

A Literature Review of Genetic Architecture of Sheep Population

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ABSTRACT

This paper focuses on quantitative genetics in sheep. Sheep were among the earliest of livestock species to be domesticated, with domestication occurring approximately 10,000 years ago along with the goat. The early domestication of the sheep may be attributed to their hardiness and versatility. Sheep are able to utilize low quality pastures and survive in adverse climatic conditions. Their hardiness is demonstrated by the wide variety of habitats in which they are found, ranging from cold mountainous regions to hot deserts.

Keywords: genetic architecture, sheep, population.

1. INTRODUCTION

This paper provides an overview of the state of quantitative genetic studies in sheep. Firstly, the genome structure of sheep is explored with emphasis on comparisons to the genomes of other species which provide a valuable resource for quantitative genetic studies. This is followed by a brief overview of methodology used in the mapping of quantitative traits loci (QTL) and a summary of QTL mapping experiments that have been performed in sheep.

In the present times, the economy of sheep farming mainly depends on more and heavier production of lambs because lamb production contributes 85-90 per cent of total income generation, whereas wool contributes only 5-10 per cent and rest comes from manure (Arora et al., 2001). The importance of wool is reduced due to the availability of synthetic wool fiber, which is more durable and easily washable than natural wool, which shifted the emphasis from wool production to production of faster growing lambs, attainment of early maturity, and to increase the number of lambs produced per unit of time. The early attainment of sexual maturity and lower age at first lambing reduces the generation interval, which increases the overall productivity of the flock by reducing the feeding and management cost. Also, weight of dam at first lambing contributes to the weight of lamb at birth, survivability and mothering ability. Average lambing interval contributes to number of lambs born per unit of time, which directly influences the economy of sheep farming.

Estimating the annual rate of change in economic traits can do a quantitative appraisal of the breeding programme. Change in the economic traits in desirable direction results from improvement in the mean breeding value and environment of the population. Accordingly, the observed change in the performance of a population for an economic trait per year, i.e. phenotypic trend consists of two components viz. genetic trend resulting from change in mean breeding value due to selection of animal and environmental trend due to change in environment. The separation of the observed change into these two components is an integral part of analysis in any breeding programme because of many reasons, like:

- a. Reliable estimate of genetic trend permits comparison of realized trend with expected one in experimental situation and assessment of progress in a particular trait.
- b. Magnitude of genetic trend must be known for comparison of sires. Daughters of younger sires are usually at disadvantage because they are compared with better herd-mate sired by older sires.
- c. These estimates help in the unbiased estimates of age correction factor.

Several methods are being developed to measure the genetic change in animal population. The early attempt of Lortscher (1937) to measure genetic change in herd performance has been criticized because the age correction factors were confounded with year effects. More recently Smith (1962) and Powell and Freeman (1974) gave methods of estimation of genetic change in field records.

Phylogenetics and Comparative Genomics

Scientific Classification: The scientific classification of the sheep is given in Table 1.1. The order Artiodactyla contains ten extant families and approximately 200 species (Franklin, 1997) making it one of the most successful mammalian orders. The suborder classification depends on what level the tragulids (mouse deer) split from the remaining (Pecoran) ruminants. Pecora could equally be considered an infraorder of Ruminantia. The family Bovidae contains important commercial species other than sheep, including cattle and goats, as well as many species native to Africa such as gazelles and wildebeest. Other families of commercial importance in the order Artiodactyla are Suidae (in suborder Suiformes) containing pigs, Camelidae (in suborder Tylopoda) containing llamas and Cervidae (in suborder Pecora) containing deer.

Table 1: Scientific classification of the domestic sheep. Adapted from Frankham, 1997.

Kingdom:	Animalia
Phylum:	Chordata
Class:	Mammalia
Order:	Artiodactyla
Suborder:	Pecora (Ruminantia)
Family:	Bovidae
Subfamily	Caprinae
Genus:	Ovis
Species:	Aries

LITERATURE REVIEW

Genetic and Phenotypic Parameters

The knowledge of precise estimates of genetic and phenotypic parameters of performance traits is essential for developing suitable selection strategies for bringing about genetic improvement in these traits.

Heritability estimates

Heritability of a trait is the fraction of total variability that is attributable to additive genetic effect. Estimates of heritability are useful for construction of selection indices, prediction of genetic response to selection and for deciding how much one can rely upon individual's own phenotype for selection. Hence, accurate estimates of heritability for different economic traits are indispensable in animal breeding programmes.

Genetic status of population

In case of plateaued populations where all the additive genetic variances have already been exhausted, then, there is very limited scope for improvement for the given trait.

In maintenance population where random mating is practiced little change will be observed. For secondary traits, (traits for which selection is not done but changes is there because of correlated responses) it depends upon magnitude and direction of their correlation with primary trait(s) under selection in a particular herd, breed or population.

Breeding practices and time period

Genetic trend also depends upon breeding policies and their implementation. For example, if we are doing crossbreeding of local low producing animals with exotic high yielder, naturally there will be steep improvement of local population initially, but gradually gain will start declining. Moreover, genetic trend gives average genetic change per unit of time during the period studied, and as we know that change may start decreasing as we reach towards selection limit, hence, longer the period studied, smaller is the trend or change per unit time.

Regarding implementation part, if there is some sort of inbreeding going on in the population, irrespective of the fact whether intentionally or unintentionally (due to small population size), naturally scope for genetic improvement will become lesser.

Method of evaluation

It is clear from various estimates of genetic trends tabulated that no method of trend estimation is absolute. Genetic trends also vary with method of trend estimation (Acharya and Lush, 1968; Gurnani and Nagarcenkar, 1974; Hingane, 1980). In some cases, even direction (Sign) of trend has also changed due to change in method. Hence, estimates of genetic trends also depend on method of estimation.

So, we can't generalize the genetic trends for a particular breed. It varies with genetic status of the herd, breeding practice, time studied for, method of trend estimation etc.

Narain and Garg (1975) utilized D^2 -statistic and analysed the data on greasy fleece weight, fibre diameter, fibre length and fleece density in crosses of different levels of Rambouillet inheritance.

Jaiswal and Jain (1988) used D^2 -statistic to study the robustness of D^2 -statistic in divergence analysis between genetic groups of crossbred cattle, when the assumption of homogeneity of covariance matrices is violated and sample sizes are unequal and revealed that D^2 -statistic is robust enough for use in such situations.

Jagtap *et al.* (1989) utilized Mahalanobis D^2 -statistic by combining three traits (18 months body weight, AFC and first lactation fat corrected milk yield) of economic importance among different genetic groups of crossbred dairy Gir cattle and formed four clusters using Tocher's method, having higher inter-cluster distance than intra-cluster distance and concluded that all crossbred groups were having maximum D^2 -value with pure bred Gir whereas they were less but significantly divergent among themselves.

Narian *et al.* (1991) utilized D^2 -values in 14-genetic grades derived from various crosses amongst Rambouillet, Chokla, Malpura and Jasalmeri and used Tocher's technique for forming different clusters of 14 genetic grades.

The information pertaining to different aspects of the present investigation available in literature has been reviewed under the following heads:

Growth traits

Growth of the lamb is a reflection of the adaptability, management and nutrition status of a flock, which finally decides the economic viability of the animal, hence may be used as a criterion for selection of individuals within a breed. The study of growth traits also helps or even guides the breeder to determine the optimum managerial practices so as to maintain body weight gain at optimum level.

Birth weight

Birth weight is the earliest available trait and can reasonably be recorded. Birth weight is the reflection of prenatal environment. Lambs with higher birth weights are expected to gain faster in life. Birth weight is influenced by a number of non-genetic factors.

Averages

Birth weights of different breeds of sheep as reported in literature are presented in Table 2.1. It varies from breed to breed and ranged from 3.02 ± 0.02 kg (Singh, 1980) to 3.18 ± 0.34 kg (Singh, 1995) in Nali crossbreds.

Jaiswal et al. (1992) utilized D2-statistic for discrimination and clustering among seven genetic groups of crossbred dairy cattle—three groups of halfbreds of Hariana with Holstein Friesian, Brown Swiss and Jersey (FH, BH and JH) and four of three-fourth with two exotic breeds (FBH, FJH, BFH and JFH) with characters age at first calving, first lactation yield, fat percentage and first calving interval and revealed that the Friesian and Jersey half-breds were statistically divergent and so were FBH and JFH groups among three-fourth and fat percentage contributed maximum discrimination, followed by age at first calving and first lactation yield.

Sangwan and Singh (1995) utilized Mahalanabis (1936) D2-statistic for locating genetically divergent groups on the basis of first lactation overall performance among Hariana and its crosses formed clusters indicating that the performance of crossbreds was similar and different from that of Hariana.

CONCLUSION

The aim of sheep breeders is to bring about genetic change in their livestock, with a view to increase profitability, sustainability and ease of management at the production level. Breeding objectives declare a desired direction for genetic change. They should be constructed in a manner which allows their rational expression as part of a Genetic Evaluation System, in order to facilitate ranking of animals on genetic merit and for effective implementation of breeding programmes.

A knowledge of change in the performance of farm livestock with time due to changes, either in the genetic structure of the population or improvement in the management and environment is of fundamental interest to the animal breeder, which is an aid in formulating breeding strategies for future genetic improvement of productivity of the flock.

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