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Prioritization of breeds for the conservation of animal genetic resources

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Abstract
The demand in conserving a breed with economic importance, genetically unique and socially or traditionally important is growing exponentially in the modern era. In focus to enhance the production, genetically diverse breeds are forgotten story in livestock production. Hence to prioritize the breed holds the key in conserving the animals. Kinship, Weitzman and combined approaches are used to analyze the genetic diversity. Thus, the extinction risk value and the conservation value are estimated to rank the breeds. The risk of extinction can be calculated by assigning definite values for each breed for different criteria, whereas conservation value is calculated as recommended by FAO. The breed should be ranked according to the utility which should include the non-genetic and genetic components affecting the conservation of the breed. The breed with the highest utility index is considered as the greatest priority for conservation.

Keywords: Prioritization, animal genetic resources, Livestock, heterozygosity

Introduction

"The maintenance of live populations of animals in their adaptive environment or as close to it as practically possible" is conservation, as defined by FAO, 2002. It is also the rational use and protection of existing genotypes and genetic introgression. Livestock with economic importance is being conserved by default. However, Genetic value, environmental effects, and traditional lifestyles are reasons for conservation of unprofitable breeds [1]. Maintenance of genetic diversity is necessary for maintaining breeding options to satisfy market demands, for evaluation of the relationship between heterozygosity and fitness. In reality, few breeds are being used extensively on a large scale for economic gain. Hence, it is necessary to estimate the uniqueness of the population and to conserve genetic variation. There is a need for the maximum risk, maximum diversity and maximum utility for the conservation of animals [2]. The risk of the population towards extinction can be assessed based on the results of livestock census, population size, the trend of the population growth, genetic composition, demographic distribution of breeds, economic importance, and their other special features. The strategies put frothed by FAO are as follows: (a) Use of more females than male, (b) selection to be practiced in large populations, (c) selection to be carried out in the native environment of the population. According to FAO, 25 breeding males and 50 females as a minimum are required for the live conservation programme with less than 1% rate of inbreeding. Conservation includes insitu and exsitu conservation. The former includes the establishment of breed societies while the later includes conservation of the biological samples like DNA, semen, tissues, ova, embryo and somatic cells. Conservation is a needed to maintain the genetic diversity along with the merit of breeds like production, adaptation, historical value or cultural importance. And it is the sole right of the genetic resource to continue in nature. On beforehand, breeds should be prioritized for their conservational value.

Conservation and prioritization

Uniqueness in traits is the result of the evolutionary forces and their interactions. And there exists a lot of genetic diversity, thus uniqueness in production, adaptability and disease resistance. However, dilutions occur due to intermixing, substructuring and as a consequence of genetic drift in a population over a longer period of time. Therefore, analysis of variations can help in analyzing these key factors and provide genetic information about the breed/population that can be further used in the conservation and improvement of breeds. Because of cost constraint in conserving the breeds, the breeds with no specific uniqueness or

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economically valuable character, with little to no historical or cultural significance and some of them have very much similar genetically. However, the conservation decisions depend on future plans. The between subpopulation diversity should be prioritized if the purpose is to use in the genetic improvement programme, cross-breeding or introgression. The within-population diversity should be prioritized if the purpose is to preserve closed population to cope with the challenging environments.

The accurate genetic information of genotypes and relationships between populations can be drawn from the microsatellite markers [3-5]. Thus, STRs/Microsatellite have proved to be an efficient tool for diversity analysis in farm animals. These are being used as efficient and standard to characterize the genetic variation among and within breeds and to estimate genetic diversity [6] and to assign individuals to breed [7]. These data provide information regarding the origin, relationships, genetic diversity, and gene pool developments of domestic animal breeds. Genetically differentiated breeds are with gene combinations of scientific and economic importance. The diversity of such important breeds needs to be conserved by insitu or exsitu methods.

Genetic Diversity
Genetic diversity is the additive genetic variance within and between breeds or populations. Information pertaining to genetic diversity is essential for genetic improvement, adaptation to the environment and conservation of breeds [8]. The two approaches for the evaluation of the genetic diversity includes quantitative approach where the additive genetic variance of the traits are estimated with the aid of pedigrees and molecular genetics approach [9].

Approaches to diversity analysis
As we have limited resources with similarities and dissimilarities in a large population, there occurs a need to set priority for conservation. This prioritization varies according to within breed component and between breed component and its relative importance. There are three approaches to identify diversity. First is the ancestry method [10], second is based on the richness of alleles and based on genetic distance [11]. Statistically, these methods aim to minimize kinship coefficient of metapopulation, to reflect between breed diversity component and to take both within and between breed component of diversity into consideration.

Kinship based methods: kinships estimated from the molecular data is the probability alleles drawn from the same locus are identical by descent. This holds value when pedigree data are missing. Mating of animals with genotypic similarity must be avoided in such cases. Kinship can be minimized to maximize genetic variability in the conserved population.

Kinship can be estimated from molecular data by a) Marker estimated kinships described [12]. (b) A variation of MEK based on log-linear regression [13]. (c) Based on log-linear regression with mixed model. (d) Average molecular coancestry (fm) based on allelic frequency [10]. The neighbor-net phylogenies of breed and breed group can be constructed using Kinship genetic distance with software SPLITS TREE 4.12.6 software. Classification of breed and groups of breed can be performed by using genetic relationships and further the contour plots of kinship coefficients with MATLAB software.

Weitzman's diversity estimation approach: The partial contributions (PC) of breed group and each breed to total diversity can be estimated by using the Weitzman method. Reynolds genetic distances can be used as a measure of between breed diversity ignoring within-breed diversity. This estimated the length reduction of a branch in maximum likelihood phylogeny. FORTRAN programme can be used to calculate the partial contributions. Alternatively, algorithm is also used to analyze breed group [14]. Pairwise Reynolds genetic distances can be used to obtain neighbor-net phylogenies by using SPLITS TREE 4.12.6 software.

Combined approaches for total diversity analysis: ideally, within and between population genetic variability should be taken in to account for prioritizing to make effective management decisions. The following approaches can be used to estimate contributions: (a) Aggregate diversity which uses Wright's FST, (b) Piyasatian and Kinghorn, (c) the method by Caballero and toro [10] and Fabuel [15]

Estimation of extinction risk
Extinction risk is an important factor in conservation by prioritizing the breeds. The risk should be prioritized within each group, the breed within the highest group should be given priority. The risk of extinction can be calculated by assigning definite values for each breed for different criteria that are related to survival like demographic distribution, change in population size, population size. Alternatively, amount of cross-breeding, the breeding male-female ratio and presence or absence of marketing programs can be included [16]. The fractional values assigned to each category to their maximum will add up to <1.0. the effective size can be determined by the rate of inbreeding, as this effective population size describe the genetic size of the population: $^\wedge F = 1/(2Ne)$. hence, the rate of inbreeding, the effective population size and rate of loss of genetic variation are parameters describing the extinction rate. If $^\wedge F > 3\%$ its considered as the critical risk, its considered as endangered if 1 to3%, vulnerable if 0.5 to 0.1%. risk i = pi + ci + gi + bi + f + 0.05. where pi is population size, ci is the change in population size, gi is demographic distribution, bi is breed program existence. Sum of all maximum values would be 0.90 and the minimum would be zero. Thus for estimation of risk and making a score, the effective population size is used estimated by using marker data with software NeEstimator [17]. To draw the conclusion and to make the final score, other information from various reliable sources can also be incorporated.

Estimation of conservation value
Genetic diversity, maximum risk, and utility are the supreme aims for prioritization. We need to determine the value of conservation of individual, breed, population, and importance of factors affecting the aims to prioritize. The simple multifactor index can be used to prioritize according to conservation values if many factors are affecting. To rank the breeds for conservation, each breed and factors are to be expressed numerically. The FAO has proposed the mode to calculate the conservation value as follows:

$$CV_i = WF1 \times (F1i - \mu F1) / \delta F1 + WF2 \times (F2i - \mu F2) / \delta F2 + \ldots + WFn \times (Fni - \mu Fn) / \delta Fn$$

Where,
Cvi = is conservation value of breed i
WF1 = is the weight of factor 1
F1i = is for factor 11 for breed I

μF1 = is the average of all breeds for factor 1

δF1 = is the std. of all breeds for factor 1

Weitzman approach for calculation of conservation value:

Weitzman's conservation potential : $CP_i = -m_iz_i$

Where,

CPi is the conservation potential of species/breeds I basis for prioritization

Mi is marginal contribution to diversity of species/breeds i

Zi is the risk of extinction of species/breeds i

CPi is amount of diversity maintained if breed i is safe completely

Breed prioritization studies in livestock

Methods have been developed to combine data on molecular genotype, phenotypic characteristics, the risk of extinction and cultural and social factors to make single value which serves as final criteria for prioritization [16, 18].

In general, genetic diversity estimated with neutral markers shouldn't be the sole criterion for conservation decisions. Several factors viz. traits with economic value, adaptive features, distinct phenotypes, resource availability, and infrastructure at the location of breed.

Cattle, sheep and goat breeds near the domestication sites in south-west Asia have high neutral genetic diversity which is measured by heterozygosity and the number of alleles of STR markers. This finding might indicate that breeds possess functional diversity in genes influencing traits. This is valuable for achieving present as well as future breeding goals. And hence the breeds with the high functional diversity should be prioritized for the conservation.

The population of unique species origin might receive higher priority if the species of unique origin is now extinct. Different evolution history may favor special combinations of genes and alleles and hence indicate uniqueness, that need to be preserved. Conservation priorities have been set up in different livestock species like cattle, sheep, and pig [18-21]. Different methodologies have been set up for prioritization. Ginja have used 19 FAO recommended microsatellite markers [19]. Different methods have been used in the past namely, Weitzman method, Kinship based, and combined. These methods rank breeds based on weight and method used. However, the need for including features like adaptation, unique traits, the cultural and historical value was emphasized. Ligda studied genetic structure by considering genetic diversity as an initial guide for conservation activities and decisions [20]. Other aspects of non-profit values like unique characters, the importance of breed in their region of habitat, cultural importance, historical heritage identity etc. Gizaw combined threat status, current breed merit and contribution to genetic diversity to rank sheep for conservation [18]. Threat analysis identified 8 breeds as threatened. It was observed that the breeds with a high probability of extinction will not have the highest priority necessarily. This is because the contribution to diversity will depend on their closeness to relative breeds. Fabuel analyzed Iberian pigs for genetic diversity and prioritization using 36 microsatellite markers by using Weizman and optimal contribution method [21]. These two approaches made different priorities as Weitzman method doesn't consider within-population diversity.

Conclusion

Different methods rank breeds differently for conservation. The same methodology should be adopted across the breeds and populations. The breed should be ranked according to the utility which should include the non-genetic and genetic components affecting the conservation of the breed. The breed with the highest utility index is considered as the greatest priority for conservation. On the other hand, A similar methodology should be adopted across different populations or breeds. The optimal approach would include using a combinatorial approach based on the weighting of the within and between breed diversity.

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