworth and Russian Charmukha breeds. Local birds shall be improved through crossbreeding/ upgrading with RIR, Black Australorp cocks. Grampriya/ Vanraja dual purpose poultry breeds shall be promoted and Hazara and Aseel breed shall be conserved under *in-situ* condition. Local ducks shall be improved by utilizing Khaki Campbell breed for improving egg production. Local ducks shall be improved by utilizing white Peking for improving meat production.

10. **Karnataka** (http://www.karnataka.gov.in/ahvs-website/en-breedingpolicy.html)

Karnataka Cattle Breeding Policy is evolved based on the National Cattle and Buffalo Breeding Policy, which envisages selective breeding of Indian cattle breeds for milk and draft, and crossbreeding of non-descript cattle with exotic dairy breeds like HF and Jersey. The state possesses the most praiseworthy draft breeds like Amritmahal, Hallikar, Khillar and dual purpose breeds like Deoni and Krishna valley etc. Along with maintaining the germ-plasm of these draft breeds, improving milk production of indigenous cattle is carried out using frozen semen of exotic dairy breeds like HF and Jersey. For crossbreeding, Jersey breed may be used in all parts of the state except eight districts where HF is used. Likewise, for the use of indigenous breeds of the state, all the breeds have been allocated different districts of the state. Surti bull/ semen may be used in all the districts of the state whereas, the use of Murrah bull / semen is restricted to selected nine districts.

11. **Kerala** (http://www.livestock.kerala.gov.in)

Intensive and structured breeding programmes taken up by the State during the last 3 and 1/2 decades considerably increased the milk production. The accepted breeding policy of the State envisages crossbreeding; limiting the exotic inheritance to around 50% followed by selection and inter-se mating. The new 'composite breed' of cattle evolved by crossing nondescript cattle with exotic donor breeds (Brown Swiss, Jersey and HF) limiting the exotic inheritance to 50% was formally named Sunandini.

12. **Madhya Pradesh** (http://www.mplivestock.com/aa.html of MP Livestock and Poultry Development corporation)

Selective Breeding of Indigenous breeds in the home tract – Malvi in Malva tract, Nimari in Nimar region and Kenkatha in ken valley of Panna district. Up-grading local cattle using indigenous milch breeds like Hariana, Tharparkar and Sahiwal etc is also a part of breeding policy of the state. Cross- breeding with exotic breeds is also practiced, however it was envisaged that the exotic blood level should be maintained up to 50% in smallholder system and up to 62.50% in organized farms. Murrah is the breed of choice for up gradation of the local buffaloes however in selected areas of Western MP (adjoining to South Gujarat) Jaffarabadi breed can also be used, if owner desires. In areas of Bhind district and adjoining areas Bhadawari Breed will be used.

13. **Maharashtra**

The cattle breeding policy of the state aims at increasing productivity of cows by genetic improvement. However, it also aims at conservation of native breeds and ensuring adequate supply of quality bullocks for animal draught power in rural areas. An area specific breeding policy will be adopted in consideration of Agro-climatic zones, available fodder resources, prevalent breeds of that area and resources available with the farmer/livestock owner. Genetic improvement of low productive non-descript cattle population in targeted areas will be achieved, after judiciously considering the resources available with the farmer, through cross-breeding programme (by using exotic germ plasm i.e. HF and Jersey) where ever it is suitable and desirable. However, in the home breeding tracts of identified indigenous breeds of the state, the non-descript animals will be continued to be upgraded with the better performing suitable recognized indigenous breeds viz. Deoni, Dangi, Red Kandhari, Gaolao and Khillar and will be subsequently bred with the germ plasm of same breed used initially. Pure bred indigenous animals in the home breeding tracts as well as in the extended breeding tracts will be continued to be bred with pure bred animals of the same breed through selective breeding to conserve and upgrade the original germplasm. In addition, pedigreed germ plasm of indigenous cattle viz. Gir, Tharparkar, Kankrej, Sahiwal etc. will be utilized suitably. An area specific buffalo breeding policy will be adopted in consideration of Agro-climatic zones/ available fodder resources, prevalent buffalo breeds of that area and resources available with the farmer/livestock owner. Buffaloes of descript breeds viz. Murrah, Jaffarabadi, Pandharpuri, Marathwadi, Nagpuri and Surti should be bred only with semen of bulls of respective breed. Non-descript buffaloes should be bred with germplasm of any one of the identified breeds mentioned above.

Breeding policy for goats primarily aims at increased meat production for meeting not only its local demand but also to explore the export avenues. As a result of the consistent use of goat milk in rural areas, the new dimension to goat farming has been incited to boost rural economy as an upcoming new horizon for breeding the goats for milch purpose also. Hence, desired genetic improvement amongst the goat population will help in reaping the benefits of dual purpose breeds through the use of identified breeds. Priority for this purpose will be given to selective breeding / up-gradation of the recognized local indigenous breeds like Osmanabadi and Sangamneri. Efforts will be made for identifying the local indigenous goat breeds through rigorous phenotypic characterization. Besides using these local indigenous breeds, a strategy will be adopted to evolve sturdy goat which would sustain and thrive in the heavy rainfall areas. Through up-gradation of the identified sturdy goat and after finalizing desired phenotypic characters, such goat will be get registered with NBAGR as a specific breed and will be used for genetic up-gradation of the local goat in heavy rainfall areas.

Breeding policy for sheep primarily aims for genetic improvement through selective breeding *I* up-gradation of the local non-descript sheep population. Extensive use of Deccani breed of sheep will be sought for this purpose. Breeding Policy for chicken breeds mainly covers the species suitable for back yard poultry and low input poultry. Breeds for commercial poultry involve import of germplasm and parent line which will be determined by Government of India's Policy in this regard and will continue to be carried out primarily by private sector initiatives. With a view to develop and proliferate backyard poultry activity in the state, a policy has already been initiated to propagate the CARI developed poultry breeds viz. Giriraja, Vanaraja, CARI Nirbhik etc. in backyard poultry as well as for genetic up-gradation of local desi poultry. State will continue to supply crossbred stocks of improved breeds like RIR and Black Australorp for low input commercial poultry. For this purpose, these types of stocks will be maintained at central hatcheries and poultry farms owned by the state. State will continue to have Duck farm for supply of foundation stock of selected duck breeds such as Khaki Campbell. Duck-fish farming shall also be tried in suitable areas. State will introduce Japanese quail also in production chain at one or more of its central hatcheries for distribution of breeding material. Suitable licensing system for farming of Japanese quail will be introduced to prevent killing of Indian Quail in violation of wild life protection Act.

14. Manipur

The breeding policy to be adopted in the State of Manipur for development of Cattle and Buffalo shall be adhered to the following characteristics.

- In order to increase milk production, crossbreeding of local non-descript cattle shall be adopted using exotic cattle breeds. Jersey shall be the breed of choice of the State of Manipur. In any case, the exotic blood inheritance shall be limited to 50% only, for which the pure local cattle shall be mated with pure Jersey only and the outcome crossbred progeny shall be mated only with crossbred cattle having 50% Jersey inheritance. In the Imphal East and Imphal West districts, the progressive farmers are serious about raising the exotic blood levels, hence they shall be encouraged to do so but the maximum admissible level shall be curtailed not to exceed beyond 75% exotic inheritance. In these districts, Holstein Friesian may be prescribed as the breed of choice. The farmers can switch over from one breed of exotic inheritance to another; i.e. from Jersey to Holstein Friesian or vice versa but in any case, the exotic blood level should not exceed the prescribed levels.
- For production of draught power, up-gradation of local cattle shall be adopted through A.I. or Natural Service using the Hariana breed and concentrating such bullock power regeneration oriented breeding programme in certain areas of Bishnupur, Thoubal, Chandel and Churachandpur districts. In the process of up-gradation, the blood level of Hariana shall be restricted to 75% only. In case of buffaloes, the policy will be selective breeding within the local animals with the objective of improving them by developing desirable characteristics of draught ability and increased milk.

15. Meghalaya

Efforts have been made in the past to increase milk production through selection and crossbreeding in cattle. A re-orientation of the cattle and buffalo breeding policy would be attempted in view of our concerns for indigenous breeds and need for Draught Animal Power. Producing quality males would be an essential component of breeding policy. Existing breeding farms, breeders associations, shall be involved in producing good quality pedigreed males for breeding purpose and for improvement of indigenous breeds shall be encouraged. An effective mechanism for providing disease free quality semen for high productivity will be put in place. Breeding services is being provided at the farmer's door. Breeding policy for small ruminants with focus on selection of rams and bucks shall be put in place and implemented through suitable programs. Preservation and development of pack animals shall also be considered.

16. Mizoram

State Breeding Policy for Mizoram: Mizoram have potential to take piggery in a more and technical approach by application of the right instrument. The concept designed is a two way, adopting the Farm Policy and the Farmers. The followings are taken into account in the Breeding Policy –(i) Pig Population Dynamics (ii) Litter size (iii) Litter Index (The litters per sow per year) (iv) Economics (v) Feed Conversion Ratio (vi) Preference and likes of the Local pigs. The breeding policy for pigs has been designed with following objectives:

- Genetic improvement through selective breeding.
- Conservation and maintenance of indigenous pig germ plasm.

- Genetic improvement by crossbreeding and gradually maintaining a desired level of exotic inheritance.
- Expansion and strengthening of Breeding Infrastructure and support mechanism to propagate elite germ plasm through A.I.
- To establish Regional Boar Semen Station for maintaining Exotic Breed in Closed Herd by import of Frozen Semen or Live Pigs.

Selective breeding for Indigenous Pigs:
Zovawk, indigenous pig breed of Mizoram, where no crossbreeding shall be applied, the germ plasm of this breed shall be established and preserved. Nucleus breeding farm for such breed shall be established. Prized animals should be collected from farmers field/State Farm to the Nucleus herd. Pedigreed animals need to be propagated only to interested farmers who want to rear indigenous germplasm. However, Govt. should ensure necessary incentive to these farmers. For this, rate of piglet and pork of Zovawk pigs may be fixed at higher values as compared to other pork by the Govt. Artificial Inseminations should be delivered through Private Inseminator who have taken training courses conducted by the Department.

Crossbreeding: Cross breeding may be propagated through selective breeds of Large White Yorkshire, Hampshire and Landrace. Import of germplasm of Large White Yorkshire, Landrace and Hampshire from sources which are free from scheduled Diseases may be done. Import of Live Animals may be considered at regular intervals at a first primary strategy with import of Semen as a secondary option, in improving and upgrading Herd Quality. As programme for breed-specific nucleus herd improvement may be developed for subsequent programmes.

17. Odisha

The Odisha Gazette No.1389 (No. 12097-3V(B)-40/2015/FARD) dated 3.10.2015

i. Basing on the type of non-descript animals in different localities of the state, genetic up-gradation programme will be taken up with introduction of germplasms of Sahiwal, Gir, Tharparkar in addition to Hariana, Red Sindhi and Binjharpuri. Hariana will slowly be eliminated by replacing with Tharparkar and Binjharpuri. Farmers' preference will be prioritized while upgrading the animals. In case of Binjharpuri, it is recommended for adoption of selective breeding for improvement of the breed. It is also appropriate that the same process may be adopted in improvement of other recognized breeds like Motu, Khariar, Ghumsuri cattle.
ii. Jersey and HF will be continued as breeds of choice for genetic improvement of the local stock through crossbreeding in areas, where infrastructure facilities for the health care and organized marketing of milk are available. In areas, where such infrastructure facilities are not available or inadequate, genetic up-gradation as indicated in sub-para (i) above would be adopted. HF is to be used in those animals with better configuration in terms of size and weight and also animals reared by resourceful farmers.
iii. The exotic blood level in crossbred and inter-se-mated population should maintained between 50 to 75%.

iv. In buffaloes, Murrah is considered as the breed of choice for up-gradation of local buffaloes. In recognized breeds like Chilika and Kalahandi it is appropriate to take up selective breeding for improvement of the stocks.

v. Efforts are to be made for preservation of native breeds of cattle including buffaloes to preserve them from their extinction or dilution.

vi. Participatory research activities on cattle and buffalo breeding like Field Performance Recording Scheme [FPRS] and Field Progeny Testing Program [FPTP] for genetic evaluation and bull production are to be taken up. Molecular characterization of native breeds may be conducted for identification of their unique characteristics in order to produce animals with high genetic merit. Technology like Embryo Transfer Technology [ETT] can be adopted.

vii. Production of quality bulls through identified elite female bovine population maintained by the farmers in the state would be taken up following procedure similar to the procedure followed by NDDB under National Dairy Plan. The database of elite s well as exotic female and male bovines would be maintained through INAPH database of NDDB to facilitate scientific management.

viii. Healthy animals are key to genetic improvement. Farmers would be sensitized for ensuring proper documentation of feeding, breeding and for systematic field performance recording system as well as use of balanced feeding (as in ration balancing system of NDDB) and use of area specific mineral mixture for better reproductive health. For this purpose, a program for capacity building and training of farmers through progressive farmers would be implemented.

18. **Punjab:** [Extract from Punjab Govt. Gaz., dated the 27th July, 2012; cited from notification of AHFandDD department, Govt. of Punjab dated 4th July 2012]

Cattle: Keeping in view the high milk production and better returns many farmers has established large dairy farms with high yielding crossbred cows, modern dairy sheds, mechanized milking/fodder harvesting. The state is not only providing large quantity of milk to the national grid but is also the major source of high yielding crossbred cows. The state has the potential to be the major source of germplasm of Holstein Friesian, Jersey crossbred, Sahiwal cattle and Murrah/ Nili Ravi buffaloes in the form of semen and bulls to other states.

Policy:

- The local/crossbred cows will be mated with Holstein Friesian bulls to produce crossbreds up to 75% exotic inheritance. Crossbred bulls with 75% exotic inheritance will be produced from the elite crossbred cows and put to progeny testing. Progeny tested crossbred bulls will be extensively used to stabilize and maintain the level of 75% exotic inheritance in crossbreds.
- The Progressive dairy farmers who have established high milk producing crossbred herds with exotic level of more than 75% and are adopting the high input technologies of dairy management and disease control can be allowed to use exotic bulls to have cows with high level more than 75% of exotic inheritance. Such farmers will be required to follow regular herd testing for specified diseases, herd registration and performance recording and will be the major sources of bull calves.

- Institutional farms may produce purebred exotic for bull production.
- The cows in the sub mountainous / Kandi and region having limited fodder resources will be improved by using Jersey.
- The Sahiwal cows/bulls available with different institutions/farmers will be identified and registered in a breed book. Sahiwal cows will be mated with the best available semen of Sahiwal bulls and the male calves from the elite cows will be procured and used in the progeny testing programme of Sahiwal breed.

Buffalo: The rate of genetic improvement in buffaloes is very low. The major source of improvement in buffaloes is selection of bulls and their extensive use through the AI. In the absence of large progeny testing programme, majority of bulls being used in the state are pedigree selected (that too on dam's peak yield estimates) mostly used through natural service. In order to bring substantial improvement in buffaloes it is necessary to develop an efficient system of bull calf production and progeny testing.

Policy:

The state has 9.63 lakh Murrah, 3.47 lakhs Nili-Ravi , 39.98 lakhs graded (crosses of M x NR) and 2.03 lakhs non-descript. In order to improve the productivity and to maintain the purity of the two breeds and also to reduce the graded population, the following breeding programme is suggested:

- Murrah buffaloes will be bred with Murrah bulls only.
- Nili-Ravi buffaloes will be bred with Nili-Ravi bullsonly.
- The graded buffaloes with predominantly Murrah characteristics shall be classified as Murrah grades and bred with Murrah bulls.
- The graded buffaloes with predominantly Nili-Ravi characteristics shall be classified as Nili-Ravi grades and bred with Nili-Ravi bulls.
- Non-descript buffaloes will be bred with the bulls of either of the predominant breed of the area i.e. Murrah or Nili-Ravi.

19. **Rajasthan (**Vide circular No. FV () ADH/Breed. Pol./07/1008 dated 19.01.2007 from Director AHD, Govt. of Rajasthan)

The important cattle breeds in the state are Gir, Rathi, Tharparkar, Hariana, Kankrej, Malvi and Nagori. Up-gradation of germplasm through upgrading and selective breeding is being proposed on priority, whereas crossbreeding of non-descript cattle and buffalo will be taken up with high yielding indigenous native breeds only and crossbreeding with exotic germplasm is restricted to animals having exotic blood only. Selective breeding of indigenous breeds of Gir, Hariana, Malvi, Rathi, Kankrej, Nagori and Tharparkar will be carried out in areas where these animals are found in their true forms. Upgrading is to be adopted in the areas where animals of the above breeds/ strains are predominately available to upgrade the breed and performance. Crossbreeding, on demand, shall be followed in the areas adjoining cities and towns subject to the condition that crossbreeding will not be done on the breeds of home tract districts area and on animals having blood of indigenous breeds. In case of crossbreeding with exotic breed is adopted, exotic blood should be maintained between 50-62.5%. Two exotic breeds will be used in Rajasthan viz. Holstein Friesian and Jersey. Murrah and Surti are two breeds to be used in the state. In Northern belt of the state i.e. Jaipur, Jodhpur, Bikaner, Kota, Ajmer and

Bharatpur region Murrah breed will be used for breeding. In the southern belt of the state i.e. Udaipur region Surti breed will be used however when the farmer demands, Murrah bulls/semen can also be used for breeding.

20. Sikkim

Cattle for milk and draft: To increase productivity, a critical area for experimentation and promotion is the "intermediate production system" which enables the small holder to gradually integrate the highly productive modern technology and management into his traditional system. Introducing crossbred milch animals (half-breds) into the traditional producer households is an excellent example of the intermediate production system, which gives the farmer some high production features but also preserves some of the ruggedness of the local animal he is used to. Crossbred cows can be promoted in the more accessible areas where trading in milk is possible; example the dairy cooperative society areas. Production of high quality half bred bulls for dairy breeding, Siri breeding bulls and AI system, are all highly specialized tasks. *Cross breeding should not be promoted in areas reserved for pure breeding of Siri Cattle.* Sikkim needs assured supply of good quality indigenous Siri breed bullocks for farm power, as crop production in Sikkim is completely dependent on work animals for farm power. To ensure a steady supply of good quality working bullocks, a good number of the Siri cattle are found in Sikkim, particularly in areas of difficult access in parts of East, West and North District, should be reserved for selective breeding. Siri cows do produce a reasonable quantity of milk, which will be used by the farmers for home consumption and / or limited trading in the village itself. All male calves born would be raised as future work animals. The demand for work animals in Sikkim is high in all four districts and therefore the selection and work animal production programme will be viable and sustainable. Selected bull calves will be raised as Breeding Bulls by identified skilled farmers for pure breeding of the Siri breed through natural service.

Breeding Swine for pork: Rearing and breeding swine for domestic consumption ranks second in the state in the food basket of Sikkim. Grading up of the indigenous pigs continuously with Large White Yorkshire/ Saddle back/ Land Race/ Middle white Yorkshire and Hampshire Boars and supply of high grades of graded boars to farmers for mating their sows may be continued.

Breeding Sheep and Goats for meat/wool: Custom bred Half-bred goat (Local x Boer) on trial basis and selective breeding between Singhari (local breed of Sikkim) in order to enhance animal productivity and support livelihood options. Banpala and Gharpala are the indigenous strains of sheep available in the state. These are dual purpose sheep that have survived the natural selection process. Selective breeding among these strains of indigenous sheep in Sikkim would assist the state in conserving the indigenous germ plasm. Breeding and improvement of sheep and goat will have to depend on natural service. This needs provision for breeding buck and ram production in very large numbers. Only participatory efforts involving large numbers of well to do and progressive farmers will succeed in providing large number of rams and bucks. The government should target these farmers for Local x Boer (half bred) bucks production on trial basis. Similarly selective breeding of local Singhari goats is tried out.

Breeding Yak and conservation of the germplasm: One disconcerting feature related to large ruminants however deserves Government's immediate attention: the growth and multiplication of domesticated herds of Yaks in the fragile eco-zones of North, East and West Districts. Notwithstanding the general view that local farmers hold yaks in small numbers is now well researched and with empirical evidence) that these fragile eco-zones above 9000 ft MSL hardly have any settlers, as the climate is extremely harsh and hostile.

21. **Tamil Nadu** (GO (Ms. No. 49 dated 15.4.2008 from Animal Husbandry Dairying and Fisheries, Department, Govt. of Tamil Nadu)

Selective breeding of native breed is to be followed in Erode, Coimbatore, Karur and Dindigul for Kangyam breed and Nagapattinam Tiruvarur and Thanjavur districts for Umblacherry breed. The lesser known breeds such as Pulikulam, Bargur, Alambadi and Malaimadu have to be surveyed, characterized and conserved. Selective breeding of these breeds in their respective breeding tract is to be followed.

Depending upon the agro-climatic conditions and availability of inputs, low yielding non-descriptive cows will be crossed with Jersey and Holstein Friesian. Jersey is the breed of choice for crossing the non-descript cows in the plains of Tamil Nadu. Holstein Friesian breed is preferred in the hilly areas, high rainfall areas, and highland area. While crossing of non-descript cows with exotic germplasm, the level of exotic inheritance should be restricted to 50%. Back crossing to the exotic breeds should be avoided. High pedigreed Indian milch breeds Red Sindhi, Sahiwal and Tharparkar may be used for crossing non-descript cows in the plains of Tamil Nadu with farmers having poor resources. The F_1 cross may further be upgraded with the same Indian milch breed or crossed with Jersey/ Holstein Friesian. Upgrading of non-descript buffaloes with Murrah is to be followed and graded Murrah buffalo are to be further upgraded with Murrah. Pure breeding of Toda buffalo is to be followed in high ranges of Nilgiris.

22. **Uttar Pradesh**

Sahiwal, Hariana, Gangatiri and Tharparkar cattle available in the state will be genetically improved by selective breeding. For crossbreeding, Holstein Friesian is the main breed of choice, however the Jersey breed will be used in the places having poor resources and small animals. The exotic blood level will be maintained around 62.5%. The state has been divided into four regions i.e. Eastern, Central, Western, and Bundelkhand. The region wise choice of breed has been mentioned in the breeding policy. Murrah breed will be used for genetic improvement of buffaloes in the state. However, in the breeding tract of Bhadawari breed i.e. Agra, Etawah, Jalaun area, this breed will be the choice of the breed for genetic improvement. The revised Breeding Policy 2018 is as below:

Revised Breeding Policy 2018 (Uttar Pradesh)					Zone	Other zone (Supply of Frozen Semen)
Species	First Breeding		Subsequent Breeding			
	Bull	Target Group	Bull	Target Group		
Cattle	Pure Sahiwal	Non- descript	Pure Sahiwal	Graded Sahiwal	Central Zone	All other zone except

	Pure Sahiwal	Graded Sahiwal	Pure Sahiwal	Pure Sahiwal		Bundelkhand (on demand)
	Pure Sahiwal	Pure Sahiwal	Pure Sahiwal	Pure Sahiwal		
	Pure Hariana	Non- descript	Pure Hariana	Graded Hariana	Western zone	Other zones except Bundelkhand
	Pure Hariana	Graded Hariana	Pure Hariana	Pure Hariana		
	Pure Hariana	Pure Hariana	Pure Hariana	Pure Hariana		
	Pure Gangatiri	Non- descript	Pure Gangatiri	Graded Gangatiri	Eastern zone	None
	Pure Gangatiri	Graded Gangatiri	Pure Gangatiri	Pure Gangatiri		
	Pure Gangatiri	Pure Gangatiri	Pure Gangatiri	Pure Gangatiri		
	Pure Tharparkar	Non- descript	Pure Tharparkar	Graded Tharparkar	Bundelkhand zone	–
	Pure Tharparkar	Graded Tharparkar	Pure Tharparkar	Pure Tharparkar		
	Pure Tharparkar	Pure Tharparkar	Pure Tharparkar	Pure Tharparkar		
	Pure Jersey	Pure Jersey	Pure Jersey	Pure Jersey	Entire state	
	Pure Jersey	Non- descript (Limited scale)	Crossbred Jersey	Crossbred Jersey		
	Crossbred Jersey	Crossbred Jersey	Crossbred Jersey	Crossbred Jersey		
	Pure HF	Pure HF	Pure HF	Pure HF	Entire state except Bundelkhand	
	Pure HF	Non- descript (Limited scale)	Crossbred HF	Crossbred HF		
Buffalo	Pure Murrah	Non- descript	Pure Murrah	Non- descript	Entire state	
	Pure Murrah	Graded Murrah	Pure Murrah	Graded Murrah		
	Pure Murrah	Pure Murrah	Pure Murrah	Pure Murrah		
	Pure Bhadawari	Non- descript	Pure Bhadawari	Non- descript	Nearby Yamuna and Chambal river bank, Agra (Bhadawar), Jalaun (Madhogarh), Etawah, Auraiya	
	Pure Bhadawari	Graded Bhadawari	Pure Bhadawari	Graded Bhadawari		
	Pure Bhadawari	Pure Bhadawari	Pure Bhadawari	Pure Bhadawari		
Note- Exotic inheritance level will be limited up to 62.5% in crossbreeding with exotic breeds.						

Genetic improvement of local sheep will be done by using Nali and Magra sheep breed of Rajasthan. In view of improving the production of carpet medium coarse wool in the state, exotic breeds having fine wool i.e. Ramboullet and Merino will be used for crossbreeding of local sheep. Genetic improvement of goat will be taken up by using Barbari breed of goat except in the districts of Etawah, Agra and Jalaun where the genetic improvement of goat is done by using Jamunapari bucks. The productivity of local pigs will be improved with the use of Middle White York shire. Local horses will be improved by using stallions of Kathiawadi breed whereas; the load carrying capacity of donkeys will be improved by using Italian donkey stallions.

23. Uttarakhand

The state is divided into four zones viz. up to 1000m height, 1000-1500m height, 1500-2400m height and above 2400m height and zone specific cattle breeding policies are evolved. In the first zone (up to 1000m height) the non-descript animals will be improved using either Holstein Friesian or Inter-se-mated HF x Sahiwal, HF x Red Sindhi and HF x Tharparkar crossbreds. In the second zone (1000-1500m height) non-descript animals will be improved by using the semen of Jersey bulls along with Inter-se-mating of Jersey x Sahiwal and Jersey x Red Sindhi crossbreds. In other two zones non-descript cattle will be genetically improved by selective breeding. The buffalo of the state will be improved using semen of Murrah bulls.

The local sheep breeds (Gaddi, Rampur Bushair black sheep) will be improved through selective breeding whereas; the crossbred sheep population of the state will be further improved using pure bred rams of Ramboullet and Merino. The local goats of plain area will be upgraded with the use of Barbari and Jamunapari bucks. In view of increasing the Mohair production in the hilly regions, the local goats will be crossed with Angora bucks. Local pigs will be upgraded by using boars of Middle/ Large white York shire breed. Local non-descript fowl will be improved by selective breeding along with conservation of indigenous breed. Selective breeding among Angora German Rabbit will be adopted for which import of germplasm will be done. To avoid inbreeding pure line breeding will be adopted, of which two lines of males and two lines of females will be maintained. The commercial hybrid poultry breeding will be encouraged under private institutions.

24. West Bengal

Up-gradation of non-descript cattle will be carried out using improved indigenous breeds like Sahiwal, Gir etc. depending upon the availability. Sahiwal breed will be used in the district of Darjeeling, Coochbehar, Jalpaiguri, Uttar Dinajpur, Dakshin Dinajpur, Malda, Murshidabad, Nadia and Hooghly. Gir breed will be used in North 24-Parganas, South 24-Parganas, Purba Medinipur, Paschim Medinipur, Birbhum, Purulia, Bankura, Bardhaman and Howrah. Up-gradation and cross-breeding will be 80% and 20%, respectively of the total cattle population. Cross-breeding will be done by West Bengal Milk Producers' Union Ltd. NGOs and Progressive farmers where adequate feed/fodder resources are available, in addition to the Government Animal Health Centers by agencies recognized by State Government. For the purpose of Cross-breeding, Jersey breed will be used. Crossing of existing cross-breeds may be taken up in a controlled manner so that exotic inheritance shall not be increased beyond 50%

in any case. Holstein Friesian, pure or its cross semen, may be made available by the Paschim Banga Go-Sampad Bikash Sanstha (PBGSBS) to those farmers who are interested in rearing Holstein cross-breed against proper indent. The improvement of the buffaloes will be brought about by grading up with high quality Murrah Buffalo semen in all districts of the state.

Note:

- *Breeding policies are subject to revision from time to time, therefore, it is advised to visit the website of Animal Husbandry/Veterinary department of respective state to know the current status of breeding policy.*
- *Breeding policies of some of the states are not available on their website, therefore could not be included in this paper.*

Gene Banks for *ex-situ* conservation of livestock assets

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The genetic resources of farm animals in India are represented by a broad spectrum of native breeds of cattle, buffaloes, goat, sheep, swine, equines, camels and poultry. The genetic biodiversity among this livestock has developed and stabilized over millions of years of evolution and endowed the indigenous breeds with capabilities to withstand hostile climate, epidemic pests and diseases, and to survive on inadequate quantities of feed, fodder and water. However, over the years due to many reasons the population size of many breeds is declining. As genetic diversity equips farmers and breeders to utilize a wide range of production environments and develop diverse products to meet the needs of local communities, the unavailability of such diversity in future may hamper sustainable development. Hence the need for conservation of animal genetic resources has been accepted in India and globally.

Conservation methods

Conservation methods can be broadly categorized as *in situ* and *ex situ*. *In situ* conservation means that animals are kept within their production system, in the area where the breed developed its characteristics. *Ex situ* conservation applies to situation where animals are kept outside their area of origin (herds kept in experimental farms, farm parks, within protected areas or in zoos) or more often, when genetic material is conserved and stored in gene banks in the form of semen, ova, embryo or DNA. Conservation through any of these methods has its own merits and demerits as explained below.

1. **Organized flocks/herds**: Maintenance of small population at a place away from the main breeding tract of the breed is the *ex situ* conservation of the live animals. This may be in the form of organized herd maintained in a research institution, bull mother farm, state owned livestock farm, zoo or breed park. This population can be used in regeneration of endangered breed, new breed development and DNA studies.
2. **Cryopreservation of embryos**: This is ideal for breed improvement, conservation and revival of lost breed. Its main importance is due to its diploid nature and containing all genes. However conserving embryos finds limited use, as its production and transfer require highly skilled manpower and large resources.
3. **Somatic cell banking**: Somatic cells can be used as genetic material for conservation of endangered animal genetic resources. They are diploid cells and contain full genetic code of an animal. Cost of maintenance of these cells is very low and can be sampled quickly even from remoter area at low cost. They can be used for production of therapeutic proteins also. However somatic cells also find less preference due to low success rate of cloning.
4. **Epididymal sperms banking:** Epididymal spermatozoa particularly caudal spermatozoa is mature and have full competence to undergo normal fertilization and cause fetal development. *In vitro* fertilization (IVF) experiments have revealed that epididymal semen

possesses binding sites for important zona pellucida proteins. Collection of cauda epididymal semen from slaughtered animals would be a rapid and cheap alternative of sperms conservation as it would obviate the requirement of time consuming and extensive training of males for semen donation. Hence epididymal spermatozoa cryostorage is promising methodology of conservation especially in small ruminants and further research efforts are needed in this direction.

5. **Cryopreservation of embryonic stem cell lines**: This can be excellent biological material for producing live animals and producing genetically modified animals. This also find usage in gene and cell therapies, and for producing vital therapeutic proteins. However so far they have limited useage as stable embryonic stem cell lines have not been successfully generated in farm animals except in human and rodents.
6. **Cryopreservation of spermatogonial stem cell lines** : The Spermatogonial Stem Cells (SSCs) are adult stem cells which transmit genetic information to the next generation and creates foundation for spermatogenesis. Transplantation of spermatogonial stem cells from a donor mouse testis into the seminiferous tubules of a recipient mouse testis results in donor-derived spermatogenesis. SSCs transplantation has also been demonstrated in goats, dog, cow, pig, baboon and bovine spermatogonial stem cells shown to be capable of colonizing recipient mouse seminiferous tubules. An *in vitro* system that supports the proliferation and maintenance of spermatogonial stem cells could be used to preserve and expand spermatogonial stem cell numbers as well as aid in genetic modification. However much needs to be done in farm animals before its potential could be utilized in domestic livestock diversity preservation.
7. **Storage of DNA**: Cryogenic storage of DNA is another method of preservation of genetic material. It has several advantages over the live germplasm as it is very easy to obtain, store, transport at low cost with no chance of disease transfer. The DNA may find use in gene conservation through their introgression by transgenesis or knock out technology, and can help in recreation of lost breeds by cross checking of different populations or genetic material used. However this has limitations due to the fact that genome maps of different farm species are not yet available and life cannot be created from DNA alone.
8. **Frozen Semen**: This is ideal for genetic resources utilization activities, providing sample half of the genetic material of preserved breeds in a form that permits convenient introgression into recipient population. However, regeneration of a cryopreserved breed from frozen semen in one generation is possible only if living females of that breed are available, otherwise several generation of up gradation are required to reestablish a conserved breed. In spite of this limitation, availability of established semen freezing technology especially in cattle and buffalo, and presence of semen freezing infrastructure across the country makes it method of choice for conserving indigenous livestock biodiversity. The National Bureau of Animal Genetic Resources (NBAGR) is playing a pivotal role in *ex situ* conservation through semen cryostorage of indigenous livestock for posterity by establishing a National Semen Bank at Karnal.

Conservation priority

High costs of collection and limited use of preserved material restricts development of *ex situ* collection. Hence it may be appropriate to prioritize breeds for undertaking them in *ex situ* programme and evaluation of many factors may make basis of such prioritization. To implement the conservation programme it is thus essential to have breed wise livestock census along with their population and production trends. However many a times the data is available species wise, there is a need to explore quick population estimates and undertake conservation efforts for threatened breeds. The unique genes possessed by a breed and the likelihood of its extinction may be an important parameter to set the priority of conserving a breed.

The quantification of relatedness among breeds can group them in different sets, each set consisting of genetically closer/ related ness breeds which are different than breeds of another set. Such arrangement will drastically reduce the conservation costs as conserving a single breed in a set will represent all breeds of respective set. Such phylogenetic differentiation of breeds is possible by mapping the genes in livestock species using microsatellite markers. The usefulness of these markers for estimation of genetic distances among closely related population in different species of livestock has been documented by numerous studies (Bowcock et al., 1994, Buchanan et al., 1994, Cianpolini et al., 1995, Bradley et al., 1996, Mac Hugh et al., 1997). Food and Agricultural Organization (1996) has well laid detailed technical programme for large scale international conservation project using microsatellite markers under MODAD project. Based upon abovementioned considerations some breeds of different species have been undertaken for *ex situ* conservation programme and for keeping their frozen semen in National Semen Bank at NBAGR (Table 1). Simultaneously ex situ conservation in form of DNA and Somatic cells has also been taken at NBAGR.

Breed population trends

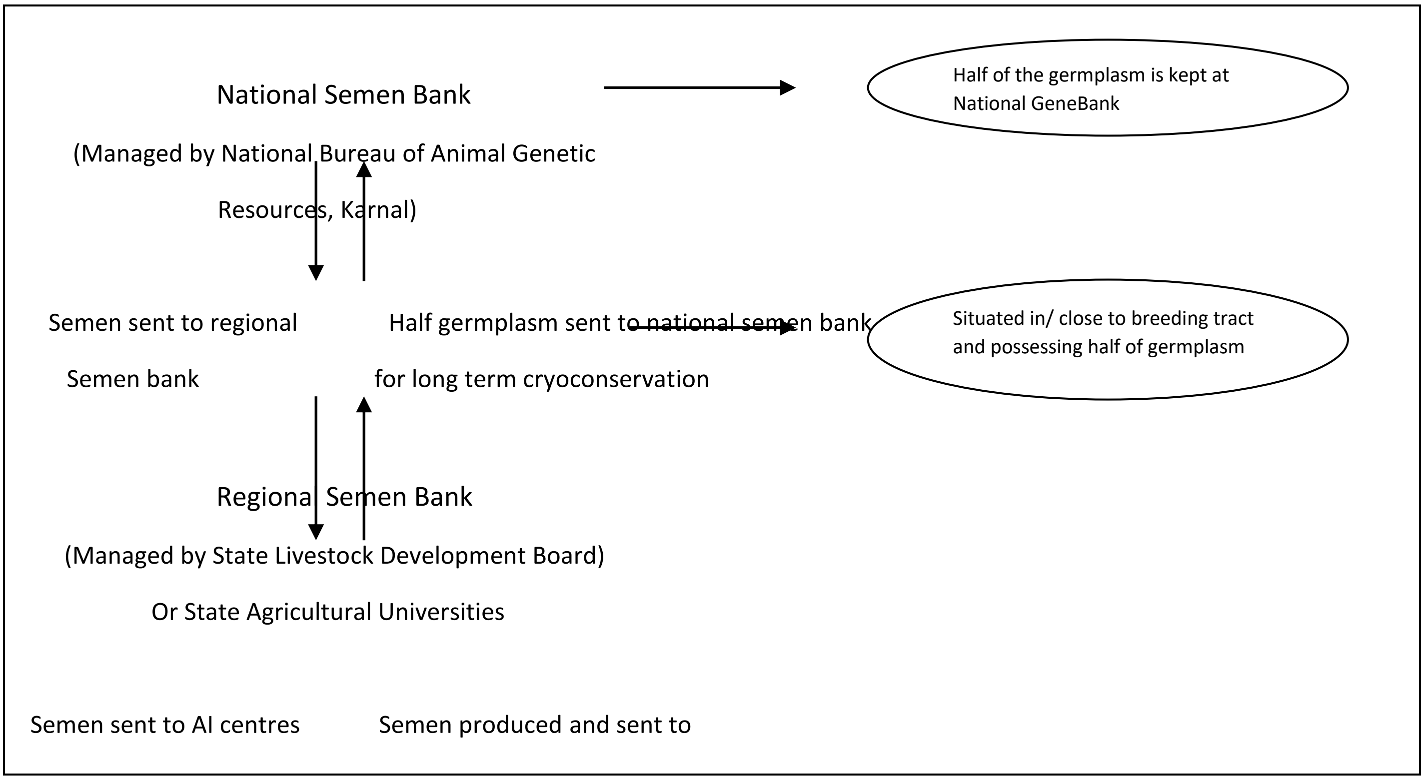
The population trend of a breed is an important parameter to suggest, whether a breed should be undertaken for its conservation. However generally breed wise census are not available. The endangered status of an animal breed can be determined by the size of breeding stock, expressed through number of breeding females and sex ratio, which may differ among different species. The endangered status of an animal breed depending upon minimum population size in different species has been suggested by different workers (Table 2). The population size, which may be applicable to Indian conditions, has also been suggested (Table 3).

Sample size in preservation programme

Sample size in preservation programs are influenced by both genetic considerations and cost. For a dominant gene, semen to produce 20 viable offspring (100 units; a unit of semen is the amount appropriate for one insemination) should suffice, but somewhat more semen (possibly 200 units) may be desirable in preserving a recessive gene. The preservation of quantitative variation within a population or breed would require about 100 units of semen from each of 10 to 20 unrelated males (CAST, 1984). As per Smith 1984, conserving collection of frozen semen from 25 sires would be adequate for all species. However it is appropriate to have frozen stores, which are large enough to provide a good representation of the conserved stock and to prevent much genetic drift or inbreeding.

Livestock conservation through participation of National/ Regional Gene Banks

Having large animal diversity and distributed over large territory of country, it becomes a gigantic task to conserve even those breeds where populations is decreasing. This situation necessitates involvement of many agencies in undertaking *ex situ* conservation programme working in a network at national level for preserving the indigenous farm resources. The AI centers in the breeding tract producing frozen semen of local livestock can deposit germplasm for long term cryopreservation in National GeneBank at NBAGR and at Regional GeneBanks managed by different state livestock development boards. The stored germplasm at these two banks may also be made available for utilization in breeding tract (Fig. 1) and replenished subsequently in the repositories.



Cattle	**Buffalo**	**Goat**	**Sheep**	**Equine**	**Yak**	**Camel**
Amritmahal	Assamese Swamp	Black Bengal	Garole	Marwari	Arunachali	Jaiselmeri
Dangi	Banni	Chegu		Zanskari		
Gangatiri	Bhadawari	Osmanabadi		Poitou (French Donkey)		
Gir	Jaffarabadi	Assam Hill		Manipuri		

Hallikar	Murrah	Gaddi		Hallari		
Hariana	Nilli-Ravi	Ganjam				
Kangayam	Pandharpuri	Jamnapari				
Kankrej	Surti	Berari				
Kherigarh	Tarai	Beetal				
Khillar	Mehsana	Sirohi				
Krishan Valley	Toda	Sangamneri				
Ongole	Nagpuri	Barbari				
Ponwar						
Punganur						
Rathi						
Red Kandhari						
Red Sindhi						
Sahiwal						
Tharparkar				**Total Species= 7** **Total Breeds= 62** **Total Semen doses= 2,88,898** **Total Males=** ***565***		
Vechur						
Frieswal						
Gaolao						
Bargur						
Nagori						
Badri						
Nimari						
Deoni						
Binjharpuri						
Ghumsari						
Khariar						

Table 2. Population estimates for endangered status of breed

Country	Cattle	Sheep	Goat	Pig	Horse	Reference
England	750	1,500	500	150	1,000	Alderson (1981)
West Germany	7,500	15,000	5,000	-	5,000	Simak (1991)
Europe	1,000	500	200	200	-	Maijala (1982)
General	10,000	10,000	10,000	10,000	10,000	FAO

Table 3. Population size of indigenous breeds for their status of endangerment (000)

Species	Normal	Insecure	Vulnerable	Endangered	Critical	Reference
Cattle	25	15-25	5-15	2-5	<2	Nivsarkar et al., 1994
Buffaloes	30	20-30	10-20	5-10	<5	
Sheep	50	30-50	15-30	8-15	<8	
Goats	30	20-30	10-20	5-10	<5	
Camels	20	15-20	5-15	205	<2	
Horses	20	15-20	5-15	2-5	<2	
Pigs	10	5-10	1-5	0.5-1.0	<0.5	
Cattle	>30	20-30	10-20	5-10	<5	Nivsarkar et al., 2000
Buffaloes	>35	25-35	15-25	10-15	<10	

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Unique attributes of indigenous AnGR - A case study on Bandur sheep

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In the last few decades, scientific efforts have been directed to enhance production, fertility and health of livestock species in India. Major breakthroughs have been achieved in production of transgenic animals for biopharming, embryo transfer technology (ETT), development of vaccines for major livestock diseases like FMD and PPR. However, a neglected but important area is the valorization of indigenous breed specific traits /products. India possesses a large number of diverse livestock breeds adapted to various ecological zones which thrive on low input. Indigenous breeds claimed to be economically important include Bhadawari buffalo (high milk fat content), Bandur, Madgyal sheep, Kadaknath poultry (meat), Black Bengal goat (skin/leather), Changthangi goat, Chokla and Magra sheep (fibre), Chilika buffalo (disease resistance) etc. However, in most cases the claims are not substantiated with scientific evidence. A scientific insight into effect of breed on product quality would be valuable for the industry, ensuring uniform or consumer defined quality. The process of valorization of breed specific traits will improve our understanding of potential genes defining these traits. This would augment value based marketing, thereby affecting and sustaining the economy of the livestock rearers directly. The identification of advantageous genes/genotype can be utilized to increase production efficiency through selective breeding or other biotechnological interventions. Scattered information in the form of a few genes and SNPs is available for some Indian livestock breeds. Comprehensive information of trait specific genes for Indian livestock is completely lacking.

Bandur sheep

Bandur is a mutton type sheep breed found in the Mandya district of Karnataka. It is also known as Mandya sheep and is one of the 44 registered sheep breeds of the country. The breed is highly acclaimed for its organoleptic mutton which fetches a higher price than other local breeds. Therefore, it is a valuable resource for unique genes/traits. Consumers are ready to pay a higher price for the unique flavor of its mutton. Meat quality depends on a large number of factors like pre and post-slaughter handling, age, nutrition, intramuscular fat, tenderness of muscle, etc. However, genetic factors also have an impact on the meat quality (Warner et al., 2010). Breed effect on meat quality in terms of intramuscular fat, shear force, water holding capacity and colour, has been documented (Waritthitham et al., 2010). In the case of Bandur mutton, the distinctive flavour has been attributed to intramuscular fat or marbling, but no systematic scientific data was available until recently to substantiate these claims. Since RNA sequencing is a reliable method for identifying known as well as novel transcripts, it has been widely used to compare transcriptomes across different tissues. RNA sequencing has led to the discovery of differentially expressed genes in *longismuss dorsi* tissue of Italian cattle (Bongiorni et al., 2015), pig (Jing et al., 2015), Chinese sheep (Sun et al., 2016). Therefore, ICAR-NBAGR initiated the investigation of the molecular genetic basis of mutton quality traits of Bandur sheep in 2016. For this purpose, the carcass traits and transcriptomes of Bandur sheep were compared with the local sheep, found in the same region. These local sheep are medium built and heavier than Bandur and are not registered as a breed. Even though the geographical and management conditions as well as available feed and fodder are similar for both populations only the Bandur mutton is preferred.

Bandur sheep

Evaluation of carcass quality

Carcass quality of Bandur sheep was evaluated by recording several characteristics like hot carcass weight, back fat thickness, fore saddle, hind saddle, foreleg, hind leg, rib eye area, pH, temperature of carcass, water holding capacity (WHC) (Kauffman *et al.* 1986). The WHC and back fat thickness was higher in Bandur sheep in comparison to local sheep. Instrumental colour studies indicated that mutton of Bandur was lighter in colour. Further, sensory evaluation of mutton, both cooked as well as fresh was also performed using the 9 point hedonic scale (Keetan, 1983), to assess attributes such as texture, appearance, flavour, mouth coating, overall acceptability and juiciness. Bandur mutton revealed a slightly higher flavour and juiciness, however, the difference between the two groups was not significant. Fat percent (of cooked meat) was significantly higher in Bandur (16.83) as compared to local sheep samples (11.16) (Arora et al 2019).

Tenderness of muscles

An important trait affecting the eating quality of mutton is tenderness of muscles. The intramuscular fat content, type of muscle fibres as well as post mortem processing determine the tenderness of meat (Renand et al., 2001; Hocquette et al., 2012). The shear force was used to measure the tenderness of several muscles viz., *longissimus dorsi, brachicephalicus, bicep, semimembranosus, psoas major, semitendinosus and triceps.* Bandur sheep muscles had an overall significantly lower shear force value (12.74N-22.65 N) as compared to those of local sheep (16.44N-26.19N) and were therefore, more tender.

Amino acid and fatty acid analysis

The mutton of Bandur and local sheep was analyzed for 17 amino acids and 12 fatty acids. Bandur had a significantly higher level of oleic acid and histidine (Arora et al., 2019). Higher content of oleic acid has been positively correlated with overall palatability while histidine is an essential amino acid required in the diet. The discovery of higher fat content, tenderness of muscles, oleic acid and histidine will add value to the mutton from Bandur sheep.

Transcriptomic studies

mRNA study

The muscle (*longissimus dorsi)* transcriptome profile of Bandur sheep was generated to identify key genes and pathways that may account for the unique mutton quality. RNA sequencing analysis revealed 602 significantly up-regulated and 1236 significantly down-regulated genes in Bandur sheep. Genes with a higher fold change between Bandur and local sheep were involved in AMPK signaling, adipocytokine signaling, PPAR signaling, biosynthesis of amino acids, calcium signaling, lipid metabolism, muscle development and differentiation and ketone body metabolism pathways that are relevant to meat quality. Enriched pathways in Bandur sheep included metabolism of proteins and lipids, PI3KAkt, EGFR and cellular response to stress. The core differentially expressed genes identified were *HSPB1, HSPA6, MAP3K14, HES1* and *COPS2* (Arora et al 2019). These genes are known to be associated with cellular stress, fatty acid metabolism and energy metabolism in skeletal muscles.

MicroRNA analysis

MicroRNAs (miRNAs) are 17- 22 nucleotides long non-coding RNA molecules that hold promise to be used as biomarkers. They are conserved across species and one miRNA molecule can target several genes. As a consequence, analysis of miRNAs delivers a wider outlook of regulatory molecular mechanisms. MiRNAs have been associated with growth, disease and metabolism (Guller and Russell, 2010). They play a significant role in development and proliferation of muscle cells in livestock species. MiRNA studies have helped to improve the understanding of regulatory factors involved in muscling traits. Several reports are available describing the miRNA expression in skeletal muscles of cattle (Goncalves et al., 2018), pig (Jing et al., 2015), goat (Guo et al., 206) and sheep (Hitachi, K. and Tsuchida, 2014; Zhao et al., 2016; Liu et al., 2019). However, no prior information on the miRNome of Indian sheep was available. The miRNA analysis of Bandur muscles led to the discovery of 400 known miRNAs. Myomirs or miRNAs specific to skeletal muscles mainly oar-mir-1, oar-mir-133b, oar-mir-206 and oar-mir-486 were enriched. The differential analysis revealed 100 differentially expressed miRNAs. The biological functions associated with these miRNAs were epithelial to mesenchymal transition, cell proliferation, immune response, apoptosis and cell differentiation. Enriched metabolic pathways were PI3K-Akt, cellular response to stress, metabolism of proteins and lipids and EGFR. Gene-microRNA interaction analysis revealed miRNA-21 at the core of the network (Kaur et al., 2020a; 2020b). miRNAs that inhibit the oxidative stress resulting in apoptosis may have potential use in improvement of mutton quality.

Conclusion

The integrated analysis of carcass and transcriptome of Bandur and local sheep of Karnataka identified genes associated with myogenesis, lipid metabolism and cellular stress, which may contribute to the uniqueness of mutton of Bandur sheep. Genes associated with tenderness (*DNAJB5, HSPA6, HSPB1*) were up-regulated in Bandur sheep. The significantly enriched genes may form potential biomarkers for unique muscle traits of Bandur. A functional genomic insight into the phenotypic differences in muscle traits of Bandur and local sheep will pave the way for elaborate studies in future. Eventually, increased valuation of mutton quality of Bandur sheep based on tenderness of muscle, histidine and oleic acid content, will improve the market value of Bandur sheep beyond the local area.

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Somatic cell banking- A technology of hope for the future

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There is a growing awareness that threats to biodiversity are increasing, whether measured in terms of extinction rate, destruction of ecosystems and habitat, or loss of genetic diversity within the species utilized in agriculture. Considering the lack of information and the unprecedented rate of extinction, the clear possibility exists that a high number of breeds are being, and will be lost in the near future, even before their characteristics can be studied and their potential evaluated. This is particularly worrying in the present scenario because of uncertainties due to rapid climate change, increasing and differentiating market demand, and human demographic expansion. In these conditions, it is more strategically important than ever to preserve as much farm animal diversity as possible, to ensure a prompt and proper response to the needs of future generations. Moreover, it is the main responsibility of a nation to preserve its genetic diversity on a long-term basis as per its agreement with the United Nations Convention on Biological Diversity (CBD).

Animal production is vital to mankind and the conservation of animal genetic diversity is a way to secure our future. The extinction of a species is an irreversible process that is imbibed in natural evolution. Human activities have influenced this process, making it much faster as compared to speciation. Keeping in view the bio, environmental, and food security, it is essential to maintain biodiversity and ultimately the alternative and potentially useful genes in the gene pool. While many developed countries counteract this phenomenon through financial incentives to threatened breeds, it is often not a viable option in the less-developed parts of the world. Successful conservation of species requires integrated management efforts to sustain available genetic diversity. These efforts include programs to protect and manage animal populations within their native habitat (*in situ* conservation) as well as supporting programs that manage populations, individuals, gametes, and/or embryos outside of natural environments (*ex situ* conservation). World conservationists recognize that the efficiency and efficacy of intensive conservation efforts can be increased many folds by applying recent advances in reproductive technology. For this purpose, cryopreservation techniques have been used for the long-term storage of gametes, embryos, gonadal tissues, and somatic cells and tissues.

Germplasm banks offer security against the loss of diversity: The role of genetic resource banks in the management and conservation of endangered species is particularly noticeable in the last decade. It includes the collection, processing, and storage of biomaterial. Under correct usage, these recourses are enough to keep up current genetic diversity in the populations and allow their reproduction in the future. A core problem in creating such banks is to determine the quantity and type of preserved genetic material. The viable options for *ex-situ* and *in vitro* conservation of endangered species at present are the protection of individual animals, semen cryopreservation, embryo, or oocyte freezing and verification, ovarian and testicular slices cryopreservation, whole ovary cryopreservation, somatic cells cryopreservation, stem cell cryopreservation, and genomic libraries. However, gametes, cells, and tissues freezing can only be performed for a limited number of species and needs customized techniques for each species. Thus, Somatic cell cryopreservation is an alternative *in vitro* option for genetic diversity maintenance.

Objectives of cryopreservation: In general, cryopreservation of genetic material from domestic farm animals can have different objectives. Although their main objective is to address long-term conservation needs, there are also short or medium-term objectives. The specific aims of a national gene bank may vary according to national strategies, availability of materials, and budgets. Objectives for cryopreservation need to be defined in terms of future use of the cryobank material:

1. To support populations conserved *in vivo*: a) as a backup in case genetic problems occur in the living population (e.g. loss of allelic diversity, inbreeding, the occurrence of deleterious genetic combinations) b) to increase effective population size of small populations and reduce genetic drift
2. To reconstruct breeds, in case of extinction or loss of a substantial number of animals
3. To create new lines/breeds, in case of breed extinction
4. As a backup, to quickly modify and/or reorient, the evolution/selection of populations
5. For research

Items 1 to 3 generally apply to endangered populations or the protection of small populations. Genetic material is stored to guarantee the survival of a breed or breed genetic variation. Gene introgression (e.g. upgrading programmes) and the creation of synthetic lines are particular examples of usage as outlined in item 3. Item 4 refers to non-endangered, selected populations, to strengthen the selection of a new target in a breed. Item 5 includes several research objectives, for example, retrospective population genetic analyses.

Somatic cell banks: Since the sheep Dolly was recreated from udder somatic cells it is well known that by cloning methods we can reestablish animals from their somatic cells. Somatic cell nuclei reprogramming allows for expanding the range of biological material used in programs for cryopreservation. Cryobanking of somatic cells as the nuclei donors for cloning is recently considered the additional approach to the preservation and improvement of agricultural animals and poultry gene pools.

Cell culture technology has become a widely used method in biology, medical research, and biomedical applications. Establishing primary cultures of fibroblasts allows researchers to obtain representative cells that have conserved most of their original characteristics and functions, which is an important foundation for further cloning, cell biology, and cell engineering. Somatic cell banks can be remarkable assets for the conservation of genetic material; by merely obtaining skin samples, it is possible to sample a large group of individuals without being limited by factors such as gender or age. Thus, techniques for somatic tissue recovery, cryopreservation, and *in vitro* culture of different farm animal species have been developed, resulting in a viable method for the conservation of species. Viable cryopreserved cell lines can be obtained from a very small amount of biopsy material, including that of dead animals, which is sufficient, but such lines contain the complete genome and proteome. In contrast to germ cells, embryos, and generative tissues, the cryopreserved somatic cells after repeated thawing are capable to regenerate, i.e. almost infinitely may serve as a source of biomaterial for use in assisted reproductive technologies and biological research, including retrospective reconstruction. Skin cells are also a source of genetic information that can be cryopreserved in a simple and efficient manner. Thus skin tissues are being used to generate cell banks which act as a source of somatic cells for different applications.

Fibroblast cell lines are very commonly used. These are mesenchymal-derived cell types important in several physiological processes such as the synthesis of extracellular matrix, epithelial differentiation, regulation of inflammation, and wound healing. In addition, fibroblasts derived from the skin are frequently used to produce induced pluripotent stem cells (iPSCs), a powerful tool that allows the production of other kinds of desired cells, and is now being widely used for disease modeling *in vitro*. Cultivation and freezing of somatic cells result in hundreds of millions of cells from an individual animal (and then preserve for many years) that are similar in number to the culture of microorganisms. Specific complex media, which consist of amino acids, vitamins, sugars, and blood serum containing sets of growth factors, are developed for effective somatic cell cultivation. The air CO_2 concentration and the temperature optimal for cultivation are specified. Developed techniques of stable line cultures allow cultivating cells for a dozen passages with no changes in karyotype and all traits of normal cells. Unlike the gametes and embryos, the somatic cells are smaller and, therefore, more resistant to cryopreservation. After decades of application and improvement, cryopreservation became a routine procedure for most cell types. It includes cell isolation from tissue, cultivation, obtaining primary cell culture, cell biomass accumulation, freezing, and storing in liquid nitrogen. In cryobanks, the samples should be stored at a temperature below −146°C, providing their high chemical and physical stability. Therefore, the stored biological material is valuable both for the conservation of genetic resources *ex-situ* and for future research projects and investigations.

The activities of Frozen Ark, the international consortium, and its members, particularly the San Diego Zoo (California, USA), LaCONES (India), and Genome Resource Bank (CGRB) for Korean Wildlife (Seoul National University), clearly demonstrated the role of cryobanks in the preservation of genetic resources of the domestic animals and wildlife. Creating somatic cell and tissue banks is a part of national programs of genetic resource conservation in Canada, Brazil, China, Germany, Poland, Spain, and Turkey. Noteworthy results were achieved when somatic cell banks and cloning technology were used to preserve the native Anatolian breeds of domestic animals.

Table 1. Cryopreservation of livestock germplasm using Fibroblast cell line

Country, Year	**Species**
UK, 2008 and USA, 2014	Equine

China, 2008-14	Luxi cattle, Simmental cattle, Jining black grey goat, Taihang black goat, Liaoning cashmere goat, Cashmere goat, Ujumqin sheep, Texel sheep, Mongolian sheep, Yorkshire pig, Sinihe horse, Wenchang chicken, Xiaoshan chicken
Spain, 2014	Iberian lynx
USA, 2014	Sheep
Netherlands, 2010	Murine
Thailand, 2014	Swamp buffalo
Iran 2014	Guinea Pig
Argentina, 2012	Przewalskii´shorse
Iran, 2016	Goat
India, 2015 onwards	Cattle, Buffalo, Sheep, Goat, Horse, Donkey, Camel, Pig, Yak

Cloning with differentiated somatic cells: Since the birth of the Dolly in 1996 (the world's first cloned farm animal produced from a differentiated adult somatic cell), many technical and scientific developments have been made in animal cloning research worldwide, and over the years, several farm animal species such as cattle, goats, sheep, buffalo, pigs, horses, and camels have successfully been cloned. Cloning means the excision of the nucleus from a mature oocyte and its replacement by the donor nucleus from a somatic cell. The donor nucleus influenced by different ooplasmic factors undergoes epigenetic reprogramming. As a result, the differentiated donor nucleus becomes active and initiates embryo development instead of somatic cell division. Cloning was first suggested in 1938 by H. Spemann who showed the pluripotency of cell nuclei until 16 cell stage in salamander embryos, but the experimental nuclei transfers in mammals were reported much later in the 1980s. As mammalian zygotes are small in size, it causes technical difficulties in manipulations. Nevertheless, the first reports about mouse cloning were dated 1981. In 1986 S.M. Willadsen reported the first successful nuclear transfer in sheep. Cloned sheep were obtained by the microsurgical enucleation of oocytes at MII with further fusion to 8 and 16-cell blastomeres. After the success with early blastomeres, there were attempts to use cultivated animal cells in cloning. Campbell et al. 1996 used donor nuclei from blastocyst inner cell mass at Scotland University. In these experiments, two lambs, Mågan and Morag, were born which became a crucial step towards obtaining clones using the somatic cells of an adult animal. The first cloned progeny via somatic cell nuclei transfer in mammals was obtained at the same university in 1997.

The birth of cloned sheep Dolly generated great scientific interest and contributed to further numerous studies in cloning other animal species using somatic cell nuclei transfer. Several wild and domestic animal species have been cloned using differentiated somatic cells. The progress involving livestock never lagged. Breakthroughs in livestock cloning are listed in Table 2.

Table 2. Famous cloned progenies of livestock species

Species	Name of cloned animal	Type of cells used	Year
Sheep	Dolly	Mammary gland epithelial	1996
Cattle	Gene	Fetal GR cells	1997

Goat	Downen TX 63 684	Fetal fibroblast	2001
Pig	Xena	Fetal fibroblast	2001
Mule	Idaho Gem	Fetal skin	2003
Horse	Prometea	Adult skin	2003
Dog	Snuppy	Adult skin	2005
Buffalo	Samrupa	Adult ear somatic	2009
Camel	Injaz	Adult ovarian	2009
Pashmina goat	Noori	Skin cells	2012
Swamp buffalo		Adult ear skin fibroblast	2014

Almost any cell type can be used in animal cloning. There are reports on cells of embryos, mammary glands, cumulus, granulosa, oviduct, liver, fibroblasts, leukocytes, and embryo stem cells being used as nuclei donors, but cloning efficacy essentially depends on the cell type. For successful embryonic development and the birth of viable animals, fetal fibroblasts are the most beneficial donors of nuclei for cloning. Low levels of mutations and high proliferation are characteristic of these cells. However, in the absence of fetal biomaterial, the tissues of adult animals could be the cell source, mainly skin, muscles, and cartilage. A disadvantage of such cells is their lower capability for reprogramming and embryo development as compared to fetal fibroblasts. Stem cells are recently considered to be the alternative source of nuclei for cloning. These cells are present in every organ of adult animals and provide structural and functional homeostasis. Proliferative ability and higher plasticity are valuable traits of stem cells in comparison to differentiated somatic cells. Experiments on the mice neural stem cells showed an easier reprogramming of stem or progenitor cells as compared to the differentiated cells. Moreover, when stem cell nuclei were used as karyoplast the number of cloned embryos significantly increased. Nowadays, mesenchymal stem cells are considered to be the most attractive source of nuclei for cloning. The adult animal cells significantly increase the potential of cloning for the conservation of animal and poultry genetic resources as well as for breeding. Controlled conditions of farms involving effective management result in the productivity of cloned animals that should differ only within a natural variability including the mitochondrial genetic variability.

Interspecies cloning: One of the biggest concerns for conservation geneticists is the effect of inbreeding on the long-term viability of an endangered species. Following a decline in population size, the risk of inbreeding increases partly because there are fewer individuals to mate with thus any two individuals are more likely to be related. Over several generations, this risk of mating between individuals that share recent ancestors increases. The problem with small populations and inbreeding is that deleterious mutations accumulate in the population. The process of cloning is substantially tweaked for conservation; specifically, instead of using the same species for both the somatic and egg cell donations, the somatic cell comes from an endangered species and the egg comes from an abundant (often domesticated) species. Then the domestic species is used as the surrogate mother for the implantation of the embryo. Thus this process is often referred to as interspecies cloning. Interspecies cloning has been tried on bantengs (*Bos javanicus*, an endangered bovine from Southeast Asia), black-footed ferrets (*Mustela nigripes*), and bighorn sheep (*Ovis canadensis*). This opens the door for several endangered species within the same genera to be candidates for interspecies cloning.

Interspecies cloning of banteng (*Bos javanicus*) is a good example of species revivalism. In 2003, measures were taken to preserve this rare species in the USA as it decreased in number by >85 %. Because of the absence of autogenic oocytes, the interspecies transformation was impossible, so the cow oocytes were used as recipients in transfer of the nuclei from adult banteng male and female skin fibroblasts. The biomaterial was received from the San Diego Zoo's Center for Reproduction of Endangered Species (CRES), where the tissues of endangered animals are stored. In this experiment, two calves were born after the transplantation of 30 blastocysts to surrogate mother cows. Intriguing progress has been achieved on the native sheep and their wild relatives, especially in the European mouflon. Somatic cell nuclei of an adult mouflon female that was found dead in a pasture, were injected into enucleated oocytes of domestic sheep. The recipient sheep were transplanted with embryos resulting in live offspring birth. Reproductive cloning has been successfully applied to the vanishing species *Ovis musimon*. In the experiment, the dead females were a source of genetic material and the efficacy was much higher than that in Dolly cloning. A cloned cub of the extinct subspecies *Capra (pyrenaica pyrenaica)* was born after the bucardo somatic cells were transferred into domestic sheep oocytes and the surrogate mothers of other subspecies or hybrids from crossing domestic and wild goats were transplanted with the embryos in Spain.

Keeping in view the phenomenal progress being made in cloning, cryobanking of somatic cells as nuclei donors in cloning is now regarded as an assisted technique for conservation and improving gene pools of agricultural animals and poultry. The domestic and wild animals of different species such as sheep, mice, cows, goats, pigs, guar, mouflon, domestic cat, rabbits, mule, horses, rats, wildcats, dogs, banteng, ferret, wolves, buffalo, deer, mountain goat, camel, and coyote have been obtained by cloning. Cattle remains the leader in cloning. The practical expansion of cloning technology, particularly the use of cryopreserved biological material, depends largely on whether there would be an acceptable relationship between the cost of implementation and economic impact.

Somatic cell bank for fulfilling national commitment under SDG: The 2030 Agenda for Sustainable Development, including the 17 Sustainable Development Goals (SDGs), were adopted by the United Nations in September 2015. It came into force on 1st January 2016 for the next 15 years covering all aspects of development. Countries were expected to implement the SDGs at the national level based on national priorities. India has been playing a prominent role in defining the contours of the 2030 agenda and is committed to achieving these goals in a time-bound manner. The central theme of SDG 2 is 'Zero Hunger' which aims to end all forms of hunger and malnutrition by 2030 and make sure that all people, especially those in vulnerable situations, have sufficient nutritious food. It also aims to double agricultural productivity by 2030 and generate decent incomes, while supporting people-centered rural development and protecting the environment. This Goal has 8 targets to measure the availability of food, improvement in nutrition, and promotion of sustainable agriculture. A total of 18 indicators have been identified to measure and monitor the progress of these targets at the national level. Two of those SDG indicators (2.5.1 and 2.5.2) are directly linked to animal genetic resources. These are:

2.5.1 Number of plant and animal genetic resources for food and agriculture secured in either medium or long-term conservation facilities

2.5.2: Proportion of local breeds, classified as being at risk of extinction

Somatic cell bank necessarily fulfills the national commitment as inherent in the SDG indicator 2.5.1:

SDG 2: Metadata: National Indicator 2.5.1 Number of (a) plant and (b) animal genetic resources for food and agriculture secured in either medium- or long-term conservation facilities	
Data Source Ministry	Ministry of Agriculture and Farmers' Welfare
Department/Ministry	Indian Council of Agricultural Research
Description of Indicator	The conservation of plant and animal genetic resources for food and agriculture (GRFA) in medium or long-term conservation facilities (ex situ, in gene banks) represents the most trusted means of conserving genetic resources worldwide. Plant and animal GRFA conserved in these facilities can be easily used in breeding programmes as well, even directly on-farm. The two components of the indicator, plant and animal GRFA, are separately counted.
Computation	**Plant component:** Number of accessions conserved in the base collection (18°C) at National Gene bank (Seeds) + Number of accessions conserved in the Gene bank (Tissue Cultures) + Number of accessions at Cryogen bank (-196°C) **Animal component:** Cryopreservation of semen at National Gene Bank + *Cryopreservation of somatic cell at National Gene Bank*
Unit of Measurement	Number
Periodicity	Annual

Conclusions

The conservation of biological resources is an interesting strategy for the maintenance of biodiversity, especially for livestock species/ breeds that are constantly threatened with extinction. Considering future developments of scientific knowledge of nuclear transfer are likely to improve the efficacy of the cloning technique. Hence, somatic cell freezing is an interesting option to create a backup repository at a faster pace under the current scenario of rapid erosion of animal genetic resources. Storage of somatic cells is a cheap and very effective method to keep a wide range of genetic variation with a limited budget. The procedure is identical for all species, sample collection is easier, and limited investment is required in both equipment and training. As a result, somatic cell cryo-conservation has the potential to be implemented rapidly in the field. Thus, the establishment of these banks has been suggested as a practical approach to the preservation of species and, when done in tandem with assisted reproductive techniques, could provide the means for reproducing endangered species.

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Insights into evolutionary relationships and domestication of livestock species

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Since evolution, animals have been an important part of human life for various utilities, apart from sources of food and nutrition. Speciation is considered a slow process, as a result of complex forces acting altogether leading to slower and stable changes in living beings which occur when populations, usually evolving in geographic isolation for extended periods, accumulate genetic differences. Species evolution is considered a continuous process, influenced greatly by the environment and surroundings, besides which genetic interactions, like horizontal gene transfer, might also affect evolutionary outcomes. Based on molecular studies, it is inferred that chicken evolved at almost 110 MYA, pig 28 MYA, bovines 24 MYA, whereas goat and sheep 18-20 MYA. Domestication of various livestock species began with the settlement of human beings as communities after giving up hunter-gatherers' lifestyle. Progressing from the first animal domestication events taking place around Fertile Crescent, today we are in a position to harness the full potential of livestock and poultry species. Among large animal species, only 14 have been domesticated: sheep, goat, cow, pig, horse, Arabian camel, Bactrian camel, llama and alpaca, donkey, reindeer, water buffalo, yak, Bali cattle, and mithun (gayal, domesticated gaur). Most of the livestock species during the process of domestication have undergone significant genetic, behavioural, and morphological changes from their wild ancestors. It is therefore important to understand the evolution and phylogenetic relationships of domestic animal species and their wild ancestors as well as closely associated species.

India possesses world's largest livestock population (535.78 million), recording an increase of 4.6% from previous census. These livestock species account for 13% of the global livestock. It has 57% of world's buffalo and 16% of cattle population. This diverse livestock is represented by a broad spectrum of 212 registered native breeds including those extant, 140 breeds, including the newly registered breeds after initiation of breed registration process by NBAGR. After including recently registered ten new breeds, total registered livestock and poultry breeds include- 53 for cattle, 20 for buffalo, 37 for goat, 44 for sheep, 7 for horses and ponies, 9 for camel, 13 for pig, 3 for donkey, 1 for yak, 19 for chicken, 2 for duck, 1 for geese, and recently 3 dog breeds also have been registered (https://nbagr.icar.gov.in/en/accession-numbers-of-registered-breeds-of-livestock-poultry). Understanding the evolution and genetic diversity of Indian livestock and classifying the populations by their evolutionary significance is essential for an appropriate conservation plan to be conceived and carried out. To comprehend the evolutionary relationships, various markers have been utilized including autosomal microsatellites, Y-chromosome sequence, and mitochondrial DNA (mtDNA) sequencing.

Out of the number of molecular markers available, the microsatellite-based genotyping is one such method of choice. Food and Agricultural Organization (1996) has laid detailed technical programme for large scale international conservation project using microsatellite markers under MoDAD project. Number of species-specific microsatellite markers have already been characterized for establishing genetic relationship and diversity among all the breeds, prescribed for global use. International comparison tests under the auspices of International Society of Animal Genetic (ISAG) to establish international standard also exists. High level of polymorphism coupled with the ease of analysis has made this type of markers being one of the most widely used for genetic analysis. Microsatellites are thus, the best available molecular markers today because of their ease of generation and highly polymorphic nature. Their use makes it possible to obtain an unprecedented understanding of the process and dynamics of biodiversity, its evolution and nature. Based on the data generated by the microsatellite characterization, clustering of different breeds is possible, which will pave the way for prioritization and further, conservation of breeds. These markers have been used for delineating the population structure based on allelic frequencies as well as genetic distinctness of the population making it suitable for registration as a new breed. Besides, admixture analysis using these tools, helps in identification of the level of mixing of other breeds into the population. The tools have helped in registration of new buffalo breeds like Banni, Gojri, Chhattisgarhi and Manda. Similarly microsatellite markers based diversity analysis of Indian cattle breeds has shown clustering of populations based on the geographical distribution and Ongole emerging as the most ancestral breed of cattle.

The mtDNA is considered ideal to study maternal evolutionary part as it possesses several favorable characters including small genome size, haploid, maternal inheritance and extremely low probability of paternal leakage, higher mutation rate than nuclear DNA, and change mainly through mutation rather than recombination. D-loop is observed as most variable portion of the mammalian mitochondrial genome and is commonly variable at the intraspecific level making it useful for phylogenetic studies, while cytochrome b usually has moderate level of intra specific level, helping to trace the maternal evolution of a species. All these features make mtDNA a useful and one of the most frequently used markers in molecular systematics and has been widely employed to address questions of genetic diversity and evolution. Workers have utilized mitochondrial D-loop sequencing for understanding the evolution of riverine as well as swamp buffaloes among various livestock species. Based on studies outcome it is pinpointed that riverine buffalo after domestication in the western region of the Indian subcontinent almost 6300 years BP, spread west up to Egypt, the Balkans and Italy. Whereas, after domestication in the China/Indochina border region almost 3000–7000 years BP, swamp buffaloes spread towards south-east Asia and China as far as the Yangtze River valley. Based on karyotype and mitochondrial D-loop sequencing studies, in has been concluded that Assam region being the evolution point of both types of buffaloes, differing in their chromosome numbers. Both riverine (2n=50) and swamp (2n=48) type buffaloes along with their hybrids (2n=49) have been documented in the region. Existence of Asiatic wild buffalo (*Bubalus arnee*), progenitor of both riverine and swamp buffaloes in the Assam region of India confirms the events. Recent studies on Chilika buffaloes of Odisha has shed a new light on the domestication of buffaloes, wherein hybrids of riverine and swamp have been identified sharing of haplotypes with both types.

Phylogenetic clustering of north-east Indian swamp buffaloes with both the lineages of Chinese swamp buffalo have been observed, revealing north-east region of India forming part of the wider hybrid zone of water buffalo that may probably extend from north-east India to South-East Asia. Studies on mitochondrial D-loop sequence data of Odisha buffaloes and other Indian riverine, swamp and hybrid buffaloes have been carried out comparing with other reported Indian riverine, Chinese and Bangladeshi swamp buffalo populations. Haplotype sharing between Chilika- an Odisha buffalo population with Indian swamp as well as Chinese swamp buffalo populations in the network analysis confirmed the presence of hybrids documented by cytogenetic analysis having 49 chromosomes in Chilika population. Phylogenetic analysis of Chilika and swamp buffaloes of India, China and Bangladesh has shown haplotypes with pre-domesticated haplogroups 'SA1', 'SA2', 'SA3' and 'SB1'. These findings thus indicate the migration of swamp buffaloes towards Bangladesh and adjoining lower parts of India and north towards the Chinese domestication sites confirming the previous reports that the northeast region of India, close to the Indo-China border, is the point of evolution of swamp buffaloes with multiple sites of domestication.

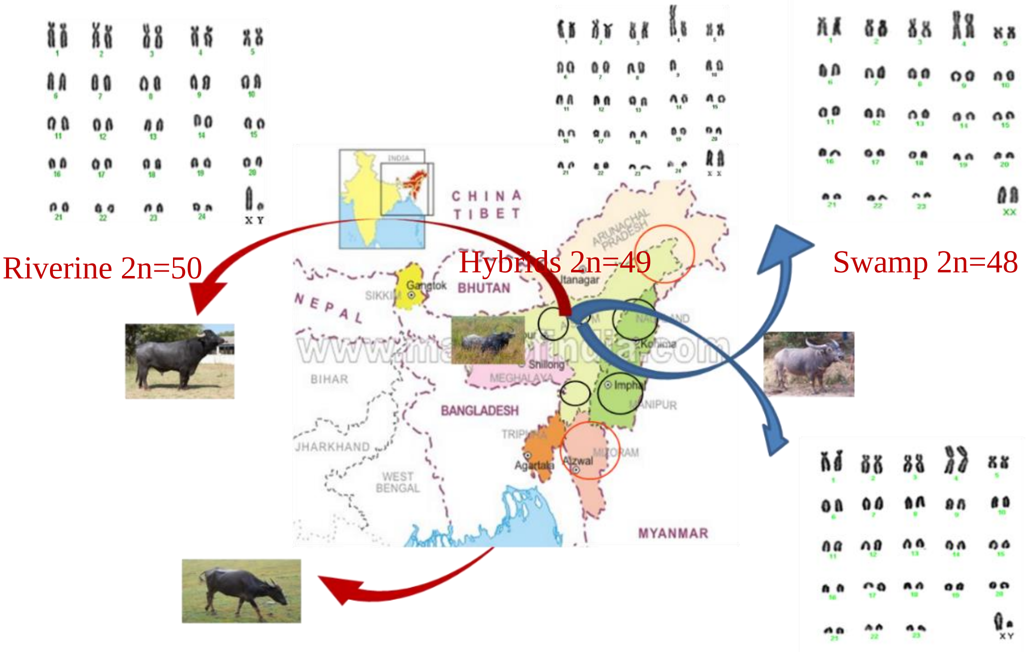

Figure 1. Evolution and spread of riverine and swamp buffaloes in India and their karyotypes

Archaeological and genomic evidences suggest that the taurine cattle (*Bos taurus*) were domesticated from its wild ancestor *Bos primigenius primigenius* in the Fertile Crescent. Later a second domestication event reported in the Indus Valley from *Bos primigenius nomadicus*, separated from the taurine branch ~250,000–330,000 YA, giving rise to the extant indicine cattle (*Bos indicus*), often also termed as zebu. It is also believed that divergent African taurine cattle arose due to third independent domestication even later happening in Northeast African region. Based on mitochondrial and Y-chromosomal DNA sequence, domestication and dispersal of three major Bos species – taurine cattle, zebu cattle and yak – and their genetic interactions has been reviewed recently, indicating population bottlenecks leading to phylogeographic differentiation of three species. Breed formation of European taurine cattle is thought to be result of isolation by distance, selective breeding and expansion of limited popular populations. Wider distribution of zebu and taurine cattle and other bovine species led to hybridization with each other showing, introgression playing a major role in environmental adaptation of these species. Molecular evidences suggest that the two species of cattle, indicus and zebu came from two independent domestication events. Zebu were first domesticated in the Indus valley region almost 8000–7500 B.P., whereas taurine cattle were domesticated in Anatolia 10,500–10,000 B.P. Sequencing of hypervariable mitochondrial DNA region on a subset of 170 Indian cattle revealed sixty haplotypes with two major star clusters for haplotypes which indicated population expansion for Indian cattle. Workers have also analysed mt DNA hypervariable region of 443 goats together with 22 reference sequences and found 341 distinct haplotypes belonging to four maternal haplogroups; A, B, C and D, with a major proportion of haplogroup A representing 90% of the individuals and concluded no genetic structuring of goats on the basis of geographical distribution.

Table 1. Mitochondrial genetic diversity in different livestock species and their potential ancestors (Bruford et al., 2003).

Domestic species	**No. of possible differentiated wild ancestors**	**No. of extant ancestor species (subspecies)**	**No. of domestication events**	**Mt cyt b (average) Sequence divergence among domestic lineages**	**Mt CR (average) sequence divergence among domestic lineages**
Cattle: taurine (*Bos taurus*) and zebu (*Bos indicus*)	2 subspecies: *B. primigenius primigenius* (*B. taurus*) and *B. primigenius namadicus* (*B. indicus*)	0	2 for *B.p. primigenius* (Eurasia and Africa) 1 for *B.P. namadicus* (Asia)	0.015 (Bradley *et al.*, 1996); between *B. taurus* and *B. indicus*)	0.057 (Steinborn *et al.*, 2002)
Sheep (*Ovis aries*)	3 species: *O. musimon*/ *O.orientalis*, *O. ammon* and *O. vignei*	3	2 for *O. musimon*/ *O. orientalis* (the mouflon)	0.007 (Townsend, 2000)	0.059 (Hiendleder *et a* 1998)
Goat (*Capra hiscus*)	2 species: *C. aegarus* and *C. falconeri*	2 (3 within *C. aegagrus*)	3 (potentially all from the *C. aegagrus* subspecies)	ND	0.035 (Luikart *e* *al.,* 2001)
Horse (*Equus caballus*)	Multiple wild populations of a single species (*E. caballus*)	0	ND	ND	0.026 (Vila *et al.,* 2001)
Pig (*Sus scrofa* domesticus)	2 species: *S. scrofa* and *S. indicus*	2	1 for *S. scrofa* and 1 for *S. indicus*	0.007 (Giuffra *et al.,* 2000)	0.018 (Watanob *et al.,* 1999)
Water Buffalo (*Bubalus bubalis*)	2 subspecies: *B. b. bubalis* and *B. b. carabanesis*	2	2 for *B. b. bubalis* and *B. b. carabanesis*	0.007 (Lau *et al.,* 1998; Tanaka *et al.,* 1996)	0.074

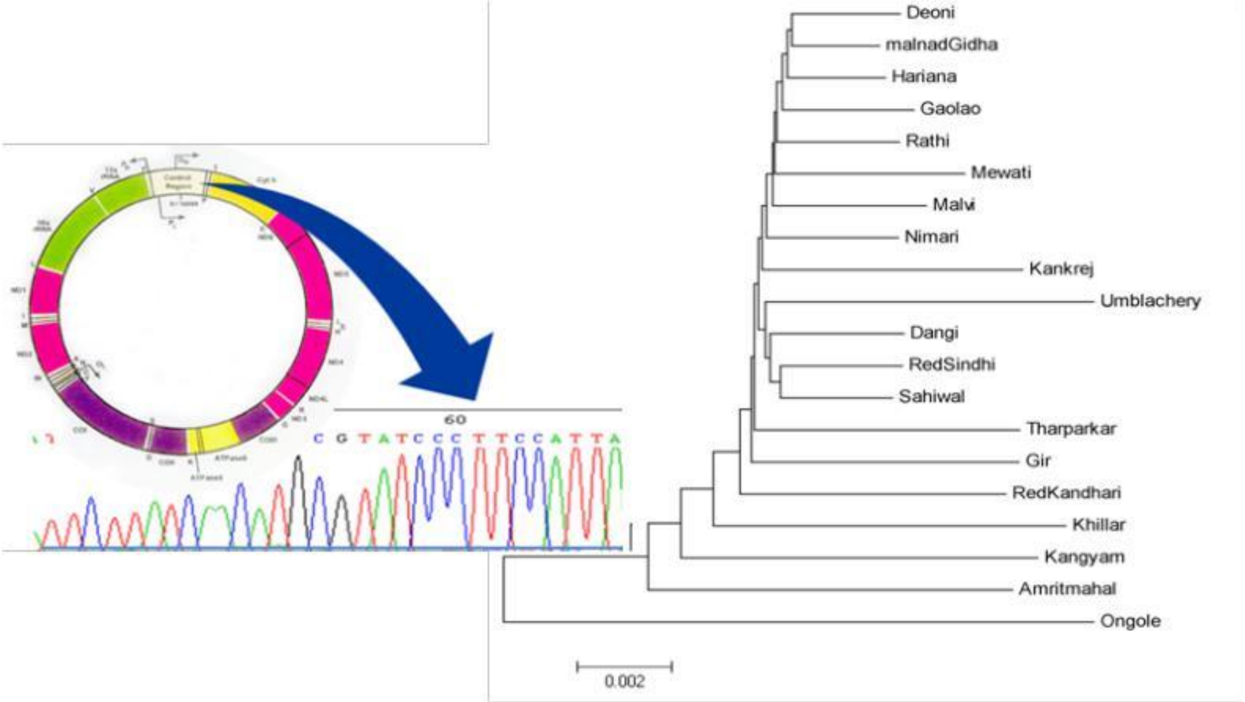

Figure 2. Phylogenetic relationship amongst Indian cattle breeds using mtDNA sequence

Present day best dairy breeds of cattle and buffaloes are from the North Western India. Moreover, it's worthwhile to explore the evolution, lineages and various genetic changes that took place during the course of evolution in Indian livestock species using high throughput genomics techniques, bioinformatics and computational biology with an interdisciplinary effort, to understand functional genomics and adaptability to the region. Recently workers have compared the whole genome sequence data generated on 79 water buffalo across seven breeds with 294 cattle genomes representing 13 global breeds. It has been observed that the genomic regions under selection between cattle breeds significantly overlap regions under selection between water buffalo breeds. Analysis of potential functional variants in the water buffalo genome identified a rare convergent domestication event down to the same mutation having independently occurred and been selected for across domesticated species. Cross-species comparisons of recent selective sweeps can consequently help identify and refine important loci linked to domestication and evolution. The output of the NGS data analyzed has shown the potential of newer technologies in better understanding the evolution of livestock species.

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Screening of breeding bulls for chromosomal and DNA based genetic disorders

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Genetic disorders are caused by any abnormal change in amount, organization or content of genetic material i.e. DNA and chromosome. Such changes, encompassing single nucleotide to chromosomal set may affect the survivability and/or fertility of an individual. Normally, genetic mutations may occur at any time inside genome; however, only a very small fraction that are occurring in functionally important regions may culminate in genetic abnormalities leading to diseased and syndromic conditions. The severity of disorder is largely subjective to the region of importance, where the defect may impair a vital function of cell or organ system. Genetic defects may be present in any of the cell, however if present in germ cells it may be inherited from parents to their progenies through gametes. The genetic defects in somatic cells capable to cause different types of anomalies mostly cancer in individual, although are not able to pass on to the next generation. Genetic abnormalities may be classified in two types- DNA and chromosomal level in broader sense. Genetic defects may also occur at any time, although, most of the *de novo* DNA mutations may occur during DNA replication and cell divisions. Chromosomal defects arise during cell division and fertilization. Although most of the affected human and animals acquire the genetic mutations and aberrations through inheritance, but extraneous environment such like mutagenic chemicals and X rays may also create the mutation in body, mostly at somatic level.

DNA Based Genetic Diseases

More than six hundred deleterious mutations have been documented in cattle, mainly in taurine breeds and among these, 193 are identified as causal variants Online Mendelian Inheritance in Animals; http://omia.angis.org.au). Interestingly, no causal variant has been found to be reported in *Bos indicus* cattle. Mutations do not seem to occur equally distributed throughout the genome, instead some genomic regions might be predisposed to higher number of deleterious mutations. The highest number of causal variants (14) are found to be present on chromosome number 19, whereas, only seven causal variants are on the first chromosome in bovines. DNA based genetic diseases seem to be population. DNA based lethal mutations are mainly reported in taurine cattle breeds. Certain mutations are even breed specific. Most of the disorders have been identified in Holstein population. Bovine leukocyte adhesion deficiency (BLAD), complex vertebral malformation (CVM), citrullinemia, and deficiency of uridine monophosphate synthase (DUMPS) are some of the most common causal variants widely present in *Bos taurus* breeds. These DNA based genetic diseases have also been reported in Indian HF cattle.

Bovine leucocyte adhesion deficiency: It is commonly referred as BLAD. This lethal autosomal recessive disorder is caused by a single point mutation (A>G) of nucleotide 383 in the CD18 gene (β2 integrin). BLAD is characterized by greatly reduced expression of β2 integrin adhesion molecules on leukocytes resulting in multiple defects in leukocyte function. BLAD affected cattle show severe and recurrent mucosal infections such as pneumonia, delayed wound healing and stunted growth; and most cattle die before one year of age. The BLAD has been reported in Holstein cattle throughout the world. with 0.8 to 3.45% of carriers in different countries.

Deficiency of uridine monophosphate synthase: It is an autosomal recessive disorder of Holstein cattle, caused by single point mutation (C→T) at exon 5 of uridine monophosphate (UMP) synthase gene. The mutation is manifested with impaired pyrimidine biosynthesis required for DNA synthesis, causing early embryonic death at around 40 days post-conception.
Citrullinemia: It is an autosomal recessive DNA mutation caused by nucleotide substitution at codon 86 of the gene coding for arginine-succinate synthase (ASS1 gene). This genetic disorder prevents the synthesis of arginino-succinate synthetase, the enzyme that catalyses the conversion of citrulline and aspartate to arginine-succinate during urea cycle. Cattle affected with Citrullinemia appear normal immediately after birth, however, the disease progresses rapidly and the calves appear to be blind and die within 7 days of age. The disease is first described in the Australian Holstein population and also observed in Indian and Chinese Holstein populations.

Factor XI deficiency: Factor XI is one of the proteins involved in blood clotting process. The factor XI deficiency in cattle arises due to insertion of a 76-nucleotide long fragment in exon 12 of FXI gene at bovine chromosome 27. The disease precipitate in form of prolonged bleeding from the umbilical cord and anaemia. Additionally, FXID causes reduced reproduction performance and the affected animals appear to be more susceptible to diseases such as pneumonia, mastitis and metritis. Affected animals may survive for years, however with higher morbidity.

Complex vertebral malformation: Also known as CVM, the disease is recessive in nature and caused by a missense mutation in SLC35A3 gene, encoding a uridinediphosphate N-acetylglucosamine transporter protein. It affects embryonic development leading to frequent abortion of affected fetuses or perinatal death associated with vertebral anomalies. Malformation of multiple vertebrae, mainly involving those at the cervico-thoracic junction, is a common feature. Typical signs are a shortened neck and contraction of carpal and fetlock joints. Affected cattle may also show cardiac anomalies. The high prevalence of CVM among Holstein populations of different countries has been reported.

Other DNA based genetic disease

Different Holstein haplotypes (HH1, HH3, HH4) have recently been reported in HF inheritance. In recent years, several recessive haplotypes have also been discovered in Holstein cattle, most of them affecting fertility due to increased embryonic mortality. VanRaden et al. (2011) discovered five new recessives that were confirmed to have produced termination of pregnancy: 3 in the Holstein breed (HH1, HH2, and HH3) and 1 each in the Jersey (JH1) and

Brown Swiss (BH1) breeds. An examination of the effects of those 5 haplotypes on fertility showed that BH1, JH1, HH2, and HH3 produced embryo losses soon after conception, but HH1 resulted in uniform losses across the entire gestation. In India, JH1, HH1, HH3 HH4 and Holstein cholesterol deficiency (HCD) have been reported in exotic cattle and their crosses. Although number of genetic defects reported in indigenous cattle and buffaloes are a few, presumably due to scarce study or non-availability of tests.

Methods for screening DNA mutation

Genetic basis of many heritable lethal mutations has largely been identified based on pedigree analysis along with the use of various molecular techniques including DNA cloning and sequencing supplemented with biochemical and physiological analyses Screening of these disorders has been carried out using various molecular approaches such as polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP), allele-specific polymerase chain reaction (AS-PCR), and amplification refractory mutation system-polymerase chain (ARMS-PCR). Among various techniques that are used to study SNPs, only a few are applicable for routine disease diagnosis. The increasing need for large-scale genotyping applications of SNPs in model and non-model organisms requires the development of low-cost technologies accessible to minimally equipped laboratories. Many techniques have been developed and are being utilized depending upon the facilities available and the number of individuals to be screened. Direct sequencing is the best way to detect as well as genotype point mutation specifically single nucleotide substitutions. In chromatogram heterozygous positions can be scored manually or by sequence alignment tools. It is possible to score homozygous as well as heterozygous alleles. Typically heterozygous position will depict double peak can help in base calling and scoring of alleles. PCR-Restriction fragment length polymorphism (RFLP) is the simplest method to detect SNPs. The specific restriction endonuclease recognizes and cleaves the DNA in the region of the point mutation of the PCR products. This technique has been widely used for screening of a number of genetic defects including BLAD, DUMPS, BC and JH1 in cattle. PCR- single strand conformation polymorphism (SSCP) is another simple, efficient, and reliable method for the detection of sequence alterations in genomic loci. The conformation is sequence dependent and most single base pair mutations alter the shape of the structure. Allele-specific polymerase chain reaction (AS-PCR) or PCR amplification of specific alleles (PASA) is a simple, fast and reliable method for detecting any mutation involving single base changes or small deletions without any post PCR processing. It works on the principle of sequence-specific PCR primers that allow amplification of test DNA only when the target allele is contained within the DNA sample and there will be no amplification if target allele is not present in the DNA. Another PCR technique called Tetra-Primers Amplification Refractory Mutation System-(Tetra-ARMS) is capable of detecting genotypes directly on gel after PCR. Two sets of primers - outer and inner primer sets – amplify the products of different lengths, depending upon the allele present. Real time PCR has proven to be a rapid, robust, accurate, and sufficiently high-throughput technique for SNP analysis. Mass spectrophotometry based MassARRAY system can genotype a group of SNPs or nucleotide mutations located in different part of the genome or chromosomes at a time through producing products of different molecular sizes for each allele. The highly efficient assay design, short lead time and easy panel modification enable users to rapidly validate those genetic markers at low reagent and labour cost. The SNaPshot® Multiplex System is also high throughput genotyping method, wherein SNPs can be multiplexed. SNaPshot® labeling chemistry relies on single-base extension and termination. With the advent of high throughput genome sequencing techniques, DNA mutations can now be identified in silico with the use of bioinformatics tools.

Chromosomal Based Genetic Diseases

Each species of domestic animals has specific chromosomal set, regarding the number as well as the form. Related species possess high chromosomal analogy. Although, differences in apparent chromosomal numbers the fundamental numbers as well structure remain same in two different but genetically close species. Cattle possess 29 pairs of autosomes acrocentric and X (submetacentric) and Y (metacentric in taurine and acrocentric in indicine cattle) sex chromosome. In buffalo, there are 5 pairs of autosomes are submetacentric, 19 pairs of autosomes and X and Y sex chromosome are acrocentric. Five submetacentric chromosomes of buffalo derived from centric fusion of 10 pairs of autosomes (1/27, 2/23, 8/19, 16/29, and 5/28) of cattle. Swamp buffalo has another fusion of 4 and 9 chromosome of riverine buffalo. Goat has 60 chromosomes. The sheep possess 54 chromosomes due to fusion of 3 pairs (1/3, 2/8 and 5/11) of chromosomes of goat.

Chromosomal abnormalities

Chromosome abnormalities usually occur when there is an error in cell division, either by mitosis or by meiosis. In both processes, the correct number of chromosomes is supposed to reach in daughter cells. Various studies reveal that about 25% of the abnormalities are attributed to the errors in recombination and separation of chromosome during meiosis at the time of gametogenesis, while rest of the abnormalities occur around the time of fertilization. Chromosomal abnormalities may account for approximately one fifth of the total embryonic and fetal loss. Chromosomally abnormal embryos have shown slow development compared to normal diploid embryos. Major deviations are rarely sustained, and such foetuses usually die and aborted. Chromosomal abnormalities can be classified in two groups- numerical and structural abnormality. Aneuploidy is condition with any deviation from normal chromosome number(s) (euploidy), or having less than or more than the normal diploid number of chromosomes. It is the most frequently observed condition of chromosomal abnormality. Monosomy is lack of one of a pair of chromosomes. Monosomy (one chromosome of a pair) is commonly seen in many species. X chromosome monosomy is common lethal during prenatal development. Trisomy is having three chromosomes of a particular type. Another type of aneuploidy is triploidy. A triploid individual has three haploid sets of chromosomes, commonly occurs by fertilization of one ova by two sperm. However, birth of a live triploid is extraordinarily rare and such individuals are quite abnormal.

Various kinds of structural abnormalities have been observed, so far. A chromosome deletion occurs when the chromosome breaks and a piece is lost. This of course involves loss of genetic information. A related abnormality is a chromosome inversion- a break or breaks occur and that fragment of chromosome is inversely rejoined. Inversions, thus do not involve loss of genetic material, however, breakpoints may disrupt the gene. Generally, individuals carrying inversions have a normal phenotype. In chromosomal translocation, chromosome(s) break and the fragments re-join to other chromosome(s). There is no loss of genetic material, although the breakpoint can cause disruption of a critical gene or may create fusion or duplication of the gene. Translocation is manifested as reductions in fertility or some time some disease conditions like cancer. When two non-homologous chromosomes break and exchange fragments, it is termed as reciprocal translocations. Individuals carrying such abnormalities may have a normal phenotype, but may show subnormal fertility. A centric fusion is a translocation in which the centromeres of two acrocentric chromosomes fuse to generate one large metacentric chromosome. They are also often called Robertsonian translocations. The best known example is fusion of chromosome 1 and 29 in cattle.

Effects of chromosomal abnormalities

Multiple congenital malformations are seen with many types of chromosomal abnormalities, particularly deletions and aneuploidy. Animals with a balanced set of chromosomes will generally be normal phenotypically. If an individual does not have a balanced set of chromosomes, this will normally be visible through more or less deviation of phenotype from normality. Animals with a non-balanced set of chromosomes will most often be sterile and have low vitality. Chromosome deviations, in animals with a normal phenotype, are normally detected due to low fertility or complete sterility. The trisomies are very rare in animals, but they occasionally occur. In cattle, normally the foetuses carrying trisomy of chromosome 28 are aborted or die straight after birth. Such animals show cleft palate and heart abnormalities. In most domestic animals less severe chromosome errors occur. The subfertility is caused by problems in chromosome pairing and segregation during meiosis. In general, however, it shows a substantial, often greater than 50% reduction in fertility. Chromosomal fusion in heterozygote form causes a slightly lower fertility. The karyotype of a bull with low fertility has shown having a 1/8 translocation. In livestock, the defects of sexual chromosomes usually influence the development and function of reproductive system. In buffaloes and some cattle reduced fertility revealed the structural and numerical aberrations of the chromosomes more frequent, specifically chromosomal gaps and deletions in autosomal and sex chromosomes as well chromatid breaks and centric fusions in autosomal chromosomes. Chromosomal disorders such as XO, XXY, translocation reported in livestock can reduce the fertility or hamper the breeding of animals. However, defects in autosomes are usually lethal except mosaicism and translocations.

Screening for chromosomal abnormalities

Cytogenetic screening involves some main steps- cell division or inducing the cell for cell division, arresting the cells at metaphase, treat the cells in hypotonic solution, and make the spread and finally staining the chromosomes. Peripheral blood is most convenient tissue and common source for the karyotype preparation in livestock species. Since, lymphocytes have the division capability; they are induced for mitosis by using suitable mitogen and allowed to propagate in suitable culture medium supplemented with essential ingredients and incubation temperature and period. Harvesting of the chromosomes is achieved by the inhibitors like colchicine or colcemid, which inhibit the tubulins and depolymerize the mitotic spindles and ultimately arrest the cell division at particular stage. Metaphase chromosomes spread make all the chromosomes to stay in the same plane on the slide. Once stained slides are prepared, they are scanned to identify "good" chromosome spreads (i.e. the chromosomes are not too long or too compact and are not overlapping), which are photographed. The images of each chromosome then are cut out and pasted to a backing sheet in an orderly manner. Alternatively, a digital image of the chromosomes can be cut and pasted using a computer. If standard staining was used, the orderly arrangement is limited to grouping like-sized chromosomes together in pairs, whereas if the chromosomes were banded, they can be unambiguously paired and numbered. Generally, several metaphases are processed because it is not uncommon for a single spread to artifact have extra chromosomes or be missing chromosomes. This is particularly important if one is to diagnose an abnormality in an individual. It also allows one to diagnose cases of mosaicism, in which an individual has multiple, cytogenetically distinct populations of cells. If abnormalities are found in peripheral blood, it is sometimes desirable to determine whether that abnormality is present throughout the individual, and further studies with tissues other than blood can be performed. It is advisable to get next blood sample and screen the chromosomal spread in any double case of chromosomal aberration(s), before giving final verdict.

Conclusion

Genetic defects in livestock although are not considered important in most of the countries, its long-term implications cause huge economic losses to the dairy industry in terms of compromised survivability, production, reproduction and fitness of affected animals. Chromosomal defects of large intensity are less frequently observed and easily identified by their physical implications in animals. However, some mild type of chromosomal defects may cause insignificant effect on animal conformation or physiology apparently but may influence reproduction. At DNA level, several genetic diseases are routinely being reported in many cattle breeds. The loci of these diseases seem to be breed specific. Earlier some of the DNA diseases reported in exotic cattle in high frequency, have now been drastically reduced after their routine screening. However, as a natural process, new DNA based lethal genetic defects, mostly causing embryonic death have emerged in recent time. Such lethal mutations have also been reported in Indian exotic and crossbred cattle populations. Therefore, routine screening of breeding bulls is mandatorily required to eradicate the genetic mutations from the dairy herds using different cytological and molecular tools. Under Minimum Standards of Protocol and Standard Operating Procedures for Bovine Breeding of DAHD, GoI, it is recommended that all bovine bulls should need to be karyotyped to rule out any chromosomal defects as well as screening for some DNA based genetic diseases.

Approaches for genetic characterization of Animal Genetic Resources

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India is fortunate to be one of the largest mega biodiversity centers of the world with livestock wealth distributed over a range of geographical, ecological and climatic regions. As per Livestock census 2019, the farm animal genetic resources in India are represented by cattle (37.28%), buffalo (21.23%), goat (26.04%), sheep (12.71%), pig (2.01%) and others such as yak, mithun, camel, horse (0.37%). ICAR-National Bureau of Animal Genetic Resources has recognized 212 breeds of different livestock/poultry species, which include 53 for cattle, 20 for buffalo, 37 for goat, 44 for sheep, 7 for horses and ponies, 9 for camel, 13 for pig, 3 for donkey, 3 for dog, 1 for yak, 19 for chicken, 2 for duck and 1 for geese. However, many unrecognized or non-descript populations also contribute significantly to India's livestock production and thus, need to be characterized.

Characterization of AnGR biodiversity

Characterization refers to defining the qualities of an individual or a population. The uniqueness of an individual or a group depends on the special character that it possesses. In livestock sector, each species has specific characters. Even within the species, a group of individuals which have uniform traits, mate to produce similar individuals with similar set of characters. Such group is considered as a 'breed'. According to FAO (2012), a domestic animal population may be regarded as a breed, if the animals fulfill the criteria of (i) being subjected to a common utilization pattern (ii) sharing a common habitat/distribution area (iii) representing largely a closed gene pool and (iv) being regarded as distinct by their breeders. The characterization of each breed/population is done on the basis of their phenotype as well as their genetic attributes. Genetic erosion of livestock diversity has emerged as a global concern over the last few decades due to preference for highly specialized breeds, neglect of the local breeds, increasing mechanization in agriculture and many unforeseen factors in different parts of the world. The introduction of exotic germplasm especially of cattle, chicken, pig and sheep from agriculturally advanced countries has contributed to severe depletion of highly adapted animal genetic resources of many developing countries including India. Additionally, shrinkage in grazing land and unavailability of breeding males of known genetic merit has further escalated the erosion of animal genetic resources. All these factors have jeopardized the sustainability of livestock production systems worldwide. Many indigenous livestock breeds have been reported to be under threat. The proportion of breeds under threat is much higher in minor species such as camel and horses. In order to ensure sustained utilization and long term preservation of farm animal diversity, a composite approach needs to be adopted which should include identification of unknown populations, their characterization and documentation, identification of breeds at risk and efforts for their conservation.

Genetic characterization

Genetic variability is a prerequisite for devising the genetic improvement strategies at present and to tackle emerging challenges such as climate change in future. Conservation of local breeds is possible only if there is a clear understanding of the genetic structure and diversity of the breeds as well as relationship between their genetic makeup and performance characteristics. FAO (Food and Agriculture Organization) included the issue of conservation, evaluation and use of animal genetic resources in its fields of interest four decades ago. There has been rapid advancement in the tools for genome analysis based on molecular markers which has generated a vast amount of information regarding variation within and between livestock breeds. They have also become extremely popular for phylogenetic analysis, thereby adding new dimension to the evolutionary theories. Other applications of molecular markers include mapping and tagging of genes, genetic distance estimation, marker assisted selection and parentage determination. Molecular markers complement morphological and productive information about the animal genetic resources of a country, thereby, contributing to an accurate assessment of the existing genetic diversity. This chapter discusses most commonly used molecular markers for genetic diversity studies of AnGR.

1. Microsatellite markers

They have proved valuable for genetic characterization of farm animals and have been recommended by FAO as first priority molecular tools for the Measurement of Domestic Animal Diversity (MoDAD). For each species of interest, International Society for Animal Genetics (ISAG) in collaboration with FAO have recommended a set of microsatellite markers to be used as the standard set for the calculation of genetic diversity. Adherence to such recommendations allows for reasonable comparison of parallel or overlapping studies and helps combine results in meta-analyses. The primer sequences and map position of each of these markers can be obtained from Domestic Animal Diversity Information System (DAD-IS-MoDAD) and are also available at site http://dad.fao.org/dadis/data/molecula/index.html. These are the most popular and versatile genetic marker with myriads of applications in population genetics, conservation biology and evolutionary biology due to co-dominant transmission, locus-specific nature, high information content, relative abundance with uniform genome coverage and higher mutation rate than standard. These markers have been used to measure genetic diversity, gene flow, migration and effective population size in livestock breeds. Besides genetic diversity, co-ancestry and kinship between breeds, past genetic bottlenecks and parentage verification are some other parameters that can be determined through the use of neutral microsatellite markers.

Microsatellites are simple sequence tandem repeats (SSTRs) and the repeat units are commonly di-, tri- tetra- or pentanucleotides. For example, AC_n, where the two nucleotides A and C are repeated in bead-like fashion a variable number of times (n could vary between 8 and 50). The dinucleotide repeats -GT and CA- are believed to be the most common microsatellites within vertebrates. These are prevalent in the non-coding regions of the DNA, although a few human genetic disorders are caused by (trinucleotide) microsatellite regions in coding regions. Flanking region on each side of the repeat unit consists of "unordered" DNA.

These are critical for designing locus-specific primers to amplify the microsatellites with PCR (Polymerase Chain Reaction). That is, for a stretch of 30-50 bp unordered DNA, the probability of finding that particular stretch more than once in the genome becomes vanishingly small (consider the four nucleotides occur with equal probability, then the probability of a given 50 bp stretch is 0.25^{50}). In contrast, a given repeat unit (say GT_{18}) may occur in thousands of places in the genome. The combination of widely occurring repeat units and locus-specific flanking regions is exploited for finding and developing microsatellite primers. The primers for PCR can be sequences from these unique flanking regions. By having a forward and a reverse primer on each side of the microsatellite, it is possible to amplify a fairly short (100 to 500 bp) locus-specific microsatellite region. Despite the growing competition from new genotyping and sequencing techniques, microsatellite markers are still regarded as the most powerful DNA tools for genetic analysis owing to their several unique characteristics and are globally being exploited to establish genetic profiles of animal genetic resources.

Advantages of microsatellites markers

1. Microsatellite loci are found in large numbers throughout the genome and are highly polymorphic.
2. They are mostly neutral which makes them compatible with the assumptions of most population genetic theories.
3. These markers follow a typical Mendelian inheritance, which usually expresses in a co-dominant fashion and are often multi-allelic giving mean heterozygosity of more than seventy percent.
4. They are PCR-based and there is need of only tiny amounts of biological material.
5. They are suitable for automated analysis.

Uses of microsatellites

Microsatellites are useful markers for a wide range of analysis due to co-dominant transmission, locus-specific nature, high information content, relative abundance with uniform genome coverage and higher mutation rate than standard.

- They serve a role in biomedical diagnosis as markers for certain disease conditions. Microsatellite alleles in these cases are associated (through genetic linkage) with mutations in coding regions of the DNA that can cause a variety of medical disorders.
- They have also become the primary marker for DNA testing in forensics, both for human and wildlife cases. The reason for popularity as a forensic marker is their high specificity. Match identities for microsatellite profiles can be very high (probability that the evidence from the crime scene is not a match with that of the suspect is < one in many millions in some cases).
- In a biological/evolutionary context, they are useful as markers for parentage analysis. They can also be used to address questions concerning degree of relatedness of individuals or groups.
- For captive or endangered species, microsatellites can serve as tools to evaluate inbreeding levels (F_{IS}). From there, we can move up to the genetic structure of subpopulations and populations (using tools such as F-statistics and genetic distances).

- They can be used to assess demographic history (e.g., to look for evidence of population bottlenecks), to assess effective population size (N_e) and to assess the magnitude and directionality of gene flow between populations.
- Microsatellites provide data suitable for phylogeographic studies that seek to explain the concordant biogeographic and genetic histories of the floras and faunas of large-scale regions. They are also useful for fine-scale phylogenies, up to the level of closely related species.

Microsatellite data analysis

Microsatellite analysis is done by individual genetic profile, determining the interrelations between different individuals and evaluating their allele frequency in populations. Microsatellite analysis involves the following steps: i) Sample collection; ii) DNA extraction, purification and evaluation; iii) PCR amplification; iv) Evaluation of amplified fragments by automatic genotyping using capillary electrophoresis and amplicons' fluorescence detection. The resulting products are compared with molecular weight standards that ensure the accuracy and precision of determinations. For a neutral marker, the degree of polymorphism is proportional to the mutational rate. Rates of mutations and their effects are important factors in the calculation of genetic distance based on data obtained from microsatellite analysis. Researchers can determine the period of time passed since the separation of two populations or measure the degree of allele transfer between them by applying theoretical models of empirical data obtained. Thus, genetic diversity and phylogenetic relationships between different populations can be assessed. Genetic diversity is determined by multiple alleles and genotypes established for a study group (population, species or species group). According to the Hardy-Weinberg equilibrium principle, allele frequencies and genotypes in a population remain constant - meaning that they are in equilibrium - from generation to generation, except in the case of outside influences. These influences could be controlled by mating, mutations, small populations, genetic drift and gene exchange. Hardy-Weinberg equilibrium is extremely important in conservation studies and genetic evolution. It provides basic information to identify random mating, occurrence of mutations or inbreeding effects. Deviations from expected values for the Hardy-Weinberg equilibrium can have several causes, such as low population size, inbreeding, or presence of null alleles among populations that can lead to an excess of false homozygosity. Analysis of a larger number of loci can provide an accurate picture of genetic diversity because each locus will contain an independent history of the population which depends on the proportion of mutations, the genetic drift or migration.

Heterozygosity is one of the most important parameters that can give us information about diversity and even the history of a population. Values vary from 0 (absence of heterozygosity) and 1 (where a large number of alleles have the same frequency). Higher values of average heterozygosity are equal to high levels of genetic variation. Conversely, if the average heterozygosity is reduced, genetic diversity is also reduced. Over time, as a result of human intervention, many populations of animals around the world have been fragmented. The impact of fragmentation on genetic diversity, inbreeding and extinction risk of these populations depends largely on the gene exchange occurring between different subpopulations. Subsequent to the fragmentation of a population, there are gradual differences between these sub-populations. The degree of differentiation between different sub-populations is directly correlated with inbreeding coefficients in both populations and inter-populations. The inbreeding coefficient of the whole population (F_{IT} = Factor of Inbreeding in the total population) can be divided into: i) inbreeding coefficient of individuals in relation to a subpopulation which includes individuals (F_{IS} = Factor of Inbreeding relative to subpopulation); ii) inbreeding coefficient due to differences between sub-populations, to the whole population at baseline (F_{ST} = Factor of Inbreeding Relative to Total Population). F_{ST} is decreased when the exchange of genes between subpopulations is large. If the exchange rate drops, F_{ST} grows and subpopulations are separated and distinguished from one another. Regarding F_{IS}, a positive value shows a deficit of heterozygosity. The deficit is even greater as the value obtained is higher, which means a high level of inbreeding. In general, the values obtained for F_{IS} vary between -1 (no inbreeding) to 1 (complete identity).

Construction of phylogenetic trees based on microsatellite frequencies

To study the phylogenetic relationships between closely related species or populations, microsatellites have been the markers of choice for a long time. Based on their frequency, genetic distances are calculated and are subsequently used to build phylogenetic trees. Some of the genetic distances used are the following: the Nei standard distance, the Cavalli-Sforza distance and the Reynolds genetic distance. The analysis of phylogenetic relationships is based on the definition of that sequence of steps (algorithms) which can build the best phylogenetic tree. A phylogenetic tree is the graphic representation of the phylogeny of a group of organisms. To obtain phylogenetic trees, the following algorithms must be followed: obtaining microsatellites data, comparing the data, selecting optimal phylogenetic methods, constructing and evaluating the trees.

2. Mitochondrial DNA based markers

MtDNA is another popular marker for resolving molecular diversity, evolutionary relationship and historical biogeography of species. Mitochondrion is the energy power plant of the cell and is a membrane-bound cytoplasmic organelle that has its own DNA. Many mitochondria are present in each cell, and the average number of mtDNA copies per cell is 500. These mitochondrial DNA molecules can differ from one another within a single mitochondrion, cell, or individual- a state referred to as heteroplasmy. The animal mtDNA is a circular molecule containing 22 tRNAs, 2rRNAs and 13 protein coding genes. The non-coding or control region (also referred to as D-loop or displacement loop), helps in replication and transcription of the mtDNA. The D-loop region is characterized by highly polymorphic regions known as hypervariable region I and II (HVI and HVII) which have proven to be useful for study of evolutionary history of vertebrates. The remarkable properties of the mtDNA which include maternal mode of inheritance, high copy number, single copy genes, rapid rate of evolution without any recombination and high variability between and within species render it suitable for phylogeographical studies. DNA barcoding for taxonomic identification is another application of mtDNA which is based on the principle that a short standardized sequence can distinguish individuals of a species because genetic variation between species exceeds that within species.

In the standardized DNA barcoding approach, identification of a specimen as belonging to a certain animal species is based on a single universal marker i.e the DNA barcode sequence (cytochrome c oxidase I). Mitochondrial DNA polymorphisms have been used to elaborate genetic variations between species, within species and within a breed. The evolution of mtDNA in various animal species has been studied using primers designed from the conserved regions.

Advantages of mitochondrial DNA markers

1. Mitochondrial genes are single copy genes, obviating the need for comparisons of paralogous genes.
2. The haploid mtDNA, carried by the mitochondria in the cell cytoplasm, has a maternal mode of inheritance (individuals inherit the mtDNA from their dams and not from their sires).
3. Uniparental inheritance also reduces the effective population size of mitochondrial genes, which means that variants tend to be fixed more quickly between speciation events.
4. High mutation rate without any recombination.
5. Mitochondrial DNA also has a much higher rate of base substitution than most nuclear genes.
6. Ease of amplification.
7. Nearly neutral nature as mitochondrial-encoded genes involved in basic metabolic functions (respiration), are less likely than other genes to be involved in adaptive processes.
8. High variability between and within species.
9. Mitochondrial DNA also has a much higher rate of base substitution than most nuclear genes.
10. Mitochondrial gene content is strongly conserved across animals, with very little duplication, no intron, and very short intergenic regions.
11. Variable regions (e.g. the control region) are typically flanked by highly conserved regions (e.g. ribosomal DNA), in which PCR primers can be designed.

Applications of mitochondrial markers

Insights into the process of livestock domestication have been provided by analyzing the polymorphisms in the sequence of the hypervariable region of the D-loop or control region of mtDNA. It has been possible to identify the wild progenitors of domestic species and also establish geographic patterns of genetic diversity. Multiple maternal lineages have been identified in cattle, goats, sheep and Asian chickens. For instance, diversity at the control region of mitochondrial DNA has been widely used to assess the origin, phylogeny, maternal lineages and population structure of sheep breeds around the world. Five maternal lineages (haplogroups A-E) have been reported to have contributed in the process of domestication of this species. These include two major (A and B) and three minor (C, D, and E) maternal lineages. Haplogroup A is of Asian origin including Chinese sheep, haplogroup B of European origin, while haplogroups C, D and E originated in the Near East. Detection of hybridization between livestock species or subspecies is another important application of mtDNA markers.

Recently, Sharma et al., 2020 evaluated the genetic structure of 34 Indian sheep breeds/populations representing all the four different agro-ecological zones of India based on the mtDNA D loop sequence. Substantial haplotype diversity, presence of three maternal haplogroups (A, B, and C) and signals of population expansion were evident in the studied populations.

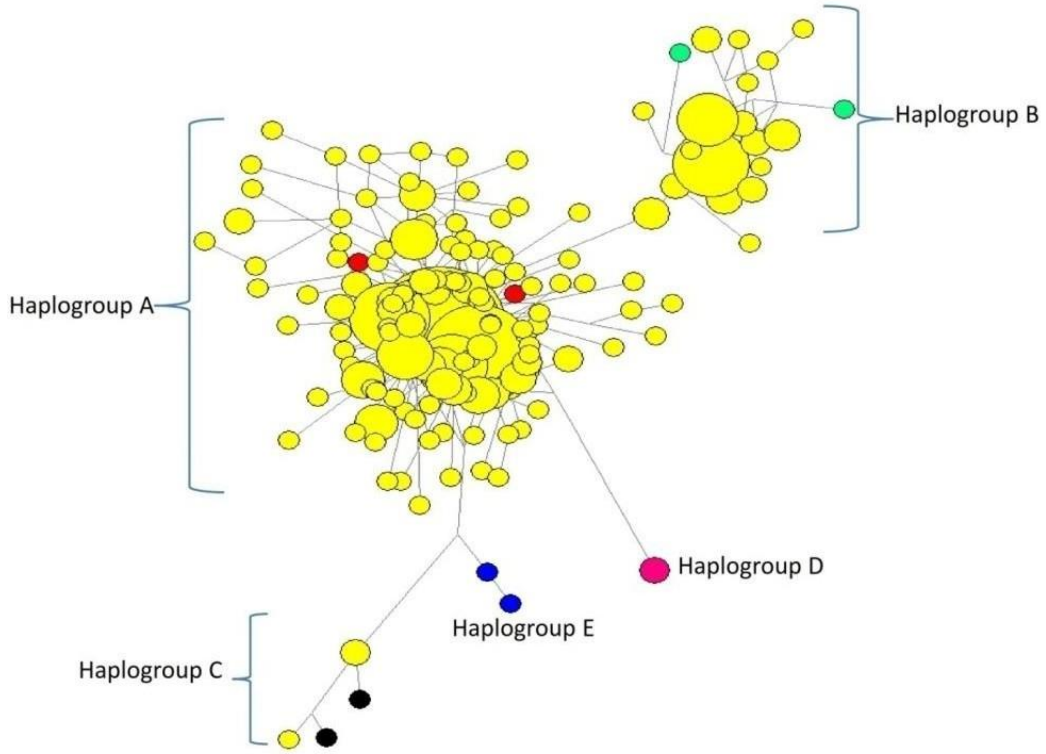

Figure 1. Median-Joining network depicting relationship of Indian sheep with 5 established haplogroups worldwide

DNA barcoding

The use of mtDNA is particularly associated with DNA barcoding for taxonomic identification and investigation of biodiversity. In DNA barcoding, a short stretch of DNA ('barcode') is commonly used to allocate an unidentified individual to a species. DNA barcoding is based on the principle that a short standardized sequence can distinguish individuals of a species because genetic variation between species exceeds that within species (Herbert et al., 2003) Several studies have demonstrated the efficiency of DNA barcoding in different animal groups. These projects have shown that >95% of species possess unique cytochrome *c* oxidase I (COI) barcode sequences; thus species-level identifications are regularly attained. The Barcode of Life project initiated in 2003, promotes the use of a standardized DNA barcoding approach, consisting of identifying a specimen as belonging to a certain animal species based on a single universal marker: the DNA barcode sequence. A 648-bp region of the (COI) gene forms the primary barcode sequence for members of the animal kingdom (Herbert et al., 2003).

3. Copy number variations (CNVs)

Copy number variations are a form of genomic structural variation, defined by DNA segments ranging from kilobases (kb) to megabases (Mb) in size, exhibiting differences in copy numbers when comparing two or more genomes. They frequently span entire genes leading to different gene copy numbers between individuals, or alter the intron/exon structure of genes by disrupting exons or fusing genes together. CNVs can lead to striking phenotypic consequences by altering gene dosage, disrupting coding sequences, or perturbing long-range gene regulation by position effects. This variation may either be inherited or caused by *de novo* mutation. CNVs are present genome-wide in the genome of humans as well as farm animals including cattle, sheep, goat, horse, pigs and poultry. About 5% to 16% of the human genome is covered by CNVs. Although CNVs are far less numerous than SNPs, they affect from 1 kb to several mega bases of DNA per event, adding up to a substantial fraction of the genome which is several magnitudes larger compared to SNPs. In terms of the total number of DNA base-pairs, CNVs are responsible for more heritable sequence differences (0.5-1%) between individuals than SNPs (0.1%). Some estimates suggest that up to 12% of the genome may be variable in copy number, and that the cumulative result of CNV inheritance may constitute more than 10% of the genome. Next generation sequencing approaches have made it possible to systematically identify CNVs at genome-wide level. CNVs can improve our understanding of genetic variation and are an important tool for deciphering the heritability of complex traits. They are emerging as a promising resource for exploring the genetic basis of phenotypic variation within and among breeds. Therefore, CNVs are increasingly being recognized as important and abundant source of genetic variation and phenotypic diversity.

4. Single nucleotide polymorphisms (SNPs)

SNPs are variations in the nucleotide present at a specific position on a chromosome. A position is referred to as an SNP when it exists in at least two variants and all the three genotypes are observed in a population. For such a base position with sequence alternative within genomic DNA to be considered as an SNP, the least frequent allele should have a frequency of 1% or greater. SNPs are becoming especially important as markers because they are very stable, i.e. have very low mutation rates; and they can be amplified with PCR. SNP can occur in genes (promoter, exons, or introns) or between genes (intergenic regions) but most are in the non-coding regions, which comprise most of the chromosomes. SNPs are inherited as co-dominant traits and are especially useful as genetic markers because of their very low mutation rate. These markers offer several advantages over other types of DNA marker systems and are rapidly becoming the markers of choice for many applications in genome analysis due to their abundance (especially important in linkage disequilibrium based mapping approaches) and also because high throughput genotyping methods are being developed for their analysis. The additional advantage offered by this approach lies in the phylogenetic information gathered through sequence variation analysis that allows drawing inferences on allele and population history that cannot be gathered with any of the other marker systems available. SNPs are also evolutionarily stable (i.e. do not change much from generation to generation) making them easier to follow in population studies. There are four major reasons for the increasing interest in the use of SNPs as markers for genetic analysis.

- They are prevalent and provide more potential markers near or in any locus of interest than other types of polymorphism such as microsatellites. For example, in human genomic DNA, there appears to be an SNP approximately every 1000 bases.
- Some SNPs are located in coding regions and directly affect protein function. These SNPs may be directly responsible for some of the variations among individuals in important traits.
- SNPs are more stably inherited than the microsatellites, making them more suitable as long term selection markers.
- SNPs are more suitable than microsatellites for high throughput genetic analysis, using DNA microarray technology or next generation sequencing approaches.

5. SNP arrays

Livestock genomics research has ventured into a new era with the introduction of SNP arrays for genetic diversity studies and genome wide association analysis. Availability of SNP arrays for different species, their accuracy, and cost-effectiveness have ensured that SNP genotyping is one of the most preferred approaches nowadays to investigate molecular diversity. The genomic data obtained for different breeds/populations of a species can be assessed to know the population structure as well as admixture level between different populations. It is also possible to detect selection signatures related to molecular mechanisms associated with various production and adaptation traits in different breeds. Some of the SNP microarrays developed for the above mentioned applications are depicted in Table 1.

Table 1. SNP chips developed worldwide for different livestock and poultry species

Species	SNP chip	Number of markers
Cattle	SNP50 v.1	54001
	GGP Indicus 50 K	54,791
	GGP *Bos indicus* HD	74,000
	Axiom Bos1	6,48,855
	Axiom Bovine	54,560
	Illumina Bovine HD 777 K	7,77,962
Buffalo	Axiom Buffalo	90,000
Sheep	SNP50 v.1	54,241
	Axiom Ovine 60 K	60,000
Goat	SNP50 v.1	53,347
	Axiom Caprine	54,236
Pig	GGPLD v.1	10,241
	SNP60 v.1	62,163
	GGP Porcine HD	70,000
	Axiom Porcine HD v1	6,58,692
Horse	SNP50 v.1	54,602
	Axiom Equine	6,70,796
Poultry	Axiom Chicken	5,80,961
	Axiom Turkey	6,43,845

Some studies have been carried out in Indian livestock for assessing the genetic diversity using the SNP genotyping arrays. For instance, the Bovine High-Density SNP has been utilized to unravel the diversity and linkage disequilibrium (LD) in Gir, Sahiwal, and Tharparkar cattle, yielding valuable information on various diversity parameters. The performance of different SNP arrays such as the Illumina BovineSNP50 BeadChip (50 K), GGP *Bos indicus* HD Array (74 K), and the Illumina BovineHD BeadChip (777 K) has been evaluated in four cattle breeds of India, including Sahiwal, Kankrej, Gir, and Red Sindhi, two *Bos taurus* breeds (Holstein and Jersey) as well as crossbred cattle. More polymorphic SNPs in Indian cattle were observed when they were genotyped with GGP *Bos indicus* HD Array, highlighting the issue of SNP ascertainment bias in the Illumina BovineSNP50 array. Thus, a need was felt to design SNP chips for the indigenous livestock. Consequently, the research efforts at ICAR-NBAGR, Karnal enabled the development of SNP arrays for Indian livestock species, which include high density chips for chicken, pig, horse, dog, and yak. Medium density chips have been designed and validated for the dromedary and Bactrian camels.

6. Whole genome sequencing

Next generation sequencing has opened new vistas to explore relationship between phenotypic and genetic diversity at genome wide scale with high precision and resolution. The complete genomes of most livestock species have been sequenced and the information is available in the public domain. The enormous wealth of data that is easily accessible has enabled the researchers across the globe to identify genetic variants at the pan-genome level. It has now become possible to delineate genomic regions that are linked to the traits of economic importance or adaptation. Distinctive genetic patterns known as “selection signatures” can be identified from the high-throughput sequencing data for breeds/traits of interest. The identification of selection signatures helps to unravel the genetic processes contributing to phenotypic differentiation among breeds within a particular species. These advances in livestock genomics have revolutionized our understanding of the genetic architecture of AnGR. Recently, in a review authored by Olschewsky and Hinrichs, 2021, changes of genotyping techniques over time have been discussed based on meta-analysis of published studies from 2005-2020. Interestingly, there has been a huge surge in studies involving SNP arrays and whole genome sequencing for assessing genetic diversity in local farm animal breeds. Although microsatellite markers and mitochondrial DNA are still relevant in the present scenario, their share since 2010 as genotyping approaches has steadily decreased (Figure 2).

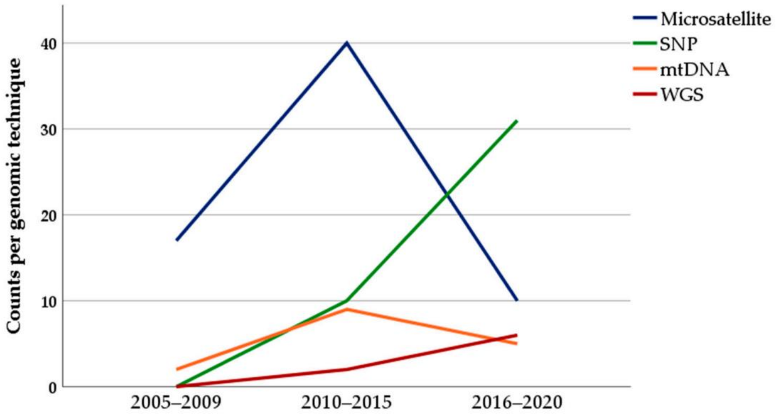

Figure 2. Adoption of various molecular approaches for genetic diversity studies in AnGR (2005-2020) based on 133 published studies

Conclusion

Indian subcontinent is home to diverse livestock germplasm but this vast biodiversity is facing the threat of erosion and dilution. So the need of the hour is to spell out clear cut conservation strategies for our precious and irreplaceable germplasm. A major stumbling block in formulation and implementation of conservation, breeding and management policies for indigenous animal genetic resources is the lack of information regarding their current genetic status. The amount of genetic divergence between populations is regarded as a major criterion for deciding their uniqueness and therefore prioritizing their conservation. Therefore, an understanding of the genetic richness is imperative to conserve our breeds. Genetic markers are useful and robust tools for analysis of genetic and functional diversity of animal genetic resources. Genetic markers for breeding and selection promise greater opportunities for improvement of farm animals.

Suggested readings

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Selection and evaluation of breeding bulls under genetic improvement and conservation programs

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Selection is one of the important tools used for improving the productivity of animals in the population. It is a favour by which the breeder permits the particular genotype to leave its progeny more in the population as compared to the average number of population. Ever since domestication, farm animals have been undergoing human-managed selection. In the beginning, there were no systematic breeding programs and probably, selection was limited to the docility and manageability of animals. But in the last 60 years breeding programmes have focused on the genetic improvement of production traits especially the milk yield in dairy cattle. This has resulted in the improved production of animals which was one of the greatest achievements of the country. Implementation of many developmental and breed improvement programmes in the past few decades had led India as the leader of milk production with an annual output of about 209.96 million tonnes of milk during 2020-21. However, the milk productivity of Indigenous/non-descript cows is very low. The ever growing human population of the country demands increase in the livestock production. Thus, it is inevitable to improve the productivity of the large population of indigenous cattle breeds. To achieve this, many developmental or breed improvement programmes are implemented in the country for their productivity enhancement and conservation for future use. Selection and mating systems are two basic tools mainly available with the breeders for bringing the genetic improvement in the population.

Importance of bull selection

Bull selection presents an important opportunity to enhance the profitability of the dairy enterprise. Bulls might make up only about 4% of a breeding herd, but they provide 50% of the genetic composition of the calves. With the advent of Artificial Insemination (AI) technology for breeding the females, the genetic contribution of a bull to the next generation has increased significantly. A good bull can produce on an average of 40000 - 45000 calves in its lifetime through AI against 400-450 calves in its life time (5-6 years) through natural service. Genetic gain for a trait in a population can be improved by altering four factors; (1) increasing the genetic variation in the population, for which we have relatively little control, (2) decreasing the generation interval by selecting younger animals as parents of the next generation, (3) increasing the accuracy of selection which is reflected by the reliability of each animal's genetic evaluation as well as the accuracy of the underlying genetic evaluation system and (4) increasing the intensity of selection. The intensity of selection refers to the degree to which the very best animals are used as parents.

Bull selection provides greatest opportunity for genetic change in a population. An informative breakdown of an opportunity for improvement by selection in an organized progeny testing plan given by Rendel and Robertson in 1950, points out the percentage of genetic improvement that can be expected from the following sources:

Path	Improvement (%)
Dams of future herd replacements	6
Dams of future young sires	33
Sires of future herd replacements	18
Sires of future young sires	43

The sire controls the 61 per cent of the improvement by selection, as shown in the last two sire pathways. So the sire is more than half of the herd. Only a small proportion of the potential males are needed with artificial insemination, and a single sire can leave thousands of progeny per year. The increased genetic gain through sire over dam is due to the greater intensity of selection that can be applied amongst male parents followed by the production of large number of daughters for use as replacement stock of the next generation. Bull selection has a permanent change with long-term impact. The favourable or unfavourable effect of a selected sire will remain for a considerable period of time. It also depends on the extend and duration at which the selected sire is used in the herd. Even though each generation dilutes his contribution, it may retain through his grand-daughters and great-granddaughters in the herd a quarter century after last sired calves. The condition becomes more critical, if the selected bull is used for the production of young bull calf. Bull selection is not only important within the herd or breed but also in grading and cross breeding programmes. Extensive programmes for planned progeny testing have been developed using artificial insemination to locate the genetically superior sires. Since so few progeny sires can be used in progeny testing programme, it is extremely important that the procedures used to select young bulls insure that that those with best potential have an opportunity to be progeny tested.

Methods of selecting a young bull

Genetic worth of the bull used as sires determines the amount of genetic progress obtained in dairy cattle over a period of time, so selection of young dairy bulls is an important step in any cattle-breeding programme. The merit of these sires is impacted by the combination of the pedigree merit of parents, number of bulls sampled, speed and accuracy of progeny testing, intensity of selection and the best use of top ranked bulls (Powel *et al.*, 2003). The selection helps to change the mean value of the trait of interest in a given population by increased frequency of desirable genotypes. Therefore, traditional selection of dairy bulls by artificial insemination organizations is based upon pedigree selection and progeny testing. In PT program, the bulls are to be selected and evaluated at their younger age itself for minimizing the generation interval and increasing the rate of genetic gain. Young bulls with outstanding pedigree merit should be put under semen collection at early age itself for distribution of their semen for breeding the animals in the herds enrolled for milk recording, which will help to evaluate them comparatively at an early age (Norman et al, 2003). It is to be noted that the bulls of specific breed should be used according to the breeding strategies for bovines as recommended by Government of India. In indigenous breeds it is recommended for selective breeding where as in non-descript cattle, grading up with improved indigenous breeds and crossbreeding with exotic dairy breeds followed by selective breeding is recommended. For crossbreeding, Holstein Friesian is the major exotic breed, while Jersey is used in less resource full areas and in high altitude areas with comparatively smaller size non-descript cattle. The level of exotic inheritance in crossbreds shall be 50%. Therefore, female crossbred offspring produced through crossing of non-descript with exotic breeds are to be mated with crossbred bulls of 50 % exotic inheritance.

The salient features of national cattle breeding policy are as follows:

1. Crossing or upgrading of low producing non-descript cattle with exotic dairy breeds viz., Jersey and Holstein Friesian.
2. Jersey and Holstein Friesian are the exotic breeds of choice for crossing the respective crossbreds
3. The level of exotic inheritance should be restricted to 50 per cent
4. Genetic improvement of nationally important indigenous breeds of cattle, both for draught and dual purposed through selective breeding in their home tract.
5. Inter se breeding among crossbred cattle using pedigreed or proven bulls.

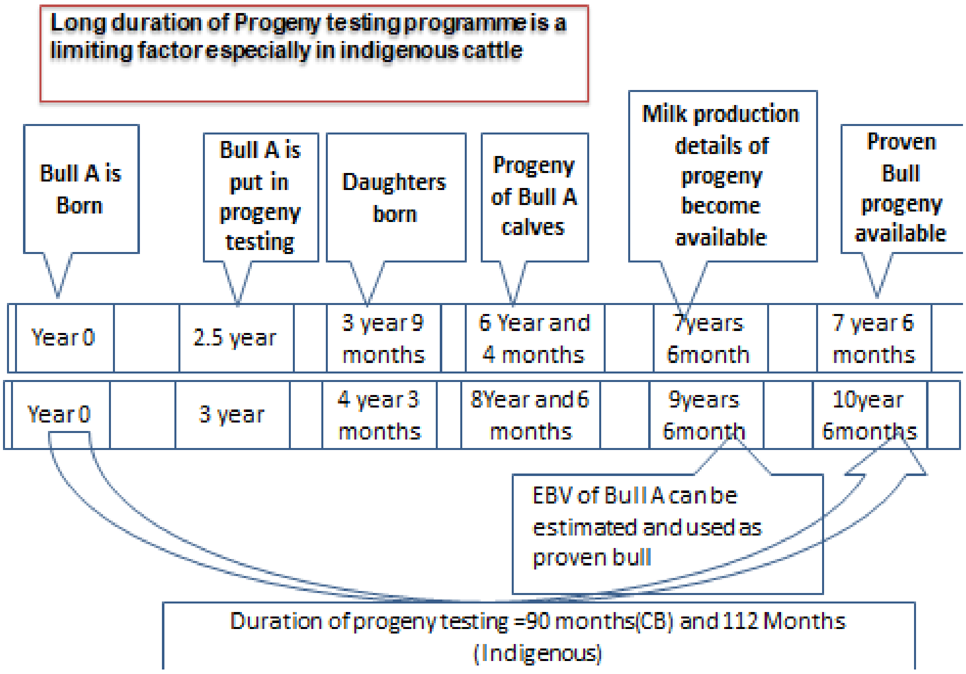


Figure 1. Time line of traditional progeny testing program of crossbred and Indigenous bulls

In practice, the phenotype of an individual and a substantial number of its relatives is recorded and used to compute the likelihood that the individual is transmitting a favourable set of alleles for the trait of interest. Even though the method is still based on phenotypic selection, it identifies variation at loci having a relatively small effect and by the application of suitable statistical methodologies an animal breeder can calculate the average of all genetic loci contributing to a trait as transmitted by the individual, which is termed as an estimated breeding value (Oltenacu and Broom, 2010). In general, for sex limited traits which are not expressed in male, selection is commonly done on the basis of the performance of its dam and daughters. Bulls are chosen first on pedigree proof then used in limited AI services for a second proof on progeny test before being selected for extensive use. The dam's performance based selection of bulls can be done at early age itself, often with the lesser accuracy. In the case of a progeny testing program, bulls produced from a nominated mating between an elite sire and proven bull only will be used. If such bulls are not available and if there are no Progeny Tested programmes for certain breeds, the procurement of bulls should be based on the dam's standard lactation yield. The requirement of dam' lactation yield either in first or best lactation and average fat per cent for different breeds are detailed in Minimum Standards for Production of Bovine Frozen Semen.

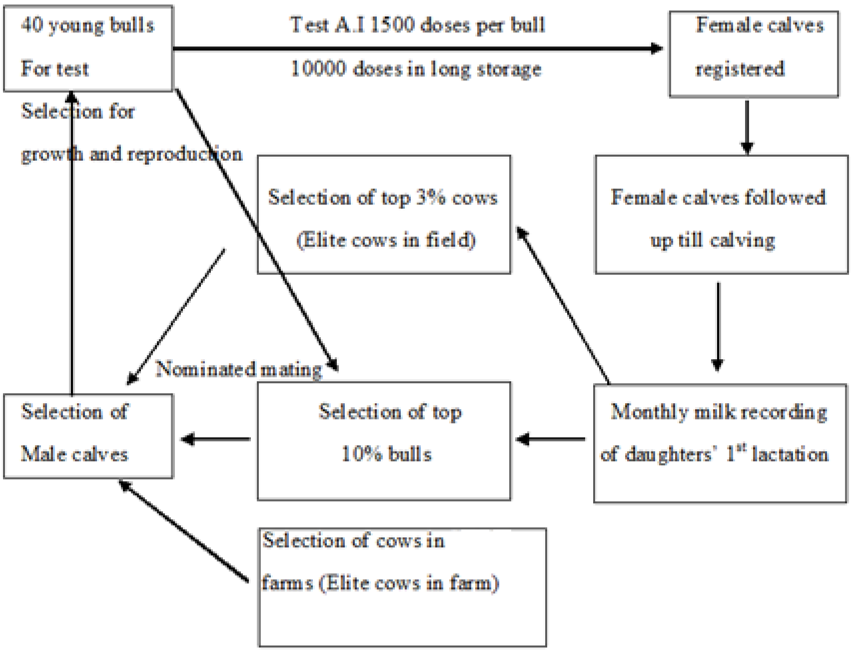


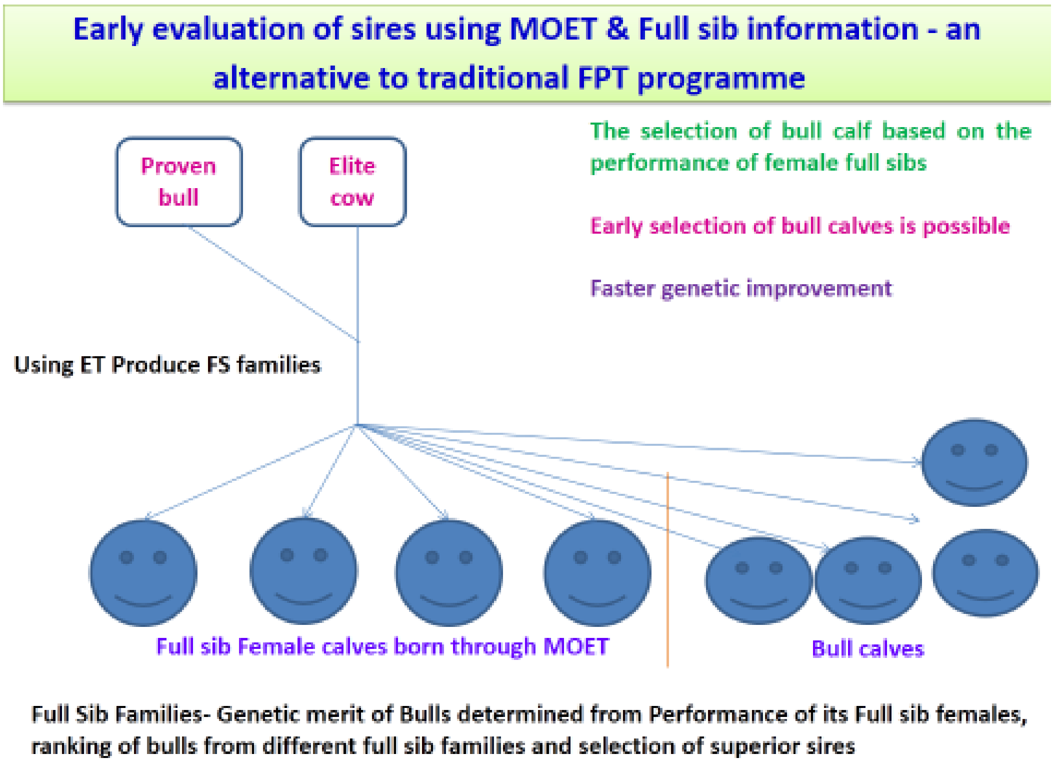
Figure 2. Operational flow diagram of young bull field progeny testing program

Before selection of bulls for a semen station or breeding purpose, a thorough physical examination shall be conducted by an accredited Official / Veterinarian to ensure that the bulls are free from abnormalities and do not display clinical symptom(s) of any infection or any contagious diseases. Screening for chromosomal defects and genetic diseases like Factor XI deficiency syndrome, Bovine Leukocyte Adhesion Deficiency (BLAD) and Citrullinemia is compulsory for all bulls selected for breeding purpose. For HF and their crossbreds, in addition to the above diseases, screening for Deficiency of Uridine Monophosphate Synthase (DUMPS) is also made mandatory to avoid spread of these genetic diseases in the population. This can be carried out at the time of birth itself.

The average daily gain also should be considered. The characteristics of the bull selected should be strictly in accordance with the breed characteristics. The bulls should be free from the infectious diseases such as Tuberculosis, Johne's disease, Brucellosis, Campylobacteriosis and Trichomoniasis. The breeding potential of the bull also should be evaluated by proper breeding soundness evaluation along with the assessment for libido, ability of achieving erection of penis, ease of mounting etc. The proper semen evaluation also should be carried out before the animal is put into the regular semen collection.

Early evaluation of sires using MOET and full sib information as an alternative to field progeny testing programme

Traditionally, in breed improvement programmes, the bulls are evaluated based on average performance of their daughters. The poor performance recording, small herd size, insufficient number of daughter records, non-cooperation of farmers, increased generation interval, etc., are some of the major constraints experience in the implementation of field progeny testing (FPT) programme. In traditional FPT program, the rate of genetic gain achieved is generally very low ranging from 0.5 to 1%. To overcome these difficulties, the MOET and full sib information model can be used as an alternative to the FPT programme. Here the full sib males and females are produced by MOET technique and the performance of full sib sisters is used as the criteria for selection of males.



Early evaluation of sires using MOET & Full sib information - an alternative to traditional FPT programme

The selection of bull calf based on the performance of female full sibs

Early selection of bull calves is possible

Faster genetic improvement

Full Sib Families- Genetic merit of Bulls determined from Performance of its Full sib females, ranking of bulls from different full sib families and selection of superior sires

Use of marker-based technologies in the selection of breeding sire

Advancement in the field of molecular biology and bioinformatics has led to the identification of variations at genomic levels which can be used as marker for selection of individuals for increasing the production. The advent of DNA sequencing and high-throughput genomic technologies together with the automated SNP genotyping resulted in a paradigm shift of selection strategies as the criteria moved from single gene/QTL to genomes, which can explain the majority of genetic variation in important traits. Molecular techniques allow the detection of polymorphisms or the variations in the specific regions of the DNA that exist among the individuals in the population.

The selection approach based on phenotype of individuals has limited scope to improve lowly heritable traits without adversely affecting production. In general, the reproduction and fitness traits are lowly heritable. Additionally, Marker Assisted Selection could be used to select the most desirable phenotypes affected by non-additive gene action or epistatic interactions between loci. Also it enables to select the breeding stock at a very early age. In Marker-assisted selection (MAS), the relative breeding value of an individual is estimated using the genotypes of markers associated with the trait. The era of genomics also brought various ways to know the full DNA sequences of animals and estimation of animals breeding value based on genotypic information became so relevant. The concept of genomic selection was introduced by Meuwissen *et al.,* 2001, which is a form of marker-assisted selection in which genetic markers covering the whole genome are used so that all QTL are in linkage disequilibrium with at least one marker. Advances in whole genome sequencing and development and utilization of high density SNP arrays made the genomic selection a reality. Implementation of genomic selection is on the base of conventional breeding techniques where recording of pedigree and phenotypic traits is very essential and routine. The main advantages of genomic selection are that it can be implemented very early in life, as there is no phenotypic information is needed once the validation of prediction equation is over. Further, it has the advantage of selecting individual of any sex for the traits recorded in the reference population. It especially provides better selection accuracy while reducing the generation interval, thereby increasing the intensity of selection.

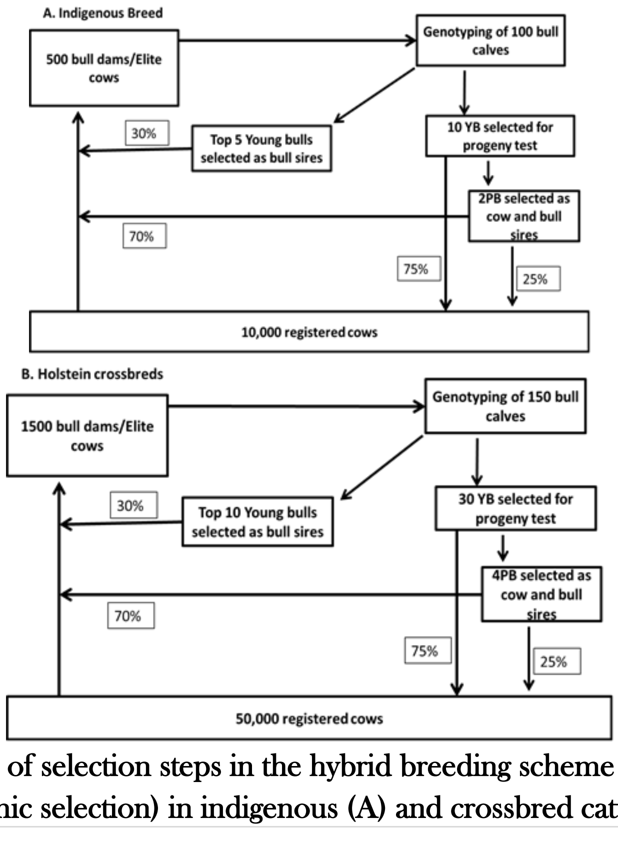


Figure 3. Illustration of selection steps in the hybrid breeding scheme (progeny testing and genomic selection) in indigenous (A) and crossbred cattle (B)

Schaeffer (2006) showed that genomic selection can double the genetic gain per year in dairy cattle with reduction of more than 90% costs for proving bulls. As the cost of sequencing decreases to a level where sequencing of each and every individual become affordable, whole genome data can be used in genetic evaluations. The a simulation study conducted by Meuwissen and Goddard (2010) revealed a 40% gain in accuracy of predicting genetic values by using the sequencing data over the data from 30,000 SNP arrays alone. The whole-genome sequence data analysis helps to predict the Genomic Estimated Breeding Values (GEBVs) of individuals more accurately.

Selection of bulls under conservation programs

The Indigenous cattle population has either decreased or diluted due to the implementation of large scale crossbreeding program in the country. In some of the breeds the size has reduced alarmingly warranting immediate attention to conserve the unique traits like disease resistance, heat tolerance, feed conversion efficiency, draftability etc., which makes them economically viable. In such cases, the bull selection program should also focus on maintaining the breed characters in addition to the maintenance of the genetic variability and other economic viability. The bulls true to the breed should be selected and used for breeding the females. Both *in-situ* and *ex-situ* conservation programs are to be followed separately or in combination. Storage of semen, ova, embryo, DNA, somatic cells etc., of at least twenty five unrelated animals of each sex are some of the ways by which we can conserve the valuable germplasm.

Evaluation of breeding bulls

Sire evaluation is one of the most important aspects of dairy breed improvement programme as the contribution of male is higher than the female for the overall genetic improvement of a trait. In addition to this, very intense selection can be made in males as very few are needed for breeding purpose. Artificial insemination technique has made easy to evaluate sires more effectively due to its wider use in a shorter span of time at multiple locations that ultimately lead to produce more number of progenies. Thus, the primary aim of animal breeders is to develop appropriate methodology for sire evaluation to bring about fastest possible genetic improvement in desirable traits. The simplest method of sire evaluation started with the use of the average performance of the daughters (simple daughter average index) and till today the average performance of daughters is considered as the major criterion in the evaluation of breeding bulls. Nearly for more than 60 years (from 1900 to 1960s) the daughter information was mainly included in the evaluation of breeding bulls. From 1925, the information on the dams was also considered in addition to the daughter's performance for the genetic evaluation of sires. Later, the information on contemporaries, herd mates and herd were also included to improve the accuracy of estimating the expected breeding value of the sire. The advances in computational power and improvement in the evaluation methods have helped to estimate the genetic merit of the bulls at higher accuracy by reducing the difference between the actual and expected breeding values. Some of the advanced methods of sire evaluation proposed by different workers are described below:

Linear model techniques

Robertson and Rendel (1954) initially proposed the least squares procedure for determining the genetic worth of sires. The procedure was based on the principle to minimize the error variance after adjusting the data for various non-genetic or environmental factors. Cunningham (1965) described the method for obtaining weighted least squares estimates of sires based on non-orthogonal data of progeny test records, where AI was practised. He reported that it was possible to classify the sires into different groups much earlier at the younger age before proofs were completed. Harvey (1966) gave the concept of least squares analysis for non-orthogonal data. In the least squares analysis, the effect of sire may be considered as random to determine its genetic merit.

The linear models should satisfy the following assumptions:

1. The dependent or response variable should follow the normal distribution
2. The variance should be homogenous
3. The sample points should be independent
4. The dependent and independent variables should have linear relationship
5. The error should be normally and independently distributed with mean zero and variance σ^2_e

   The general form of linear model is as follows:

   $Y_{ijkl} = \mu + H_i + G_j + S_{jk} + e_{ijk}$

where

Y_{ijkl} represented the age-month adjusted first lactation production by the 1^{th} daughter of the k^{th} sire (S) in the j^{th} group (G) made in the i^{th} herd-year-season (H) and μ is herd average. The μ, H_i and G_j were considered as fixed effects, and the S_{jk} and e_{ijk} were considered as random with means zero and variance-covariance matrices as $I\sigma^2s$ and $I\sigma^2e$, respectively.

The different methods used for simre evaluation are

1. Least squares method (LS)
2. Simple regressed least squares (SRLS)
3. Best Linear Unbiased Prediction (BLUP)
4. Restricted Maximum Likelihood Method (REML)
5. Random Regression Model (RRM):

Use of animal model in breeding value estimation:

Henderson in 1952 gave the concept of animal model in which the records and relationships of all the animals in a herd will be used to evaluate each animal. He explained the advantages of using relationship among sires in addition to some female ancestors.

1. Increases the prediction accuracy particularly for sires with few or no progeny.
2. Helps in early evaluation of sires through the use of sires of dam, parental sisters of dam and their own parental sisters.
3. The genetic trends and genetic differences among populations or sub populations can be estimated from fewer groups.

He also enumerated the advantages of utilizing all known relationships among animals as it increase the accuracy of selection, the genetic trend can be accounted for most efficiently and necessity of grouping can be eliminated.

The sire model utilizes the performance records of daughters only and do not include the information of dams and relationship between females and so the predicted estimates may be biased due to non-random mating or selection of cows. On the contrary, animal model utilizes the information on all the animals included in the analysis and evaluates both the sires and cows simultaneously. In the animal model, animals without records are also evaluated from the performance records of their relatives. Thus, the animal model takes into account all the available information and relationships and adjusts the records for non-random mating, selection bias to increase the accuracy of prediction.

Conclusion

Bulls are considered as half of the herd and hence identification of genetically superior bulls is of utmost importance. The traditional progeny testing programme allows the transmission of superior germplasm in a large population, which was one of the major contributory factors in the increase in the world milk production. Incorporation of broader selection goals giving due weightages for production, health, fertility and longevity traits in the breeding strategy will be suitable for a sustainable breeding programme. The application of genomic selection can also augment the selection programmes. The top ranked/progeny tested bull semen should be used for nominated mating to elite females to produce young bull calves. These young bull calves will be used in the breeding program for the genetic improvement of cattle.

Methodology for phenotypic characterization of livestock and poultry genetic resources through field survey

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Characterization is defining the phenotypic qualities/characters of an individual or group of individuals or a population. The special character which is confined to an individual or a group establishes its uniqueness. In livestock sector each species is having specific characters. Within species also a group of individuals, which have uniform traits, mate true to produce similar individuals with similar set of characters. Such group is designated by 'breed'. The "World Watch List for Domestic Animal Diversity" report (3rd ed.) of FAO documents more than 6400 breeds of livestock belonging to 30 domestic species. FAO's (1999) broad definition of the breed concept states that "either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity".

Hence, "A domestic animal population may be regarded as a breed, if the animals fulfil the criteria of

(i) being subjected to a common utilization pattern
(ii) sharing a common habitat/distribution area
(iii) representing largely a closed gene pool and
(iv) being regarded as distinct by their breeders" (FAO, 2012).

The term "breed" is used in phenotypic characterization to identify distinct animal population and this diversity in animal genetic resource population can be measured in terms of inter-population diversity (between breeds), intra-population relationship diversity (within breeds) and inter-relationships between populations. This diversity of domesticated livestock and poultry breeds was developed due to years of evolution within the specific ecological niche. Several complex and interactive factors like human needs, adaptability of a species, agro-climatic conditions, selection and animal husbandry practices ultimately culminate in the emergence of a breed. Several valuable strains of more efficient and high producing breeds/farm animals have also been developed over the years to meet the ever increasing demand for animal products. These indigenous livestock breeds possess unique genes and combinations of genes which are responsible for different phenotypes like difference in body confirmation, disease resistance, stress resistance, quality animal products, feed efficiency and many more traits of economic importance, which are studied/characterized through phenotypic or genetic characterization or combination of both. As FAO states because of a lack of comprehensive information on population fragmentations or substructures and geographical distributions, many animal populations in the developing regions of the world are commonly referred to as “non-descript” or “traditional”. The inventory of breeds in these regions is thought not to be exhaustive, and new breeds continue to be identified.

Survey and identification of breeds Animal Genetic Resource Characterization involves generating information on phenotypic, genetic and historical aspects of a breed under study and the weightage given to each aspect depends on the objective of the study. Phenotypic characterization of animal genetic resources is the practice of systematically documenting the observed characteristics, geographical distribution, production environments and utility of these resources. It also refers to the process of identifying distinct breed populations and describing their physical, body biometry and production parameters within a particular environment where it was evolved. The term “environment” includes not only the “natural” environment, but also management practices, utility of the animals, as well as social and economic factors such as market orientation, niche-marketing opportunities and gender issues. Recording and describing the geographical distribution of breed populations is also makes an integral part of phenotypic characterization. The study unraveling the genetic basis of phenotypes and their inheritance from generation to generation and to establish relationships between breeds are referred to as molecular genetic characterization, which is complementary to phenotypic characterization (FAO, 2011b). The phenotypic and molecular genetic characterization of AnGR is used to measure and describe genetic diversity in these resources which will be a basis for understanding and sustainably utilizing the genetic resources.

Objectives

- To identify new breeds/populations.
- To know the geographical distributions of the breeds/populations.
- To know the status of breeds in terms of population, characteristics, etc. in native environments.
- To document unique characteristics of the breed.
- To identify elite animals to be used in breed improvement/genetic improvement programmes.
- To develop monitoring mechanisms for conservation and sustainable use of the genetic resources.
- To create public awareness regarding the importance of AnGR.
- To document animal genetic resources.

The phenotypic characterization can be taken as two different levels or phases viz.,

a. Primary characterization.
b. Secondary characterization.

Primary characterization- refers to the activities that can be carried out in a single field visit (e.g. measurement of animals’ morphological features, interviews with livestock keepers, observation and measurement of some aspects of the production environment, mapping of geographical distribution).

Advanced characterization- refers to the activities that require repeated field visits which includes the measurement of the productive capacities (e.g. growth rate, milk production) and the adaptive capacities (e.g. resistance or tolerance to specific diseases) of breeds in specified production environments.

Depending on the background information available, phenotypic characterization can be approached in two ways

a. Exploratory approach
b. Confirmatory approach

Exploratory approach shall be undertaken when there is no reliable background information is available for a breed or population. Here the objective of the study shall be to investigate the existence of the breed in the area under study. Whereas the confirmatory approach shall be undertaken when there is some basic information available about the breed identity and area of distribution. The objective of the study shall be to validate the breed identity and to provide systematic descriptions of the breeds. When the secondary information available is insufficient to undertake the phenotypic characterization, preliminary field data on breed identity, geographical distribution and relative significance of the AnGR in the study area needs to be collected. This is to decide whether an exploratory or confirmatory approach is required.

Preliminary data collection activities may include

- Mapping expeditions- a journey has to be undertaken by the survey team to have an idea about the geographical distribution of different population.
- Rapid appraisals – this is to collect information from the local people. This involves discussions in group meetings, discussion with focus groups, semi-structured interviews with individual livestock keepers, key informants and direct observation. Specific techniques like mapping exercises, seasonal calendars', ranking and scoring exercises, transect walks, progeny history etc., can be used to discuss about the local production system with groups or individuals.

Study team

A typical study team might be composed of the following members:

- Lead investigator
- Specialist in livestock production and/or genetics
- Sociologist or anthropologist
- Data management specialist
- Data entry staff
- Data analyst
- Statistician
- Enumerators

Survey Plan

Survey plan should be devised for collecting information from farmer's herds/flocks for phenotypic characterization of breeds. Surveys of breeds/animal types must ensure mandatory recording of the following types of information:

- Demographical and geographical distribution of the breed.
- The native environment.
- Enumeration of breeds in terms of age and sex in a popula¬tion.
- Management practices and utility.

- Qualitative and quantitative characterisation of breeds in relation to morphological traits, production potential and reproductive status etc.
- Qualitative and quantitative description of unique ani¬mals, elite producers and rare or unusual characteristics in certain specimens.

Sampling design

On the assumption that the breeding tract of a breed is spread over adjoining/contiguous districts in one or more states, stratified two stage sampling design can be adopted. Different zones within a district shall be identified which will constitute the different strata. Villages within the stratum would constitute the first unit and houses within the village, the second unit. The survey should be conducted in three districts. Within each district 4 strata should be randomly selected. From each stratum, 5 villages would be randomly selected with a total of 20 villages in the breeding tract.

Work force

Each district would have one supervisor and four enumerators. One enumerator should carry out the survey work in 5 villages of a stratum and each district should be monitored by one supervisor covering a total of 20 villages.

Duration of survey

During first 3 months the data on general information viz. population enumeration, management practices and socio-economic status of the farmers should be completed. During this phase, the households and animals for detailed data recording should be identified. Subsequently, the enumerators would continue recording information on morphological characteristics, performance and utility traits as per the questionnaires. The duration of the survey may be 18 months for small ruminants (sheep and goats) and 24 months for large ruminants.

Demographical and Geographical Distribution

Complete enumeration of selected villages should be done for the purpose of deriving the demographic distribution of the breed. This study should cover the following information: age wise and sex-wise distribution, group-wise enumeration and geographical distribution of the breed. When the complete information is obtained by stratified survey, the data regarding group wise, sex-wise and breed wise total population in the breeding tracts would be enumerated by superimposing the proportion obtained by a survey on the livestock census data.

Production Environment

The field work phase of a phenotypic characterization study is an opportunity both to directly collect data on the production environments of the targeted AnGR populations and to collect data on the socioeconomic profile of livestock keepers. This information should be related to datasets obtained from other sources like geographical distribution.

Data Collection and recording

Data collection and recording on phenotypic traits, production parameters vary between species and also the number of animals available in the breeding tract. Information on Physical traits, feeding, management practices and growth traits have to be collected from different sex and age group animals. In a phenotypic characterization study, four levels of sampling may be required:

Region (applicable only in a country wide characterization)
Study sites or communities within the region targeted by the study
Households keeping the targets species or communities
Individual animals within the sample households

Total number animals to be recorded for different livestock species is given in table1.

Table 1. Data Recording

Species	No. of districts to be covered	Total no. of animals to be recorded
Cattle, buffalo, sheep, goat and pig	3 (covering four randomly selected zones of each district)	3000
Horse and donkey	3 (covering four randomly selected zones of each district)	1200
Camel	3 (covering four randomly selected zones of each district)	1200
Chicken	3 (covering four randomly selected zones of each district)	3000 birds

Group classification, and study coverage for phenotypic characterization of different species of livestock

Cattle and buffalo breeds

Group	Study coverage
a. Calves (up to 1 year)	Physical traits, feeding, management practices and growth traits.
b. Stock (1 - 3 years)	Physical traits, feeding, management practices and growth traits.
c. Milking females	Physical traits and feeding and management practices, production, reproduction and growth traits.
d. Working males	Physical traits, and feeding and management practices and utility.
e. Breeding bulls	Physical and reproductive traits, and feeding and management practices.

Sheep breeds

Group	Study coverage
a. Lamb (1-3 months)	Physical traits, feeding, management practices & growth traits.
b.Young Stock (6-12 months)	Physical traits, feeding, management practices, and

	growth traits.
c. Milking ewes	Physical, productive and reproductive traits, feeding and management practices.
d. Stud rams	Physical and reproductive traits, and feeding and management practices.

Goat breeds

Group	Study coverage
a. Kids (1-3 months)	Physical traits, feeding, management practices & growth traits.
b.Young Stock (6-12 months)	Physical traits, feeding, management practices, and growth traits.
c. Yearlings	Physical and reproductive traits, and feeding management practices and growth traits.
d. Milking Does	Physical, productive and reproductive traits, feeding and management practices.
e. Stud Bucks	Physical and reproductive traits, and feeding and management practices.

Horse and donkey breeds

Group	Study coverage
a. Foal (up to 1 year)	Physical traits, feeding, management practices and growth traits.
b. Young stock (1 - 3 years)	Physical traits, feeding, management practices and growth traits.
c. Adult female (>3Year)	Physical traits and feeding and management practices, production, reproduction and growth traits.
d. Adult male (>3Year)	Physical traits, reproductive traits, and feeding and management practices, utility.

Camel breeds

Group	Study coverage
a. Camel calves (up to 1 year)	Physical traits, feeding, management practices and growth traits.
b. Young stock (1 - 4 years)	Physical traits, feeding, management practices and growth traits.
c. Milking females	Physical traits, feeding and management practices, production, reproduction and growth traits.
d. Adult males Physical	traits, reproductive traits, and feeding and management practices, utility

Pig breeds

Group	Study coverage
a. Piglets (0-2 months)	Physical traits, feeding, management practices & growth traits.

b.Young Stock (2-8 months)	Physical traits, feeding, management practices, and growth traits.
c. Sows	Physical, productive and reproductive traits, feeding and management practices.
d. Boar	Physical and reproductive traits, and feeding and management practices.

Chicken breeds

Group	Study coverage
a. Cockerels (up to 5 months)	Physical traits, feeding, management practices and growth traits.
b. Pullets (up to 5 months)	Physical traits, feeding, management practices and growth traits.
c. Cock (above 5 months)	Physical and reproductive traits, feeding and management practices, growth traits.
d. Hen (above 5 months)	Physical traits and feeding and management practices, utility, egg production traits, growth traits.

Breed Descriptors

The breed descriptor of a breed includes the minimum information in a summarized form so as to describe the breed in all respects. The breed descriptors generally have five major parts, i.e. General description, physical characters, performance traits, physiology of the animal and disease. Under general description the name of the breed, its origin, communities rearing the breed with their socioeconomic status, different kind of management practices including feeding, grazing, housing, breeding and health management, the native tract of its distribution along with the native environment and the population status of the breed is described. Physical characters include the qualitative and quantitative physical traits and biometric observations of the animals belonging to different ages and sex. The performance of the animals is generally recorded in terms of growth, production, reproduction and draft ability of the animals besides these factors, the uniqueness of the animals and adaptive traits should also be mentioned in the breed descriptors. It will also be appropriate, if the photographs of a typical mature breeding male and female is given along with the breed descriptor. National Bureau of Animal Genetic Resources, Karnal, India has developed format for breed descriptors of cattle, buffalo, sheep, goat, horse and pony, poultry, pig and donkey.

Network project on AnGR Characterization in India

ICAR-National Bureau of Animal Genetic Resources (Indian Council of Agricultural Research), Karnal involved in detailed phenotypic characterization of indigenous livestock breeds through a network approach involving state veterinary/agriculture universities, state animal husbandry departments and other NGO's by providing funds and technical program.

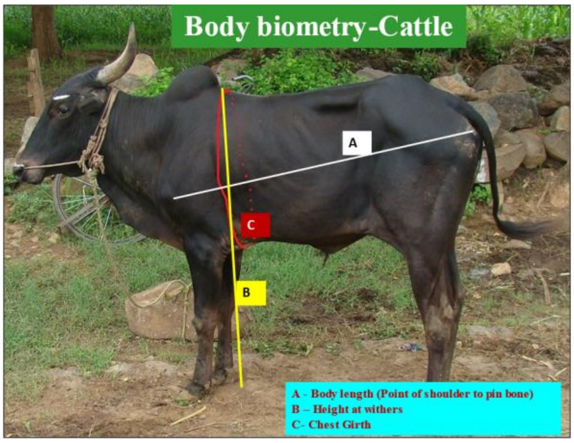
Documentation of Livestock breeds Biodiversity in India

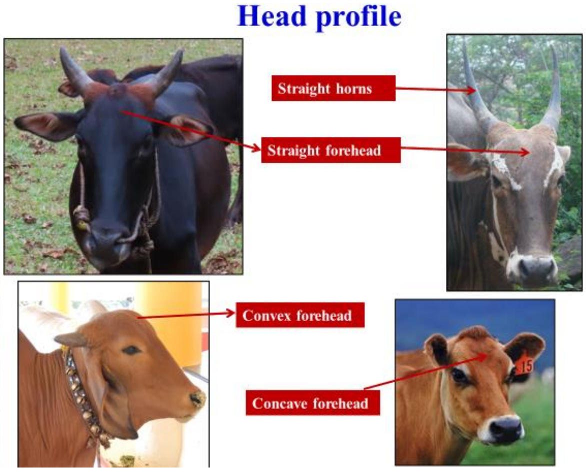
ICAR-National Bureau of Animal Genetic Resources, Karnal has been authorized for registration of all livestock and poultry breeds of the country. Until now 212 breeds belonging to cattle, buffalo, sheep, goat, horse & ponies, poultry, pig, gheese, dog, yak and donkey had been registered with accession number.

Precautions taken during survey for characterization of the breed

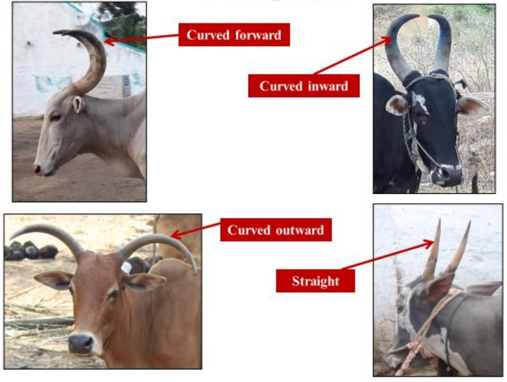
Following precautionary measure should be taken at the time of collecting information during the survey:

- The survey formats should be thoroughly studied before going for the survey.
- Try to get information about management, physical traits, production and reproduction by personal observation before asking them from the farmers.
- The preliminary questions to be asked from the farmers should be of general interest.
- Minimum questions should be asked to the farmers and questions should be designed in such a way that farmers may understand them and correct information may be generated.
- Leading questions should be avoided.
- Survey visits may be made during the early hours of the day.
- Make informal discussions with the farmers and some problems may be removed regarding feeding, breeding or disease control measures.
- While taking the measurements of animals, it should be well restrained on dry and kachcha ground floor and the animals should be squarely placed with straight head.
- All the measurements should be accurately taken and immediately recorded.
- After completing the survey of the village, try to have a meeting with the farmers and the livestock owners so as to know the traditional husbandry practices and ground level realities of animal husbandry in the village.



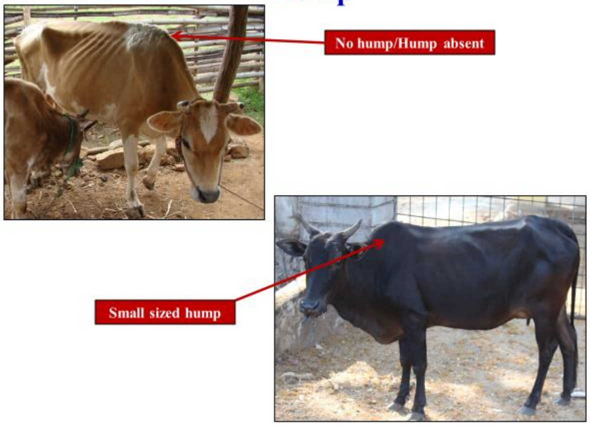


Horn pattern

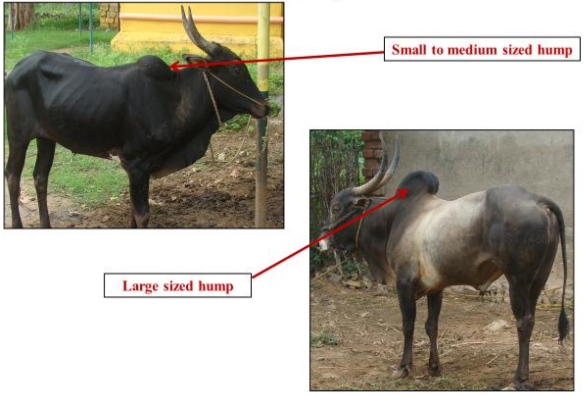


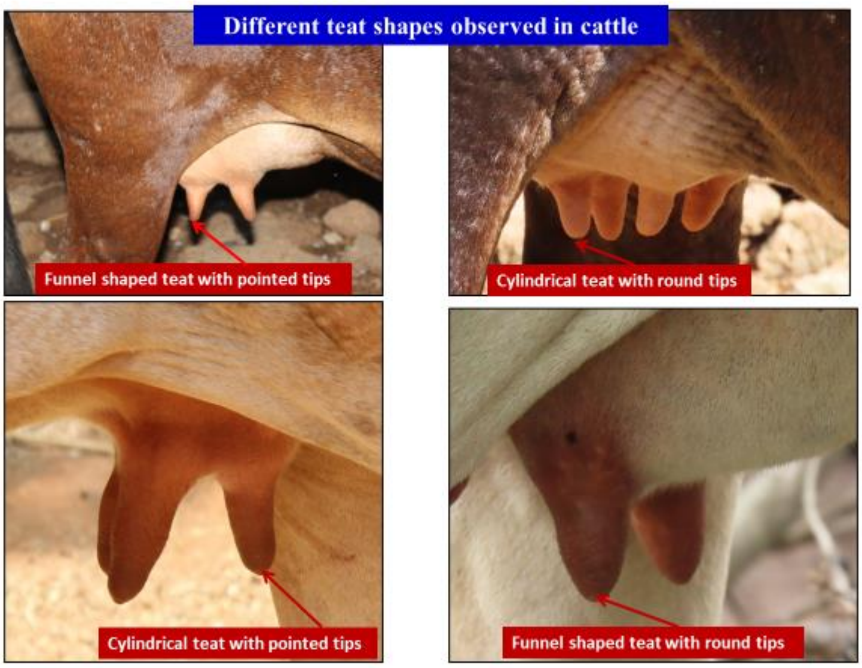
Different ear orientation

Hump



Hump




Different teat shapes observed in cattle

Prioritization of breeds for conservation

Conservation of livestock breeds is an act of preserving, protecting, management and improvement of breeds for present and future need of human beings. Before initiating the process of conservation the first and foremost step needs to be consider is the population structure of any particular breed which includes the cultural or historical value of the breed, population dynamics in the past, geographical distribution of the breed within the country, effective population size, number of breedable male and female for any particular breed genetic variability within the breed, relative value, unique traits and the market preference of the breed. The major five factors considered for prioritizing the breeds for conservation can be

- Population size
- Change in population size
- Geographic distribution
- Presence of formal breeding programmes
- Farmer satisfaction.

Other criteria may also be included like amount of cross-breeding, ratio of male to females, presence or absence of marketing facilities etc., and accordingly the fractional value should be assigned.

Breed risk classification

The assessment of risk status of livestock breeds or populations is an important factor in planning of AnGR management, conservation and genetic improvement. This will tell the policy planner and stakeholders whether, and how urgently, actions need to be taken for conservation. Considering various aspects, following categories has been evolved for risk classification of a livestock breed. These definitions can be further refined in future, if needed. Department of Animal Husbandry, Dairying and Fisheries, Govt. Of India started breed wise census for livestock and poultry species which also provides the sex and age wise counts also. The information available in the Livestock census may be utilized for calculating the effective population size and there by assessing the rate of inbreeding then keeping other factors into consideration the risk status of the breed may be defined. The effective population size (Ne) and rate of inbreeding (▲F) are interrelated (▲F=1/2Ne). Hence, two major criteria may be followed for evaluating the risk status of a breed

Demographics

Genetic parameter (Ne)

The breed risk status can be classified as under:

Extinct (any of the following condition)

- No breeding males (or stored semen),
- No breeding females (or oocytes) nor embryos remaining.
- No longer possible to easily recreate the breed population.

Critical

Cattle, Buffalo, sheep, goat, horse and camel (any of the following condition)

- Total number of breeding females is less than 500
- Total number of breeding males is less than or equal to approximately 5

Pig and poultry (any of the following condition)

- Total number of breeding females is less than 250
- Total number of breeding males is less than or equal to approximately 5

Endangered

Cattle, Buffalo, sheep, goat, horse and camel (any of the following condition)

- Total number of breeding females is between 5000 and 500.
- Total number of breeding males is approximately between 20 and 5.

Pig and poultry (any of the following condition)

- Total number of breeding females is between 2500 and 250.
- Total number of breeding males is approximately between 20 and 5.

Vulnerable

Cattle, Buffalo, sheep, goat, horse and camel (any of the following condition)

- Total number of breeding females is between 10000 and 5000.
- Total number of breeding males is approximately between 40 and 20.

Pig and poultry (any of the following condition)

- Total number of breeding females is between 5000 and 2500.
- Total number of breeding males is approximately between 40 and 20.

Not at risk

- When population status of the breed is known and does not fall in the any risk categories.

Once the breed risk status has been assigned the prioritization of breeds for conservation needs to be undertaken. All the breeds under risk status may not be considered for conservation. The following steps may be followed for prioritizing the breeds for conservation.

- Assessing the conservation value of the breed
- Subjective prioritization
- Conservation value index
- Formal prioritization

For assessing the conservation value the factors like characterization of a breed, productivity, uniqueness, cultural value, genetic variability within the breed, pedigree, population history, etc., needs to be considered for accessing the conservation value of a breed. Based on the conservation value a subjective ranking of breeds may be done for determining the priority.

Using the conservation value index the breeds may be ranked for its priority for conservation. Under Indian scenario breeds for conservation may be prioritized based on the conservation value calculated using the information on population dynamics (particularly effective population size), socio-economic utility, preferences of the farmers, cultural value of a breed etc., For example Toda buffalo of Tamil Nadu reared by the Toda tribe in Otacamund has its cultural value in terms of its milk and other milk products among the people rearing. Apart from the phenotypic characters, risk of extinction, cultural and social values, the data on molecular genotypes (like genetic diversity within and among breeds, genetic distances, genetic markers on unique characters etc.,) can also be considered altogether to get a single value for each breed which can serve as a final criterion for prioritization.

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Registered Livestock and Poultry Breeds of India

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Animal Genetic resources of our country is represented by 212 indigenous registered breeds belonging to cattle, buffalo, sheep, goat, camel, pig, horse and ponnies, donkey, dog, yak, gheese and poultry. FAO's (1999) broad definition of the breed concept states that "either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity". Hence, "A domestic animal population may be regarded as a breed, if the animals fulfil the criteria of (i) being subjected to a common utilization pattern (ii) sharing a common habitat/distribution area (iii) representing largely a closed gene pool and (iv) being regarded as distinct by their breeders" (FAO, 2012).

A mechanism for "Registration of Animal Germplasm" was initiated by Indian Council of Agricultural Research, New Delhi with a coordinating unit at National Bureau of Animal Genetic Resources (NBAGR), Karnal. This would provide protection to the valuable animal genetic diversity and facilitate its access for genetic improvement of animal breeds. This mechanism is the sole recognised process for registration of "Animal Genetic Resources" material at national level. Initially 129 breeds have been registered as extant breeds followed by 83 breeds of different livestock and poultry species in the subsequent years until 2022 and an accession number has been given to each breed. The important phenotypic characters and area of distribution for the registered livestock breeds are as follows:

Registered Cattle breeds of India

1. Amritmahal

Amritmahal has its breeding tract in the districts of Chikmagalur, Chitradurga and Hassan in Karnataka. They are gray in colour but varies from white to almost black. White grey markings are present on face and dewlap in some animals. Horns are long and emerge from the top of the poll fairly close together in backward and upward direction, turn in and end in sharp black points - sometime touching each other. They also have a long head tappering towards muzzle.

2. Bachaur

Sitamarhi district (Nepal border comprising Bachaur and Koilpur sub divisions of Sitamarhi district) of Bihar is the breeding tract of the animals. They are gray in colour with horns that medium in size, stumpy, curving outward and upward. The animals are medium sized compact animals with straight back with flat or slightly convex forehead.

3. Badri

Badri belongs to hilly areas of Uttarakhand. The animals are black, brown, red, white or gray. Their horns are small in size. They have long legs with a prominent hump and small udder tucked up with the body. Their hooves and muzzle are black or brown in colour.

4. Bargur

Bargur hills in Bhavani taluk of Erode district of Tamil Nadu is the breeding tract of this breed. They are brown with white markings and have horns are closer at root and are inclined backward, outward and upward with a forward curve; sharp at the tip. The horns are light brown in colour. The animals are medium in size and light brown in colour with white markings.

5. Belahi

The breed belongs to Naraingarh, Ambala, Panchkula, Morni, Chandigarh, Mohali, Shivalik foot hills districts in the hilly regions of Haryana and Chandigarh. The animals are red while the face, lower abdomen and feet are white in colour with black muzzle. Horn are curved upward and inward like a sickle. They are medium sized strong dual type and migratory animals of lower Himalayas with white face along with some region of hump, neck, and dewlap being white. In males, hump and neck region are dark in colour.

6. Binjharpuri

The animals are found in Bhadrak, Kendrapara and "Binjharpur" of Jajpur district in Orissa. They are mostly white in colour while some animals are gray, black or brown. Horns are curved upward and inward. Male animals have horns that are 21.17±2.85cm on an average while female animals have 12.70±1.31cm. The animals are medium sized, strong and dual type. Hump, neck, and some region of face and back are black in colour irrespective of coat colour in males.

7. Dangi

The animals are spread in Dangs district of Gujarat and Thane, Nashik, Ahmadnagar (Akola taluka of Ahmadnagar district, Sinner and Igatpuri taluka of Nashik districts) of Maharashtra. Generally these animals are found near the hilly tract where forest is available in the ranges of Sahyadri. Dangi cattle have distinct white coat colour with red or black spots distributed unevenly over the body. Horns are short (12-15 cm) and thick with lateral pointing tips. Animals with inward and downward pointing horn tips are also available in sizable numbers. Uneven distribution of black or red spots over the body is also not uncommon. Forehead is slightly protruding.

8. Deoni

Deoni breed is the native of Bidar district in Karnataka and Parbhani, Nanded, Osmanabad, Latur (Deoni, Udgir and Ahmadpur taluks of Latur district districts of Maharashtra. Body colour is usually spotted black and white. This breed has three strains viz. 1- Complete white animal (balankya). 2.- Comlete white with partial black face (wannera). 3-Black and white spotted animal (waghyd orshevera). Horn emerge from the side of the poll behind and above the eyes in out ward and upward direction, slightly backward and again curving upward. Horn size is small and the tips are blunt. Black and white spotted body colour, drooping ears, prominent and slightly bulging forehead are their characteristics.

9. Gangatiri

Eastern UP and Bihar are the breeding tract of this breed. Animals are white or light gray in colour. Bulls have a relatively dark or dark gray colour in between fore and hind quarters. Horns are small to medium in size.

10. Gaolao

Gaolao breeds is found in Balaghat, Chhindwara, Seoni, and Durg districts of Madhya Pradesh and Rajnandgaon, Wardha,and Nagpur districts of Maharashtra. Gaolao animals are white or light grey. Males are generally grey over the neck. Horns are short and stumpy, blunt at the points and curve slightly backward. Head is markedly long and narrow tapering towards muzzle. Forehead recedes at the top giving a slightly convex appearance. Eyes are almond shaped and placed slightly at angles.

11. Ghumusari

The breed is native to Ganjam and Phulbani districts of Odisha. The animals are mainly white in colour but sometimes gray. Horns are curved upward and inward. Some animals have straight horns. The average size of horns in male animals is 8.72±1.54 cm while in female it is 7.47±1.67cm. The animals are small sized, strong and draft type animal with small head, flat forehead, broad and depressed in between the eyes

12. Gir

Amreli, Bhavnagar, and Junagadh districts of Gujarat is the home to this breed. Most of the Gir animals are pure red through some are speckled red. Horns are peculiarly curved; starting at the base of the crown they take a downward and backward curve and again incline a little upward and forward taking a spiral inward sweep, finally ending in a fine taper- thus giving a half moon appearance. Long and pendulous ears folded like a leaf and hang all the time with their inside facing forward. Forehead is bulging and convex.

13. Hallikar

The breeding tract of the breed is Chitradurga, Hassan, Kolar, Mandya, Mysore and Tumkur districts of Karnataka. The animals vary from gray to dark gray colour with deep shadings on forehead and hind quarters. Frequently, there are light gray markings on face, dewlap and under the body. Horns emerge near to each other from top of poll and are carried backward, each in a straight line for nearly half their length and then with gentle and graceful sweep bend forward and slightly inward towards the tips which are black and sharp.

14. Hariana

The animals are native to Hissar, Rohtak, Jind, and Gurgaon (widely spread in Indo Gangetic plains) districts of Haryana. Animals are white or light gray in colour. In bulls, colour in between fore and hind quarters is relatively dark or dark gray. Horns are small in size. Animals have white colour, long and narrow face, well-marked bony prominence at the center of poll.

15. Kangayam

Coimbatore, Erode, Dindigul, Karur, and Namakkal districts of Tamil Nadu is the native tract of Kangayam. Coat is red at birth, but changes to gray at about 6 month of age. Bulls are gray with dark coloured hump, fore and hind quarters, face and legs. Bullocks are gray. Cows are gray or white and gray. However, few animals (1-2 %) with red, black and fawn colour are also found. Horn are long and strong, taking backward, outward and upward sweep and then curving inward with tips tending to meet each other nearly completing a circle. Animals have a large hump and strong body.

16. Kankrej

Kankrej animals are distributed in Ahmadabad, Banas Kantha, Kheda, Mahesana, Sabar-Kantha, and Kutchchh districts of Gujarat and Barmer, and Jodhpur districts of Rajasthan. Colour varies from silver-gray to iron gray or steel gray. In males, fore quarters, hind quarters and hump are slightly darker than the rest of the body. Horn are strong and curved outward and upward in a lyre shaped fashion. They are curved to a longer distance compared to other breeds. Kankrej is the heaviest breed of cattle with large pendulous and open ears.

17. Kenkatha

Kenkatha breed is found in Tikamgarh district of Madhya Pradesh and Lalitpur, Hamirpur, and Banda (bred along the banks of river Ken in the area of Bundelkhand) districts of Uttar Pradesh. Colour varies from gray on the barrel to dark gray on the rest of body. Horns emerge from the outer angles of the poll in markedly forward direction and terminate in sharp points. They are small, sturdy and fairly powerful animal.

18. Khariar

The animals are distributed in Balangir, Kalahandi, and Nowpara districts of Odhisa. They are mainly brown sometimes gray. Horns are straight, quite often upward and inward. The average size of horns in male animals is 12.34±0.21cm, and female is 10.12±0.27cm. The animals are small sized, strong and draft type. Hump, neck, and some region of face and back are dark in colour.

19. Kherigarh

Kheri district of Uttar Pradesh is the native tract of this breed. Animals have white coat colour. Some animals have grey colour distributed all over body especially on face. Horns are upstanding, curving outward and upward; thick at the base. Horn formation is typical of lyre-horned Malvi type. Horns are medium in size (15 cm). The animals are small but active animal.

20. Khillar

Khillar is present in Belgaum, Bijapur, Dharwad, Gulbarga, and Bagalkote districts of Karnataka and Pune, Satara, Sholapur, Sangli, Kolhapur, and Osmanabad districts of Maharashtra. Khillaris of Deccan plateau - the Mhaswad and the Atapadi Mahal type are grayish-white. Males are dark over the fore and hind quarters with peculiar gray and white mottled marking on face. The Tapti Khillariis are white with carroty nose and carroty hooves. Horn are bow shaped, long and pointed and follow the backward curve of the forehead. They are placed close together at the root, grow backward for half of the length and then turn upwards in a smooth bow shape peculiar to this breed. The horns are thick at the base and taper. A distinct groove in the centre of forehead from the nasal bridge to the centre of the poll. Sharp and prominent nasal bridge.

21. Konkan Kapila

Konkan Kapila is also called Konkan Gidda, and Konkan. Thane, Raigadh, Ratnagiri, Sindhudurg and Palghar districts of Maharashtra is the breeding tract of the breed. Animals are of various coat colours, predominant being reddish brown followed by black. However white/gray, mixed, brown or fawn coat colour animals are also available. Horns are generally straight and emerge from side of the poll behind and above eyes in outward direction and going upwards and backwards ending with pointed tips with an average size of 18.45cm in males and 18.30cm in. The animals have small to medium sized and compact body with horizontal ears and straight forehead. Eyelids, muzzle, hoof and tail switch are generally black.

22. Kosali

Kosali is present in Raipur, Durg, Bilaspur, and Janjgiri districts of Chhattisgarh. They are mainly light red (60-55%), followed by whitish gray (30-35%). Few animals (3-5%) having black coat colour or red with white patches also seen. Horns are stumpy and straight; grows outward, upward and inward with an average size of 21cm in males and 12cm in females. Muzzle, eyelids, tail switch and hooves are black. Head is broad, flat and straight. Hump is small to medium in size. Udder is small and bowl shaped.

23. Krishna Valley

Satara, Sholapur, and Sangli districts of Maharashtra is the home to Krishna Valley breed. The common colour is grey- white with a darker shade on fore and hind quarters in males. Adult females are more whitish in appearance. Brown and white, black & white, and mottled colors are often seen. Horns are small in size, curved and usually emerge in an outward direction from the outer angles of the poll curving slightly upward and inward. Massive body with a distinct bulge in the forehead.

24. Ladaki

Ladaki is present in Leh and Kargil district of Jammu and Kashmir. They are mostly black followed by brown. Horns are mostly curved, directed slightly upward and forward ending with pointed tips over the forehead with an average size of 16cm in male and 11cm in female. Small hairy, forehead with slightly long face with a small hump. They are small statured with short legs.

25. Lakhimi

Assam is the native breeding tract of Lakhimi cattle. They are brown and gray in colour. Horns are straight at average of 17 cm. Animals are small sized, horned and have relatively short legs. Coat colour is variable mainly brown and gray. Hump is medium in size and the backline is slightly curved. Udder is small and bowel shaped.

26. Malnad Gidda

Malnad Gidda is found in Chikmagalur, Dakshina Kannada, Hassan, Kodagu, Shimoga, Uttar Kannada, and Udupi districts of Karnataka. The animals are black with light shades of fawn on thigh and shoulder region. Horns are generally small and straight; grows outward, upward and inward. Gidda means dwarf and Malnad means a place receiving heavy rainfall. They are small in size with compact body frame weighing around 80- 120 Kg. Tail switch is black, with a small humpand small udder that is bowl shaped.

27. Malvi

The animals are spread over Rajgarh, Shajapur, Ujjain, Ratlam, Mandsaur, Dewas, and Indore district of Madhya Pradesh and Jhalawar district of Rajasthan. Malvi cattle are gray in colour; darker in males, with neck, shoulders, hump and quarters almost black. Cows and bullocks become nearly pure white with age. Horns are strong and pointed, emerge from the outer angle of the poll in an outward and upward direction with an average size of 20 - 25 cm in length. Strong well-built whitish gray animal with lyre shaped strong and pointed horns.

28. Mewati

The animals are native to three states namely, Haryana (Gurgaon, Faridabad), Rajasthan (Alwar, Bharatpur) and Uttar Pradesh (Mathura). Mewati cattle are usually white with neck, shoulders and quarters of a darker shade. Horns emerge from the outer angles of poll and are inclined to turn backward at the points.

29. Motu

Malkangiri district of Odhisa is the breeding tract of Motu. The animals are mainly brown (reddish) sometimes gray. Few animals are white in colour. Horns are straight, upward with rounded tip with average of 6.23±0.21cm in male and 3.35±0.18cmin female. They are small sized, strong and draft type cattle. Animals are mostly polled and brown in colour.

30. Nagori

The breeding tract of the breed is Nagore, Bikaner, and Jodhpur districts of Rajasthan. They are generally white or light grey. In some cases head, face and shoulder are slightly grayish. Horns emerge from the outer angles of poll. They extend in an outward direction and are carried upward with gentle curve to turn in at points. Horns are medium in size. White, upstanding, very alert and agile animals with long and narrow face like that of a horse.

31. Nimari

Nimari cattle are found in Khandwa (East Nimar), Khargaon (West Nimar), and Badwani in Madhya Pradesh and Jalgaon in Maharashtra. Nimar cattle are red with large splashes of white on various parts of the body. Horns usually emerge in a backward direction from the outer angles of the poll, somewhat in the same manner as in Gir cattle, turning upward, outward and finally backward at the points. Massive body structure that is typical red in colour with large splashes of white and bulging forehead.

32. Ongole

The breed is spread over Vizianagaram, Vishakhapatnam, East& West Godavari, Guntur, Nellore, Kurnool, Anantapur, Cuddapah, Chittoor, Mahbubnagar, Nalgonda, and Khammam districts of Andhra Pradesh. Ongole have a glossy white coat called padakateeru by the breeders. Males have dark gray markings on head, neck and hump, black points on knees and pasterns, black muzzle and black eye lashes. Horns are short and stumpy, growing outward and backward from the outer angles of the poll, thick at the base and firm without cracks. In cows, horns are thinner than in bulls. Horns in cows generally extend outward, upward and inward. The animals have majestic gait, stumpy horns, large fan shaped and fleshy dewlap serrated with smooth flowing folds instead of narrow constrictions.

33. Ponwar

Pilibhit district of Uttar Pradesh is the native tract of Ponwar. Ponwar cattle are usually brown or black with white patches. There is no particular pattern but black and white patches are intermixed. Horns emerge outward, upward and then curve inward with pointed tips. Sometimes horns curve backward in the end. Horns are medium in size.

34. Pullikulum

Madurai, Sivagangai and Virudhunagar district of Tamil Nadu is where these animals are found. Males are dark gray and females are white or gray. Horns grow outwards, upwards, backwards and inwards ending with pointed tips, tips are wide apart with an average size of 34.34cm in males and 37.22cm female. The animals are small sized with compact body and short legs. Muzzle, eyelids, tail switch and hooves are black. Fore Head is broad and level with groove at center. Hump large in males and small in females. Udder is not well developed.

35. Punganur

Chittoor district of Andhra Pradesh is the home to this cattle. Punganur cattle are white, grey or light brown to dark brown. White mixed with red or black colour animals are also available. Combination of white with brown or black patches is not uncommon. Horns are crescent shaped and often loose curving backward and forward in males and lateral and forward in females. Horns are stumpy in males and slightly longer in females. Horn size is small (10-15 cm). Animals are very short / small sized.

36. Rathi

Bikaner, Ganganagar, and Jaisalmer districts of Rajasthan. The animals are usually brown with white patches all over the body, but animals having completely brown, or black coat with white patches are often encountered. The lower body parts are generally lighter in colour as compared to the rest of body. Horns are curving outward, upward and inward. Horns are short to medium in size. Body colour and horns type are significant characteristic of this breed.

37. Red Kandhari

The breed is present in the Ahmednagar, Beed, Nanded, Prabani, and Latur districts of Maharashtra. The colour is uniform deep dark red, but variations from a dull red to almost brown are also found. Bulls as a rule are a shade darker than cows. Horns are evenly curved and medium sized. Body colour and horns type are significant characteristic of this breed.

38. Red Sindhi

Red Sindhi is found only at organized farms of Odisha, Tamil Nadu, Bihar, Kerala and Assam States. This breed has distinctly red coloured body. Red shades vary from dark red to dim yellow. Though patches of white are seen on dewlap and sometime on forehead, no large white patches are present on the body. In bulls, colour is dark on the shoulders and thighs. Horns are thick at the base and emerge laterally and curve upward. Body colour and horns type are significant characteristic of this breed.

39. Sahiwal

Sahiwal animals are present in Amritsar, and Ferozepur in Punjab and Ganganagar in Rajasthan. Coat colour is usually reddish dun but pale red or brown occasionally mixed with white spots is also seen in few animals. Horns are stumpy and short. Large and loose skin of Dewlap / neck are significant characteristic of this breed. They have large and pendulous teats and are pale red in colour with short horns.

40. Siri

Darjeeling in West Bengal; Gyalshing, Namchi, Gangtok, North, East, West, and South Sikkim in Sikkim is the home to this breed. Animals are either black with white patches or brown with white patches. In some cases they are totally black or brown. Horns are curved outward, forward and slightly upward, and are medium in size. Colour pattern similar to that of Holstein Friesian, Cervico - thoracic type of hump.

41. Tharparkar

Tharparkar is found in Kutchchh, Barmer, Jaisalmer, and Jodhpur districts of Rajasthan. Animals are white or light grey. Face and extremities are of a darker shade than the body. In bulls neck, hump, and fore and hind quarters are also dark. Horns are set well apart curving gradually upward and outward in the same line as that of the poll, with blunt points inclined inward, moderately thick at the base i.e. Average size 12.5 -17.5 cm in circumference just above the skin. In males, horns are thicker and short. White colour, convex forehead, large skin of dewlap/neck are significant characteristic of this breed.

42. Umblachery

The breed is found in Thanjavur, Nagapatinam, and Thiruvarur districts of Tamil Nadu. Calves are generally red or brown at birth. This colour changes to grey at about 6 months of age. In adult females, the predominant coat colour is grey with white markings on face and legs. The intensity of colour varies from grey with admixture of black. Horns are curving outward and inward and sometimes spreading laterally. These are thick in bulls and thin in cows. Horns are very small in size. White markings are present on face, limbs and tail. All the legs below hocks have white marks either as Socks or as Stockings. Even a portion of hooves is white.

43. Vechur

Kottayam district of Kerala is the native tract of this breed. Animals are light red, black or fawn and white. Horns are small, thin curving forward and downward. In some cases they are extremely small and are hardly visible. They are eextremely small sized animal with compact body.

44. Poda Thurpu

Poda Thurpu (Poda locally means spotted/ speckles/blotches) is the first cattle breed registered from Telangana state, has breeding tract within Nagarkurnool district. The animals have light brown to dark brown patches on white coat. Their horns are mostly straight, sometimes curved backward and upward or forward pointing with broad base. The animals are medium sized with compact body. Forehead is bulging/convex with a depression in the middle/centre. It has the excellent tolerant capacity to drought conditions and can sustain during less fodder and water availability. Wild and aggressive in nature.

45. Nari

Foothill areas of Aravalli hills of Rajasthan mainly in Sirohi and Pali districts and Sabar Kantha and Banas Kantha districts of Gujarat is native of this breed. Coat colour varies from white to greyish white and bulls are either white, greyish white or black. Horns are spirally curved and outward/ forward in orientation. widespread, long, and thick at bottom and pointed at tips. Highly adopted to hot climate and excellent in draught within plains and hilly forest areas.

46. Dagri

Dagri in colloquial language means ‘Deshi’ or old or native, mainly draught purpose breed found within Godhara/Panch Mahals, Dahod, Narmada, Chhotaudepur and Mahisager districts of Gujarat. Breed with predominantly white, sometimes with grey shade, small sized, compact body and straight forehead. Body length is proportionally more than height. Head is straight with prominent supraorbital groove. Horns are short, thin, curved upward in a lyre shaped or in straight fashion with pointed tip. Bullocks were used for agricultural operations mainly ploughing, inter culturing, sowing etc.

47. Thutho

Only beef breed of India, from Nagaland, well adapted to hilly region and able to graze on hill slopes even during rainfall. Coat colour is black or brown, sometimes white patches on face and body. The horns are short and stumpy and curved outward and upward. They are medium in size, hardy, well-built and docile. Fore-head is small and straight. Backline is uneven, slopes behind the small hump, and rises to peak between hipbones and then drops sharply to the tail head.

48. Sweta Kapila

Animals are spread over North and South Goa, mainly maintained in Gaushalas and considered to have medicinal properties. The coat colour is white, and white colour extends from muzzle to tail switch including eyelashes and muzzle (whitish brown). Horns are mostly straight and maybe slightly curved upward and outward. Short to medium statured animal have straight face and small to medium hump. Fore head is straight and triangular shaped, having slight furrow at centre. Reared mainly for milk purpose.

49. Himachali Pahari

Chamba, Kangra, Kinnaur, Kullu, Mandi, Shimla, Sirmaur, Lahul and Spiti districts of Himachal Pradesh are the breeding tract of this breed. They are highly adapted to mountain topography, extremely cold climate, and fodder scarcity. Animals have black and blackish brown coat colour, small to medium sized, compact cylindrical body, short legs, medium hump, horizontally placed ears, long tails, small udder with medium sized horns, mainly curved lateral and upward directions.

50. Purnea

Purnea is breed from Bihar spread over Madhepura, Purnia, Katihar, Araria, Kishanganj, and Supaul districts. It is rea reared for milk, draught, and manure; has very good drought and heat tolerant capabilities. Purnea animals adapted to harsh native environment, resistance to tropical diseases and external parasites and sustenance on low quality roughages and grasses. Coat colour is primarily grey followed by red and black. Horns are straight and carried upwards sometimes laterally. Face is triangular in appearance and head profile is straight in females but budged in males. These are small sized animals. These cattle have medium hump, small to medium dewlap, small naval flap and small to medium sized udder.

51. Kathani

It is a dual purpose cattle. It is distributed in mainly Vidarbha region of Western Maharashtra. The Kathani cattle possesses good draft ability, suited to marshy land for paddy cultivation.

52. Sanchori

It is a medium sized, good milk producing cattle. It is distributed in Jalore district of Rajasthan. Majority of animals are white in colour. Average daily milk yield is about 9 kg with 2769kg milk in a lactation.

53. Masilum

It is a small sized but well-built and sturdy cattle of Meghalaya. It is well adapted to the hill ecosystem. These cattle are reared by the Khasi and Jaintia communities for sports, manure and socio-cultural festivals.

Registered Buffalo Breeds of India

1. Banni

Banni buffaloes belong to Kachchh, Sabarkantha, Surendranagar, Kheda, and Banaskantha districts of Gujarat. They are mainly black in colour; sometimes copper. Horns are curved, medium to large, heavy with 24 to 30 cm diameter in adult animals. Horns are vertical and upward in direction with inverted double/single coiling.

2. Bargur

Malai Erumai or Malai Emmai are other names for Bargur buffaloes. They are found in Erode (Hamlets of Bargur village A & B of Anthiyoor taluk, and Gundri & Kadamboor village of Sathyamangalam taluk). The animals are brownish black and brown. Horns are curved backward and inward. The horn is medium sized in males and medium to long in females. They are medium in size with black muzzle and eyelids, brownish black tail switch and gray hooves.

3. Bhadawari

The breeding tract of the breed lies in Etawah district- Chakranagar and Barhpura blocks Bah tehsil of Agra district in Uttar Pradesh and Mahangaon tehsil of Bhind Ambah and Porsa tehsil of Morena district in Madhya Pradesh. The animals are blackish copper to light copper. Colour of legs is usually like wheat straw. Horns are black curling slightly outward, downward before running backward parallel and close to neck and finally turning upward. Two white lines "Chevron" locally called as Kanthy are present on the lower side of the neck is a distinguishing character of this breed.

4. Chhattisgarhi buffalo

Chhattisgarh is the home to this buffalo breed. The animals are black in colour with medium to large sized horns that are directed laterally backwards and then upwards with pointing tips. Animals are medium built with proportionate body. 'Peda' made from buffalo milk is a famous milk product; Better preference over cow's bullocks for ploughing rice fields.

5. Chilka

Kurda, Puri and Ganjam districts of Odisha is the home to this breed. They are brownish black or black in colour. Horns are curved upward and inward. The average size of horns in male is 48.32±0.24cm while it is 50.75±0.12cm in female. The animals are medium sized with compact body, strong legs and small udder.

6. Gijri

Gojri distributed in Punjab and Himachal Pradesh. Compact body, brown or black skin, and coat colour, and typical horn pattern. Horns are heavy medium-sized with curved orientation which moves backward and then towards the front to complete the loop, locally called 'Pattih wale seengh'.

7. Jaffrabadi

Jaffrabadi breed is spread in Saurashtra region - Gir forest, Junagarh, Bhavnagar, Jamnagar, Porbandhar, Amreli and Rajkot districts of Gujarat. The animals are black but some animals having gray colour or white spots on forehead, feet and tail switch are also seen. Horns exhibit wide variation, but usually emerge out by compressing the head, go downward sideways, then upward and inward finally forming a ring like structure. It makes eyes look small, and is termed as study eye, especially in males. The bulky head and horn shape is peculiar to this breed.

8. Kalahandi

Kalahandi and Raygada districts of Odisha is the breeding tract of this breed. Coat colour is usually blackish gray, sometimes gray. Horizontal going backwards, upward, and inward. It is curved to make half circle appearance and is about 50cm long. Muzzle, eyelids, tail and hoofs are black. The other characteristics are convex head, small hump, round and medium sized udder. Tail extends below hock with coarse hairs on switch.

9. Luit (Swamp)

The Luit buffaloes are also called Assamese Swamp. They are found in Tinsukia, Dibrugarh, Sibsagar, Jorhat, Golaghat, Dhemaji, Majuli, Lakimpur and Biswanath districts of Assam. The animals are black in colour. Horns are curved laterally backward and then upward forming a semi-circle; average size being 60.13cm in male and 57.13cm in female. These swamp buffaloes are medium sized strongly built animals with prominent wither and short tail. The animals are characterized by broad and concave fore head with prominent eyes and wide muzzle, and distinct semi-circular horns in both sexes. They possess light white stocking up to the knee in both fore and hind legs.

10. Marathwadi

The animals belong to Aurangabad, Nanded, Latur, Jalna, Beed, Parbhani, Osmanabad, and Hingoli districts of Maharashtra. The animals are greyish black to jet black. Some animals have white markings on forehead and lower parts of the limbs. Horns reach up to shoulder but never beyond shoulder blade. Length of horns differentiate these buffaloes from Pandharpuri buffaloes. Horns reach up to shoulder unlike in Pandharpuri buffaloes where these may reach up to pin bones.

11. Mehsana

Mehsana animals are distributed in Mehsana, Sabarkantha, and Banaskantha districts of Gujarat. They are mostly black, a few animals are black brown or brown. Horns are generally sickle shaped with the curve more upward then in the Surti breed and less curved then in the

Murrah breed. They are generally bent downward and then take a curve like the horns of a ram. Eyes are very prominent, black and bright bulging from their sockets with folds of skin on upper lids.

12. Murrah

Rohtak, Jind, Hisar, Jhajhar, Fatehabad, Gurgaon and union territory of Delhi in Gujarat is the home tract of Murrah buffaloes. The animals are jet Black /pure black in colour. Horns are tightly curved in a spiral form and short in size. Thin Skin, Jet black colour, tightly curled horns are the distinguishing characters of this breed.

13. Nagpuri

Nagpuri animals are found in Vidarbha region - Amravati, Akola, Bhandara, Buldana, Chandrapur, Gadchiroli, Gondia, Nagpur, Wardha, Washim, and Yavatmal districts of Maharashtra. They are black colored animals with white patches on face, legs and tail tips. Puranthadi strain is slightly brownish. Horns are flat, curved and carried back on side of the neck nearly to shoulders. Horns are heavier in males than in the females. Horns are long (50-65 cm). Flat, curved and long horns on side of neck is the distinguishing character of this breed.

14. Nilli-Ravi

Nili-Ravi is found in Gurdaspur, Amritsar, and Ferozpur districts of Punjab. They are mostly black with white markings on forehead, muzzle, tail switch and legs. Horns are tightly curved and circular in cross section, small in size. They are usually walled eyed with white markings on forehead, face, muzzle, legs and tail. The most desired character of female is the possession of these five white markings known as "Panch Kalyani".

15. Pandharpuri

Solapur, Kolhapur, and Sangli districts of Maharashtra is the home to Pandharpuri buffaloes. Colour is usually black but varies from light to deep black. White markings are found on forehead, legs and tail in few animals. Horns are very long and extend beyond shoulder blade, sometimes up to pin bones. These are of three types i.e. 1. Bharkand - curving back ward and usually twisted. 2. Toki - curving backward, upward and usually twisted outward. 3. Meti - flat running down. Very long horns, prominent, long and straight nasal bone is a distinguishing character of this breed.

16. Surti

Surti buffaloes are present in Kheda, Baroda, Bharuch and Surat districts of Gujarat. Coat colour varies from rusty brown to silver- grey. Skin is black or brown. Horns are flat, sickle shaped and are directed down ward and backward, and then turn upward at the tip to form a hook. The horns are medium in size. They are medium sized animal, brown in colour, with two white bands below the neck and sickle shaped horns.

17. Toda

Nilgiri hills and south of Tamil Nadu is the home to Toda buffaloes. Calfs are generally fawn at birth; at about 2 months, the fawn colour changes to ash gray. In adult buffaloes the predominant coat colours are fawn and ash-gray. Horns long and are variable in shape. They are usually set wide apart, outward, slightly downward and upward with the points being re-curved inward, forming characteristically a crescent shape or semicircle. Horns are thick at the base, and are tapering. A narrow band of dense hair covering the top line from the crest of neck to the point of origin of tail, two chevron markings - one just around the jowl and the other anterior to the brisket are the distinguishing characters of this breed.

18. Dharwadi

Dharwadi is a medium sized buffalo breed from Karnataka with black coat colour. Milk of this breed is used for the preparation of Dharwad peda which is having the GI recognition. Average lactation milk yield is 972 litre; Daily milk yield ranges from 1.5 to 8.7 litre. Head is straight with semi-circular horns and almost touching to wither. Ears are erect. Udder is medium in size with cylindrical shaped teats.

19. Manda

Manda buffalo is distributed in Koraput, Malkangiri and Nawarangapur districts of Odisha. Body colour is mostly ash grey and grey with copper coloured hairs. Horns are broad, emerging slight laterally, extending backward and inward and making half circle. Both male and female buffaloes are utilised in agriculture, particularly for ploughing and preparing agricultural land.

20. Purnathadi

Purnathadi buffalo is distributed in Vidarbha region of Maharashtra state. It is medium in size with whitish to light brown coat. Leg extremities and tail switch are white. Horns are long with hook like appearance at end. Milk yield ranges from 353 to1533 kg in a lactation. Milk fat percentage ranges from 6.5 to11.5.

Registered Sheep Breeds of India

1. Balangir

Balangir, Sambalpur and Sundargarh districts of Odisha is the home to Balangir sheep. Animals are medium sized; white or light brown or of mixed colours. Few animals are also black. The ears are small and stumpy. Tail is medium long and thin. Fleece is extremely course, hairy and open. Legs and belly are devoid of wool. Horns are found in male only.

2. Bellary

Bellary sheep are present in Bellary, Davangere and Haveri districts of Karnataka. They are strongly built and medium sized animals with body colour ranging from white through various combinations of black and white. Ears are medium long, flat and drooping. Horns are found in 30% male only.

3. Bhakarwal

They are completely migratory throughout the state of Jammu & Kashmir. They are medium-sized animals, with a typical roman nose. The animals are generally white, although colored fleece are occasionally observed. All animals are spotted fawn or grey. Rams are horned; ewes are polled. Ears are long and drooping. T ail is small and thin. Fleece is coarse and open.

4. Bonpala

Southern part of Sikkim is the home to this breed. Tall, leggy, well-built animals. Fleece colour ranges from completely white to completely black with a no. of intermediary tones. Ears are small and tubular. Tail is thin and short. Fleece is course hairy and open. Belly and legs are devoid of wool.

5. Changthangi

Changthangi sheep are found in Changthang region of Ladakh in Jammu & Kashmir. Strong built, large-framed animals with good fleece cover and extra ordinarily long staple.

6. Chevaadu

Chevaadu is also called Arichevaadu and is found in Tirunelveli district of Tamil Nadu. They are light brown in colour while some are dark brown and few tan. Horns are highly corrugated, curved horizontally outward, backward with blunt conical apex having few thick ridges with an average size of 10 - 42 cm. Dorsal part of the body is light brown in colour and the ventral part, from the jaw to inguinal region, is lighter than the dorsal part of the body and these animals are called as "Arichevaadu". Head is erected and high in disposition.

7. Chokla

In limited area at juncture of Churu, Sikar, and Nagaur districts of Rajasthan, Chokla breed is preset. They are light to medium-sized animals. Face is generally devoid of wool, dark brown and the colour may extend up to the middle of the neck. Head profile is straight. Ears small to medium in length and tubular relatively fine. Tail thin and medium length. Coat colour is white, dense, relatively fine, covering the entire body including the belly and greater part of legs.

8. Chottanagpuri

The home tract of chottanagpuri is Ranchi, Saraikhela- Kharsawa, West Singhbhum and Dhanbad districts of Jharkhand and Purulia, western part of Banpura and west of Midnapur district in West Bengal. The animals are small, light-weight; light grey and brown in colour. Ears are small and parallel to the head (Horizontal). Pendulous in some cases. Tail is thin and short. Fleece is course hairy and open.

9. Coimbatore

Coimbatore, Madurai districts of Tamil Nadu is the breeding tract of this breed. They are medium-sized animals, white with black or brown spots. Ears are medium sized and directed outward and backward. Tail is small and thin. Fleece is white, coarse, hairy and open.

10. Deccani

Deccani sheep is found in Maharashtra, Andhra Pradesh and Karnataka. The animals are medium sized, colour is black with white marking. Ears are medium in length, flat and drooping. Tail short and thin. Fleece coarse hairy and open.

11. Gaddi

Kistwar and Bhadarwati tehsils of Kashmir, Udhampur and Kullu valleys of H.P. and Dehra Dun, Nainital districts of Uttarakhand is the home to this breed. They are medium sized animals usually white, although tan brown and mixtures of these are also seen. Tail is small and thin. The fleece is relatively fine and dense.

12. Ganjam

Ganjam breed is found in Ganjam, Gajapati, Rayagada Koraput, parts of Phulbani, Nayagarh, Khorda and Puri districts of Odisha. Some animals of this breed, though in less pure form are also found in the Cuttack district. The animals are medium sized with brown to dark tan coat; some have white spots on face and body. Ears are medium sized and drooping. Nose line is slightly convex or straight. Tail is medium long and thin. Fleece is hairy and short.

13. Garole

They are found in Sunderban region of South 24- Parganas district in West Bengal. Some animals are also found in the parts of North 24- Parganas and Midnapore district adjoining the South- Parganas district. Animals are small sized with relatively low body weight. Body is compact and square with small head, medium ears and short and thin tail. Grey and white are predominant colours in this breed. The udder is fairly developed and twins can easily be sustained on the milk available from the ewes. Fleece is open, coarse and very dense. Multiple births are common.

14. Gurez

Gurej and Tulial blocks of Gurej subdivision in the Baramulla district Kashmir. In north Gurej's habitat overlaps with the breed tract of Karnah sheep in Kupwara district, while in west as well as eastern sides border with Pakistan occupied Kashmir. Gurez is the largest of the sheep breeds in Jammu and Kashmir. The animals are generally white, brown or black or have brown or black spots. Tail is thin and short. Fleece is generally coarse and hairy. Ears are long, thin and pointed.

15. Hassan

Hassan district of Karnataka is the breeding tract of thisbreed. They are small animals having white body with light brown or black spots. Ears are medium-long and alert. Fleece is white, extremely coarse and open; legs and belly are devoid of wool.

16. Jaisalmeri

Jaisalmer district of Rajasthan is the main breeding tract. However, this breed is also found in the adjoining areas of Barmer, Jodhpur and Pali districts. Animals are fairly built square, deep and tall in appearance. Black or dark brown face, the colour extending up to the neck. Typical

Roman nose. Long drooping ears, generally with a cartilaginous appendage. Both sexes are polled. The tail is medium to long. The fleece is white, of medium carpet quality and not very dense.

17. Jalauni

Jalaun, Jhansi and Lalitpur districts of U.P. Tikamgarh and Datia districts of Madhya Pradesh is the breeding tract of Jalauni breed. They are medium sized animals, with a straight nose line. Ears are large flat and drooping. Tail is thin and medium in length. Fleece is coarse, short-stapled and open, generally white. Belly and legs are devoid of wool.

18. Kajali

A sheep population of Punjab (India) is primarily reared for mutton production along with wool and manure. Derive their name from the black circle around the eyes. Large with a well-built body having a Roman nose, long and pendulous ears, and long tail touching ground. Kajali sheep has two colour variants based on the coat color, White (Chitti) and Black (Kali). Both sexes are typically polled. Kajali is one of the heaviest sheep breeds of India.

19. Karnah

Karnah sheep are found in Tangdhar and Teetwal blocks of Karnah tehsil of Kupwara district in North Kashmir in the state of Jammu & Kashmir. The animals are medium sized with round and compact body. The rams have large curved horns with pointed tips and a prominent nose line (Roman nose). The predominant coat colour is creamy white. Ears are pendulous and medium. Tail is thin, straight and medium.

20. Katchaikatty Black

Katchaikatty Black is also known by other names like Katchaikatty Karuppu Aadu and Muttaadu. They are found in Madurai district of Tamil Nadu. The animals are black in colour with large horns (32±2.0cm) that are widespread and twisted outwards. Animals are medium in size with compact body. Face is of moderate length; concave with depression; forehead moderately broad. Tail is short and slender.

21. Kendrapada

Cuttack, Puri, Jagatsinghpur, Jajpur, Bhadrak and Kendrapada districts of Odisha is the home to this breed. They are also known as Deshi and Kuzi. The animals are brown with button type horns present only in few males. Head, face, belly and legs are bare. Rest of the body is covered with non-lustrous hair. Animals have horizontal ears; short, straight and drooping tail.

22. Kenguri

Raichur and Koppala district of Karnataka is the home to Kenguri sheep. The animals are medium sized and dark brown or coconut colored, but colors ranging from white to black with spots of different shades are also observed. Ears are medium long and drooping. Tail is short and thin.

23. Kilakarsal

Kilakarasal is found in Ramnathapuram, Madurai, and Tanjavur districts of Tamil Nadu. Coat is dark tan, with black spots on head, belly and legs. Ears are medium sized. Tail is small and thin. Males have thick twisted horns. Most of the animals have wattle.

24. Madras Red

Chengalpattu and Madras in Tamil Nadu is the home tract of this sheep breed. Body colour is predominant brown, the intensity varying from light tan to dark brown; some animals have white markings on the forehead, inside the thigh and on the lower abdomen. Ears are medium, long and drooping. Rams have strong corrugated horns.

25. Magra

This breed is distributed in Bikaner, Nagaur, Jaisalmer and Churu districts of Rajasthan. The animals are medium to large in size having a white face with light brown patches around the eyes, which is the characteristic of this breed. Skin colour is pink. Ears are small to medium and tubular. Both sexes are polled. Tail is medium in length and thin. Fleece is of medium carpet quality, extremely white and lustrous and not very dense.

26. Malpura

The major breeding tract of Malpura sheep comprises of, Tonk, Sawaimadhopur, Jaipur, Dausa while minor breeding tract includes Ajmer, Bhiwara, Chittorgarh, Bundi and Kota districts of Rajasthan. They are fairly well-built animals with long legs. The typical colour of the face is light brown extending up to the neck. Ears are short and tubular, with a small cartilaginous appendage on upper side. Both sexes are polled. Tail is medium to long and thin. Fleece is white, extremely coarse and hairy. Belly and legs are devoid of wool.

27. Mandya

Mandya sheep are found in Mandya district and also in the bordering area of Mysore and Bengaluru in the state of Karnataka. They are relatively small animals that are white in colour, but in some cases face is light brown and this colour may extend up to the neck. Compact body with a typical reverse U shaped conformation from the rear. Ears are long leafy and drooping. Tail is short and thin. Slightly Roman nose. Both sexes polled. Fleece is extremely coarse and hairy.

28. Marwari

Jodhpur, Jalore, Nagaur, Pali, Sirohi, Barmer and Udaipur districts of Rajasthan, Jeoria region of Gujarat are the breeding tracts of this breed. The animals are medium-sized with black face colour extending to the lower part of neck. Ears extremely small and tubular. Both sexes are polled. Tail is short to medium and thin. Fleece is white and not very dense.

29. Mecheri

Mecheri sheep is distributed in Salem, Namakkal, Erode and Coimbatore districts of Tamil Nadu. They are medium sized animals. Light brown in colour. Ears are medium sized. Tail is short and thin. Body is covered with very small hair.

30. Muzaffarnagri

The native tract of Muzaffarnagri is spread across Muzaffarnagar, Bulandshahar, Saharanpur, Meerut, Bijnor districts of UP, Dehradun district of Uttarakhand and parts of Delhi and Haryana. They are medium to large animals with slightly convex face line. Face and body are white with occasional patches of brown or black. Ears are occasionally black. Males occasionally have rudimentary horns. Ears long and drooping. Tail is extremely long and reaches fetlock. Fleece is white, coarse and open. Belly and legs are devoid of wool.

31. Nali

Ganganagar, Sikar, Hanumangarh, Churu & Jhunjhunu districts of Rajasthan, southern part of Rohtak & Hissar districts of Haryana is the home to Nali sheep. They are medium sized animals. Face colour is light brown, skin colour is pink. Both sexes are polled. Ears are large and leafy (pendulous). Tail is short to medium and thin. Fleece is white, coarse, dense and long-stalped. Forehead, belly and legs are covered with wool.

32. Nellore

Nellore breed is distributed in Nellore, Prakasham and Ongole districts of Andhra Pradesh. The animals are relatively tall with little hair present all over the body except at brisket wither and breech. Ears are long and drooping. Tail is short and thin.

33. Nilgiri

Nilgiri hills in Tamil Nadu is the native breeding tract of Nilgiri sheep. They are medium sized animals. Body colour is white; exceptionally there are brown patches on face and body. Face line is convex giving a typical roman nose. Ears are broad, flat and drooping. Males have horn buds and scars; females are polled. The tail is medium and thin. The fleece is fine and dense.

34. Panchali

Baraiya, Dooma, Dumma, and Panchali-Dumma are other names for Panchali sheep. They are found in Surendranagar, Rajkot, Botad, Bhavnagar and Kutchchh districts of Gujarat. The animals are white in colour with light brown, blackish brown, brown and black head or facial parts which is continued on the ventral part of neck and in some animal on whole neck and below knee joint on foreleg and below hock joint on hind leg. Horn are absent. Head is convex. Ears are long and pendulous. Tail is long. Udder is well-developed. Head, face and belly are devoid of wool while legs are covered up to elbow joint of fore leg and stifle joint of hind leg. Tuft of fiber/hair on ears is found in some animals.

35. Patanwadi

Saurashtra, Kutch and Mehsana districts of Gujarat is the breeding tract of Patanwadi sheep. Animals ae medium to large with relatively long legs. They have a typical Roman nose with brown and spotted tan face. Ears are medium to large and tubular with a hairy tuft. Tail is thin and short. Both sexes are polled. White fleece is of medium carpet quality, not very dense.

36. Poonchi

Poonch and Rajori districts of Jammu province in Jammu and Kashmir is the home to this breed. They look similar to Gaddi, but lighter in weight. Animals are predominantly white, including the face, but spotted sheep are also seen, varying from brown to light black. Ears are medium long. Tail is short and thin; legs are also short, giving a low-set conformation.

37. Pugal

Pugal sheep are distributed in Bikaner and Jaisalmer districts of Rajasthan. They are fairly well-built animals having black face with small light-brown stripes on either side above the eyes; lower jaw is typically light brown. The black colour may extend up to neck. Ears are short and tubular. Both sexes are polled. Tail is short to medium and thin. White fleece, of medium carpet quality, not very dense.

38. Ramnad White

Ramnathapuram district of Tamil Nadu is the native tract of this sheep. They are medium sized animal, predominantly white; some animals have fawn or black markings over the body. The ears are medium size and directed outward and downward. Tail is short and thin.

39. Rampur Bushair

Shimla, Kinnaur, Bilaspur and Lahaul spiti districts of H.P. and Dehra Dun, Rishikesh, Chakrota and Nainital district of Uttarakhand is the home tract of this breed.

40. Shahabadi

Shahabadi sheep are distributed in Shahbad, Patna and Gaya districts of Bihar. The aimals are medium-sized and leggy. The fleece colour is mostly gray, sometimes with black spots. Ears are medium sized and drooping. Tail is extremely long and thin. Fleece is extremely course, hairy and open. Legs and belly are devoid of wool.

41. Sonadi

Udaipur, Dungarpur, Chittorgarh and Banswara districts of Rajasthan is the home to Sonadi sheep. Fairly well built animals, somewhat smaller than Malpura, with long legs. White or light brown face with colour extending to the middle of the neck. Ears are large, flat, drooping and generally have a cartilaginous appendage. Tail is thin and medium in length. Both sexes are polled. Udder is fairly well developed. Fleece is white, extremely coarse and hairy. Belly and legs are devoid of wool.

42. Tibetan

The breeding tract of Tibetan sheep is Sikkim and Kameng districts in Arunachal Pradesh. The animals are medium-sized, mostly white with black or brown face; brown and white spots are also observed on the body. The nose is convex, giving a typical roman nose. The ears are small broad and drooping. The fleece is relatively fine and dense. The belly face and legs are devoid of wool.

43. Tiruchi Black

Tiruchy, Arcot, Salem and Dharmapuri districts of Tamil Nadu is the home to this breed. They are small animals with completely black body. Ears are short and directed down and forward. Tail is short and thin. Fleece is extremely coarse, hairy and open.

44. Vembur

Vembur sheep are distributed Vembur, Melakharandhai, Nagalpuram, Achangulam villages of Tirunelveli district in Tamil Nadu. They are tall animals, white in colour with irregular red and fawn patches all over the body. Ears are medium sized and drooping. Tail is thin and short. Body covered with short hair.

Registered Goat Breeds of India

1. Assam Hill

Assam state is home tract for this breed. Usually found white with occasional balck patches on backline and legs. Horns are small, mainly straight but sometime backward, cylindrical, tapering toward the end and pointed at the tip. Short legs, small body size, medium size ears, short and hairy tails with both buck and does are bearded. The breed is prolific in nature. Incidence of Singlet, twins, Triplets and quadruplets are 51.17, 41.92, 6.69 and 0.22 percent, respectively.

2. Attapady Black

Attapady Black is found in Palakkad/Palghat district of Kerala. The animals are small and black in colour with curved horns that are oriented backwards. Extremities are black. Tail is bunchy type.

3. Barbari

Bharatpur district of Rajasthan and Aligarh, Agra, and Etawah districts of Uttar Pradesh are the breeding tracts of Barbari goat. Their colour is white with tan spots/dark red spots. Horns are twisted, directed upward and outward and medium in size. They are small sized animals with short erect horns having small tubular and prick ears.

4. Beetal

Beetal goats are distributed in Amritsar and Gurdaspur districts of Punjab. Black coat is mostly common while brown with white spots of different sizes is also seen. Horns are medium in size (about 12 cm), carried horizontally with slight twist, directed backward and upward. Beetal goats are tall animals, having Roman nose and long ears (24.8 cm).

5. Berari

Akola, Amravati, Wardha, and Nagpur district of Maharashtra is the native breeding tract of Berari goat. Coat colour is light to dark tan (reddish colour). Horns are flat, small, oriented upward and backward. Black colored ring around neck in adult male is a distinguishing characteristic. Black hair line along the vertebral column extending up to tail in both sexes is evident.

6. Bhakarwali

Kagani is another name given to Bhakarwali goat. The animals are distributed in Poonch, Rajouri, Udhampur, Jammu, Kathua, Doda, Reasi, Kishtwar and Ramban districts of Jammu & Kashmir. They are white n colour while some have black face or hind quarters are also seen. Horns are curved and screw like; directed upward and backward being an average of 15cm in size. They are large sized goats having convex head. Body is covered with very long hairs. Udder is pendulous and medium in size.

7. Bidri

Bidar and Gulbarga districts of Karnataka is the native tract of this breed. The animals are black, some have white spots on ears, forehead, neck and knees. Horns are curved and directed backward, outward and downward. The average length of horns in female is 13.72 cm and male is 16.44cm. Forehead is straight. Muzzle, eyelids and hooves are black. Ears are pendulous. Udder is hairy and small in size.

8. Black Bengal

Black Bengal goat is distributed in the states of West Bengal, Odisha, Assam, Manipur, Meghalaya, Tripura, and Arunachal Pradesh. Colour is predominantly black, brown, grey and white are also found. Horns are small to medium in size (5.8 to 11.5 cm), directed upward and sometime backward. They are small-legged goat with short and lustrous hair coat. Nose line is slightly depressed.

9. Changthangi

Leh and Ladakh districts of Jammu & Kashmiris the major breeding tract of this breed. About 50% of the animals are white while rest hve black, gray or brown coat colour. Horns are large, turned outward, upward and inward to form a semi-circle. They are medium sized animals and sturdily built.

10. Chegu

Chegu is distributed in Himachal Pradesh (Chamba, Kinnaur, Lahul, and Spiti districts) and Jammu & Kashmir (Ladakh). The animals have compact body that is commonly white, black, gray, brown and mixture of these colours. Horns are long, cork shaped, directed upward, backward and inward/outward. Average length of horns is is about 59 cm in males and 33 cm in females. Reddish/tan/black coloration mostly around head, neck, and abdominal areas is the characteristic of this breed. Face and muzzle are tapering; possess long hair below with a second coat of pashmina wool.

11. Gaddi

Chamba, Kangra, Kullu, and Shimla districts of Himachal Pradesh and Jammu district of Jammu & Kashmir is the home tract of Gaddi breed. White is dominant colour while black coloured animals are also present. Horns are long, directed upward and backward and occasionally twisted. Skin is very tough, covered with coarse long hair measuring 17 to 25 cm. Ears are drooping and pointed (12 cm).

12. Ganjam

Ganjam breed of goats are present in Ganjam, and Koraput districts of Odisha. The animals are black or brown black in colour. White, brown and spotted animals are also found. Horns are twisted and curved; long, parallel and pointed backward and upward. Males usually have beards. Head is convex, ears are pendulous and medium in size (14.50 cm), wattles mostly absent.

13. Gohilwadi

Amreli, Bhavnagar, and Junagarh districts of Gujarat is the native tract of this breed. Coat colour of this breed is black. Horns are slightly twisted and turned backward. Horns are 8 to 10 cm long in female and 12 to 15 cm in males. Nose line is slightly convex. Ears are tubular and drooping. Body is covered with coarse long hairs.

14. Jakhrana

Jakhrana is predominantly present in Alwar district of Rajasthan. The coat colour is black with white spots on ears and muzzle. Horns are broad and flat, going backwards with a straight face line. Forehead is narrow and slightly bulging. Udder size is large with conical teats.

15. Jamunapari

Agra, Mathura, and Etawah districts of Uttar Pradesh and Bhind and Morena distrcits of Madhya Pradesh is the breeding tract of Jamunapari breed. The coat is white with patches of tan or black mostly on head and neck. Horns are short, sword shaped. Face is large and convex having tuft of hairs. Ears are large, pendulous, drooping and about 30 cm long.

16. Kahmi

Kahmi is also known by the name Desi and is distributed in Rajkot, Jamnagar, Junagadh and Devbhoomi Dwarka districts of Gujarat and Bareilly, Budaun, Pilibhit and Shahjahanpur districts of Uttar Pradesh. Coat color is unique; neck and face are reddish brown while rear abdominal part is black. Muzzle, eyelids and hooves are black in colour. Horns re curved upward and backward. The animals are medium in size with unique coat color (Cranial Reddish brown and Caudal black coat, locally called Kahmi) and convex forehead. Ear type (long, tubular and coiled, locally called veludi), wattles are found in majority of goats.

17. Kanni Adu

Kani adu is found in Tirunelveli and Thoothukudi/Tuticorin districts of Tamil Nadu. The animals are black with white markings on face and legs. Horns are broad, small and going backwards. White stripes extending on either side of the face from the base of the horn to corner of the muzzle is the unique characteristic of this breed.

18. Kodi Adu

Porai adu is another name for Kodi adu. They are distributed in Ramanatahpuram and Thoothukudi districts of Tamil Nadu. The animals are white with splashes of black or reddish brown colour. Horns are directed upward, backward and curved downward or upward and sharp at the tip with an average size of 15-25cm. Kodi Adu goats are tall, long, lean and leggy animals with compact body. Females have short, straight and sleek hairs on almost all parts of the body. Males have fairly long, straight and rough hairs on the neck and withers.

19. Konkan Kanyal

Sindhudurg district of Maharashtra is the home tract of Konkan Kanyal. The animals are black with white marking on collar, lower jaw and ventral surface. Horns are cylindrical, backward and medium in size (15-25cm). The animals have bilateral white strips from nostrils to ear. Legs are long, laterally black, medially white and white from knee to fetlock joint. Tail is dorsally black and ventrally white.

20. Kutchi

Kutchi goats are found in Ahmedabad and Kutchchh districts of Gujarat and Barmer, Bikaner, Jaisalmer, Jalore, Jodhpur, Pali, and Nagaur districts of Rajasthan. Coat/body colour is predominantly black but a few white, brown and spotted animals are also seen. Horns are short (10.6 cm), thick and pointed upwards. They have long and coarse hair, slightly roman nose, and short and thick horns.

21. Malabari

Malappuram, Kannur, and Calicut districts of Kerala is the home to Malabari goats. The animals are black, brown, white or mixture of these colors. Horns are slightly twisted horns directed outward and upward. The animals are small in size with medium sized ears, directed outward and downward.

22. Marwari

Marwari goats are distributed in Barmer, Bikaner, Jaisalmer, Jalore, Jodhpur, Pali, and Nagaur districts of Rajasthan. The animals are predominantly black in colour. In few animals white or brown patches are present. Horns are pointed and short (about 10 cm), directed upward and backward. The hair coat is long and shaggy. Ears are flat, medium sized and drooping.

23. Mehsana

The native tract of Mehsana goats is Ahmedabad, Banas Kantha, Gandhi Nagar, Mehsana, Sabar Kantha, and Patan districts of Gujarat. The animals are black with white ear base. Horns are screw type, twisted slightly, curved upward and backward and pointed at the tips (12-15 cm in males and 8- 12 cm in females). Ears have white spots ranging from a few white spots to complete white with few black spots at the base. White spots are present on the upper part of upper muzzle and look like a ring in some of the animals. Hair coat is long and shaggy.

24. Nandidurga

Nandi and Bilimeke are other names for Nandidurga breed. Chitradurga, Tumkur and Davanagere districts of Karnataka. The aimals are white in colour; some have black/brown spots on ears, forehead, neck and knees. Horns are curved, directed backward, downward, inward and touching neck in few. Average size of horns in male is 20.33cm and female is 15.79cm. Muzzle, eyelids and hooves are black. Ears are leafy and pendulous. Udder is hairy and pendulous. Teats are funnel shaped.

25. Osmanabadi

Ahmadnagar, Solar, Prabhani, Beed, Osmanabad, and Latur districts of Maharashtra is the native tract of this breed. Predominant colour is black. White colour is noticed only on ears and some spots on neck and forehead. Some animals are reddish in colour. Horns are straight, curved and small in size (about 13 cm). Five types of animals are available: 1. Entirely black with horns. 2. Entirely black with white ears and horns. 3. Entirely black and polled. 4. Entirely black, white ears and polled. 5. Combination of black, white and brown patches or irregular ridges on ears.

26. Pantja

The animals are also known as Pantuja. They are distributed in Udhamsingh Nagar and Nanital areas of Uttarakhand. The animals are fawn to brown in colour, which becomes lighter ventrally. Horns are small sized (<15cm), triangular, twisted, slightly upwards and backwards, pointed tip. White streak is present on either side of face. Head is slightly convex. Ears are pendulous.

27. Rohilkhandi

Desi and Chheri are other names for Rohilkhandi. They are distributed in Bareilly, Budaun, Pilibhit and Shahjahanpur districts of Uttar Pradesh. The animals are mostly black. Few animals are brown, fawn or mixed. Horns are slightly curved and directed laterally and outwards. Forehead is slightly convex. A tuft of hair (black or brown) is present in thigh region. Tail is bunchy. Ears mostly pendulous.

28. Salem Black

Karuppadu (In vernacular Tamil language) is another name for Salem Black goat. The animals are found in Salem, Dharmapuri, Erode and Krishnagiri districts of Tamil Nadu. The animals are completely black with glossy hair coat. No typical horn pattern however mostly directed upward and backward and sharp at the tip (Males: 20cm; Females: 13.7cm). Salem Black goats are tall, long, lean and leggy animals with compact body. Head is medium in length. The eyes are small and bright and the eyelashes are black in colour. The ears are medium in length, leaf-like and semi-pendulous. Neck is thick, broad and well set to the thorax in males.

29. Sangamneri

Ahmednagar and Pune in Maharashtra is the native tract of Sangamneri. The animals are white, black or brown. Spotted animals are also seen. Horns are directed backward and upward. Hair coat is extensively coarse and short.

30. Sirohi

The breed is distributed in Sirohi district in Rajasthan. Coat colour is predominantly brown with light or dark brown patches. Few individuals are completely white. Horns are curved upward and backward, small in size. Flat and leaf like drooping ears is the unique characteristic of this breed.

31. Sumi-Ne

Apu-Asu-Ne are Nagaland Long Haired are other names for this breed. The animals are found in Zunheboto district in Nagaland. White colour with characteristic black markings on head, neck and legs is the colour of this breed. Horns are small and slightly curved backward. Head is straight. Ears are horizontal. Horns are pointed. Beard is present. Presence of long hair in adult animals is the most important phenotypic character. The length of the fibre, however, is more in case of male compared to that of females.

32. Surti

Vadodra and Surat districts of Gujarat is the breeding tract of this breed. The animals are mostly white. Horns are directed backward, small in size (about 12 cm). Ears are medium sized and udder is well-developed with large conical teats.

33. Teressa

Teressa goats are also called Pookore. They are distributed in Nicobar district of Andaman & Nicobar Islands. They are dark tan, brown, white and brown mixed, black and brown mixed, females mostly light brown and white mixed. Horns are small, flat at base and pointing towards tip, starting from base and bending back along with/behind the head or straight with slight curvature towards back/ side wards. (11.5cm in male and 10.5cm in females). Peculiar white patch/line starting from inner canthus of both eyes or from eye brows and extending up to nostrils or mouth is a characteristic of this breed. Black hairs on dorsal midline up to the tail.

34. Zalawadi

Rajkot and Surendranagar districts of Gujarat is the native tract of this breed. Body is covered with black, lustrous, shining hairs. Some animals have white or brown hairs. Horns are cork-screw type moving straight upwards, backwards and slightly outward with pointing tips. Long, wide leaf like and drooping ears and well-developed udder with large conical teats.

35. Sojat

It is a large sized dual-purpose goat; reared for both meat and milk purpose. Sojat is mainly distributed in Pali, Jodhpur, Nagaur and Jaisalmer districts of Rajasthan. Average adult weight is about 60.0 kg in males. Average milk yield in female is about 1 kg per day.

36. Karauli

Karauli is a medium to large sized goat, reared for meat and milk. It is distributed in Sawai Madhopur, Kota, Bundi, and Baran districts of Rajasthan. Average adult weight in males is about 52.0 kg. Average daily milk yield is 1.530 Kg.

37. Gujari

This goat is a large sized, dual-purpose breed of Rajasthan. Coat colour is mixed of brown and white with white face, leg and abdomen. Average adult weight is about 69.0 kg in males and 58.0 kg in females. Average daily milk yield is 1.616Kg.

Registered Poultry Breeds of India

1. Ankleshwar

Ankleshwar, Jambusar, Zagadia, Bharuch, Hansot and Valia talukas of Bharuch and Narmada districts of Gujarat is the native tract of this breed. Their plumage is normal; white and light gray to brown and golden and is stripped or spotted with golden yellow feathers. They have single or rose comb with yellow or pinkish skin. The shank is yellow in colour. The birds lay cream brown to white shelled eggs. They are medium sized birds.

2. Aseel

Khammam districts of Andhra Pradesh;, Koraput and Malkangiri districts of Odisha and Bastar and Dantawara districts of Chhattisgarh are the breeding tracts of Aseel. The plumage is normal type and shows a patchy pattern. Plumage colour is red or/and black. The Aseel birds have pea comb. The skin and shank colour is yellow. The egg shell colour is brown. The birds hav small but firmly set comb, bright red wattles and ear lobes. The birds have long and slender face devoid of feathers. The general feathering is close, scanty and almost absent on the breast. The plumage has practically no fluff and the feathers are tough.

3. Busra

The breeding tracts of this breed include Dangs and Surat districts of Gujarat and Dhule and Nandurbar districts of Maharashtra. The plumage type is normal while the pattern is spotted. Plumage colour is white mixed with black or brown. The comb type is single. The skin colour is pinkish while shank is yellow. The eggs have light brown shells. The birds are small in size and wide variation in body colour. Black feathers are found in neck, back, tail, and reddish brown on shoulders and wings. Eye ring is red. Earlobe is white. Wattles are red in colour.

4. Chittagong

North eastern States of India is the home to Chittagong. The plumage type is normal and plumage is white with splash of golden markings on wings. They have pea comb. Adult birds are very strong and hardy. Head is long; beak is long and yellow, legs are yellow and featherless, plumage is close to the body, firm and glossy. Wattles are red in colour and very small. Ear lobes very small and usually red. Eyebrows are overhanging.

5. Danki

Srikakulam, Vizianagaram, and Vishakhapatanam districts of Andhra Pradesh is the breeding tract of Danki chicken. Plumage type is normal and pattern is patchy. The birds have brown plumage and pea comb. Skin colour is pinkish white and shank colour is yellow. Egg shell colour is brown. Cocks have shinning bluish black feathers on wings, breast, tail and thighs. Earlobe is red in color. Eyes are sharp. Eye ring is red in color. Comb is red in color. Beak is yellow in color. Wattles are absent. Spur is long and sharp in cocks.

6. Daothigir

Daothigir chicken are found in Dhuburi, Kokarajhar, Barpeta, Bongaigaon, and Nalbari districts of Assam. The birds have normal plumage with stripped or spotted pattern. The colour of the plumage is black interspersed with white. They have single comb with creamish white skin which is towards pinkish colour. Shank is yellow in colour. The egg shell is brown in colour. The birds are small sized, compact and has long legs. Wings and tail has black or brown feathers. Neck and back has golden yellow or brown feathers in some birds. Comb red and erect. Wattles are red. Tail is short and almost in level with the back.

7. Ghagus

Chittoor distrct in Andhra Pradesh and Kolar and rural Bangalore in Karnataka is the home to Ghagus breed. Plumage type is normal ad has a patchy pattern. The comb is single or pea type with white skin and yellow shank. Egg shell colour is light brown. Cocks have shinning bluish black feathers on breast, tail and thighs. Neck is covered with golden feathers. Throat in some cases is loose and hanging. Wattles are small and red in colour. Ear lobes are mostly red.

8. Hansli

Hansli chicken are found in Keonjhar and Mayurbhanj districts of Odisha. The birds have normal plumage type that are in solid pattern and black in colour. The comb is pea type with pink skin and yellow shank. They lay cream or light brown shelled eggs. Wings are medium to large in size, situated close to the body, well folded and carried horizontally.

9. Harringhatta Black

West Bengal is the home to this breed. Plumage is of normal type and black in colour. The birds have small body.

10. Kadaknath

Kadaknath is found in Dhar and Jhabua districts in Madhya Pradesh. Plumage type is normal and ranges from silver to gold spangled to blue black. The skin is dark gray in colour and the shank is gray in colour. The birds lay light brown shelled eggs. The colour of day old chicks is bluish to black with irregular dark stripes over the back. In the adults, comb, wattles and tongue are purple. The shining blue tinge of the ear lobes adds to its unique features.

11. Kalasthi

Nellore, Cuddapah and Chittoor districts of Andhra Pradesh is the home to Kalasthi chicken breed. The birds have normal type plumage which has a patchy pattern. The plumage colour is bluish black. They have pea or single comb. Skin is white or pinkish and shank is gray. The chicken lays brown shelled eggs. Neck is long and is covered with golden feathers. Brown colored birds have dark brown feathers on neck and bluish black or dark brown on tail. Wings are dorsally set exposing thighs covered with smooth feathers.

12. Kashmir Favrolla

Srinagar, Baramulla, Anantnag, Budgam, Kupwara, and Pulwama districts of Jammu and Kashmir is the breeding tract of Kashmir Favrolla. They have normal plumage with solid, stripped, patchy, spotted, barred pattern. Plumage colour is mixed shades of black, red, green, gold. They have single comb. The skin colour is white and shank colour is yellow. The birds lay light brown shelled eggs. The unique characteristic is feathered cap on head.

13. Kaunayen

Kaunaen chicken are found in Ukhrul, Tamenglong, Bishnupur, Thoubal, Imphal West, Chandel, Churachandupur, Senapati and Imphal East districts of Manipur. Birds have normal plumage type with a pattern that is patchy in males and solid in females. The plumage colour is black. The comb type is pea; skin is white and shank is yellow. Egg shell colour is brown.

14. Mewari

Ajmer, Banswara, Bhilwara, Chittorgarh, Dungarpur, Jaipur, Sirohi, Udaipur and Rajsamand districts of Rajasthan is the breeding tract of Mewari chicken. The plumage is normal type with stripped pattern that are brown in colour. They have single comb. They have yellow skin and shank. The eggs are brown shelled. The plumage is light to dark brown or gray with pencil lining. Males have bright gold and bronze feathers forming a shawl or cape over the back. Tail is composed of long arching feathers that initially look black but shimmer with blue, purple and green in good light.

15. Miri

Sibsagar, Lakhimpur, and Dhemaji districts of Assam is the native tract of this breed. The birds have normal plumage and the pttern is solid. The plumage colour is white and brown. They have single comb with white or yellow coloured skin and shank. Egg shell colour is light brown and the birds have brown eyes.

16. Nicobari

Nicobari breed is found in Andaman and Nicobar. The birds have normal plumage having solid pattern and brown in colour. The comb is single type. The skin is yellow in colour and shank is white pink. The egg shell colour is white or creamy. The birds are short legged. Shank length at 10 weeks of age varies from 3.50 to 3.85 cm.

17. Punjab Brown

Punjab and Haryana is the home to Punjab Brown chicken. Their plumage is normal with solid brown pattern and is brown in colour. Single comb is the characteristic of this breed. The skin colour is white while shank is yellow. Egg Shell Colour is brown. Plumage pattern is sometimes spotted or striped. Males in particular have black spots/stripes. Ear lobes are mostly brown. Wattles are red, large sized in males and small in females. Eye ring is red. Comb is red, and erect in position. Beak is yellow.

18. Tellichery

Tellichery chicken are found in Kerala and Malappuram, Kannur/ Cannanore, Calicut, Mahe districts of Pondicherry. Their plumage is normal type with solid pattern. The plumage is black with shining bluish tinge. They have single comb. The skin is gray and shank is blackish gray. The birds lay light brown shelled eggs. Shining bluish tinge on hackle, back and tail can be seen. Comb is red and large in size. It is erect in cocks and drooping on the rear side in hens. Wattles are red in colour. Ear lobe is mostly red in colour. Eye ring is blackish red. Beak is blackish.

19. Uttara

Uttara belongs to Nanital, Almora and Pithoragarh districts of Uttarakhand. The birds have normal solid black plumage. The comb is single type. The skin colour is white while shank colour is yellow. The birds lay light brown shelled eggs. About 18 % of birds have feathered shank and bunch of feather on head (crown structure).

Registered Horse & Pony Breeds of India

1. Bhutia

Darjeeling district of West Bengal and Sikkim is the home tract of this breed. Bhutia horses are distributed in Sikkim and Darjeeling. They are usually gray or bay colored and similar to the Tibetan pony. It has a compact body, short neck, round muscular quarters, coarse hairy legs, long tall and mane.

2. Kachchhi-Sindhi

Kachchhi and Sindhi are the other names of this breed. They belong to Surat, Kutchchh and Navsari districts of Gujarat and Barmer and Jaisalmer districts of Rajasthan. They are generally used for transportation of goods or other materials like fodder, raw construction materials, etc. Majority of the Kachchhi-Sindhi horse owners maintain and keep these horses for riding purpose, as these are excellent for long distance riding because of special type of Horse gait called Rewal Chal and also used for horse safaris. Unique features include roman nose appearance of face, ears curved at tips but not touching each other, short back, short pastern bone length, broader hoof for better grip and docile temperament.

3. Kathiawari

The breeding tract of the breed is Saurashtra province of Gujarat which comprises of Rajkot, Bhavnagar, Surendranagar Junagarh and Amreli. It is hardy, vigorous, well known for its space and speed and possesses good endurance power. The most prominent body colors in Kathiawari horses are chestnut, bay, gray and dun (light chestnut). They have concave forehead (mostly), long neck, short leg and squared quarters. Their face is dry and short, triangular from pole to forehead with small muzzle, big nostrils. The edge of the nostril is thin. Ears are small, fine and curved upright ears on 90 degrees axis that can rotate at 180 degrees, broad forehead and large expressive sensitive eyes. Tail is long, not bushy, curved well and touching to the ground. The hooves are round and broad. Height at withers is 150 cm or more.

4. Manipuri

Manipur is the native breed tract of Manipuri ponies. They are one of the purest and prestigious breed of equines of India. It is a strong and hardy breed and has very good adaptability to extreme geo-climatic conditions. Manipuri ponies are intelligent and extremely tough, and have tremendous endurance. Perhaps all these good qualities made it suitable for polo game for which it is globally famous. Generally the Manipuri ponies are of 130 cm high (Average) at withers with a good shoulder, short back, well developed quarters and strong limbs. Mane is generally coarse and upright. It has small pointed pricked ears; eyes are alert and slightly slant. The area between the nostrils is flat not crispy. Withers are not prominent. Face is concave and tall is well set and commensurate with height. Common body colours are bay, dark bay, brown, reddish brown, gray, chestnut and roan.

5. Marwari

The Marwari breed is derived from the Marwar region of the Rajasthan which is the natural habitat of the breed. The Marwar region includes Udaipur, Jalor, Jodhpur and Rajasamand districts of Rajasthan and some adjoining areas of Gujarat. The Marwari horses are reared mainly for riding and sports and no attempts are being made to prepare them as thoroughbred race animals. The predominant body colour is brown where as other body colors are roan, chestnut, white and black with white patches. The Marwari horses are longer and taller than Kathiawari and other breed of horses. Average height at withers is 150 cm or more.

6. Spiti

Spiti valley and adjoining areas of Kullu and Kinnaur divisions of Himachal Pradesh is the breeding tract of this breed. These horses are smaller in height. The Spiti ponies have two strains, Spiti pure and Konimare. The Konimare ponies are comparatively taller. They are capable of thriving in cold regions under adverse conditions of scarcity of food, low temperature and long journeys at high altitude. The predominant body colour is gray, followed by brown, black, bay. Chestnut, Roan, Piebald (black and white) and skewbald (white and any colour other than Black). The Spiti horses are hardy and surefooted. Body is well developed with fairly strong bones. The legs are thick and covered with long coarse hairs. The mane is longer having 20 to 30 cm long hairs. Solid and compact body, convex face, erect ears, black eyes, straight back, long and straight tail, alert looking and short height are some of the important breed characteristics. Average height at withers is 130 cm. The horses are nervous in temperament. Ear length of Spiti equines is higher than rest of the breeds.

7. Zanskari

Zanskari horses are native to Zanskar Valley of Ladakh in Jammu and Kashmir. The horses are known for their ability to work, run and carry loads at high altitude. The predominant body colour is gray followed by black and copper. Horses are medium in size, well-built and are 120 to 140 cm tall. The Zanskari horses have predominant eyes, heavy and long tail and uniform gait. The body hairs are fine, long and glossy.

Registered Camel Breeds of India

1. Bikaneri

Bikaneri camels are predominantly bred in Bikaner and nearby districts, such as Sriganganagar, Hanumangarh, Churu, Jhunjhunu, Sikar and Nagaur of Rajasthan and adjoining parts of Haryana and Punjab State. The breeding tract extends in east from 71°53' to 78°15' longitude and in north from 24°37' to 30°30' latitude. The home tract of this breed is arid and sandy with extreme hot and cold climates. Bikaneri camels are well known for its draught potential and endurance. They are heavily built with attractive look. The colour varies from brown to dark blackish brown; some animals show reddish tinge. Head is dome shaped and forehead is marked with depression above the eyes. Nose is long and extends up to head. Some camels of this breed have tuft of hair around eyes, ears, below the neck, thick eye lashes. Body in general is symmetrical, massive. Ears are small, hairy and erect. Neck is medium to long, thick, fairly marked curved giving a graceful carriage head. Fore and hind limbs are long, strong and muscled. Tail is short to medium with small tufts of hair at the end. The udder is well developed in females.

2. Jaisalmeri

Jaisalmer, Barmer and part of Jodhpur district in Rajasthan is the breeding tract of Jaisalmeri and extends in east from 69°30' to 73°04' longitude and in north from 24°37' to 28°15' latitude with very poor vegetation. Sand dunes are the typical features of the tract. This medium sized breed of camel is well adapted to riding and race potential. Jaisalmeri camels are gracious, lightly lean and thin in appearance, quite tall with long and thin legs. Head and mouth are small with narrow muzzle, the eyes are prominent. The forehead is not dome shaped and is without any depression above eyes ("STOP"). Body colour is predominantly light brown. Also, there is no luxuriant growth of hairs on their eyebrows, eyelids and ears. The Jaisalmeri camels have thin skin and short hairs on body. The udder is mostly round in shape.

3. Jalori

Jalore and Sirohi District of Rajasthan is the breeding tract of Jalori camels; predominantly found in the Noon region of Jalore and adjoining areas of Sirohi District. They are medium size with well developed udder and prominent milk vein. Female used predominantly for milk and male for carrying loads. The animals are brown to dark brown.

4. Kharai

Kharia and Dariya Vara Unt are the other names for this camel breed. They are found in Kutchchh district of Gujarat. Khara means salty; he animals graze on mangroves in costal belt and also aline sp. of hrubs, so they were named Kharai. This camel is also used for draught purpose, transportation, border security, police services, and tourism. The colour varies from gray, dark brown, light red, light brown, black, and dark red. Kharai camel has typically thick neck region and medium body size than Kachchhi camel. Chest pad is short and does not touch humerus of fore legs during walking. Wool is smooth, soft and long. Generally, during monsoon, Kharai camel stays in island (locally called bets) 3-5 km away from the mainland for 2-3 months at a stretch as sweet water is available in those islands as rainwater store. They graze primarily on mangroves in the island. In summer and winter, Kharai camel are taken to nearby creeks for grazing on mangroves for 2-3 days and then to the mainland for watering. During low tide, camels swim through sea water to reach island. Besides mangroves, Kharai camel feed on other saline trees, shrubs and grass species like kharijar (Salvadora persica), Lano (Suaeda sp.)

5. Kutchi/Kachchhi

The Kachchhi breed inhabits the rann of Kachchh in Gujarat State. The major breeding tract encompasses the Kachchh and Bansakantha districts of Gujarat. The breeding tract extends in east from 68°20' to 74° longitude and in north from 22°51' to 24°37' latitude. The land is marshy with abundant salt bushes. The camels of this breed are generally brown to dark brown in colour with absence of hair on eyelids and ears. The body hairs are coarse. Head is of medium size without distinct "stop". Body size is medium. Ears are small. Camels of this breed are heavy and dull in appearance. They are stouter and little shorter. They have strong hindquarters, heavy legs, hard and thick foot pads and are well adapted to the humid climate and marshy land of Kachchh. In some animals the lower lip is droopy due to which the teeth are visible from a distance. The udder is well developed and mostly round in shape. They are good in milk producers.

6. Malvi

They were have been named after Malwa (Malwa) region, a distinct physiographic and historic-cultural area in Central India (between 27°70' -25" lO'N and 73"45'- 79"14'E) mostly occupies the plateau in western Madhya Pradesh, but also extends into South-eastern Rajasthan and into northern Maharashtra. Body colour very light to off-white with a pronounced convex forehead. Lower lip is extremely pendulous and is longer and protrudes further than upper lip. Body size small and probably the smallest of all Indian Camel.

7. Marwari

Marwar region of Rajasthan (Jodhpur, Nagaur and Pali districts) is the home to Marwari camels. They tends to be of medium height, medium build, and of fairly dark colour.

8. Mewari

Udaipur, Chittorgarh, Rajsamand districts and adjoining Neemuch and Mandsour districts of Madhya Pradesh and Bhilwara, Banswara, Dundarpur districts and Hadoti region of Rajasthan is the breeding tract and it extends in east from 73°02' to 77°20' longitude and in north from 22°55' to 25°46' latitude with fairly good vegetation and rainfall. Average height from main sea level is about 575 meters. The tract consists of hills of the Aravali in Mewar area. Mewari camels are adapted to the hilly tracts of Arawali. Mewari camels are stouter and a little shorter than Bikaneri. They have strong hindquarters, heavy legs, hard and thick foot pads. Well adapted to travel and carry loads across hills. The body hairs are coarse, which protects them from the bites of wild honeybees and insects. The body colour varies from light brown to dark brown but some animals are almost white in colour, such variation in body colour is generally not seen in other breeds of camel. The head is heavy, set on a thick neck. Unlike the Bikaneri camel, the Mewari camel has no 'stop', but its muzzle is loose. Luxuriant hair growth (Jheepra) on ears and neck is generally absent. Ears are thick and short, set well apart, tail is long and thick. The milk vein is prominent and the udder is well developed.

9. Mewati

Mewat of Haryana and Alwar and Bharatpur of Rajasthan is the home to Mewati camel. Heavily built animals that are sturdy and have heavy load carrying capacity. These are specific characteristics of this breed.

Double Humped (Not a registered breed)

This breed has breeding tract in Nubra valley of Jammu and Kashmir, mainly used for the transport and wool (hair). It is believed that these camels belong to the stock originally native to Gobi Desert of Asia and introduced by traders of Yak through silk route and widely used for transportation in silk route. These camels are suitable for cold desert areas.

Registered Pig Breeds of India

1. Agonda Goan

Agonda Goa pigs are found in North and South Goa. They are mostly black. Few animals (both male and female) have white patches on legs and face. These are small sized animals having short ears, short snout, pot belly and are wild in nature with rough bristles.

2. Doom

Dhuburi, Kokarajhar and Bongaigaon districts of Assam is the home to Doom pigs. They are black in colour with short concave snout. They are large; flat belly type with short erect ears. Top line is straight with long bristles extending up to thoraco-lumber area.

3. Ghoongroo

Ghoongroo pigs are found in Darjeeling, Jalpaiguri, Cooch Behar, Dakshin Dinajpur and Uttar Dinajpur districts of West Bengal. The animals are black but occasionally hooves and metapodials are white. Ear are pendulous and snout is concave. They posses thick coarse and long hair coat, long tail, upwardly curved snout, broad and flattened face with large and heart shaped ears resembling those of elephant. They have seven pairs of Thoraco-abdominal teats.

4. Ghurrah

Ghurrah pigs are also known by other names like Deshi and Bareilly Loca. They are found in Bareilly, Budaun, Pilibhit, Shahjahanpur and Sitapur districts of Uttar Pradesh. The animals are black but few are greyish black or brownish in colour. The animals are medium sized with flat belly, angular body and long straight snout. Legs below hock joint are white. Thick line of hairs is present from neck to shoulders. Head is elongated with triangular face and short leaf shaped vertically erected ears.

5. Niang Megha

Meghalaya is the home state to Niang Megha pigs. The pigs are black with star shaped white patches at forehead and sometimes hock joint. They have short ears and a long snout that is tapering, partially white at nostril. Bristles are long on midline, uniformly placed at other places. Hoof placement is partial. Top line is straight in male, concave in female. Female has 4-6 pairs of mid ventral teats.

6. Nicobari

They are found in Nicobar district of Andaman & Nicobar Islands. They are called Ha-un/Naut which means pig in local Nicobari language. They are mostly black and brown bu few are creamy-white, reddish-brown and black and brown mixed. The animals are sturdy and short with long body. They have medium to short snout and short erect ears. Marked bristle crest (mane) on the back extending from mid head/shoulder to base of the tail. Facial profile varied from flat to concave. Neck is short with very large jowl. No curling is the characteristic feature of the tail.

7. Tenyi Vo

Votho, Naga Local, and Suho are other names for Tenyi Vo pigs. They are distributed in Kohima, Phek and Dimapur districts of Nagaland. The pigs are mostly black in both sexes. These are potbellied animals with sagging back and pendulous belly touching the ground in females, straight tail ending with white switch reaching the hock joint, white stocking, white markings on the forehead and ventral body. Tenyi Vo pigs have strong and long tapering snout, small erect ears and bright alert eyes.

8. Zovawk

They are called Mizo local. They are found in Aizawl, Lunglei, Lawngtlai, Champhai, Saiha, Kolasib and Mamit districts of Mizoram. They are predominantly black but white spot on the forehead (star), white patches on belly (sometimes) and white boot are also common. They have rect ears, concave snout, pot belly, concave top line and long bristles on mid-line are characteristics of the Zovawk pig.

9. Mali

Mali is also famous as 'Tripura Desi Pig' preffered for slaughtering as rituals of the local community found within Tripura. Medium sized with pot belly. Medium to small bristles are ubiquitosly distributed throughout the body. Animals are characterized with short erect ears lying perpendicular to body axis and concave snout.

10. Purnea

Purnea is pig breed from Bihar state. Animals have mainly black coat colour, few animals have white spot at the lower limbs. These pigs have compact body and pot belly. Thick line of bristle is present on topline from neck to shoulders giving the animal a wild look. Animals are characterized with round face; short conical and erect ears; and small, thick and slightly concave snout. Skin is thick with neck folds in mature animals.

11. Banda

A pig breed found in Jharkhand, mainly reared for pork and manure. Animals are black coloured, having short and erect ear. Average adult body weight is 28.0 kg in male and 27.0 kg in females. Litter size ranges from 4 to 7.

12. Manipuri Black

It is native pig of Manipur state, mainly reared for meat. Adult body weight averages about 96.0 kg in males and 93.0 kg in females. Litter size ranges from 6 to 11 at birth. Meat is preferred for its taste by local people.

13. Wak Chambil

Small sized pig breed with round and pendulous belly. It is mainly distributed in Garo Hills of Meghalaya. Pork is known for its unique flavour and taste and cherished during religious and ceremonial occasions by local people. Average adult body weight is32.0 kg in males. Litter size at birth ranges from 4 to 11.

Registered Donkey Breeds of India

1. Halari

Jamnagar and Devbhoomi Dwarka distrcits of Gujarat is the major breeding tract of Halari donkeys. They are white in colour with black muzzle and hooves. Mane is white. Forehead and nasal bone are mostly convex. Ears are mostly erect. Back is mostly concave. Halari donkey has a strong built and large size.

2. Spiti

Spiti donkeys are found in Kinnaur, Lahul and Spiti districts of Himachal Pradesh. The animals are mainly brown, also brown-black and black. Major white markings are mostly found around muzzle and sometimes around eyes. The face is also covered with long hairs like rest of the body. The head is comparatively broader and shorter. Tail extends up to hocks. Tail switch is not distinguishable due to presence of long hair on rest of the tail.

3. Kachchhi

Only donkey breed used for Agricultural activities like Inter cultivation in field crops found within katch district of Gujarat. Coat colour is mainly grey followed by white, brown and black with dorsal and shoulder stripes and Zebra marking in few animals. Forehead is convex. Nasal bone is straight. Docile in temperament.

Registered Yak Breed of India

1. Arunachali Yak

Arunachali yak is distributed in West Kameng and Tawang districts of Arunachal Pradesh. Majority of the animals are black; few animals have white forehead/white face/white strip from hump to tail. Horns are mostly curved forward followed by backward with pointing tips. Some animals have upward or inward or lateral or downward pointing horns. The average size of horn in male animal is 28-35cm while it is 18-24cm in female. They have a medium sized compact body with short and stocky legs. Horizontal ear is typical characteristic of Arunachali Yak. Poll is prominent with convex head. Udder mostly trough shaped with cylindrical teats. Brisket, belly, ribs, lateral parts and legs are covered with long hair.

Registered Duck Breed of India

1. Pati

Pati duck belongs to Assam. The plumage type is normal and brown in colour while the pattern is select. The comb is select type. Skin and shank are yellow in colour and they lay white shelled eggs.

2. Maithili

These are native to the 'Mithila region' of Bihar state and thrive under a free-range management system. These ducks are raised both for meat and eggs. These ducks have uniform light/dark brown feathers all over their body. Ducks are unique in their morphological characteristics with attractive colour patterns in the mosaic plumage; circular feather patches (mosaic pattern) in ducks and dark brown to ash gray in ducks. The head is glossy black to greenish black in ducks and brown in ducks. The tail is brown to black. The posture is slightly vertical and the shape of the beak is horizontal.

Registered Geese Breed of India

1. Kashmiri Anz

Kashmiri Anz is also known by the name Anz. Srinagar, Baramulla, Budgam, Bandipora and Ganderbal distrcits of Jammu & Kashmir is the native tract of this breed. They have normal plumage pattern with select plumage pattern. They have white and cinnamone coloured pattern with select comb type and select skin colour. The shank is orange in colour. They lay white shelled eggs. The birds are complete yellow through all intermediate grades. Knob present in 45%, dewlap in 3% and paunch in 14% geese. Eye colour is either gray or brown. Sexual dimorphism on basis of plumage and eye colour is absent.

Registered Dog Breed of India

1. Rajapalayam

Medium size dogs from Tamil Nadu with compact body and coat colour is white. Height at wither ranges from 55 to 72 cm in males. Adult body weight 14 to 32 kg. Utilized for guarding of farms and houses. Highly obedient and easily trainable. Estimated population is 3,000–4,000.

2. Chippiparai

Chippiparai dogs from Tamil Nadu are also called as Kanni (virgin) or vettainaai (hunting dog). Medium in size, coat colour varies from fawn to dark brown, brownish black and black. Height at wither ranges from 60 to 76 cm in males. Utility is guarding and hunting. Estimated population is about 6,000.

3. Mudhol Hound

Also known as Pissouri Hound or Lahori Hound from Karnataka, is having aerodynamic body with high stamina and endurance. Head is small, skull is long and narrow. Ears are medium, thin, triangular and set high. Abdomen is tucked. The tail is long and tapering. Height at wither ranges from 73 to 80 cm in males. Used for guarding and shepherding. Estimated population is ~1,500.

Source: Breed monographs published on each breed and Animal genetic resources of India-Information System (AGRI-IS).

Registration of Animal Genetic Resources (AnGR) to protect the legal rights of stakeholders

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India as a signatory of the CBD, and also promulgated legislation for protection of biodiversity in form of The Biological Diversity Act in 2002. Protection of AnGR per se got the momentum after developing The Global Plan of Action for AnGR by the Food & Agriculture Organization (FAO) as Interlaken Declaration in 2007 and subsequently CBD-Nagoya protocol for Access & Benefit Sharing and Indigenous Knowledge in 2010. Further, various targets specially CBD's Aichi Biodiversity Targets (2010) and the UN's Sustainable Development Goals (SDGs) have been further crusaded the global efforts for the protection of AnGR diversity. SDG 2 (Zero Hunger) envisioned the proper management of all kinds of genetic resources to promote sustainable agriculture and achieving food security and oriented towards the preservation of farm animal biodiversity. 'Delhi Declaration' in 2016 is another milestone framework for protection of valuable germplasm globally.

India possesses a huge AnGR diversity distributed over a large range of geographical, ecological and climatic regions. A range of farm animal species like zebu cattle, riverine buffalo, swamp buffalo, sheep, goat, pig, horse, donkey, camel, yak mithun, chicken, duck and geese are natively inhabited in the region for centuries. In any given geographical regions in the world, none of country is that much rich in farm animal diversity. These species are further diversified in form of unique populations called breeds specific utility and unique attributes of adaptation. The animal breeds have been evolved through of various evolutionary processes including man made selection for different needs. Creating inventory of animal breeds, with their unique attributes is important to recognise their characteristics and uniqueness. In fact, the characterization and inventory have been recognized as the foundation of proper management of AnGR.

Registration of animal breeds

'Animal breed' is considered as a referral point for the farm animal diversity, and as per FAO, it can be defined as "sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within same species. Moreover, breed is a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity. Each breed serves a specific purpose to the food and agriculture for the mankind within a well-defined geographical region.

Registration of native breeds of livestock and poultry has been envisioned to protect and check the bio piracy of indigenous AnGR and our country has developed the mechanism for recognising breeds with known characteristics in form of authentic national documentation system. Indian Council of Agricultural Research (ICAR) initiated "Registration of Animal

Germplasm" specifically indigenous livestock and poultry breeds in the country in the year 2007. In the year, 2008, ICAR-National Bureau of Animal Genetic Resources (NBAGR), Karnal was given the temporary authority for the registration of germplasm related to livestock and poultry in the country. Subsequently, in 2008, ICAR constituted a Breed Registration Committee (BRC) under the chairmanship of Deputy Director General (Animal Science), ICAR for the registration of new breeds. This mechanism is the sole recognised process for registration of "Animal Genetic Resources" material at national level.

Breed registration process

The registration of Indian livestock and poultry germplasm revolves around the concept of a breed. Breeds of domesticated animals, which are unique, stable and uniform, and have potential attributes of academic, scientific, or commercial value can be registered. Any livestock population which has been characterized must be documented and inventoried, if having the breed characters. First, all of the information recorded during phenotypic characterization, should be formatted in a shape of breed descriptor. Such an physical characterization along with management practices can be published in different scientific journals. After phenotypic characterization, it should be clear that If the population is found distinct, then only it should to be registered as breed.

First, all of the information recorded during phenotypic characterization should be shaped as a breed descriptor. Such a physical characterization along with management practices can be published in different scientific journals. The registration involves a process for screening of the applications submitted for registration as per Guidelines developed for this purpose. The application can be submitted by any citizen of India / breed society / NGO / Govt. Agency. The application must be accompanied by a complete description of the breed using standard descriptors. All claims concerning the material submitted for registration should accompany scientific evidence for uniqueness, reproducibility, and value. The population, for consideration of registration should have at least 1000 animals. The breed should complete a minimum of 10 generations. A detailed history of the breed, Difference, distinction, and details that are specific for that breed should also be provided. Representative photographs, a list of the registered animals of the breed, letters explaining certain questions about the breed from at least three different breeders/owners of the breed should also be submitted. After registration, NBAGR provides the unique Accession number to each breed after registration. The newly registered breeds are also notified through Official Gazetted published by the Government of India. Detailed guidelines, descriptors and application form for registration of new breeds can be accessed at www.nbagr.res.in/guidelines.html.

Breed registration criteria

- Unique, stable and uniform population with potential attributes of academic, scientific or commercial value
- Population: at least 1000 animals and also maintained in field conditions for minimum of 10 generations
- Breed application, with standard descriptors
- Accompanying with scientific evidence
- Signed by the applicant
- countersigned by Director, AHD of concerned state with rubber seal
- A detailed history of the breed
- List the difference, comparison to other breeds
- Photographs of the breed
- Letters from at least three different breeders/owners of the breed.

Present status of breed registration

Initially, the known breeds of livestock and poultry were registered as extant breeds, and simultaneously process for registration of new breeds was initiated. First time in the year 2008, all 129 extant breeds of livestock and poultry were registered by the ICAR-NBAGR. Further 83 new breeds were added and by 2022, the number reached 212; which included 187 breeds of livestock and 22 of poultry and 3 of dog. The breeds include 53 of cattle, 20 of buffalo, 37 of goat, 44 of sheep, 7 of horses and ponies, 9 of camel, 13 of pig, 3 of donkey and one of yak in livestock and 19 of chicken, one of geese and two of duck in poultry and three for dog species. Breeds Registered by ICAR-NBAGR during different years are presented in table 1.

The Gazette Notification of registered breeds

After realizing the need to protect the valuable agricultural genetic resource biodiversity specific to indigenous farm animal germplasm in the country and claiming its sovereignty over the germplasm, the Gazette notification for the livestock and poultry breeds was initiated by the Government of India in October, 2019. To provide legal safeguards for germplasm protection, notification of indigenous breeds being registered by ICAR has started in the year 2019 through publishing the Official Gazette by the Government of India. All registered breeds up to that year (total 184 breeds) were first time notified by the Government of India to provide statutory recognition of and claiming sovereignty over the native germplasm [Gazette Notification: Ministry of Agriculture and Farmers' Welfare, No. 3364 (S.O. 3699(E)) (October 14, 2019)] and further all newly registered breeds (28 breeds) in subsequent years were notified through five Gazette notifications. These breeds got the statutory recognition; and shall be the notified breeds for the whole of India for purposes of animal husbandry, production, breeding, conservation, utilization, consumption and trade from the date of publication of the notification in the official Gazette of Govt. of India. The notified breeds of the specified States received the statutory recognition; and were recognised as notified breeds for the whole of India for keeping and rearing for various purposes as mentioned in the notification.

Impact of breed registration

Registration of breeds of native livestock and poultry has a broader impact through modulating various policies and programs and affecting all stakeholders of the livestock sector in the country. Most importantly, it enabled to conduct breed wise livestock census by the Govt. of India which could ensure the precise population of each of the breed in the country. This has come to be much useful for suitable policy formulation for their conservation and development if the breed is endangered. A total of 83 new breeds were added after the initiation of the registration process, which has put about 25 million livestock and poultry into the descript category in the country. In the 19th Livestock Census (2012), a total of 143 breeds were included in breed wise survey. Further, 20th Livestock Census was carried out on 184 registered breeds in the country. Based on breed wise census, it is imperative to define the risk status of the breeds and as per preliminary data about 24 breeds are a risk in the country. Breeding policies have been formulated for many newly registered breeds in many states with recent example of Haryana, Odisha, Nagaland, Ladakh (UT). At national level, National Kamdhenu Breeding Centre, An initiative by Govt. of India has covered all NBAGR registered breeds of cattle (41) and buffalo (13) for conservation, promotion, and development. Farmers are best benefitted by the registration process. After breed recognition, superior quality germplasm of the breed becomes available to the livestock owners. Various governmental facilities for animal-based farming, small to large /commercial scale become available to the farmers when the animal farming is based on the registered breeds. Breed societies have been developed for various native livestock breeds in their native tract by the local livestock keepers, which ensured improvement of germplasm, strengthening of the production system and marketing of the products and benefit-sharing among the society. As an example, benefits of Ongole embryo germplasm export were disseminated among the society of the breed.

The Gazette Notification also provided legal support to germplasm protection of the registered breeds and for developing mechanisms for sharing benefits among the animal keepers. In an era of globalization, there remains a constant threat of germplasm piracy as well as forged patenting and IP rights to the inherent characteristics. Registration and notification would keep the proper check for such spurious activities related to precious native germplasm. Notification of breeding areas of registered breeds also enables to develop suitable breeding strategies for the genetic improvement and development programme of low productive native animals. As defined in Livestock Breeding Policy, such breeds can be improved by their own germplasm through selective breeding and no other germplasm can be introduced in the notified breeding tract of registered breeds. In this way, registration of native breeds would be helpful in not only the protection of our germplasm but also their improvement as well as avoiding genetic dilution. Breeding policies for many newly registered breeds are being developed by the respective state departments.

Nevertheless, the framework of breed registration and the gazette notification has certainly broadened its impact through modulating various policies and programmes. Along with preserving the biodiversity as mandated, the stakeholders specially Farmers would be the best benefitted. After breed designation, superior quality germplasm of the breed become available to the livestock owners. This sui generis system would also provide the legal support to Intellectual Property Rights of the registered breeds and for developing mechanism for sharing benefits among the animal keepers.

Future action points

- New breeds of indigenous livestock and poultry with unique characters may be explored and registered specifically from remote and inaccessible regions of the country.
- Synthetic populations of livestock species evolved by different organizations in India may also be registered.
- A legislation may be promulgated for animal breed protection and farmers rights in this direction.

Reference

FAO (2007) Global plan of action and the Interlaken declaration commission on genetic resources for food and agriculture food and agriculture organization of the United Nations Rome.

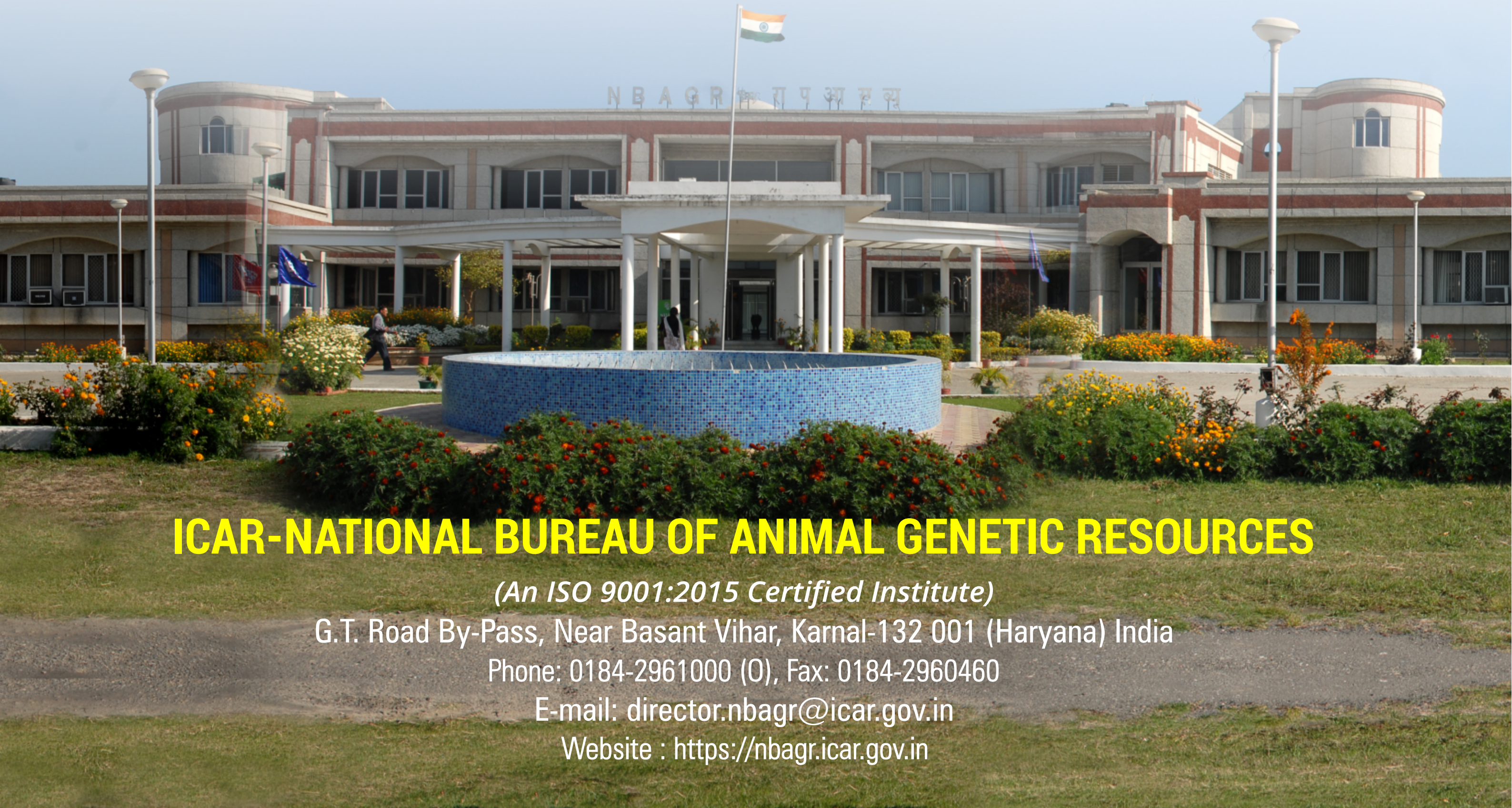
ICAR-NBAGR (2016). Guidelines for Management of Animal Genetic Resources of India, National Bureau of Animal Genetic Resources (ICAR), Karnal, http://www.icar.nbagr.gov.in/guidelines

Table 1 Breeds Registered by ICAR-NBAGR during different years

Species	Extant breeds	2010-11 (12.04.2010)	2012-13 (14.05.2012)	2014-15 (06.01.2015)	2016-17 (21.06.2016)	2017-18 (04.08.2017)	2018-19 (05.9.2018)	2019-20 (24.1.2020)	2020-21 (16.09.2020)	2021-22 (16.08.2021)	2022-23 (31.08.2022)	New reg. breeds	Total
Cattle	30	1. Motu, 2. Ghumusari 3. Binjharpuri 4. Khariar	1. Kosali, 2. Pulikulam 3. Malnad Gidda	1. Belahi 2. Gangatiri	1. Badri	1. Lakhimi	1. Ladakhi 2. Konkan Kapila	1. Poda Thurpu 2. Nari 3. Dagri 4. Thutho 5. Shweta Kapila 6. Himachali Pahari (Gauri) 7. Purnea			1. Kathani 2. Sanchori 3. Masilum	23	53
Buffalo	10	1. Banni, 2. Chilika	1. Kalahandi	-	-	-	1. Luit (Swamp) 2. Bargur 3. Chattisgarhi	1. Gojri		1..Marwadi 2. Manda	1. Purnathdi	10	20
Sheep	39	-	-	1. Kachaikatty Black	1. Chevaadu 2.Kendrapada	-	1. Panchali	1. Kajli				5	44
Goat	21	-	1. Konkan Kanyal 2. Berari	1. Pantja	1. Teressa 2. Kodi Adu	1. Salem Black 2. Sumi-Ne	1. Kahmi 2. Rohilkhandi 3. Assam Hill 4. Bidri 5. Nandidurga 6. Bhakarwali				1.Sojat 2.Karauli 3.Gujari	16	37
Horse	6	-	-	-	-	1. Kachchhi-Sindhi	-					1	7
Pig	0	-	1. Ghoongroo 2. Niang Megha	1. Agonda Goan	1. Tenyi Vo, 2. Nicobari 2. Doom	1. Zovawk	1. Ghurrah	1. Mali 2. Purnea			1. Banda 2. Manipuri Black 3. Wak Cahmbil	13	13
Camel	8	-	-	1. Kharai	-	-						1	9

Donkey	0	-	1. Spiti	-	-	-	1. Halari	1. Kachchhi				3	3
Yak	0	-	-	-	-	1.Arunachali						1	1
Chicken	15	-	-	1. Mewari	1. Kaunayen	1. Hansli	1. Uttara					4	19
Duck	0					1. Pati		1. Maithili				2	2
Geese	0					1. Kashmir Anz						1	1
Dog	0					2.			1. Rajapalayam 2. Chippiparai 3. Mudhol Hound			3	3
Total	129	6	9	7	9	9	15	13	3	2		83	212
Chicken Line	0			PD1 (Vanaraja male line)				PD-2 (Vanraja female)				2	2

गौरवशाली भारतीय पशु जैव-विविधता
का सजग एवं सतत् प्रहरी....



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