

Origin, Assessment Type, Forces Influence and Loss of Genetic Diversity -review

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Abstract

This review objective is to review the origin of domestic livestock, type of assessment, forces influence and loss of genetic diversity. Genetic diversity is crucial for species and breeds to adapt to changing environmental conditions and to respond to market demands, socio-economic changes and changes in consumer preferences. It provides the buffering capacity for breeds or populations to survive disease outbreaks or dramatically emerging environmental challenges. However, there is loss through inbreeding, mutation, genetic drift, selection and migration, these can be assess by concepts of diversity measurement, molecular-marker approach, morphological-marker approach (phenotypic assessments), pedigree-based approach and survey-based approach.

Keywords: - genetic diversity, assessment of genetic diversity, loss of genetic diversity

1. INTRODUCTION

Biological diversity or biodiversity, which comprises the variability within and among genes (genetic diversity), species (species diversity) and habitats (ecosystem diversity), decreases drastically within agricultural production and adjacent, natural and semi-natural systems (Godfray *et al.*, 2010). Each living organisms have developed specific genetic characteristics according to its particular natural ecosystem, environmental and socioeconomic conditions. Collectively, these characteristics constitute the earth's species diversity (Rollefson, 2000). Genetic variation is the raw material for evolutionary change within wildlife populations. It allows populations to evolve in response to environmental change, whether that be new or changed diseases, pests, parasites, competitors or predators or greenhouse waning, ozone layer depletion, or pollution. Consequently, the world conservation union has recognized genetic diversity as one of three levels of biological diversity requiring conservation (McNeely *et al.*, 1990). During the subsequent history of livestock, the main evolutionary forces of mutation, selective breeding, adaptation, isolation and genetic drift have created an enormous diversity of local populations. During the last decades, development and increased focus on more efficient selection programmes have accelerated genetic improvement in a number of breeds. Artificial insemination and embryo transfer have facilitated the dissemination of genetic material. In addition, progress in feed technology has allowed optimal nutrition, while enhanced transport and communication systems have led to uniform and strictly controlled production environments. As a result, highly productive breeds have replaced local ones across the world. This development has led to growing concerns about the erosion of genetic resources (FAO, 2007).

The level of genetic variation within a species represents a balance between mutation, drift, and natural selection. Genetic variation is generated by mutation and is lost from populations by genetic drift due to finite population size. Natural selection may either erode genetic variation by leading to fixation of alleles or promote its retention as a result of balancing or diversifying selection (Crow & Kimura, 1970). Genetic diversity provides the raw material for breed improvement and for the adaptation of livestock populations to changing environments and changing demands. Information on the origin and history of animal genetic resources (AnGR) is essential to the design of strategies for their sustainable management (Ajmone-Marsan *et al.*, 2010; Felius *et al.*, 2014). Genetic improvement under relatively intense unidirectional selection may involve both increases in the frequency of favorable additive alleles as well as the progressive breakdown of homeostatic regulatory mechanisms established under the stabilizing selection that is characteristic of natural populations. Recombination among closely linked regulatory loci and new, potentially favorable mutations are possible sources of long-term genetic variation. A greater understanding of the potential that these alternative mechanisms have for supporting long-term genetic improvement and of genetic relationships among global livestock populations are priorities for managing farm animal genetic diversity (Notter, 2017).

Genetic diversity is crucial for species and breeds to adapt to changing environmental conditions and to respond to market demands, socio-economic changes and changes in consumer preferences. It provides the buffering capacity for breeds or populations to survive disease outbreaks or dramatically emerging environmental challenges (FAO, 2007). Livestock diversity in Ethiopia has suffered considerably due to the many wars, civil strife and cyclical famines. Growing transhumance and migrations in the lower altitude areas have resulted in massive interbreeding between traditionally isolated livestock populations. In the highlands, government sponsored crossbreeding programmes have severely compromised the sustenance of genetic diversity in indigenous livestock, especially cattle and poultry (FOA, 1984). Therefore, the objective of this paper is to review on the genetic diversity, origin, type and assessment driving force that affects genetic diversity.

2. Genetic Diversity

Genetic diversity, i.e. the diversity within species and populations, represents the most fundamental level of agrobiodiversity. It comprises the diversity of crop species and husbandry animals, the corresponding cultivars and breeds (modern breeding lines, hybrids, clones, etc.), and landraces (farmers' varieties, traditional, local or heritage varieties or breeds) (Newton *et al.*, 2010). Also genetic diversity can be defined as the variability of alleles and genotypes occurring within a population or species which drives all morphological and physiological differences among individuals that are based on genetic inheritance (Kumar *et al.* 2006). Different breeds have specific genetically determined characteristics. It is possible, but very rare, there is no genetic variation in a population. This occurs in populations that are fully inbred: animals are genetically completely identical to each other. The number of alleles that are present in a population is a measure of genetic diversity. The frequency at which these alleles occur in the population also have an influence on the size of genetic diversity. The more equal the allele frequencies are, the larger the diversity (Waaij, 2014). Diversity can be defined as the genetic variation between and within different breeds, so it is essential to characterize a breed for its conservation. Microsatellites markers are the best genetic marker have been used successfully to define genetic structures and genetic relationships among different breeds. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary (Kumar *et al.* 2006).

Genetic diversity can be haploid (DNA of the mitochondria), diploid, or even polyploid. Genetic traits can be based on the alleles at a single locus or many dozens of loci (Frankham *et al.*, 2002). Allelic diversity is important for a population's long- term ability to adapt, while heterozygosity is important for more immediate individual health (Allendorf, 1986). Accordingly, populations lacking genetic diversity often exhibit an increased rate of extinction (Markert *et al.*, 2010). Inbreeding, genetic drift, restricted gene flow, and small population size all contribute to a reduction in genetic diversity. Fragmented and threatened populations are typically exposed to these conditions, which is likely to increase their risk of extinction (Madsen *et al.*, 1999; Frankham *et al.*, 2010). Genetic theory predicts that levels of genetic variation should increase with effective population size. Compiled the first convincing evidence that levels of genetic variation in wildlife were related to population size, but this issue remains controversial (Sould, 1976).

In 2010, the Commission on Genetic Resources for Food and Agriculture reported a global total of 8,054 breeds, of which 7,001 were local breeds and 1,053 were transboundary breeds (CGRFA, 2010). These breeds, which vary with respect to morphological traits, production and reproductive performances, and unique characteristics, are the outcome of evolution, mutation and natural selection. The varying climatic conditions across the world have caused animals to develop adaptive attributes for the local environment (Paterson and Coleman; 1982). The genetic diversity has also been enhanced by the differences in the selection practices for economically and culturally important traits among countries and communities. These factors as well as genetic drift have also contributed to vast variations in genetic makeup among populations of the same breed at different locations.

The hypothesis that genetic variation is related to population size leads to the following predictions:-

- ❖ Genetic variation within species should be related to population size
- ❖ Genetic variation should be related to population size within taxonomic groups
- ❖ Widespread species should have more genetic variation than restricted species
- ❖ genetic variation in animals should be negatively correlated with body size
- ❖ Genetic variation should be negatively correlated with rate of chromosome evolution
- ❖ Genetic variation across species should be related to population size
- ❖ Vertebrates should have less genetic variation than invertebrates or plants
- ❖ Island populations should have less genetic variation than mainland populations
- ❖ Endangered species should have less genetic variation than non-endangered species (Sould, 1976).

3. Origin and Domestication of Livestock

Domestic animals possess a wide variety of similar morphological traits despite the lack of close evolutionary relationships between their wild progenitors (Darwin, 1868). Phenotypic convergence, which includes, variations in coat color and texture, docility, shifts in reproductive timing, alterations in skull shape and tooth crowding, dwarf and giant varieties, and floppy ears, has intrigued scholars for the past 150 years (Larson and Fuller, 2014). Livestock domestication is thought to have occurred in at least 15 areas of the world (Larson and Burger, 2013). On the other hand, early animal domestication is associated with perhaps only 3 regions (the Near East, central China, and the Andes) (Larson and Fuller, 2014). Close genetic relationships between domestic and wild populations in other parts of the world (i.e. outside the recognized domestication centers) are considered to indicate introgression (Larson and Burger, 2013). The domestic animals important today for food and agriculture production are a consequence of processes of domestication that have existed for almost 12,000 years (Beate, 2008). The total number of animal domesticates doubled in the middle Holocene (8,000–4,000 years BP) several thousand years after the first domestication episodes, the majority of domestic animals on Earth have been

domesticated in the past few centuries (Larson and Fuller, 2014). The genetic differentiation of domestic and wild populations can be framed within the context of two key considerations. The first distinguishes between domestication traits, presumed to have been essential at the early stages of domestication, and improvement traits, those that have appeared since the split between wild and domestic populations (Olsen and Wendel, 2013).

The recognizing and formally three separate pathways that animals followed into a domesticated relationship with humans: a commensal pathway, a prey pathway and a directed pathway. The only pathway that began with a deliberate objective to domesticate a species is the directed pathway (Zeder, 2012). The majority of modern domestic animals have arisen in the past few hundred years because of the directed pathway (Larson and Fuller, 2014). Information on the origin and history of animal genetic resources (AnGR) is essential to the design of strategies for their sustainable management (Ajmone-Marsan *et al.*, 2010; Feliuss *et al.*, 2014). Only 15 out of 148 non-carnivore terrestrial mammalian species weighing more than 45 kg have been domesticated. From the 10000 avian species, only very few (chicken, turkey, pheasant, guinea fowl, duck, Muscovy duck, goose, pigeon, quail and ostrich) have been domesticated as a source of food. According to Diamond (2002), successful domestication depends on the presence of several traits in the target species:-

- Behavioural traits that facilitate management by humans (e.g. a lack of aggression towards humans, a tendency not to panic when disturbed and strong social instincts)
- Reproductive traits, such as the ability to breed in captivity, short intervals between births and (preferably) large litter sizes
- Physiological traits, such as rapid growth and a non-carnivorous diet. Domestication may have been triggered by climatic changes at the end of the Pleistocene (12000 to 14000 BP) that led to localized expansion of human populations and the emergence of crop farming (Larson and Burger, 2013).

3.1. Historical phases in gene flows

Evolutionary processes such as speciation result from mutations within genetic information. The exchange of alleles from one individual or population to another by reproduction and recombination is called gene flow and leads to new genotypes which increase genetic variability (Freeland *et al.*, 2011). Gene flow' means the movement of genes. In some cases, small fragments of DNA may pass from one individual directly into the germline of another, perhaps transduced by a pathogenic virus or other vector, or deliberately via a human transgenic manipulation (Mallet, 2001). Developments in England during the late eighteenth century marked the beginning of a new era and had major consequences for the future of livestock diversity throughout the world. Systematic performance recording, identification of animals and pedigree recording, managed by breeders' associations and documented in herd books, led to the development of more homogenous breeds.

In the developed world the past two hundred years have seen several phases of genetic change. In phase one, the development of more intensive agriculture and changes in demand for agricultural products in the last 18th and early 19th century led to the stabilization of many breeds as distinct genetic entities and purity. Railways increased mobility and facilitated the long-distance transportation of livestock. This developments initiated what is referred to in the first SoW-AnGR as the "second phase of global gene flow", which lasted from the nineteenth to the mid-twentieth century and saw a large expansion in the geographical distribution of several successful breeds (Valle Zárate *et al.*, 2006; Feliuss, 2015). Breeds very often originated from a regional population that contained diverse genetic origins. In phase two as agricultural system continued to intensify through the late 19th and early 20th century, breeds better adapted to modern production system became more widespread and other breeds reduced in numbers, many others breeds reduced in numbers, many becoming extinct. In phase three, as smaller number of breeds came to dominant production system in the middle to late 20th century, modern within breed genetic improvement programs became widely established coupled with extensive use of crossbreeding and the rise of breeding companies (Gibson, 2005). Artificial insemination became common in cattle and pig breeding. As a result of these developments, a limited number of transboundary breeds have become very widespread and increasingly dominate livestock production throughout the world (FAO, 2011). The breeding companies often abandoned the concept of breed, creating their own synthetic populations from crosses among existing breeds and then practicing intense selection for desired characteristics within these new populations (Gibson, 2005).

To date mainly using neutral markers (i.e. markers that have no known effect on the phenotype) (Groeneveld *et al.*, 2010). Different categories of polymorphic DNA markers reveal different aspects of the history of livestock:-

- ❖ Mitochondrial DNA (mtDNA) is transmitted maternally and has been instrumental in identifying ancestor species, estimating the number of female founders (Bollongino *et al.*, 2012).
- ❖ Identifying the geographic regions of domestication (Naderi *et al.*, 2008) and reconstructing migration routes (Groeneveld *et al.*, 2010; Lenstra *et al.*, 2012).

The importance of gene flow, the successful movement of genes among populations, has been controversial (Zimmer, 2010). According to the classical view, gene flow among populations of a species is an

essential factor in maintaining species integrity (Mayer, 1970). Moderate to high rates of gene flow among populations help prevent sub-population isolation, thereby maintaining genetic variation and preventing inbreeding depression (Franklin, 1980).

4. Importance of Genetic Diversity

Animal genetic diversity is critical for food security and rural development. Animal genetic diversity allows farmers to select stocks or develop new breeds in response to environmental change conditions, including new or resurgent disease threats, new knowledge of human nutrition requirements and changing market conditions /societal needs– all of which are largely unpredictable. What is predictable is the future human demand for food. Demand of felt most acutely in developing countries, where 85% of the increased food demand is expected. Given the above facts, domestic animal diversity is critical for food security (FAO/UNEP, 2000). Genetic diversity serves as a way for populations to adapt to changing environments (Kumar *et al.* 2006) and it has been identified as an important factor influencing a population's long-term potential for survival (Bouzat, 2010). The contribution of genetic diversity has been recognized in numerous aspects of population persistence, and is critical for long-term fitness and adaptation (Frankham, 2005). Genetic diversity provides the genetic resources for animal breeders to design selection and breeding programmes to further enhance animal productivity and ensure food security. These needs of the future and increasingly diminishing genetic diversity have gained global attention and concern (FAO, 2007).

Genetic diversity allows for flexibility in a population. If circumstances change, different genotypes may be more suitable and selection pressure will change. If the alleles required to adapt to the new circumstances are no longer present, or only at very low frequency than adaptation of the population will be very difficult. Inbreeding (increase in homozygosity) causes inbreeding depression. Inbred animals tend to be less healthy, live shorter, and have reduced reproductive capacity. Related to that: reduced genetic diversity results in increased homozygosity, also of alleles that have deleterious effects. More inbred animal's means more animals that suffer from monogenic recessive disorders (Waaaj, 2014).

Genetic variation present in a population today may not be entirely beneficial in the current environment. A few alleles may be directly harmful for the individuals carrying the alleles under the present circumstances (Lundqvist *et al.*, 2008). Farm animal genetic diversity is required to meet current production needs in various environments, to allow sustained genetic improvement, and to facilitate rapid adaptation to changing breeding objectives. Production efficiency in pastoral species is closely tied to the use of diverse genetic types, but greater genetic uniformity has evolved in intensively raised species. In poultry, breeding decisions are directed by a few multinational companies and involve intense selection, the use of distinct production lines, and very large populations. In dairy cattle, the Holstein breed dominates production. Intensive sire selection is leading to relatively rapid inbreeding rates and raises questions about long-term effects of genetic drift. Key questions in management of farm animal genetic diversity involve the distribution of potentially useful quantitative trait locus alleles among global livestock breeds (Notter, 2017).

The total diversity of animal genetic resources available to farmers and the resulting diverse products make it possible for humans to survive in a wide range of environments, from the hot and humid tropics to arid deserts and extremely cold arctic or mountainous regions. Genetic diversity also enables livestock to adapt to diseases, parasites, wide variations in the availability and quality of food and water, and other limiting factors (FAO, 1999).

5. Monitoring and Assessment of Genetic Diversity

Monitoring of diversity should address both the level of between-breeds diversity, with setting up conservation programmes for endangered populations, and the level of within-breed diversity with updating rules for the genetic management of the population (Fikse and Philippon, 2007). Monitoring programmes need to ensure that feedback is provided to farmers, researchers and other stakeholders.

Today's efforts to estimate genetic diversity within natural and domesticated populations of animal species have more various goal:-

- 1) Estimations have to provide insight into evolutionary biology for basic information. This information is fundamental for understanding the importance of genetic diversity and its impact on higher levels of organization and vice versa (Templeton, 1994).
- 2) Investigations will help to assess, evaluate and predict consequences resulting from natural and anthropogenic impacts and disturbances on population genetics (Peter-Schmid *et al.*, 2008).
- 3) Investigations of genetic diversity provide information for evaluation and utilization of genetic resources as well as targeted breeding strategies and efforts (Kölliker *et al.*, 2005). This includes information, which support and improve the management and storage of genetic material such as germplasm collections (Fjellheim *et al.*, 2007). Especially in breeding and agriculture, the knowledge of genetic constitution helps to detect and maintain the most valuable genes from highly variable gene

- pools (Mohammadi and Prasanna, 2003).
- 4) Genetic diversity assessments will help to target biological conservation and management efforts and support decision making in order to conserve and create biodiversity (Gustafson *et al.*, 2004; Zhang *et al.*, 2010). This includes prevention from further loss of genetic diversity by, for example, securing and conserving genetic information (ex situ/in situ), natural variations and material for the future (Ranatunga *et al.*, 2009).
 - 5) The assessment of already lost genetic information – the genetic erosion (Teklu and Hammer, 2006). The analysis and evaluation of genetic diversity of livestock as well as natural populations are the most fundamental steps to achieve all listed goals.

5.1. Methods of genetic diversity assessment

5.1.1. Concepts of diversity measurement

Concepts for the estimation of genetic diversity in natural and anthropogenic systems are diverse and do address the current state as well as spatial and temporal trends of genetic diversity and erosion at multiple levels (Meng *et al.*, 2000). Those concepts rely on the analysis of molecular and biochemical data (Boettcher *et al.*, 2010), phenotypic data (Dias *et al.*, 2008; Cortese *et al.*, 2010), pedigree data (van Beuningen and Busch, 1997) or diversity indices such as the Shannon's diversity index calculated using demographic data such as total numbers and the percentage of varieties and breeds used by farmers (Goffaux *et al.*, 2011). Regardless of the origin of data, diversity is basically measured as either richness, i.e. the number of entity; evenness, i.e. the equitability of entities; genetic dissimilarity, i.e. genetic distance; or is based on diversity indices addressing heterogeneity or dominance of an entity (Cardinale *et al.*, 2012).

5.1.2. Morphological-marker approach (phenotypic assessments)

Genetic diversity within and among populations of animals can be estimated using phenotypic, e.g. morphological, phenological or agronomic characters, i.e. the physical form and structure of an organism or populations visible by eye such as color, growth habit or height (Chang *et al.*, 2012). Morphological marker are useful tools to identify valuable traits in populations for the improvement of breeding programs (Fjellheim *et al.*, 2007). Furthermore, they are of great importance for the detection of valuable genetic resources and provide an important basis for their conservation. Nonetheless, compared to molecular markers, they are limited, influenced by environmental condition at the locality, quantitative, i.e. related to multiple genes and their assessment requires multiple replications, space and time (Boller and Greene, 2010).

5.1.3. Molecular-marker approach

Molecular markers are of major importance for the detection of intra-specific genetic diversity. Genetic diversity can be detected directly at gene level while excluding the impact of environmental factors. Multiple marker systems, which can be used to investigate a wide range of natural and domesticated animal species. The potential applications are diverse and range from genetic diversity assessments within and among populations (quantification), structure of genetic diversity (partitioning), genetic distance between individuals and populations (relatedness), genome mapping, or for the identification of single alleles, genes or genotypes which are of interest for specific breeding purposes (Agarwal *et al.*, 2008; Freeland *et al.*, 2011). Current species systematics rely on high resolution which has been provided by molecular and biochemical markers (Soltis *et al.*, 2009).

5.1.4. Pedigree-based approach

Another approach to address latent genetic diversity is based on pedigree-data analysis. The Coefficient of Parentage (COP) can be measured as relative estimate of genetic similarity or distance between varieties based on pedigree information (Malécot, 1947). The COP is based on the assumption that a random allele taken from a random locus of two varieties is identical by descent (Kempthorne, 1957). It is used to measure genetic diversity within husbandry animal species as well as for the improvement of breeding strategies (Singh *et al.*, 2007; Melka and Schenkel, 2011). Although this method excludes environmental impacts, it is quite restricted due to complicated and incomplete pedigree-data of varieties, lacking pedigree-data for landraces or unrealistic basic assumption which this calculation is built. For example, complete pedigrees, ancestors are per se assumed to be unrelated and alleles are exclusively identical by descent and not by state (Meng *et al.*, 2000).

5.1.5. Survey-based approach

Genetic diversity detected at inter-varietal diversity level, i.e. diversity among livestock populations, based on demographic data such as the total number as well as the percentage of the livestock breeds occurring at different spatial or temporal scale (Meng *et al.*, 2000). This concept assumes a variation that is related to a population or accession name, which are per se supposed to be genetically different. Genetic diversity can either be estimated using demographic data of crop and livestock accessions that are stored ex situ/in vitro (Clerc *et al.*, 2006) or managed in situ/in vivo (Jarvis *et al.*, 2008). On-farm surveys are predominantly conducted using questionnaires or interviews directed at crop and livestock populations on-farm (FAO, 2011). Although the survey-based approach does neither address genetic diversity at gene nor at intra-varietal level, general trends of genetic

erosion can be detected and data bases, e.g. germplasm collections or registers, can be completed using this approach (Cebolla-Cornejo *et al.*, 2007). Furthermore, valuable information of farmer perceptions and knowledge of on-farm genetic diversity and its maintenance can be surveyed (Jarvis *et al.*, 2011).

6. Forces Influence and Loss of Genetic Diversity

Genetic erosion, i.e. the loss of genetic diversity in livestock due to natural and anthropogenic processes in agricultural development, resulted from two major events which occurred during the history of livestock-breed development (van de Wouw *et al.*, 2010). There are a number of forces that influence genetic diversity. At population level there are forces that increase genetic diversity, and forces that decrease it. Evolutionary change proceeds via four different phenomena, often called “evolutionary forces” or “evolutionary mechanisms”: mutation, selection, drift, and gene flow. Working separately or together, they affect the change of allele frequencies in a population from generation to generation (Zimmer, 2010). Mutations are events that create new alleles. When it happens in germ cells it has an increasing effect on genetic diversity. Also migration may have an increasing effect, but only immigration (new animals moving into the population). Emigration (animals moving out of the population) usually has a decreasing effect on genetic diversity, especially when the population size is small. Also selection has a decreasing effect, only animals with a specific genetic make-up are allowed to breed, at the expense of others. This will have an effect on allele frequencies, away from the equal frequencies. A final force with a decreasing effect on genetic diversity is the force of coincidence (genetic drift), and related to that is inbreeding. Genetic drift cannot directly be influenced by our selection decisions. Forces that influence genetic diversity -direction of change in genetic diversity

Genetic Drift and inbreeding -

Selection -

Migration - or +

Mutation + (Waaij, 2014).

The status in risk is still unknown for more than 30 % of the collected inventory (FAO, 2007). During the past century (1882 to 1992), the disappearance of 617 breeds due to extinction has been noticed worldwide (World Conservation Monitoring Centre, 1992). Within the current century (2000 to 2006), the extinction rate even increased, reaching a monthly rate and within six years more than 60 breeds are registered as extinct (CBD, 2010). Worldwide, 35 species of domesticated animal species (birds, mammals) are represented by more than 7'000 breeds of which one quarter is under risk status (CBD, 2010). In Europe, approximately 130 cattle breeds are at risk of extinction or have been lost (FAO, 2013). In the Netherlands, local breeds were reduced by 95 % within the past 30 years (Buiteveld *et al.*, 2009).

A loss of genetic diversity has been shown to affect individual fitness with decreased sperm quality, reduced litter size (Hedrick and Fredrickson, 2010), increased juvenile mortality (Ralls *et al.*, 1988), and increased susceptibility to disease and parasites (Coltman *et al.*, 1999). Alleles can be lost from the population by coincidence. One reason for allele loss can be that not all animals mate and produce offspring, irrespective of selection decisions, because animals selected for breeding may not all manage to produce offspring. Consequence of this not producing offspring despite being selection candidates does influence the allele frequencies in the offspring generation and alleles that were present at low frequency may be lost (Waaij, 2014). As the genetic diversity of low-production breeds is likely to contribute to current or future traits of interest (Bruford *et al.*, 2003; Toro *et al.*, 2008), they are considered essential for maintaining future breeding options. The existing FAO definitions of breed risk status (extinct, critical, endangered and not at risk) are based on numbers of breeding females and males, but do not relate to how matings are handled (e.g. random or high selection intensity within breeds, use of crossbreeding) (Fikse and Philippon, 2007). Populations can show low levels of genetic diversity or be genetically impoverished in different ways:

- ❖ Many alleles may have become rare or are absent from the gene pool because of genetic drift
- ❖ The proportion of homozygotes may have increased at the expense of the heterozygotes due to inbreeding in the population
- ❖ The gene pool may be fixed for alleles that decrease the viability and fertility of the individuals or the population (FAO, 1999).

7. Genetic diversity indicators

Indicators for the assessment of genetic diversity are considered to be important tools and they can be defined as a parameter which simplifies, quantifies, standardizes and communicates the rather complex state or level of a system (CBD, 2003). Indicators have been proposed to be used for genetic diversity monitoring to evaluate ecosystem conditions and corresponding environmental factors (Bagley *et al.*, 2002). They can also be used to monitor and evaluate the contribution and the effectiveness of policies, e.g. addressing agrobiodiversity issues, while assisting the identification and improvement of policies and management strategies for the conservation of biological diversity in agriculture (Layke, 2009).

Recent research suggests that several issues need to be taken into account for the development of indicators for animal genetic diversity

- the concept of the breed as a genetic entity for measuring diversity would benefit from the use of molecular markers for the assignment of individuals to breeds
- the assessment of breed risk status should not rely on population size alone, but would benefit from more accurate parameters calculated on the basis of extensive pedigree analysis, such as inbreeding coefficients of current breeding animals, or the number of ancestors with a cumulated contribution of 50 percent of the total gene pool
- In the absence of pedigree recording, loss in diversity may be monitored using molecular markers, particularly on the basis of the adjusted mean number of alleles calculated for reference sets of microsatellite markers
- Occurrence of introgressions or fragmentations may be monitored with molecular markers, combining nuclear markers and mtDNA, provided that reference data sets for a range of populations are available for comparative analysis within a country or region.

A compromise has to be found between the ideal list of indicators needed to provide accurate information, and the cost of collection and ease of interpretation. As stated by OECD (2001), four main criteria may be used to assess the value of indicators

- ✚ Policy relevance
- ✚ Analytical soundness
- ✚ Measurability and interpretation

In general, a small number of indicators is preferable in terms of measurability and communication, but relevant information needs to be captured in order to support sound decisions.

Major drivers of change can lead to rapid changes in the population size and structures of locally adapted breeds. Regular monitoring is therefore required, at least for those breeds classified as critical or endangered. At present, most national livestock censuses do not contain breed-level data; therefore, regular reporting of breed population numbers does not usually take place. In addition to population size, the number of farms and number of breeding organizations could be considered. The number of breeding males should be made available. Such a monitoring scheme can serve as the basis for national early warning, so that timely management interventions can be planned (Fikse and Philippson, 2007).

8. CONCLUSION

Genetic diversity is crucial for species and breeds to adapt changing environmental conditions and to respond to market demands, socio-economic changes and changes in consumer preferences. It provides the buffering capacity for breeds or populations to survive disease outbreaks or dramatically emerging environmental challenges. Diversity in animal genetic resource (AnGR) populations is measured in three forms: inter-population diversity (between breeds), intra-population diversity (within breeds) and the inter-relationships between characterization is therefore fundamental to the establishment of national inventories of AnGR, to effective monitoring of AnGR populations and to the establishment of early-warning and response systems for AnGR. Genetic drift and inbreeding, selection, migration and mutation are forces that influence genetic diversity. A loss of genetic diversity has been shown to affect individual fitness with decreased sperm quality, reduced litter size, increased juvenile mortality and increased susceptibility to disease and parasites. Molecular markers are of major importance for the detection of intra-specific genetic diversity. Genetic diversity can be detected directly at gene level while excluding the impact of environmental factors. Multiple marker systems, which can be used to investigate a wide range of natural and domesticated animal species.

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