Scientific Research Publishing

Open Journal of Animal Sciences, 2021, 11, 304-332
https://www.scirp.org/journal/ojas
ISSN Online: 2161-7627
ISSN Print: 2161-7597

# Cattle Conservation in the 21st Century: A Mini Review

**Umar-Faruq Olayinka Bolaji[1], Afees Abiola Ajasa[2], Ridwan Olawale Ahmed[3], Semiu Folaniyi Bello[4*], Obiajulu Emenike Ositanwosu[5,6]**

[1]Department of Animal Production, College of Food Science and Agriculture King Saud University, Riyadh, Saudi Arabia
[2]Department of Animal Husbandry, University of Debrecen, Debrecen, Hungary
[3]Department of Animal and Avian Sciences, University of Maryland, College Park, USA
[4]Department of Animal Genetics, Breeding and Reproduction, College of Animal Science, South China Agricultural University, Guangzhou, China
[5]Department of Agricultural Electrification and Automation, College of Mathematics and Informatics, South China Agricultural University, Guangzhou, China
[6]Department of Computer Science, Nnamdi Azikiwe University, Awka, Nigeria
Email: ubolaji@ksu.edu.sa, afees@mailbox.unideb.hu, ahmedridwan341@gmail.com, *sfbello70@yahoo.com, ositanwosuobiajulu@yahoo.com

**How to cite this paper:** Bolaji, U.-F.O., Ajasa, A.A., Ahmed, R.O., Bello, S.F. and Ositanwosu, O.E. (2021) Cattle Conservation in the 21st Century: A Mini Review. *Open Journal of Animal Sciences*, **11**, 304-332.
https://doi.org/10.4236/ojas.2021.112023

**Received:** March 13, 2021
**Accepted:** April 27, 2021
**Published:** April 30, 2021



## Abstract

Cattle are arguably the most important livestock species. Since the beginning of this century, the loss of genetic diversity within this species has been a major concern as this could have serious consequences on the ability of this species to respond to future production constraints. Genetic diversity has traditionally been accessed from pedigree, however, with the advances in molecular genetics new opportunities have emerged. We examined different methods for accessing genetic diversity and estimating genetic diversity parameters at the genomic level. We also examined criteria and strategies for the conservation of animal genetic resources. Finally, we examined genomic studies on some endangered cattle breeds.

## Keywords

Genetic Diversity, Conservation, Genetic Diversity Parameters, Cattle

## 1. Introduction

Arguably the biggest threat to biodiversity across the planet is habitat degradation, resulting from direct or indirect human activities [1] [2]. As the human population increases rapidly, we modify the landscape to meet our increasing need for the resources to sustain our modern lifestyles. Presently, the world's

population is currently growing at 1.5 percent per annum [3]. Corresponding to this increase is a rise in energy consumption that is driving climate change across the globe. The rapid pace of the changing climate will outpace the natural ability of some species to respond to survival [4].

A temporal analysis reported by [5] suggests that loss of biodiversity indicates that the Earth is on the path to its sixth mass extinction event, with the rate of extinction in the last century conservatively estimated to be 22 times faster than the historical baseline rate as reported by [6]. It is even more austere when we analytically examine population declines, rather than the complete loss of species, as 32% of known vertebrate species are showing substantial population deterioration [7]. The continuous increase in the human population coupled with rising incomes and urbanization necessitates the need to conserve the genetic potential of animals to avoid or lower the consequences of biodiversity loss.

During the spread of livestock species across Europe, Asia, and Africa, numerous geographically separate populations of livestock species emerged, where each of these populations is expected to have adapted to their respective environment. Mutation, random genetic drift due to geographical separation, population size bottleneck, and genetic reshuffling (recombination); also, adaptation to a diverse selection pressure imposed by climate, nutritional factors, disease, and parasites are natural agents that discern the species and breeds of livestock [8]. Over the years, human-imposed breeding strategies led to the development of essentially closed populations—with members distinguished based on visible phenotypic traits; described as breeds [9].

Consequently, conservation of farm animal breeds had been for several reasons, for example, to retain potentially useful genes and gene combinations such as the Booroola fecundity gene in sheep [10], the exploitation of heterosis, and to overcome selection plateaus, in addition to cultural motivations, research, and food security. Sustaining genetic diversity also offers indemnification against climate change, disease, changing availability of feedstuffs, social change, selection errors, and unexpected catastrophic events such as the Chernobyl where many local breeds' diversity became threatened [11].

A large number of wild species and domesticated breeds of animals now require human intervention to maintain their survival and to study the diversity within the genome which is an important aspect of conservative genetics [12] [13] [14] [15]. As stated by [16], the conservation of genetic diversity is, however, a form of guarantee against possible unexpected environmental conditions because it is a means of maintaining potential adaptation abilities. Hence, the conservation of biological (genetic) diversity in animals has attracted a great deal of attention.

Cattle are important livestock species for human survivability, but certain breeds are at the risk of extinction [17]. According to a report by [18] on the state of animal genetic resources, 17% of the world livestock breeds are on the verge of extinction despite an increasing number of actions to preserve biodiver-

sity. Sequel to the rigorous activities of human-induced selection, highly productive cattle breeds have replaced less productive ones resulting in the extinction of some and numerous others on the verge of extinction [12] [19].

Artificial selection criteria imposed by man (back-crossing of domesticated animals with their wild ancestral species) are factors that have made livestock breeds evolve and have created numerous cattle breeds that display broad phenotypic and genetic variation [20] [21]. As reported by [22], artificial selection has proved to have a rapid and significant effect on the phenotype and genome of organisms; and has resulted specifically to diverse cattle breeds that are specialized for either milk or meat production or raised as dual-purpose breeds and consequently the neglect of the inferior ones [23]. Studying the estimation of diversity within these populations is therefore an important aspect in conservation genetics to retain the potential and economic traits of the animals from going into extinction.

Therefore, the objectives of this review are to examine different methods for accessing genetic diversity and estimating genetic diversity parameters at the genomic level. To discuss the criteria and strategies for the conservation of the animal genetic resources and examine genomic studies on some endangered cattle breeds using here strategies.

## 2. Estimating Genetic Diversity in Livestock Breeds

In livestock science, conservation genetics is based on estimating diversity by pedigree relatedness and choosing those animals that maximize genetic diversity [24]. One of the main research priorities for the threatened species includes the characterization of genetic diversity and population structure which leads to more effective conservation and management strategies that are necessary to estimate genetic diversity [25] [26]. Also, the identification of the genomic regions affected by natural and artificial selection is a relevant research niche in livestock population genetics and useful in genetic diversity conservation [27].

These diversities are unravelled by statistical techniques and the knowledge about the relationship between the animals. Generally, half of the total genetic variation within species is estimated to be between breeds, hence the loss of breeds can substantially reduce genetic variation within species [28]. The genetic diversity observed within breeds is, therefore, defined as the allelic variation in a group of individuals. Genetic diversity of domestic cattle can be divided into two components; differences occurring between species from different breeds and those differences between individuals within a single breed measured as differences in their DNA [15] [29] which has a significant contribution to the sustainability of animal production [30]. Remarkably, genetic diversity is usually related with heterozygosity in population genetics [31].

Previously, the selection of breeds for conservation has been difficult until a more operational theoretical framework was developed by [32]. This analytical framework was adopted by animal geneticists using a diversity function to eva-

luate the biochemical polymorphism of 19 European cattle breeds including 18 French breeds and the British Shorthorn Cattle breeds [33]. More recently, the development of molecular biological techniques for the detection of variation in the DNA facilitates a more accurate description of genetic variation. Repetitive sequences of genomic DNA have opened a great means to estimate the genetic information associated with a particular organism [34]. It becomes easier to study genetic diversity with the help of these repetitive sequences. Molecular markers offer numerous advantages over conventional phenotype-based alternatives as they are stable and detectable in all tissues despite growth, differentiation, discrimination, defence, or development status of cells. The greater the genetic diversity within species, the greater the chances of long-term survive for such species [35].

Furthermore, mitochondrial DNA analysis, Nuclear DNA (Y-chromosomal haplotypes, and autosomal), and microsatellites analysis provide more viable alternatives as compared to the conventional blood groups, enzyme polymorphisms, transplantation antigens, and RFLP analysis. The collection of molecular data using microsatellite markers is a useful way of investigating the genetic diversity and differentiation among species and breeds of cattle [18]. These methods have also been used to investigate the genetic diversity of breeds in developing countries such as in Ankole longhorn breeds [36] [37] and, Afrikaner cattle breeds [38]; as well as several indigenous cattle breeds in Mozambique [39], Cuba [15], Cameroon [40] and India [41]. More recently, Single Nucleotide Polymorphisms (SNPs) [19], Copy Number Variants, Whole Genome Sequencing Analysis are the newly adopted techniques to study genetic diversity.

## 3. Parameters for Estimating Genetic Diversity

### 3.1. Effective Population Size

The primary factor responsible for the rate of loss of genetic diversity as well as the rate of increase of inbreeding and genetic drift in a biological population is the effective population size ($N_e$) [42] [43] [44].

As defined by Wright [45], $N_e$ is defined as the size of an idealized population undergoing the same rate of genetic drift as the population under study. The effective population size is not usually equal to the census size (N) of the population. Discrepancies can sometimes be extreme, for instance in the case of the Holstein cattle breed [46]. Despite being a worldwide dairy cow breed with a census size of millions of individuals, the $N_e$ of the whole population is about 100 [47]. This implies that the Holstein breed accumulates inbreeding at the same rate as an ideal population of only 100 individuals [46]. Fluctuations in census population size, breeding sex ratio, and variance in reproductive success are the factors that influence the size of $N_e$ [48].

Estimation of $N_e$ can be achieved using approaches that fall into three methodological categories which are demographic, pedigree-based, or marker-based [49]. Demographic method occasionally provides crucial Ne estimate which is

based on simplified population models and limited population data [49] The pedigree-based approach provides a complete population description [49] but has a problem with incomplete pedigree records [48] [49]. However, the use of genomic information (*i.e.* marker-based approach) has been proposed to overcome the challenge of incomplete pedigree [48] by estimating Ne from information on linkage disequilibrium [50] [51]. $N_e$ is an important measure to preserve diversity and it explains genetic variability [52]. It is also an important parameter to control unfavourable events such as inbreeding and bottleneck effects in a population [53] [54] $N_e$ can be used to evaluate the threat status of a population and to design breeding programs for both wild/captive populations and autochthonous livestock breeds [46] As a "rule of thumb", it has been suggested that a minimum $N_e$ of 50 is required to avoid the effects of inbreeding depression in the short-term [55], and larger than 500 if the interest is to maintain the evolutionary potential of the population over the long term [56].

### 3.2. Linkage Disequilibrium

Linkage disequilibrium (LD) is the non-random assortment of alleles at different loci [57] [58], which occurs when chromosomes are mosaics, and this occurrence depends on recombination rate, mutation rate, population size, and natural selection. A better understanding of LD is very important for genetic studies [59]

The information on the degree of LD in livestock populations is important to determine the minimum distance between the markers required for effective coverage when conducting genome-wide association studies (GWAS), marker-assisted selection (MAS) and genomic studies [60], and gene mapping and evolutionary inferences [58]. Furthermore, the pattern of LD is a powerful indicator of the genetic forces shaping a population [58]. However, the terms linkage and LD are puzzled.

LD is population-specific and is difficult between populations depending on the demographic history of the populations [61] [62] [63]. Also, the LD of genome markers is related to various evolutionary forces such as inbreeding, non-random mating, population bottleneck, drift, recombination, and mutation [64].

Considering the economic importance of domesticated animals, the knowledge of the dimension of LD enables the planning and execution of successful genomic breeding programs to achieve global food security.

### 3.3. Hardy-Weinberg Equilibrium

In 1908, the British mathematician Godfrey H. Hardy and German physician Wilhelm Weinberg independently discovered the relationship between gene and genotype frequencies, known as the Hardy-Weinberg principle, or Hardy-Weinberg equilibrium (HWE) [65] [66]. This discovery marked the beginning of the field of population genetics and has become a powerful research tool in both theoretical and applied research in population and quantitative genetics [67].

HWE is the relationship between the allelic and genotypic frequency that holds for most genetic markers. Also, HWE is not simply a theoretical law; deviations can signal important problems, errors, or peculiarities in the analyzed data sets [68] [69].

The theory of HWE has played a critical and powerful role in the development of population genetics and has frequently been used as a basis for genetic inferences [70]. Tests for differences from Hardy-Weinberg proportions are often used to confirm random mating in populations, and the deviations from the expected frequency of homozygotes are used to evaluate inbreeding coefficients [71]. Moreover, the validity of genetic association studies depends considerably on the use of appropriate controls such as HWE [72]. In recent decades, there has been a greater interest in retrieving and conserving local breeds, especially their capacity to adapt in marginal areas and for their importance as a reservoir of genetic diversity [64].

### 3.4. Heterozygosity

One of the parameters commonly used as an estimate of genetic diversity is Heterozygosity—Observed and Expected heterozygosity. In a population at hardy-Weinberg equilibrium, Expected Heterozygosity can be defined as the proportion of heterozygous individuals in that population with equal allelic frequencies as that observed in the population [25]. It is estimated with the formula: $H_e = 1 - \Sigma P^2$, where P is the frequency of alleles at the locus. The higher the $H_e$ value is, the more genetically diverse the population.

Because the populations we work with are usually finite and not at hardy-Weinberg equilibrium, expected heterozygosity usually varies from the Observed heterozygosity. Observed heterozygosity is the actual proportion of heterozygotes in the population. Microsatellite marker [73] and SNP chips have been used to estimate heterozygosity in cattle [74].

### 3.5. Homozygosity

Homozygosity increases in a population where closely related animals are mated. It is estimated with a parameter called runs of Homozygosity (ROH). ROH is defined as a continuous stretch of the genomic segment without heterozygosity in the diploid animal [75]. Concerning effective population size, it has been observed that smaller populations tend to have a higher number of ROH and vice versa [75]. In terms of inbreeding, populations with a high inbreeding coefficient are associated with longer ROHs segment [75]. ROH can be estimated with the use of microsatellites [75] and SNP array [76].

### 3.6. Genetic Distance and Population Differentiation

The standard genetic distance (*D*) is often used as a common parameter for classification and evolutionary studies [77]. It is the accumulated number of gene differences per locus and across the genome. The expression that estimates the

genetic distance between two randomly mating diploid populations (X and Y) in which multiple alleles segregate at a locus is given as; $D = -\log_e I$, where $I = J_{XY} \Big/ \sqrt{J_X J_Y}$; $J_X$, $J_Y$, and $J_{XY}$ are the arithmetic mean of $j_X$, $j_Y$, and $j_{XY}$ respectively.

However, the above formula holds if the rate of gene substitution per locus is the same for all loci. Rather data on amino acid substitution in some proteins indicates that the rate of substitution varies considerably among loci [78]. So, when the rate of gene substitution varies among locus, a more appropriate measure of genetic distance [79] is given as; $D' = -\log_e I'$, where $I' = J'_{XY} \Big/ \sqrt{J'_X J'_Y}$ in which $J'_X$, $J'_Y$, and $J'_{XY}$ are the geometric means of $j_X$, $j_Y$, and $j_{XY}$ respectively. The formula can also be expressed as; $D' = \left(\sum_{j=1}^{n} d_j\right) \Big/ n$, where $d_j$ is the value of $-\log_e I_j$ at the $j$th locus and $n$ is the number of loci examined.

Concisely, a measure of the genetic distance (D) based on the identity of genes between populations is expressed as $D = -\log_e I$, where $I$ is the normalized identity of genes between two populations which is equivalent to protein identity. If the rate of gene substitution per year is constant, it is linearly related to the divergence time between populations under sexual isolation. It is also linearly related to geographical distance or area in some migration models. It is important to note that population differentiation is estimated as the genetic distance between isolated populations and the distance between incompletely isolated populations. Further clarifications as to how genetic distance can be estimated in these forms of populations can be found in Nei's (1972) report. Since $D$ is a measure of the accumulated number of codon differences per locus, it can also be estimated from data on amino acid sequences in proteins even for a distantly related species. Thus, if enough data is available, the genetic distance between any pair of organisms can be measured in terms of $D$. This measure applies to any kind of organism without regard to the ploidy or mating scheme [79].

There had been several variations of $D$ that have been proposed and used over time, for example, $D_C$ [80], $D_A$, $D_m$ [77], $D_{SW}$ [81], and $D_{LR}$ [82]. A comparison between some conventional parameters of genetic distance [e.g., $D$, $F_{ST}$, $R_{ST}$, and $(\delta\mu)^2$], and newly introduced ones [e.g., $D'$, $D_K$, $D_{CSE}$, and $D_{SA}$] *have also been conducted* [62] [83].

## 4. Setting Priorities for Conservation

Though conservation decisions rely upon a range of information including the degree of endangerment, adaptation to a specific environment, possession of traits of current or future economic importance, possession of unique traits of scientific interest, and the cultural or the historical value of the breed. Moreover, accurate assessment of populations concerning their contribution to national and overall genetic diversity is an important step in determining priorities for conservation [84].

It is imperative to note that, to retain or maximize among-breed diversity, it

might be predictable that genetically divergent breeds are given the highest priority. However, when objective measures of genetic relationships among breeds are obtainable, other criteria for setting priorities may be classified as; 1) risk of breed extinction, 2) measure of "merit" of the breed, 3) within breed variation [85] [86]. Breeds at the peril of extinction are mostly classified as being threatened, based on their current population numbers (numbers of males and females), alterations in population size, and the degree of crossbreeding with other breeds [87]. The probability of extinction for each breed can be estimated by simply relating the current population size to a critical effective size and accounting for other demographic and environmental risk factors. These risk factors may include a decreasing number of breeding females; reduced population size; high level of crossbreeding; alteration in the production environment and so on [9].

The measure of traits unique to each breed (which may include adaptive, production, and other quality traits of sociocultural and ecological value) may be classified as breed merits. Ideally, objective information about these phenotypic traits should be available, nevertheless, subjective information relating to the adaptation or unique features from the local animal owners should be considered. Besides, a decision-making system that takes both the phenotypic merit and measures between and within breeds' genetic diversity into account was developed by [88]. Though sociocultural and ecological values may be difficult to define, therefore, it is important to consider the opinions of indigenous owners.

While it is important to measure genetic variability among populations, the measure of within-population variability would not be out of place in priority decision-making. The measure of within-population variability has been described above. Though there are differences in opinions of which method best measures the within-population variability, in the context of conservation and minimizing loss of diversity, "the number of alleles per locus" is most appropriate [89]. A more detailed analogy of these steps can be found in a report published by [18].

## 5. Categories/Strategies for Farm Animal Genetic Resources Conservation

### 5.1. *In Situ* Conservation

At large, *in situ* conservation or conservation by utilization is an ideal mechanism to conserve breeds, in a way that diversity is optimally utilized in the short-term and maintained for the long-term [18]. A breed has to evolve and acclimatize to changing environments and efforts to fashion a need for products or functions of the breed should be encouraged. However, continuous conservation deprived of further development of the breed or without expected future use is not an essential strategy. This approach is expensive, and unless the breed can be used for production, it is not likely to succeed [90]. Activities relating to *in*

*situ* conservation may include performance recording, schemes, development of breeding programs, and management of diversity within populations. It also includes steps taken to ensure sustainable management of ecosystems [91] [92] concluded that the conservation of traditional systems may depend on the conservation of the breeds that resides in them.

Furthermore, in addition to in situ conservation, practices to maintain live animals outside their production or natural environment (*ex-situ* live) or through cryopreservation of germplasm (*ex-situ*) are established to preserve germplasm of rare breeds as well as the more commonly used commercial breeds in the case of cattle and other livestock species [93] [94]. Besides, cryopreservation of germplasm is the current state of the art in *ex-situ* strategy and an integral part of conservation strategies employed to conserve existing allelic diversity for future use [95].

## 5.2. *Ex-Situ* Conservation

### 5.2.1. *Ex-Situ in Vivo* Conservation

Occasionally, there might be uneconomical reasons for conservation and management may however be demanding. Nevertheless, cultural, historical, or ecological values may exist. Breeds in this category can rationalize roles in zoos, farm parks, and natural parks. Since the cost is relatively low, breeds are kept out of their production environment to which they are adapted [28]. In the context of domestic animal diversity, *ex-situ* conservation means conservation away from the habitat and production systems where the resource is developed. This category includes both the maintenance of live animals (*in vivo*) and preservation of their genetic properties through cryopreservation of their reproductive organs (*in vitro*).

### 5.2.2. Cryoconservation or Cryopreservation

*Ex-situ* (*in vitro*) conservation programs of livestock genetic resources have focused efforts on cryopreservation of gametes, embryos, and somatic cells as well as the testis and ovarian tissues, effectively lengthening the genetic lifespan of individuals in a breeding program even after their death [96] [97]. It also gives us the ability to reconstitute live animals at a later date. One of the major issues surrounding genome banks is the amount and type of material that needs to be stored, which is a function of the intended future use of the material [13]. To avoid inbreeding, a gene bank of male and female genetics formed from the largest number of individuals would be ideal [98].

**1) Gonadal Cryopreservation**

Testicular tissue cryopreservation is a possibility in livestock production. There are reports of successful cryopreservation of immature testicular tissues in goat [99], pig [100] [101], cattle [102], and sheep [103]. However, it is important to note that the developmental stage of the testis plays an important role in the cryopreservation and subsequently on the semen product [104]. Successful cryopreservation of gonadal tissue is an important factor that guarantees fertility

preservation [93]. With the advent of the Assisted Reproductive Technique (ART) and an improved understanding of cryobiology, strategies have been developed to allow the long-term storage of gametes and embryos [105] which would help in conserving animals with genetic potentials. Similar reports have been documented in Ovarian tissues in sheep [106] [107], rabbit [108], bovine [109], and in porcine [110].

**2) Sperm**

Systematic cryopreservation and storage of male gametes from threatened species skirt the problem of homozygosis in secluded populations by introducing new genetic material across populations and facilitates genetic interactions between captive areas/zoos/research centers or countries [111]. Sperm is one of the most practical means of storing germplasm due to its abundance and ease of application [112]. Preserved frozen-thawed semen of superior males of endangered livestock could be reintroduced into the population either through *in vitro* fertilization (IVF) or artificial insemination (AI). It has the potential to retain existing diversity and maintain heterozygosity while minimizing live animal transport [111]. Semen from most mammalian and few avian species have been successfully frozen in the past [112].

However, [113] contested the efficiency of sperm cryopreservation due to physiological damage leading to loss of fertility after freezing and thawing sustained by a large number of sperm cells. [114] concisely state the stressors influencing the cells during cooling and freezing stages as follows: 1) exposure to harmful effects while cooling like metabolism decoupling, ionic imbalance, activation of proteases, cellular acidosis, deprivation of energy, membrane phase transition, destabilization of the cytoskeleton and production of free radicals or reactive oxygen species (ROS); 2) during freezing, sperm cell are predisposed to effects of ice crystal formation, hyperosmolarity, alteration in the cell volume and protein denaturation [115]. These and other factors form the hindrance to the full exploitation of sperm cryopreservation in farm animal species.

However, an appealing success is being recorded in the cattle AI industry, where bulls are selected for "freezing ability" of their semen, exhibiting good post-thaw semen quality, ranging from 50% - 70% motile spermatozoa. Pregnancy or calving rate is similar to that of fresh semen provided that higher sperm dosages are used for frozen sperm [116]. This depicts the prospect and efficacy that cryopreserved sperm cells can contribute to the conservation of genetic diversity in this industry.

**3) Oocytes**

Female gametes (ova) can be obtained through follicle puncture, ovarian tissue biopsies, unilateral or bilateral ovariectomy, or ovary collection immediately after an animal's death, irrespective of its age [117]. Abattoir harvested ovaries are at the germinal vesicle (GV) stage in which the genetic material is confined within the nucleus. Since this stage has no spindle present, GVs are assumed to be less prone to chromosomal and microtubular damage during cryopreserva-

tion. However, oocytes can also be cryopreserved at the metaphase II (MII) stage of maturation. During the MII stage, the cumulus cells surrounding the oocyte are expanded, microfilaments of actin are involved in cell shape and movements, and microtubules form the spindle apparatus [118].

Oocytes collected by *in vivo* pickup or at slaughter, ovarian tissue, isolated follicles, and mature or immature oocytes [119] can all be stored by cryopreservation for extended periods for subsequent *in vitro* fertilization (IVF) to produce embryos. Oocyte banks would enlarge the gene pool, facilitate several assisted reproductive procedures, salvage female genetics after an unexpected death, and avoid the controversy surrounding the preservation of embryos [120] [121]. Like semen, oocyte cryopreservation is beneficial for the international exchange of germplasm, as it avoids injury and sanitary risks involved in live animal transportation [122]. Oocytes are extremely sensitive to chilling, and the technique is not as established as in semen or embryos, because oocytes tend to have large cells that have a low surface-to-volume ratio and a low permeability coefficient, both of which hinder the migration of water and cryoprotectants (CPAs) through the cell [90] [123].

It is, however, important to note that, [124] had stated that immature oocytes at the germinal vesicle stage that is yet to form the spindle lack cortical granules and have a higher membrane permeability, which makes them more resistant to chilling injury than mature metaphase II oocytes. The major differences between oocytes and embryos are the plasma membrane, presence of cortical granules, and spindle formation at the metaphase II (MII) stage of meiosis [125]. However, [126] concluded that cryopreserving ovarian tissue helps to circumvent many restrictions encountered in mature oocyte preservation, from a limited number of mature oocytes available in the ovaries to conceivable lethal effects of its conservation under low temperatures, and the need for a super-ovulation procedure. The main constraint of its use is the difficulty in preserving ovarian tissue, given the diversity of cell types and tissue components in it [127].

Two procedures have been defined for female gametes preservation: slow freezing (SF) and vitrification. Slow freezing or conventional freezing refers to the exposure of the tissues/cells to a low concentration of CPA and cooling them slowly in a programmable freezer [128]. CPA concentration and exposure time before freezing need to be balanced to reach sufficient dehydration; however, it has to be low enough to avoid cytotoxic damages [129]. Although this procedure is widely accepted, however, sophisticated and expensive programmable freezers are required for the cooling procedure, those of which are generally not available [126].

Alternatively, vitrification is considered a cheap technique that can be performed under field conditions with no need for special equipment [130], including after animal death [131]. This method involves the use of high concentrations of CPAs and rapid cooling (−20,000˚C/min −40,000˚C/min) to achieve a glass-like highly viscous solution without the formation of ice crystals [132].

Vitrification promotes the viscosity state of the solution, but without water crystallization [133].

To date, there is no consistent oocyte cryopreservation method established in any species, although, there has been significant progress and offsprings have been produced from frozen-thawed oocytes in cattle [134], sheep, and horses [123] [135]. During the process of cryopreservation, oocytes suffer considerable morphological and functional damage, although the extent of cryoinjuries depends on the species and the origin (*in vivo* or *in vitro* produced). The mechanism of cryoinjuries is yet to be fully understood and until more insight is gained, improvement of oocyte cryopreservation will be difficult [122].

**4) Embryos**

Embryo cryopreservation allows the preservation of the full genetic complement of both dam and sire and has incredible opportunities for preserving heterozygosity and population integrity. However, it is a more complex and costly procedure than semen cryopreservation. Moreover, a large number of embryos would be required for the complete reconstruction of a population and are unlikely to be available from donor females of threatened breeds [98]. Embryos of virtually all mammals have been successfully frozen, thawed, and transferred to synchronized recipient females in the past; however, embryos from species such as swine or equine are much more sensitive to cryopreservation when compared to bovine or ovine embryos [136].

Currently, the widespread use of embryo cryopreservation is limited to cattle, sheep, and goats [137]. In the year 2015, almost 700.000 IVP embryos were produced, surpassing for the first time, the number of bovine embryos produced *in vivo*. In this context, 269.353 bovine OPU IVP embryos were transferred in Brazil alone [138], which is considered the world's largest producer of bovine embryos. An advantage of *in vitro* embryo preservation is that they are more resistant than gametes when subjected to high body temperatures due to thermal stress [139]. Thus, the pregnancy rates are better in embryo transfer (ET) than artificial insemination (AI) throughout the year [140] [141] [142]. Another benefit of this method is the smaller number of viable sperms required for fertilization, therefore, more efficient results are recorded by using sex-sorted semen [143] [144].

Despite the advantages of embryo cryopreservation, the greatest challenge is its low resistance to the cryopreservation process [145] [146] reported that its high sensitivity to cooling is due to the accumulation of lipids in their cells, arranged in the form of cytoplasmic lipid droplets that are constituted mainly of triglycerides [147]. However, indications that this high lipid content is because of the medium in which the embryos cultured has been confirmed [148] [149] reported some strategies for refining post-cryopreservation survival capacity which produce more cryotolerant embryos.

## 6. Genomic Studies on Some Endangered Cattle Breeds

The Wild Gaur (Bos gaurus) is a critically endangered species in Vietnam with a

reported population size of just 500 individuals (http://www.iucnredlist.org). [150] revealed the genetic status of Vietnamese wild guar by amplifying 130 bovine microsatellite markers in these species. Out of the 130, only 117 markers were efficiently amplified. Sixty-eight of them were polymorphic, which resulted in a total of 264 alleles. It was noted that three cattle Y-chromosome specific microsatellite markers were also highly expressed in the wild gaur. Their result revealed that bovine microsatellites are highly conserved in the wild gaur genome. This indicates the possibility of using bovine microsatellites for genetic characterization and studies in the Wild Guar. Also, low genetic diversity was observed occasioned by a mean Polymorphic Information Content (PIC) of 0.252, Observed Heterozygosity ($H_o$) of 0.269, Nei's unbiased mean heterozygosity of 0.298. In general, the study obtained genomic information that highlighted the risk of extinction facing the species and the potential to use genomic information from cattle to design breeding strategies that will help preserve these species.

Chikso is a beef cattle breed in Korea and classified as an endangered breed by the [18]. To obtain genomic information that could help in conservation efforts, [151] conducted whole-genome sequencing on the Chikso cattle using the parallel sequencing method of the Illumina HiSeq 2000 sequencing platform. When compared to the bovine reference genome sequence, the authors identified 5,874,026 SNPs and 551,363 insertions/deletions. 45% and 75% of the variations were identified in the autosomes and X-chromosome, respectively, which were previously unknown. In total, 16,273 missense mutations were identified in 7111 genes throughout the genome. With the breed having a very small population at the brink of extinction and the potential of SNPs identified contributing to variation in economically important traits, the information provided by [151] could be beneficial in crafting a genomic breeding program that will facilitate conservation of the cattle breed.

Gayal (Mithan) is another bovine breed with a rapidly dwindling population size that has been classified as endangered (https://www.iucnredlist.org//). This bovine specie is found in China, India, and Bangladesh [152]. It is a dual-purpose breed with better body size and meat quality traits than most indigenous cattle breed in those regions [153]. To gain insight into the valuable genetic resource of this species for conservation, Mei *et al.* (2016) sequenced the whole genome of Gayal together with two controls (Red Angus and Japanese Black cattle breeds). When compared with the bovine reference genome, 23,828,562 SNPs were identified, of which 62.24% were novel in Gayal, which is higher than the 2.53% and 5.10% novel SNPs identified in Red Angus and Japanese Black cattle breeds, respectively. I6901 non-synonymous SNPs were identified that might be associated with variation in physical traits in Gayal. The genomic information provided could be a guide to conservationists in the design of breeding programs for Gayal to prevent its extinction.

It is widely known that the knowledge of population size and structure can shed light on the risk status of cattle breeds. In this regard, [154] genotyped eight

Iranian cattle breeds (Sarabi, Kurdi, Najdi, Taleshi, Mazandarani, Pars, Kermani, and Sistani breeds) for 777,962 SNPs. Apart from the Mazandarani breed that had an effective population size of 107, the Mean effective population size for other breeds was 24. The lowest effective population size was 13, found in the Sarabi breed. Runs of homozygosity (ROH) in Sarabi, Pars, and Sistani breeds were of higher proportion. The study revealed the critical status of Sarabi, Sistani, Pars, Teleshi, and Kermani cattle breeds in Iran and suggests the urgent need for conservation efforts to prevent the Sarabi breed from becoming extinct. **Table 1** at the end of this review has a list of some threatened cattle breeds in different locations; information on researches that had been done concerning the molecular markers used, and the genetic parameters calculated to estimate diversity.

**Table 1.** List of some threatened cattle breeds in different locations.

| Country | Breed(s) | Molecular marker(s) used | Genetic parameters estimated | References |
|---|---|---|---|---|
| Spain | Betizu | Microsatellite | Allele frequencies | [159] |
| | Mallorquina | | Population size | |
| | Menorquina | | Nei's genetic distances | |
| | Monchina | | Hardy-Weinberg equilibrum | |
| | Serrana de Teruel | | Linkage disequilibrum | |
| | | | Heterozygosity | |
| | | | Inbreeding coefficient | |
| | Berrenda en Negro | rob(1;29) chromosome translocation | Translocation distribution | [160] |
| | Berrenda en Colorado | | Translocation frequencies | |
| | Cardena Andaluza | | F statistic | |
| | Pajuna | | Hardy-Weinberg equilibrum | |
| | Negra Andaluza | | Heterozygosity | |
| Western Pyrenees | Betizu | DNA Microsatellite | Heterozygosity | [161] |
| | Terrena | | Allele frequencies | |
| | Monchina | | Hardy-Weinberg equilibrum | |
| | | | Parentage exclusion power | |
| | | | Mean PIC value | |
| | | | F statistic | |
| Germany | Pustertaler–Sprinzen | DNA Microsatellite | Heterozygosity | |
| | | | Allele frequencies | [162] |
| | | | Genetic distance | |

**Continued**

| | | | | |
|---|---|---|---|---|
| Portugal | Cachena | Microsatelite | Heterozygosities | [163] |
| | | | inbreeding coefficient (Fis) | |
| | | | Hardy weinberg equilibrum | |
| | | | Mean number of allele | |
| | Garvonesa | Microsatelite | Heterozygousity | [164] |
| | | | Total Number of Allele | |
| | | | Mean number of allele | |
| | | | Hardy weinberg equilibrum | |
| Italy | Maremmana | Single nucleotide Polymorphism | Heterozygousity | [19] |
| | | | Runs of homozygousity | |
| | | | Linkage disequilibrium decay | |
| | | | Nucleotide diversity | |
| | Modicana | Single nucleotide Polymorphism | Wright Fixation Index | [165] |
| | | | Runs of Homozygosity (ROH) | |
| | | | Heterozygousity | |
| Scotland (UK) | Native Aberdeen Angus | Microsatellites | Expected/observed heterozygosity | [166] |
| | | | Gene diversity | [167] |
| | | | PIC | |
| | | | Allele frequencies | |
| | | | homozygosity | |
| | | | Nei's genetic distance | |
| | Chillingham Wild Cattle | SNPs | Fraction of polymorphic loci | [168] |
| | | | observed homozygosity | |
| | | | Inbreeding coefficient | |
| | | | linkage disequilibrium | |
| | | | ROHom and ROHet | |
| | | | heterozygosity | |
| Ireland | Irish Moiled (Kerry) | SNPs | Effective population size | [169] |
| | | | Runs of Homozygosity | |
| | | | Maximum Likelihood | |
| | Lincoln Red | | Effective population size | [169] |
| | | | Runs of Homozygosity | |
| | | | Maximum Likelihood | |
| Nigeria | Muturu Cattle | SNPs | Nei's genetic distance | [170] |
| | | | Rsb Analysis | |
| | | | Homozygosity selection tests | |
| | | | Integrated haplotype score | |

**Continued**

| | | | | |
|---|---|---|---|---|
| Tanzania | Maasai<br>Tarime<br>Sukume | SNPs | Integrated haplotype score<br>runs of homozygosity (ROH)<br>Identical by state (IBS)<br>Pairwise distance (FST) | [171] |
| African | N'dama,<br>Ankole<br>Boran<br>Kenana<br>Ogaden | SNPs | Fixation index (Fst)<br>linkage disequlibrium<br>population differentiation and structure,<br>maximum livelihood (ML) approach,<br>Allelic frequency<br>Population size | [172] |
| Senegal | Gobra Zebu,<br>Maure Zebu<br>Djakore<br>N'dama | Autosomal microsatellite markers | Allelic frequencies,<br>observed number of alleles per locus<br>observed heterozygosity (Ho)<br>unbiased expected heterozygosity<br>Gene diversity of Nei's (Hs),<br>Inbreeding coefficient<br>Shannon's information index (I)<br>effective number of alleles (Ne)<br>Genetic distance<br>Hardy-weinberg equilibrium (HWE)<br>Genotypic linkage equilibrium. | [173] |
| Tanzania | Local Zebu | Polymorphic DNA marker | Interbreed dissimilarities | [174] |
| South Africa | Nguni | Microsatellite markers | Population structure<br>genetic distance<br>number of alleles<br>Genetic Relationship<br>heterozygosity values | [175] |
| Bangladesh | Red Chittagong | SNPs | Popolation Structure<br>Observed Heterozigosity (Ho)<br>Expected Heterozygosity (He)<br>Hardy-Weinberg equilibrium | [176] |
| Korea | Brindle Hanwoo | SNPs | Linkage disequilibrium | [176] |
| | Jeju Black Hanwoo | SNPs | Hardy-Weinberg Equilibrium | [177] |

SNPs: Single nucleotide polymorphism; Mean PIC value: Mean Polymorphic information Content value.

Crossbreeding is a common technique used in the livestock industry. Although beneficial, it has the potential to cause loss of breed-specific characteristics, thereby threatening the existence of natural genetic resources of certain breeds [155]. To avoid extinction, it is expedient that the original genetic backgrounds of those breeds are recovered [156] by removing exogenous genetic materials in a process called de-introgression.

[157] used the Merino and Poll Dorset sheep breeds as models to investigate a genomic approach to identify and recover chromosome segments of endangered breeds whose genetic materials have been mixed with other breeds. First, the full genomic data was obtained from pure Merino and Poll Dorset breeds, after which the breeds were crossed to produce F1 crossbred. The authors tested the efficiency of two genome-wide methods adapted from [158] and [129] to detect Merino segments and Poll Dorset segments in the F1 crossbred. The methods used are either genomic prediction or identification of breed-specific haplotypes. Their results showed that both approaches could efficiently identify genomic segments belonging to different origins in the admixture. Also, both methods were able to restore the full Merino genetic background in a controlled breeding program. Although the sheep breeds used are not threatened breeds, this study has potential application in breed conservation efforts, by helping to identify and restore genetic resources from endangered cattle breeds that have been indiscriminately crossed with other breeds.

## 7. Conclusion

Genomics has allowed for genetic diversity study on a wider scope. This has helped to gain better insight into the genetic diversity in cattle which would allow for effective management and conservation of this species.

## Acknowledgements

The authors would like to thank Dr. Jimoh Saheed and Mr. Oyekunle John Oladosu for their extensive contributions and corrections to the manuscript.

## Authors' Contribution

BU, AA, RO, and BS conceived ideas. All authors contributed equally during the drafting of the paper. BU, AA, and RO corrected the final draft. All authors read and approved the paper for publication.

## Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

## References

[1] Haddad, N.M., *et al.* (2015) Habitat Fragmentation and Its Lasting Impact on Earth's Ecosystems. *Science Advances*, **1**, e1500052.

https://doi.org/10.1126/sciadv.1500052

[2] Newbold, T., *et al.* (2015) Global Effects of Land Use on Local Terrestrial Biodiversity. *Nature*, **520**, 45-50. https://doi.org/10.1038/nature14324

[3] Roser, M., Ritchie, H. and Ortiz-Ospina, E. (2013) World Population Growth—Our World in Data. https://ourworldindata.org/world-population-growth

[4] Hoffmann, A.A. and Sgró, C.M. (2011) Climate Change and Evolutionary Adaptation. *Nature*, **470**, 479-485. https://doi.org/10.1038/nature09670

[5] Barnosky, A.D., *et al.* (2011) Has the Earth's Sixth Mass Extinction Already Arrived? *Nature*, **471**, 51-57. https://doi.org/10.1038/nature09678

[6] Ceballos, G., Ehrlich, P.R., Barnosky, A.D., García, A., Pringle, R.M. and Palmer, T.M. (2015) Accelerated Modern Human-Induced Species Losses: Entering the Sixth Mass Extinction. *Science Advances*, **1**, e1400253. https://doi.org/10.1126/sciadv.1400253

[7] Ceballos, G., Ehrlich, P.R. and Dirzo, R. (2017) Biological Annihilation via the Ongoing Sixth Mass Extinction Signaled by Vertebrate Population Losses and Declines. *Proceedings of the National Academy of Sciences of the United States of America*, **114**, E6089-E6096. https://doi.org/10.1073/pnas.1704949114

[8] Lynch, M., *et al.* (2016) Genetic Drift, Selection and the Evolution of the Mutation Rate. *Nature Reviews Genetics*, **17**, 704-714. https://doi.org/10.1038/nrg.2016.104

[9] Barker, J.S.F., Tan, S.G., Moore, S.S., Mukherjee, T.K., Matheson, J.L. and Selvaraj, O.S. (2001) Genetic Variation within and Relationships among Populations of Asian Goats (*Capra hircus*). *Journal of Animal Breeding and Genetics*, **118**, 213-233. https://doi.org/10.1046/j.1439-0388.2001.00296.x

[10] Mishra, A.K., Arora, A.L., Kumar, S. and Prince, L.L.L. (2008) Studies on Effect of Booroola (FecB) Genotype on Lifetime Ewes' Productivity Efficiency, Litter Size and Number of Weaned Lambs in Garole × Malpura Sheep. *Animal Reproduction Science*, **113**, 293-298. https://doi.org/10.1016/j.anireprosci.2008.06.002

[11] Patterson, D.L. and Silversides, F.G. (2003) Farm Animal Genetic Resource Conservation: Why and How? Canadian Farm Animal Genetic Resources Foundation. http://www.fao.org/3/a1250e/annexes/CountryReports/Canada.pdf

[12] Notter, D.R. (1999) The Importance of Genetic Diversity in Livestock Populations of the Future. *Journal of Animal Science*, **77**, 61-69. https://doi.org/10.2527/1999.77161x

[13] Boettcher, P.J., *et al.* (2010) Objectives, Criteria and Methods for Using Molecular Genetic Data in Priority Setting for Conservation of Animal Genetic Resources. *Animal Genetics*, **41**, 64-77. https://doi.org/10.1111/j.1365-2052.2010.02050.x

[14] Markert, J.A., *et al.* (2010) Population Genetic Diversity and Fitness in Multiple Environments. *BMC Ecology and Evolution*, **10**, 205. https://doi.org/10.1186/1471-2148-10-205

[15] Acosta, A.C., *et al.* (2013) Genetic Diversity and Differentiation of Five Cuban Cattle Breeds Using 30 Microsatellite Loci. *Journal of Animal Breeding and Genetics*, **130**, 79-86. https://doi.org/10.1111/j.1439-0388.2012.00988.x

[16] Toro, M.A. and Caballero, A. (2005) Characterization and Conservation of Genetic Diversity in Subdivided Populations. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **360**, 1367-1378. https://doi.org/10.1098/rstb.2005.1680

[17] Öner, Y., Yilmaz, O., Eriş, C., Ata, N., Ünal, C. and Koncagül, S. (2019) Genetic Diversity and Population Structure of Turkish Native Cattle Breeds. *South African Journal of Animal Science*, **49**, 628-635. https://doi.org/10.4314/sajas.v49i4.4

[18] Boettcher, P., Oldenbroek, J., Sponenberg, D., Gandini, G., Martin, J. and Joshi, B. (2013) *In Vivo* Conservation of Animal Genetic Resources. FAO, Rome.

[19] Upadhyay, M., *et al.* (2019) Deciphering the Patterns of Genetic Admixture and Diversity in Southern European Cattle Using Genome-Wide SNPs. *Evolutionary Applications*, **12**, 951-963. https://doi.org/10.1111/eva.12770

[20] Gautier, M., Laloë, D. and Moazami-Goudarzi, K. (2010) Insights into the Genetic History of French Cattle from Dense SNP Data on 47 Worldwide Breeds. *PLoS ONE*, **5**, e13038. https://doi.org/10.1371/journal.pone.0013038

[21] Jimenez, D.E., de Lima Lins, T.C., Taveira, P.O. and Pereira, R.W. (2014) A Prospective Screening of Gene Copy Number Variation in Brazilian Admixed Population Sample. *Hereditary Genetics*, **3**, Article ID: 1000125. https://doi.org/10.4172/2161-1041.1000125

[22] Kim, K., *et al.* (2018) Artificial Selection Increased Body Weight but Induced Increase of Runs of Homozygosity in Hanwoo Cattle. *PLoS ONE*, **13**, e0193701. https://doi.org/10.1371/journal.pone.0193701

[23] Zhao, F., McParland, S., Kearney, F., Du, L. and Berry, D.P. (2015) Detection of Selection Signatures in Dairy and Beef Cattle Using High-Density Genomic Information. *Genetics Selection Evolution*, **47**, Article No. 49.

[24] Windig, J.J. and Engelsma, K.A. (2010) Perspectives of Genomics for Genetic Conservation of Livestock. *Conservation Genetics*, **11**, 635-641. https://doi.org/10.1007/s10592-009-0007-x

[25] Allendorf, F.W., Hohenlohe, P.A. and Luikart, G. (2010) Genomics and the Future of Conservation Genetics. *Nature Reviews Genetics*, **11**, 697-709. https://doi.org/10.1038/nrg2844

[26] Höglund, J. (2009) Evolutionary Conservation Genetics. Oxford University Press, Oxford. https://doi.org/10.1093/acprof:oso/9780199214211.001.0001

[27] Moravčíková, N., Trakovická, A., Kadlečík, O. and Kasarda, R. (2019) Genomic Signatures of Selection in Cattle through Variation of Allele Frequencies and Linkage Disequilibrium. *Journal of Central European Agriculture*, **20**, 576-580. https://doi.org/10.5513/JCEA01/20.2.2552

[28] Oldenbroek, J.K. (1999) Genebanks and the Management of Farm Animal Genetic Resource. Institute of Animal Science and Health, Lelystad, 119 p.

[29] Oldenbroek, J.K. (2007) Utilisation and Conservation of Farm Animal Genetic Resources. Wageningen Academic Publishers, Wageningen. https://doi.org/10.3920/978-90-8686-592-5

[30] Makanjuola, B.O., Miglior, F., Abdalla, E.A., Maltecca, C., Schenkel, F.S. and Baes, C.F. (2020) Effect of Genomic Selection on Rate of Inbreeding and Coancestry and Effective Population Size of Holstein and Jersey Cattle Populations. *Journal of Dairy Science*, **103**, 5183-5199. https://doi.org/10.3168/jds.2019-18013

[31] Jost, L., Archer, F., Flanagan, S., Gaggiotti, O., Hoban, S. and Latch, E. (2018) Differentiation Measures for Conservation Genetics. *Evolutionary Applications*, **11**, 1139-1148. https://doi.org/10.1111/eva.12590

[32] Weitzman, M. (1993) What to Preserve? An Application of Diversity Theory to Crane Conservation? *The Quarterly Journal of Economics*, **108**, 157-183. https://doi.org/10.2307/2118499

[33] d'Arnoldi, C., Foulley, J.-L. and Ollivier, L. (1998) An Overview of the Weitzman Approach to Diversity. *Genetics Selection Evolution*, **30**, Article No. 149. https://doi.org/10.1186/1297-9686-30-2-149

[34] Groeneveld, L.F., *et al.* (2010) Genetic Diversity in Farm Animals—A Review. *Animal Genetics*, **41**, 6-31. https://doi.org/10.1111/j.1365-2052.2010.02038.x

[35] FAO (2007) The State of the Art in the Management of Animal Genetic Resources.

[36] Ndumu, D.B., *et al.* (2008) Genetic and Morphological Characterisation of the Ankole Longhorn Cattle in the African Great Lakes Region. *Genetics Selection Evolution*, **40**, 467-490. https://doi.org/10.1051/gse:2008014

[37] Kugonza, D.R., *et al.* (2011) Genetic Diversity and Differentiation of Ankole Cattle Populations in Uganda Inferred from Microsatellite Data. *Livestock Science*, **135**, 140-147. https://doi.org/10.1016/j.livsci.2010.06.158

[38] Pienaar, L., *et al.* (2014) Genetic Diversity of the Afrikaner Cattle Breed. 10*th World Congress on Genetics Applied to Livestock Production*, Vancouver, BC, Canada, 17-22 August 2014.

[39] Bessa, I., Pinheiro, I., Matola, M., Dzama, K., Rocha, A. and Alexandrino, P. (2009) Genetic Diversity and Relationships among Indigenous Mozambican Cattle Breeds. *South African Journal of Animal Science*, **39**, 61-72. https://doi.org/10.4314/sajas.v39i1.43548

[40] Ngono Ema, P.J., *et al.* (2014) Genetic Diversity of Four Cameroonian Indigenous Cattle Using Microsatellite Markers. *Journal of Livestock Science*, **5**, 9-17.

[41] Sharma, R., *et al.* (2015) Genetic Diversity and Relationship of Indian Cattle Inferred from Microsatellite and Mitochondrial DNA Markers. *BMC Genetics*, **16**, Article No. 73. https://doi.org/10.1186/s12863-015-0221-0

[42] Frankham, R., Ballou, J.D. and Briscoe, D.A. (2010) Introduction to Conservation Genetics. 2nd Edition, Cambridge University Press, Cambridge. https://doi.org/10.1017/CBO9780511809002

[43] Ewens, W.J. (1990) The Minimum Viable Population Size as a Genetic and a Demographic Concept. Oxford University Press, New York/Oxford.

[44] Charlesworth, B. (2009) Fundamental Concepts in Genetics: Effective Population Size and Patterns of Molecular Evolution and Variation. *Nature Reviews Genetics*, **10**, 195-205. https://doi.org/10.1038/nrg2526

[45] Wright, S. (1931) Evolution in Mendelian Populations. *Bulletin of Mathematical Biology*, **52**, 241-295; Discussion 201-207. https://doi.org/10.1016/S0092-8240(05)80011-4

[46] Jiménez-Mena, B., Hospital, F. and Bataillon, T. (2016) Heterogeneity in Effective Population Size and Its Implications in Conservation Genetics and Animal Breeding. *Conservation Genetics Resources*, **8**, 35-41. https://doi.org/10.1007/s12686-015-0508-5

[47] Flint, J. and Mott, R. (2001) Finding the Molecular Basis of Quantitative Traits: Successes and Pitfalls. *Nature Reviews Genetics*, **2**, 437-445. https://doi.org/10.1038/35076585

[48] Barbato, M., Orozco-terWengel, P., Tapio, M. and Bruford, M.W. (2015) SNeP: A Tool to Estimate Trends in Recent Effective Population Size Trajectories Using Genome-Wide SNP Data. *Frontiers in Genetics*, **6**, 223-243. https://doi.org/10.3389/fgene.2015.00109

[49] Flury, C., *et al.* (2010) Effective Population Size of an Indigenous Swiss Cattle Breed Estimated from Linkage Disequilibrium. *Journal of Animal Breeding and Genetics*, **127**, 339-347. https://doi.org/10.1111/j.1439-0388.2010.00862.x

[50] Crow, J.F. and Kimura, M. (1970) An Introduction to Population Genetics Theory. Harper and Row, New York.

[51] Hill, W.G. (1981) Estimation of Effective Population Size from Data on Linkage Disequilibrium. *Genetics Research*, **38**, 209-216. https://doi.org/10.1017/S0016672300020553

[52] Toro Ospina, A.M., *et al.* (2019) Linkage Disequilibrium and Effective Population Size in Gir Cattle Selected for Yearling Weight. *Reproduction in Domestic Animals*, **54**, 1524-1531. https://doi.org/10.1111/rda.13559

[53] Goddard, M.E. and Hayes, B.J. (2012) Genome-Wide Association Studies and Linkage Disequilibrium in Cattle. In J. E. Womack, Ed., *Bovine Genomics*, John Wiley & Sons, Oxford, 192-210. https://doi.org/10.1002/9781118301739.ch13

[54] Hedrick, P.W. (2005) A Standardized Genetic Differentiation Measure. *Evolution*, **59**, 1633-1638. https://doi.org/10.1111/j.0014-3820.2005.tb01814.x

[55] Soulé, M.E. (1980) Thresholds for Survival: Maintaining Fitness and Evolutionary Potential. In: Soulé, M.E. and Wilcox, B.A., Eds., *Conservation Biology*: *An Evolutionary-Ecological Perspective*, Sinauer, Sunderland, MA, 151-169.

[56] Franklin, I.R. (1980) Evolutionary Change in Small Populations. Sinauer Associates. Inc., Sunderland, MA, 135-150.

[57] Prasad, A., *et al.* (2008) Linkage Disequilibrium and Signatures of Selection on Chromosomes 19 and 29 in Beef and Dairy Cattle. *Animal Genetics*, **39**, 597-605. https://doi.org/10.1111/j.1365-2052.2008.01772.x

[58] Qanbari, S. (2020) On the Extent of Linkage Disequilibrium in the Genome of Farm Animals. *Frontiers in Genetics*, **10**, 1304. https://doi.org/10.3389/fgene.2019.01304

[59] Maloy, S. and Hughes, K., Eds. (2013) Brenner's Encyclopedia of Genetics. 2nd Edition. Academic Press, Cambridge, MA.

[60] Makina, S.O., *et al.* (2015) Extent of Linkage Disequilibrium and Effective Population Size in Four South African Sanga Cattle Breeds. *Frontiers in Genetics*, **6**, 337. https://doi.org/10.3389/fgene.2015.00337

[61] McKay, S.D., *et al.* (2007) Whole Genome Linkage Disequilibrium Maps in Cattle. *BMC Genetics*, **8**, 74. https://doi.org/10.1186/1471-2156-8-74

[62] Séré, M., Thévenon, S., Belem, A.M.G. and De Meeûs, T. (2017) Comparison of Different Genetic Distances to Test Isolation by Distance between Populations. *Heredity* (*Edinb*), **119**, 55-63. https://doi.org/10.1038/hdy.2017.26

[63] Edea, Z., *et al.* (2014) Linkage Disequilibrium and Genomic Scan to Detect Selective Loci in Cattle Populations Adapted to Different Ecological Conditions in Ethiopia. *Journal of Animal Breeding and Genetics*, **131**, 358-366. https://doi.org/10.1111/jbg.12083

[64] Fabbri, M.C., Dadousis, C. and Bozzi, R. (2020) Estimation of Linkage Disequilibrium and Effective Population Size in Three Italian Autochthonous Beef Breeds. *Animals*, **10**, 1034. https://doi.org/10.3390/ani10061034

[65] Hardy, G.H. (1908) Mendelian Proportions in a Mixed Population. *Science*, **28**, 49-50. https://doi.org/10.1126/science.28.706.49

[66] Weinberg, W. (1908) Über den Nachweis der Vererbung beim Menschen. *Jahreshefte des Vereins für vaterländische Naturkunde in Württemberg*, **64**, 368-382.

[67] Crow, J.F. (1988) Eighty Years Ago: The Beginnings of Population Genetics. *Genetics*, **119**, 473-476. https://doi.org/10.1093/genetics/119.3.473

[68] Sham, P. (2001) Statistics in Human Genetics. Arnold Publishers, London.

[69] Morton, N.E. (1994) Fundamentals of Genetic Epidemiology, M. J. Khoury, T. H. Beaty, and B. H. Cohen, New York: Oxford University Press, 1993, 383 pages, $55.00. *Genetic Epidemiology*, **11**, 389-390.

https://doi.org/10.1002/gepi.1370110409

[70] Guo, S.-W. and Thompson, E. (1992) Performing the Exact Test of Hardy-Weinberg Proportion for Multiple Alleles. *Biometrics*, **48**, 361-372. https://doi.org/10.2307/2532296

[71] Robertson, A. and Hill, W.G. (1984) Deviations from Hardy-Weinberg Proportions: Sampling Variances and Use in Estimation of Inbreeding Coefficients. *Genetics*, **107**, 703-718. https://doi.org/10.1093/genetics/107.4.703

[72] Salanti, G., Amountza, G., Ntzani, E. and Ioannidis, J. (2005) Hardy-Weinberg Equilibrium in Genetic Association Studies: An Empirical Evaluation of Reporting, Deviations, and Power. *European Journal of Human Genetics*, **13**, 840-848. https://doi.org/10.1038/sj.ejhg.5201410

[73] Ginja, C., *et al.* (2019) The Genetic Ancestry of American Creole Cattle Inferred from Uniparental and Autosomal Genetic Markers. *Scientific Reports*, **9**, Article No. 11486. https://doi.org/10.1038/s41598-019-47636-0

[74] Kleinman-Ruiz, D., Villanueva, B., Fernández, J., Toro, M.A., García-Cortés, L.A. and Rodríguez-Ramilo, S.T. (2016) Intra-Chromosomal Estimates of Inbreeding and Coancestry in the Spanish Holstein Cattle Population. *Livestock Science*, **185**, 34-42. https://doi.org/10.1016/j.livsci.2016.01.002

[75] Peripolli, E., *et al.* (2018) Assessment of Runs of Homozygosity Islands and Estimates of Genomic Inbreeding in Gyr (*Bos indicus*) Dairy Cattle. *BMC Genomics*, **19**, Article No. 34. https://doi.org/10.1186/s12864-017-4365-3

[76] Mastrangelo, S., *et al.* (2017) Genome-Wide Scan for Runs of Homozygosity Identifies Potential Candidate Genes Associated with Local Adaptation in Valle del Belice Sheep. *Genetics Selection Evolution*, **49**, Article No. 84. https://doi.org/10.1186/s12711-017-0360-z

[77] Nei, M. (1987) Molecular Evolutionary Genetics. Columbia University Press, New York. https://doi.org/10.7312/nei-92038

[78] Dayhoff, M. and Eck, R.V., Eds. (1972) Atlas of Protein Sequence and Structure. National Biomedical Research Foundation, Washington, D.C.

[79] Nei, M. (1972) Genetic Distance between Populations. *The American Naturalist*, **106**, 283-292. https://doi.org/10.1086/282771

[80] Cavalli-Sforza, L.L. and Edwards, A.W. (1967) Phylogenetic Analysis. Models and Estimation Procedures. *The American Journal of Human Genetics*, **19**, 233-257.

[81] Shriver, M.D., Jin, L., Boerwinkle, E., Deka, R., Ferrell, R.E. and Chakraborty, R. (1995) A Novel Measure of Genetic Distance for Highly Polymorphic Tandem Repeat Loci. *Molecular Biology and Evolution*, **12**, 914-920.

[82] Paetkau, D., Waits, L.P., Clarkson, P.L., Craighead, L. and Strobeck, C. (1997) An Empirical Evaluation of Genetic Distance Statistics Using Microsatellite Data from Bear (Ursidae) Populations. *Genetics*, **147**, 1943-1957. https://pubmed.ncbi.nlm.nih.gov/9409849 https://doi.org/10.1093/genetics/147.4.1943

[83] Wang, R., Zheng, L., Touré, Y.T., Dandekar, T. and Kafatos, F.C. (2001) When Genetic Distance Matters: Measuring Genetic Differentiation at Microsatellite Loci in Whole-Genome Scans of Recent and Incipient Mosquito Species. *Proceedings of the National Academy of Sciences of the United States of America*, **98**, 10769-10774. https://doi.org/10.1073/pnas.191003598

[84] Bao, W.B., Shu, J.-T., Wu, X.S., Musa, H., Ji, C.L. and Chen, G.H. (2009) Genetic Diversity and Relationship between Genetic Distance and Geographical Distance in 14 Chinese Indigenous Chicken Breeds and Red Jungle Fowl. *Czech Journal of*

*Animal Science*, **54**, 74-83. https://doi.org/10.17221/1666-CJAS

[85] Eding, H. and Laval, G. (1999) Measuring the Genetic Uniqueness in Livestock. In: Oldenbroek, J.K., Ed., *Genebanks and the Management of Farm Animal Genetic Resources*, DLO Institute for Animal Science and Health, The Netherlands, 33-59.

[86] Ruane, J. (2001) A Critical Review of the Value of Genetic Distance Studies in Breed Conservation. *Journal of Animal Breeding and Genetics*, **116**, 317-323. https://doi.org/10.1046/j.1439-0388.1999.00205.x

[87] Barker, J.S.F. (1994) A Global Protocol for Determining Genetic Distances among Domestic Livestock Breeds. 5*th World Congress on Genetics Applied to Livestock Production*, **21**, 501-508.

[88] Piyasatian, N. and Kinghorn, B. (1999) Use of Genetic Markers to Aid Conservation Decisions for Groups of Rare Domestic Breeds. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*, **13**, 365-368.

[89] Marshall, D. and Brown, A. (1975) Optimum Sampling Strategies in Genetic Conservation. In: Frankel, O.H. and Hawkes, J.G., Eds., *Crop Genetic Resources for Today and Tomorrow*, Cambridge University Press, Cambridge, 53-80.

[90] Prentice, J.R. and Anzar, M. (2011) Cryopreservation of Mammalian Oocyte for Conservation of Animal Genetics. *Veterinary Medicine International*, **2011**, Article ID: 146405. https://doi.org/10.4061/2011/146405

[91] FAO (2012) Cryoconservation of Animal Genetic Resources.

[92] Hall, S.J.G. and Bradley, D.G. (1995) Conserving Livestock Breed Biodiversity. *Trends in Ecology & Evolution*, **10**, 267-270. https://doi.org/10.1016/0169-5347(95)90005-5

[93] Jahnukainen, K., Ehmcke, J., Hergenrother, S.D. and Schlatt, S. (2007) Effect of Cold Storage and Cryopreservation of Immature Non-Human Primate Testicular Tissue on Spermatogonial Stem Cell Potential in Xenografts. *Human Reproduction*, **22**, 1060-1067. https://doi.org/10.1093/humrep/del471

[94] Mara, L., Casu, S., Carta, A. and Dattena, M. (2013) Cryobanking of Farm Animal Gametes and Embryos as a Means of Conserving Livestock Genetics. *Animal Reproduction Science*, **138**, 25-38. https://doi.org/10.1016/j.anireprosci.2013.02.006

[95] Blackburn, H. (2004) Development of National Animal Genetic Resource Programs. *Reproduction, Fertility and Development*, **16**, 27-32. https://doi.org/10.1071/RD03075

[96] Holt, W. (1999) Role of Reproductive Technologies and Genetic Resource Banks in Animal Conservation. *Reviews of Reproduction*, **4**, 143-150. https://doi.org/10.1530/ror.0.0040143

[97] Andrabi, S.M.H. and Maxwell, W.M.C. (2007) A Review on Reproductive Biotechnologies for Conservation of Endangered Mammalian Species. *Animal Reproduction Science*, **99**, 223-243. https://doi.org/10.1016/j.anireprosci.2006.07.002

[98] Demirci, B., Lornage, J., Salle, B., Poirel, M.T., Guerin, J.F. and Franck, M. (2003) The Cryopreservation of Ovarian Tissue: Uses and Indications in Veterinary Medicine. *Theriogenology*, **60**, 999-1010. https://doi.org/10.1016/S0093-691X(03)00121-3

[99] Honaramooz, A., Snedaker, A., Boiani, M., Schöler, H., Dobrinski, I. and Schlatt, S. (2002) Sperm from Neonatal Mammalia Testes Grafted in Mice. *Nature*, **418**, 778-781. https://doi.org/10.1038/nature00918

[100] Yang, Y., Steeg, J. and Honaramooz, A. (2010) The Effects of Tissue Sample Size and Media on Short-Term Hypothermic Preservation of Porcine Testis Tissue. *Cell*

*and Tissue Research*, **340**, 397-406. https://doi.org/10.1007/s00441-010-0946-z

[101] Zeng, W., *et al.* (2009) Preservation and Transplantation of Porcine Testis Tissue. *Reproduction, Fertility and Development*, **21**, 489-497. https://doi.org/10.1071/RD08235

[102] Wu, J.Y., Sun, Y.X., Wang, A.B., Che, G.Y., Hu, T.J. and Zhang, X.M. (2014) Effect of Newborn Bovine Serum on Cryopreservation of Adult Bovine Testicular Tissue. *Andrologia*, **46**, 308-312. https://doi.org/10.1111/and.12084

[103] Pukazhenthi, B.S., *et al.* (2015) Slow Freezing, but Not Vitrification Supports Complete Spermatogenesis in Cryopreserved, Neonatal Sheep Testicular Xenografts. *PLoS ONE*, **10**, e0123957. https://doi.org/10.1371/journal.pone.0123957

[104] Devi, L. and Goel, S. (2016) Fertility Preservation through Gonadal Cryopreservation. *Reproductive Medicine and Biology*, **15**, 235-251. https://doi.org/10.1007/s12522-016-0240-1

[105] Picton, H.M., Kim, S.S. and Gosden, R.G. (2000) Cryopreservation of Gonadal Tissue and Cells. *British Medical Bulletin*, **56**, 603-615. https://doi.org/10.1258/0007142001903418

[106] Courbiere, B., Caquant, L., Mazoyer, C., Franck, M., Lornage, J. and Salle, B. (2009) Difficulties Improving Ovarian Functional Recovery by Microvascular Transplantation and Whole Ovary Vitrification. *Fertility and Sterility*, **91**, 2697-2706. https://doi.org/10.1016/j.fertnstert.2008.03.012

[107] Isachenko, V., Isachenko, E., Sanchez, R., Dattena, M., Mallmann, P. and Rahimi, G. (2015) Cryopreservation of Whole Ovine Ovaries with Pedicles as a Model for Human: Parameters of Perfusion with Simultaneous Saturations by Cryoprotectants. *Clinical Laboratory*, **61**, 415-420. https://doi.org/10.7754/Clin.Lab.2014.140919

[108] Chen, C.H., Chen, S.G., Wu, G.J., Wang, J., Yu, C.P. and Liu, J.Y. (2006) Autologous Heterotopic Transplantation of Intact Rabbit Ovary after Frozen Banking at −196˚C. *Fertility and Sterility*, **86**, 1059-1066. https://doi.org/10.1016/j.fertnstert.2006.04.019

[109] Gerritse, R., *et al.* (2008) Optimal Perfusion of an Intact Ovary as a Prerequisite for Successful Ovarian Cryopreservation. *Human Reproduction*, **23**, 329-335. https://doi.org/10.1093/humrep/dem384

[110] Imhof, M., *et al.* (2004) Cryopreservation of a Whole Ovary as a Strategy for Restoring Ovarian Function. *Journal of Assisted Reproduction and Genetics*, **21**, 459-465. https://doi.org/10.1007/s10815-004-8763-5

[111] Johnston, L.A. and Lacy, R.C. (1995) Genome Resource Banking for Species Conservation: Selection of Sperm Donors. *Cryobiology*, **32**, 68-77. https://doi.org/10.1006/cryo.1995.1006

[112] Rischkowsky, B. and Pilling, D. (2007) The State of the World's Animal Genetic Resources for Food and Agriculture. FAO, Rome.

[113] Bailey, J., Bilodeau, J.-F. and Cormier, N. (2000) Semen Cryopreservation in Domestic Animals: A Damaging and Capacitating Phenomenon. *Journal of Andrology*, **21**, 1-7.

[114] Baust, J.G., Gao, D. and Baust, J.M. (2009) Cryopreservation: An Emerging Paradigm Change. *Organogenesis*, **5**, 90-96. https://doi.org/10.4161/org.5.3.10021

[115] Ugur, M.R., *et al.* (2019) Advances in Cryopreservation of Bull Sperm. *Frontiers in Veterinary Science*, **6**, 268. https://doi.org/10.3389/fvets.2019.00268

[116] Hiemstra, S.J., van der Lende, T. and Woelders, H. (2007) The Potential of Cryo-

preservation and Reproductive Technologies for Animal Genetic Resources Conservation Strategies. *The Role of Biotechnology*, Villa Gualino, Turin, 5-7 March 2005, 25-36.

[117] Domingues, S.F.S., Caldas-Bussiere, M.C., Martins, N.D. and Carvalho, R.A. (2007) Ultrasonographic Imaging of the Reproductive Tract and Surgical Recovery of Oocytes in *Cebus apella* (Capuchin Monkeys). *Theriogenology*, **68**, 1251-1259. https://doi.org/10.1016/j.theriogenology.2007.08.023

[118] Massip, A. and Donnay, I. (2003) Cryopreservation of Bovine Oocytes: Current Status and Recent Developments. *Reproduction Nutrition Development*, **43**, 325-330. https://doi.org/10.1051/rnd:2003024

[119] Lermen, D., *et al.* (2009) Cryobanking of Viable Biomaterials: Implementation of New Strategies for Conservation Purposes. *Molecular Ecology*, **18**, 1030-1033. https://doi.org/10.1111/j.1365-294X.2008.04062.x

[120] Ledda, S., Leoni, G., Bogliolo, L. and Naitana, S. (2001) Oocyte Cryopreservation and Ovarian Tissue Banking. *Theriogenology*, **55**, 1359-1371. https://doi.org/10.1016/S0093-691X(01)00487-3

[121] Checura, C.M. and Seidel, G.E. (2007) Effect of Macromolecules in Solutions for Vitrification of Mature Bovine Oocytes. *Theriogenology*, **67**, 919-930. https://doi.org/10.1016/j.theriogenology.2006.09.044

[122] Pereira, R.M. and Marques, C.C. (2008) Animal Oocyte and Embryo Cryopreservation. *Cell and Tissue Banking*, **9**, 267-277. https://doi.org/10.1007/s10561-008-9075-2

[123] Woods, E.J., Benson, J.D., Agca, Y. and Critser, J.K. (2004) Fundamental Cryobiology of Reproductive Cells and Tissue. *Cryobiology*, **48**, 146-156. https://doi.org/10.1016/j.cryobiol.2004.03.002

[124] Tucker, M.J., Morton, R.C., Wright, G., Sweitzer, C.L. and Massey, J.B. (1998) Clinical Application of Human Egg Cryopreservation. *Human Reproduction*, **13**, 3156-3159. https://doi.org/10.1093/humrep/13.11.3156

[125] Chen, S.U., Lien, Y.R., Chao, K.H., Ho, H.N., Yang, Y.S. and Lee, T.Y. (2003) Effects of Cryopreservation on Meiotic Spindles of Oocytes and Its Dynamics after Thawing: Clinical Implications in Oocyte Freezing—A Review Article. *Molecular and Cellular Endocrinology*, **202**, 101-107. https://doi.org/10.1016/S0303-7207(03)00070-4

[126] Santos, R.R., *et al.* (2010) Cryopreservation of Ovarian Tissue: An Emerging Technology for Female Germline Preservation of Endangered Species and Breeds. *Animal Reproduction Science*, **122**, 151-163. https://doi.org/10.1016/j.anireprosci.2010.08.010

[127] Hovatta, O. (2005) Methods for Cryopreservation of Human Ovarian Tissue. *Reproductive BioMedicine Online*, **10**, 729-734. https://doi.org/10.1016/S1472-6483(10)61116-9

[128] Naik, B.R., Rao, B.S., Vagdevi, R., Gnanprakash, M., Amarnath, D. and Rao, V.H. (2005) Conventional Slow Freezing, Vitrification and Open Pulled Straw (OPS) Vitrification of Rabbit Embryos. *Animal Reproduction Science*, **86**, 329-338. https://doi.org/10.1016/j.anireprosci.2004.07.008

[129] Amorim, C.A., Rondina, D., Lucci, C.M., Gonçalves, P.B.D., de Figueiredo, J.R. and Giorgetti, A. (2006) Permeability of Ovine Primordial Follicles to Different Cryoprotectants. *Fertility and Sterility*, **85**, 1077-1081. https://doi.org/10.1016/j.fertnstert.2005.09.041

[130] Saragusty, J. and Arav, A. (2011) Current Progress in Oocyte and Embryo Cryopreservation by Slow Freezing and Vitrification. *Reproduction*, **141**, 1-19. https://doi.org/10.1530/REP-10-0236

[131] Amorim, C., Curaba, M., Van Langendonckt, A., Dolmans, M.-M. and Donnez, J. (2011) Vitrification as an Alternative Means of Cryopreserving Ovarian Tissue. *Reproductive BioMedicine Online*, **23**, 160-186. https://doi.org/10.1016/j.rbmo.2011.04.005

[132] Rodriguez-Wallberg, K.A. and Oktay, K. (2012) Recent Advances in Oocyte and Ovarian Tissue Cryopreservation and Transplantation. *Best Practice & Research*: *Clinical Obstetrics & Gynaecology*, **26**, 391-405. https://doi.org/10.1016/j.bpobgyn.2012.01.001

[133] Mukaida, T. and Oka, C. (2012) Vitrification of Oocytes, Embryos and Blastocysts. *Best Practice & Research*: *Clinical Obstetrics & Gynaecology*, **26**, 789-803. https://doi.org/10.1016/j.bpobgyn.2012.07.001

[134] Otoi, T., Yamamoto, K., Koyama, N., Tachikawa, S. and Suzuki, T. (1996) A Frozen-Thawed *in Vitro*-Matured Bovine Oocyte Derived Calf with Normal Growth and Fertility. *The Journal of Veterinary Medical Science*, **58**, 811-813. https://doi.org/10.1292/jvms.58.811

[135] Maclellan, L.J., Carnevale, E.M., Coutinho da Silva, M.A., Scoggin, C.F., Bruemmer, J.E. and Squires, E.L. (2002) Pregnancies from Vitrified Equine Oocytes Collected from Super-Stimulated and Non-Stimulated Mares. *Theriogenology*, **58**, 911-919. https://doi.org/10.1016/S0093-691X(02)00920-2

[136] Hölker, M., *et al.* (2005) Duration of *in Vitro* Maturation of Recipient Oocytes Affects Blastocyst Development of Cloned Porcine Embryos. *Cloning and Stem Cells*, **7**, 35-44. https://doi.org/10.1089/clo.2005.7.35

[137] Niemann, H. and Rath, D. (2001) Progress in Reproductive Biotechnology in Swine. *Theriogenology*, **56**, 1291-1304. https://doi.org/10.1016/S0093-691X(01)00630-6

[138] Perry, G. (2018) 2013 Statistics of Embryo Collection and Transfer in Domestic Farm Animals.

[139] Chebel, R.C., Demétrio, D.G.B. and Metzger, J. (2008) Factors Affecting Success of Embryo Collection and Transfer in Large Dairy Herds. *Theriogenology*, **69**, 98-106. https://doi.org/10.1016/j.theriogenology.2007.09.008

[140] Stewart, B.M., *et al.* (2011) Efficacy of Embryo Transfer in Lactating Dairy Cows during Summer Using Fresh or Vitrified Embryos Produced *in Vitro* with Sex-Sorted Semen. *Journal of Dairy Science*, **94**, 3437-3445. https://doi.org/10.3168/jds.2010-4008

[141] Ferreira, G. (2013) Reproductive Performance of Dairy Farms in Western Buenos Aires Province, Argentina. *Journal of Dairy Science*, **96**, 8075-8080. https://doi.org/10.3168/jds.2013-6910

[142] Sanches, B.V., Zangirolamo, A.F., da Silva, N.C., Morotti, F. and Seneda, M.M. (2017) Cryopreservation of *in Vitro*-Produced Embryos: Challenges for Commercial Implementation. *Animal Reproduction*, **14**, 521-527. https://doi.org/10.21451/1984-3143-AR995

[143] Pontes, J.H.F., *et al.* (2010) Large-Scale *in Vitro* Embryo Production and Pregnancy Rates from *Bos taurus*, *Bos indicus*, and *indicus-taurus* Dairy Cows Using Sexed Sperm. *Theriogenology*, **74**, 1349-1355. https://doi.org/10.1016/j.theriogenology.2010.06.004

[144] Morotti, F., *et al.* (2013) Pregnancy Rate and Birth Rate of Calves from a Large-Scale

IVF Program Using Reverse-Sorted Semen in *Bos indicus*, *Bos indicus-taurus*, and *Bos taurus* Cattle. *Theriogenology*, **81**, 696-701. https://doi.org/10.1016/j.theriogenology.2013.12.002

[145] Sudano, M.J., *et al.* (2011) Lipid Content and Apoptosis of *in Vitro*-Produced Bovine Embryos as Determinants of Susceptibility to Vitrification. *Theriogenology*, **75**, 1211-1220. https://doi.org/10.1016/j.theriogenology.2010.11.033

[146] Abe, H., Yamashita, S., Satoh, T. and Hoshi, H. (2002) Accumulation of Cytoplasmic Lipid Droplets in Bovine Embryos and Cryotolerance of Embryos Developed in Different Culture Systems Using Serum-Free or Serum-Containing Media. *Molecular Reproduction and Development*, **61**, 57-66. https://doi.org/10.1002/mrd.1131

[147] McKeegan, P.J. and Sturmey, R.G. (2009) The Role of Fatty Acids in Oocyte and Early Embryo Development. *Reproduction, Fertility and Development*, **44**, 50-58. https://doi.org/10.1111/j.1439-0531.2009.01402.x

[148] Sanches, B.V., *et al.* (2013) Cryosurvival and Pregnancy Rates after Exposure of IVF-Derived *Bos indicus* Embryos to Forskolin before Vitrification. *Theriogenology*, **80**, 372-377. https://doi.org/10.1016/j.theriogenology.2013.04.026

[149] Sudano, M., *et al.* (2013) Improving Postcryopreservation Survival Capacity: An Embryo-Focused Approach. *Animal Reproduction*, **10**, 160-167.

[150] Nguyen, T.T., *et al.* (2007) Genomic Conservation of Cattle Microsatellite Loci in Wild Gaur (*Bos gaurus*) and Current Genetic Status of This Species in Vietnam. *BMC Genetics*, **8**, 77. https://doi.org/10.1186/1471-2156-8-77

[151] Choi, J.W., *et al.* (2013) Massively Parallel Sequencing of Chikso (Korean Brindle Cattle) to Discover Genome-Wide SNPs and InDels. *Molecules and Cells*, **36**, 203-211. https://doi.org/10.1007/s10059-013-2347-0

[152] Mondal, M., Dhali, A., Rajkhowa, C. and Prakash, B.S. (2004) Secretion Patterns of Growth Hormone in Growing Captive Mithuns (*Bos frontalis*). *Zoological Science*, **21**, 1125-1129. https://doi.org/10.2108/zsj.21.1125

[153] Giasuddin, M., Huque, K.S. and Alam, J. (2003) Reproductive Potentials of Gayal (*Bos frontalis*) under Semi-Intensive Management. *Asian-Australasian Journal of Animal Sciences*, **16**, 331-334. https://doi.org/10.5713/ajas.2003.331

[154] Karimi, K., Esmailizadeh Koshkoiyeh, A., Asadi Fozi, M., Porto-Neto, L.R. and Gondro, C. (2015) Prioritization for Conservation of Iranian Native Cattle Breeds Based on Genome-Wide SNP Data. *Conservation Genetics*, **17**, 77-89. https://doi.org/10.1007/s10592-015-0762-9

[155] Taberlet, P., *et al.* (2008) Are Cattle, Sheep, and Goats Endangered Species? *Molecular Ecology*, **17**, 275-284. https://doi.org/10.1111/j.1365-294X.2007.03475.x

[156] Morais, J., Oom, M.M., Malta-Vacas, J. and Luís, C. (2005) Genetic Structure of an Endangered Portuguese Semiferal Pony Breed, the Garrano. *Biochemical Genetics*, **43**, 347-364. https://doi.org/10.1007/s10528-005-6775-1

[157] Amador, C., Hayes, B.J. and Daetwyler, H.D. (2014) Genomic Selection for Recovery of Original Genetic Background from Hybrids of Endangered and Common Breeds. *Evolutionary Applications*, **7**, 227-237. https://doi.org/10.1111/eva.12113

[158] Bolormaa, S., Hayes, B.J., Hawken, R.J., Zhang, Y., Reverter, A. and Goddard, M.E. (2011) Detection of Chromosome Segments of Zebu and Taurine Origin and Their Effect on Beef Production and Growth. *Journal of Animal Science*, **89**, 2050-2060. https://doi.org/10.2527/jas.2010-3363

[159] Martín-Burriel, I., *et al.* (2007) Genetic Diversity and Relationships of Endangered Spanish Cattle Breeds. *Journal of Heredity*, **98**, 687-691. https://doi.org/10.1093/jhered/esm096

[160] Rodero-Serrano, E., Demyda-Peyrás, S., González-Martinez, A., Rodero-Franganillo, A. and Moreno-Millán, M. (2013) The Rob(1;29) Chromosome Translocation in Endangered Andalusian Cattle Breeds. *Livestock Science*, **158**, 32-39. https://doi.org/10.1016/j.livsci.2013.10.001

[161] Rendo, F., *et al.* (2004) Analysis of the Genetic Structure of Endangered Bovine Breeds from the Western Pyrenees Using DNA Microsatellite Markers. *Biochemical Genetics*, **42**, 99-108. https://doi.org/10.1023/B:BIGI.0000020465.62447.00

[162] Edwards, C.J., Loftus, R.T., Bradley, D.G., Dolf, G. and Looft, C. (2000) Relationships between the Endangered Pustertaler-Sprinzen and Three Related European Cattle Breeds as Analysed with 20 Microsatellite Loci. *Animal Genetics*, **31**, 329-332. https://doi.org/10.1046/j.1365-2052.2000.00651.x

[163] Ginja, C., Telo Da Gama, L. and Penedo, M.C.T. (2010) Analysis of STR Markers Reveals High Genetic Structure in Portuguese Native Cattle. *Journal of Heredity*, **101**, 201-210. https://doi.org/10.1093/jhered/esp104

[164] Mateus, J.C., Penedo, M.C.T., Alves, V.C., Ramos, M. and Rangel-Figueiredo, T. (2004) Genetic Diversity and Differentiation in Portuguese Cattle Breeds Using Microsatellites. *Animal Genetics*, **35**, 106-113. https://doi.org/10.1111/j.1365-2052.2004.01089.x

[165] Cesarani, A., *et al.* (2018) Genome-Wide Variability and Selection Signatures in Italian Island Cattle Breeds. *Animal Genetics*, **49**, 371-383. https://doi.org/10.1111/age.12697

[166] Klocker, V., Tambasco-Talhari, D., Pozzi, P., Coutinho, L. and Regitano, L. (2003) Genetic Characterization of Aberdeen Angus Cattle Using Molecular Markers. *Genetics and Molecular Biology*, **26**, 133-137. https://doi.org/10.1590/S1415-47572003000200005

[167] Wiener, P., Burton, D. and Williams, J.L. (2005) Breed Relationships and Definition in British Cattle: A Genetic Analysis. *Heredity* (*Edinb*), **93**, 597-602. https://doi.org/10.1038/sj.hdy.6800566

[168] Williams, J.L., *et al.* (2015) Inbreeding and Purging at the Genomic Level: The Chillingham Cattle Reveal Extensive, Non-Random SNP Heterozygosity. *Animal Genetics*, **47**, 19-27. https://doi.org/10.1111/age.12376

[169] Browett, S., *et al.* (2018) Genomic Characterisation of the Indigenous Irish Kerry Cattle Breed. *Frontiers in Genetics*, **9**, 51. https://doi.org/10.3389/fgene.2018.00051

[170] Tijjani, A., Utsunomiya, Y.T., Ezekwe, A.G., Nashiru, O. and Hanotte, O. (2019) Genome Sequence Analysis Reveals Selection Signatures in Endangered Trypanotolerant West African Muturu Cattle. *Frontiers in Genetics*, **10**, 442. https://doi.org/10.3389/fgene.2019.00442

[171] Msalya, G., *et al.* (2017) Determination of Genetic Structure and Signatures of Selection in Three Strains of Tanzania Shorthorn Zebu, Boran and Friesian Cattle by Genome-Wide SNP Analyses. *PLoS ONE*, **12**, e0171088. https://doi.org/10.1371/journal.pone.0171088

[172] Kim, J., *et al.* (2017) The Genome Landscape of Indigenous African Cattle. *Genome Biology*, **18**, Article No. 34. https://doi.org/10.1186/s13059-017-1153-y

[173] Ndiaye, N.P., Sow, A., Dayo, G.K., Ndiaye, S., Sawadogo, G.J. and Sembène, M. (2015) Genetic Diversity and Phylogenetic Relationships in Local Cattle Breeds of Senegal Based on Autosomal Microsatellite Markers. *Veterinary World*, **8**, 994-1005. https://doi.org/10.14202/vetworld.2015.994-1005

[174] Gwakisa, P.S., Kemp, S.J. and Teale, A.J. (1994) Characterization of Zebu Cattle Breeds in Tanzania Using Random Amplified Polymorphic DNA Markers. *Animal*

*Genetics*, **25**, 89-94. https://doi.org/10.1111/j.1365-2052.1994.tb00433.x

[175] Sanarana, Y., Visser, C., Bosman, L., Nephawe, K., Maiwashe, A. and van Marle-Köster, E. (2016) Genetic Diversity in South African Nguni Cattle Ecotypes Based on Microsatellite Markers. *Tropical Animal Health and Production*, **48**, 379-385. https://doi.org/10.1007/s11250-015-0962-9

[176] Edea, Z., Bhuiyan, M.S.A., Dessie, T., Rothschild, M.F., Dadi, H. and Kim, K.S. (2014) Genome-Wide Genetic Diversity, Population Structure and Admixture Analysis in African and Asian Cattle Breeds. *Animal*, **9**, 218-226. https://doi.org/10.1017/S1751731114002560

[177] Khatun, M.M., Hossain, K.M. and Mahbubur Rahman, S.M. (2012) Molecular Characterization of Selected Local and Exotic Cattle Using RAPD Marker. *Asian-Australasian Journal of Animal Sciences*, **25**, 751-757. https://doi.org/10.5713/ajas.2011.11331