Exploring genetic variability and selection of Garole × Indigenous crossbred sheep (F₁) for various traits under semi-intensive systems in the southwestern coastal areas of Bangladesh

Minhazul Abedin Sun, Sarder Safiqul Islam*, Nayema Akter, Sanjana Karim, Md. Shafiqul Islam, S. M. Abdullah Al Mamun and Md. Mustajabur Rahman

Agrotechnology Discipline, Khulna University, Khulna-9208, Bangladesh
*Corresponding author: sardersislam@at.ku.ac.bd

Abstract

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The research aimed to assess the genetic diversity among Garole × Indigenous crossbred sheep (F₁) for various quantitative traits, to enhance the selection process to improve their productivity and reproductive capabilities. Additionally, the study sought to pinpoint the top-performing sheep genotypes for potential commercialization. Twenty nondescript indigenous ewes were mated with two pure-line Garole rams under semi-intensive rearing conditions. Among the traits, gain between the birth and weaning period and weaning weight were highly and positively correlated (r = 0.984). In contrast, the weight at maturity and growth between the first lambing and maturity exhibited higher but hostile relations (-0.460) with each other. Principal component analysis (PCA) extracted four principal components, which explained 81.84% of the total variation. The first principal component accounted for 30.46% of the total variation. The cluster analysis revealed the presence of wide genetic variations among the sheep genotypes, grouping them into four distinct clusters. Cluster III contained the genotypes with the best response to most of the traits under study, and the maximum cluster distance was found between Cluster II and Cluster IV. The selection of genotypes from Cluster III for commercial purposes may enhance the economic return of sheep farmers. In contrast, selecting parents from distant clusters (II and IV) for hybridization may harness hybrid vigor to produce the best-performing sheep breeds. The study provided new and valuable insights into the genetic diversity of crossbred sheep, identifying the best-performing genotypes for both breeding purposes and commercial applications.

Keywords: crossbred F₁ sheep; genetic diversity; principal component analysis; productive and reproductive performance; selection

Introduction

Approximately 32% of Bangladesh's sheep population is found in the Barind, Jamuna basin, and Coastal areas, with the remaining segment distributed throughout the country (Bhuiyan, 2006). About 98% of the sheep are reared by landless and marginal farmers in Bangladesh. The sheep production in Bangladesh is primarily based on indigenous nondescript breeds; however, an exotic Muzaffarnagar crossbreed is also widely reared in field farms, mainly in Chuadanga, Chapainawabganj, and Meherpur districts, and is gaining attention in other districts as well. The country's native sheep are sporadically scattered, although they are concentrated in a few agro-ecological zones, including the Barind tracts, coastal areas, northeastern wetlands, Jamuna River basin areas, and Sundarbans-delta regions (Pervage et al., 2009). Among vari-

ous sheep breeds, Garole stands out as a promising option, and it is found in West Bengal, India, as well as in the Sundarbans region and the southern part of Bangladesh (Khan et al., 2009; Sharma et al., 1999). The Garole sheep breed, renowned for its resilience and adaptability to various environmental conditions, has long been prized by farmers for its prolificacy and robustness. In the quest to enhance the productivity and adaptability of local sheep populations, crossbreeding strategies have gained prominence, particularly in regions such as the southwest coastal area of Bangladesh, where agricultural systems face unique challenges due to the impact of climate change. In this context, the present study delves into the genetic variability and selection processes of Garole × Indigenous crossbred sheep (F_1) under semi-intensive management systems. The semi-intensive approach strikes a balance between traditional extensive grazing and intensive management practices, making it a pragmatic choice for farmers seeking optimal productivity while effectively leveraging natural resources.

Sheep farmers mostly followed the traditional natural mating system (95.90%) at the study areas, where rams were permitted to mate with heated ewes without consideration of the relationship between ram and ewes (Islam et al., 2016). At the study site, where a traditional mating system was maintained, farmers permitted their rams to breed with half-sibs, full-sibs, and also allowed them to breed with first-cousin sisters and second-cousin sisters. The herd could mate freely with their grand dam or even with an ewe that is four generations senior to them (Islam et al., 2016). A cross-breeding program of sheep, i.e., crossbreeding male Garole and indigenous female sheep, is very rarely practiced in Bangladesh. Very little research is available regarding the selection of superior-quality breeding sheep. Considering these factors, the objectives of the research program were set:

To determine the genetic variability of crossbred sheep under semi-intensive management conditions.

To select the best performing genotypes for commercial rearing and/or for use as parents in the next hybridization program.

Materials and Methods

Experimental site
The study was conducted at the Dr. Purnendu Gain Field Laboratory of Agrotechnology Discipline at Khulna University, Khulna. The Ganges Tidal Flood Plain's Agro-Ecological Zone (AEZ) contains the experimental site (Rahaman et al., 2019). The latitude and longitude of the research unit are 22º80′ N and 89º53′ E.

Housing and management of sheep
The experimental sheep were housed in a wooden slatted flooring system. There were adequate ventilation systems in the sheep shed. Regular cleanings were done for the waterer, feeder, and shed. All sheep were provided with a similar environment and facilities. It also minimizes variations that can affect research results. The sheep house was located near the pastures. Washing was done at regular intervals to remove waste materials and dung, and to eradicate ectoparasites such as lice and ticks.

Feeding and nutrition
Throughout the day, sheep were permitted to graze at regular intervals. Sheep were let out at eight in the morning and taken in at six in the evening. Every sheep had unlimited access to clean drinking water.

Vaccination and healthcare
Every sheep was dewormed with an anthelminthic injection (A-mectin plus), and the procedure was repeated every three months. Every sheep received the infectious disease (PPR) vaccinations listed in Table 1. To prevent diseases, appropriate biosecurity precautions were implemented.

Description of parental population
A total of 20 female and two male sheep were used as the experimental material for the study. The females were non-descript and were collected from the local markets of the southwest coastal region of Bangladesh. However, the male was a pure Garole breed, which was obtained from a designated farm in the Chuadanga district of Bangladesh. A crossbreeding program involving the mating of purebred Garole male sheep with non-descript female sheep was conducted in the field laboratory. There was no restriction in the mating process, which allowed natural crossbreeding based on selective preferences.

Data collection and analysis
Data on performance parameters of the sheep were collected and recorded. The information included parameters

Table 1. Vaccination schedule of sheep

Vaccine's name	Quantity/sheep	Vaccination route	Interval
A-mectin plus (Deworming)	0.5cc	Sub-cutaneous	3-months
Peste des petits ruminants (PPR)	1ml	Sub-cutaneous	6-months

Source: Authors' own elaboration

for reproductive performances of sheep such as sex of lambs, age at maturity (days), weight at maturity (kg), weight at first lambing (kg), gain between maturity and first lambing (kg), gestation period (days), birth weight of lamb (kg), weaning age (day), weaning weight (kg) and gain between birth and weaning period (kg). The data were analyzed using the R programming language (version 2.14.0).

Results and Discussion

Sex of lamb

Figures 1 and 2 indicate the sex of lambs in number and percentage, respectively. The number of male and female lambs was four and two, respectively, in cluster I. Male lambs represented 66.67 % of the total number of lambs, and female lambs were 33.33% under cluster I. Cluster II consisted of 40% male lambs and 60% female lambs. In cluster III, male and female lambs were equal in number (4). In cluster IV, there were two male lambs (66.67%) and one female (33.33%). The ratio of male lambs was higher in cluster I and cluster IV. Overall, males and females contributed 54.55% and 45.45%, respectively. Asaduzzaman et al. (2020) reported that, in Muzaffarnagar, the sex ratio of male and female lambs was 58.9% and 41%, respectively. This distribution, with a higher percentage of males, supports the findings of the current study. However, in the Jamuna Basin, the male-to-female ratio of indigenous sheep was found to be 41.9% and 58.1%, respectively, indicating a higher proportion of female lambs in this context. Siminska et al. (2008) noted that the Pomeranian sheep had a sex ratio of 53.5% for females and 46.5% for males. This was natural, and no visible cause was identified for the increase in the number of female sheep. The results of Ashebir et al. (2016) in Begayt sheep, where the male-to-female ratio was 50.33% and 49.69%, respectively, are consistent with the current study. According to Skjervold (1979), variables such as the dam's age, the flock's nutritional status, the size of the litter, and the lambing season may influence the variance in the sex ratio.

Correlation coefficients among morphometric traits of sheep

The phenotypic correlations between the various biometric parameters are presented in Figure 3. The magnitude of the correlation coefficient varied from -0.460 (weight at maturity and growth between the first lambing and maturity) to 0.984 (gain between the birth and weaning periods and weaning weight). Two were found to be highly significant ($p < 0.01$) and three to be substantial ($p < 0.05$) out of the total 36 correlation coefficients evaluated. Figure 3 showed a negative correlation (-0.064) between maturity weight and maturity age. First lambing weight and maturity age also had a negative correlation (-0.129). Age at maturity was also negatively correlated with gain between maturity and first lambing, gestation period, and birth weight of lambs, with values of -0.090, -0.122, and -0.055, respectively. Age at maturity was positively and significantly ($p < 0.05$) correlated with weaning age ($r = 0.462$). Still, it was negatively correlated with weaning weight ($r = -0.009$) and positively correlated with gain between the birth and weaning periods ($r = 0.001$).

Weight at maturity was positively and significantly ($p < 0.01$) correlated with weight at first lambing (0.818). Weight at maturity was negatively and significantly correlated ($p < 0.05$) with gain between maturity and first lambing (-0.460) and also negatively correlated with gestation period (-0.271). Weight at maturity was significantly ($p < 0.05$) correlated with the birth weight of the lamb (0.444). Weight at maturity showed a negative correlation with weaning age and gain between the birth and weaning periods, with values of -0.339 and -0.059, respectively. It was positively correlated with weaning weight ($r = 0.026$). Weight at first lambing was positively correlated with gain between maturity and first lambing, birth weight of the lamb, and weaning weight,
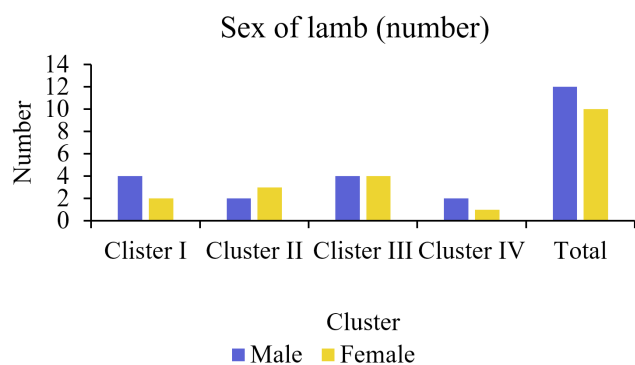

Fig. 1. Sex of lamb (number)
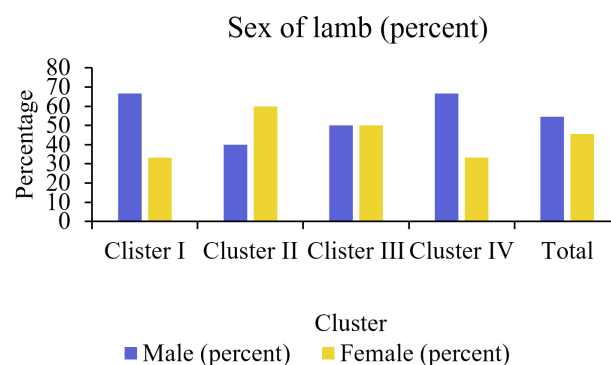*Source*: Authors' own elaboration

Fig. 2. Sex of lamb (percentage)
Source: Authors' own elaboration

with correlation coefficients of 0.133, 0.422, and 0.014, respectively. It was negatively correlated with gestation period, weaning age, and gain between the birth and weaning periods, with values of -0.145, -0.269, and -0.067, respectively.

The gain between maturity and first lambing was positively correlated with gestation period (r = 0.243) and weaning age (r = 0.169). It was negatively correlated with the birth weight of the lamb (-0.113), weaning weight (-0.023), and the gain between the birth and weaning periods (-0.002).

The gestation period was negatively correlated with the birth weight of the lamb (-0.208), and it was positively correlated with other components, such as weaning age (0.135), weaning weight (0.191), and gain between birth and weaning period (0.244). The birth weight of the lamb was negatively correlated with weaning age (-0.274), but it was positively correlated with weaning weight (0.417) and the gain between the birth and weaning periods (0.250). Weaning age was negatively correlated with both components, including weaning
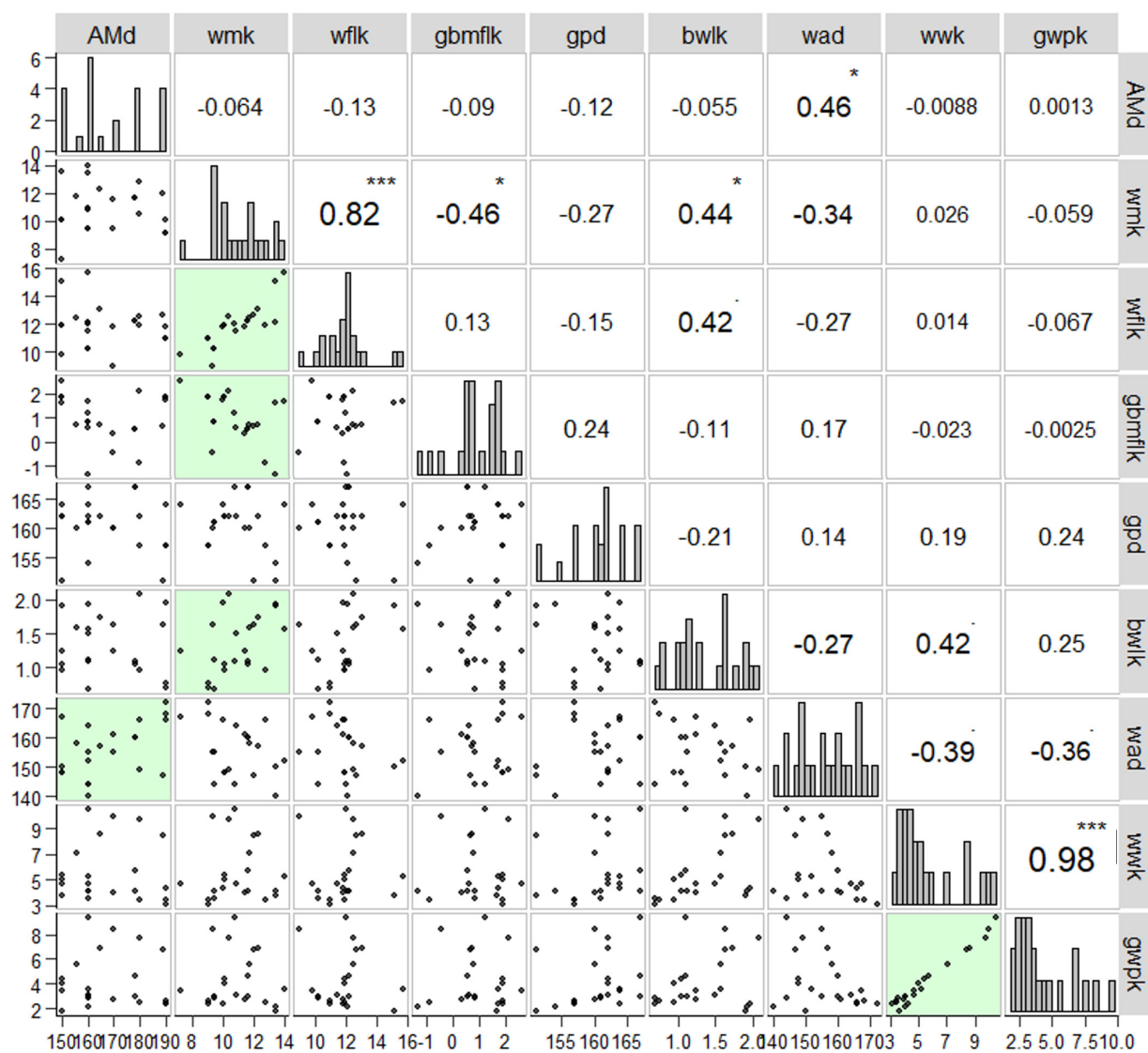

Fig. 3. Correlation coefficients among the morphometric traits of sheep
*** = significant at p < 0.01 and p < 0.05; *= significant at < 0.05; AMd = age at maturity (days); wmk = weight at maturity (kg); wflk = weight at first lambing (kg); gbmflk = gain between maturity & first lambing (kg); gpd = gestation period (days); bwl k= birth weight of lamb (kg); wad = weaning age (days); wwk = weaning weight (kg); gwpk = gain between birth & weaning period (kg)
Source: Authors' own elaboration

weight and gain between the birth and weaning periods, with correlation coefficients of -0.390 and -0.362, respectively. Weaning weight was positively and significantly correlated (p < 0.01) with gain between the birth and weaning periods (r = 0.984).

The high correlation between weight at maturity and weight at first lambing was to be expected due to their natural relationship. Similar findings were also noted by other researchers (Kunene et al., 2009; Yakubu and Ayoade, 2009). The hypothesis proposed by Kunene et al. (2009) that weight at maturity could be a good indicator of first lambing weight is well supported by the highly significant link between maturity weight and first lambing weight. In our findings, we found that weight at maturity was significantly positively correlated (p < 0.01) with weight at first lambing (r = 0.818). The birth weight of the lamb increased with the high weight at maturity. Therefore, similarities exist in both the findings. In a related study, Salako (2006) proposed correlations as high as 0.99 between body measurement parameters.

Selecting parameters with lower correlations for breeding programs would not significantly improve weight at maturity and other biometric traits, as Mavule et al. (2013) found that these parameters were influenced by non-additive genetic effects, suggesting a less significant impact from environmental factors. A lower correlation was found between age at maturity and gain during the birth-to-weaning period (p = 0.001). These findings are similar to Malvule et al. (2013). High predictability is indicated by the positively significant (p<0.01) correlations between these biometric characteristics. Yunusa et al. (2013) reported substantial correlations for the majority of these parameters, which are similar to the present findings.

Principal component analysis (PCA)

According to Mavule et al. (2013), principal component analysis (PCA) assesses the variability of individual parameters and their respective contributions to the total morpho-structural variance in animals. Principal component analysis is more suitable for analyzing morphometric traits than the simple correlation method. PCA is primarily used to identify the most important morphometric traits with greater variation, which facilitates the formulation of breeding plans and selection criteria for prime animals. Table 2 shows that to determine the number of principal components, four principal components (PCs) were selected from an initial set of eleven. Four components accounted for 81.84% of the total variance and had eigenvalues greater than one. For PC1, the variance was 30.46%, and for PC4, it was 12.41%. In dispersion plots, principal component scores are often used to highlight any trends or clustering within the data.

The PC1 showed highest value for weight at maturity (0.43) birth weight of lambs (0.43), weaning age (-0.43) where the PC2 showed highest value for gestation period (-0.37), weaning weight (-0.49) and gain between birth & weaning period (-0.54) and PC3 showed no highest value for any trait but PC4 showed highest value for most of the trait e.g., age at maturity (0.45), weight at maturity (0.68), weight at first lambing (0.44), gain between maturity & first lambing (0.54). The PC1 differentiated the genotype of lambs based on their birth weight. The PC2 differentiated the genotype of weaning weight and gain between the birth and weaning periods. The PC4 accounted for weight at maturity, weight at first lambing, and gain between maturity and first lambing. One technique to lend significance to the extracted PC data in relation to the original variables is to analyze the eigenvalue structure.

Table 2. Principal component analysis for the first four principal components

Traits	PC1	PC2	PC3	PC4
Age at maturity (days)	-0.15	0.02	-0.66	0.45
Weight at maturity (kg)	0.43	0.41	-0.05	0.68
Weight at first lambing (kg)	0.37	0.34	0.28	0.44
Gain between maturity & first lambing (kg)	-0.16	-0.19	0.52	0.54
Gestation period (days)	-0.10	-0.37	0.31	0.17
Birth weight of lamb (kg)	0.43	0.05	-0.11	0.27
Weaning age (day)	-0.43	0.06	-0.24	0.43
Weaning weight (kg)	0.38	-0.49	-0.17	0.09
Gain between birth & weaning period (kg)	0.32	-0.54	-0.16	0.04
Standard deviation (SD)	1.65	1.47	1.15	0.06
Eigen value	2.74	2.17	1.33	1.11
Variance (%)	30.46	24.18	14.78	12.41
Cumulative variance (%)	30.46	54.65	69.43	81.84

Source: Authors' own elaboration

The PC1 presented the highest value at 30.46% compared to the other PCs. The PC2 explained 24.18%, and the third and fourth principal components explained 14.78% and 12.41% of the total variability, respectively. The biplot of the current study summarized the matrix's values in PCs, where the correlation coefficient between traits was proportional to the cosine of the angle between the vectors linking those traits to the origin (Fig. 4). In the current study, four PCs for the genotypes of sheep described the entire breed variability. These findings could suggest that a large number of variables with higher correlation levels contribute to explaining the overall variability.

Mishra et al. (2017) identified three components that exhibited eigenvalues greater than one, accounting for 68.66% of the total variance. In Balami and Uda sheep, Yunusa et al. (2013) observed 66.911% and 57.426 % of the total variation, respectively. Whereas Mavule et al. (2013) identified four components that contributed to 62.13% of the overall variation in adult Zulu sheep and Gojri buffalo, the present study's four principal components were extracted with eigenvalues larger than one and accounted for 81.84% of the entire variance. The present results are nearly identical to those of Salako (2006) and da Silva et al. (2015). Salako (2006) discovered two components from a set of 10 attributes ob-

served in Uda sheep, which accounted for 75% of the overall variations, while da Silva et al. (2015) found three principal components with eigenvalues greater than one, contributing to 72.28% for the Morada Nova breed of sheep.

Two main components, accounting for 72% of the total variance and having an eigenvalue greater than one, were reported by Putra and Ilham (2019) for Katjang sheep. The findings of the current study, which account for 80% of the variance, were in line with those of Yakubu et al. (2011) for Uda sheep. According to Brooks et al. (2010), the unexplained variation may be caused by measurement errors, random allele separation at relevant loci, or external environmental variables. According to Yunusa et al. (2013), PC1 in Balami and Uda sheep explained 54.81% and 48.07% of the variance, respectively. According to Mishra et al. (2017), PC1 accounted for 36.04% of the total variance. The first principal component (PC1) in this study explained 30.46% of the total variance, supporting the findings of Mishra et al. (2017), as the genotypes, feeding, and environmental conditions were nearly identical. According to the current study, PC2 and PC3 accounted for 24.18% and 14.78% of the variance, respectively, which aligns exactly with the observations of Mishra et al. (2017). According to their reports, PC2 accounted for 21.26% and PC3 for 11.36% of the overall variance. PC2 and PC3
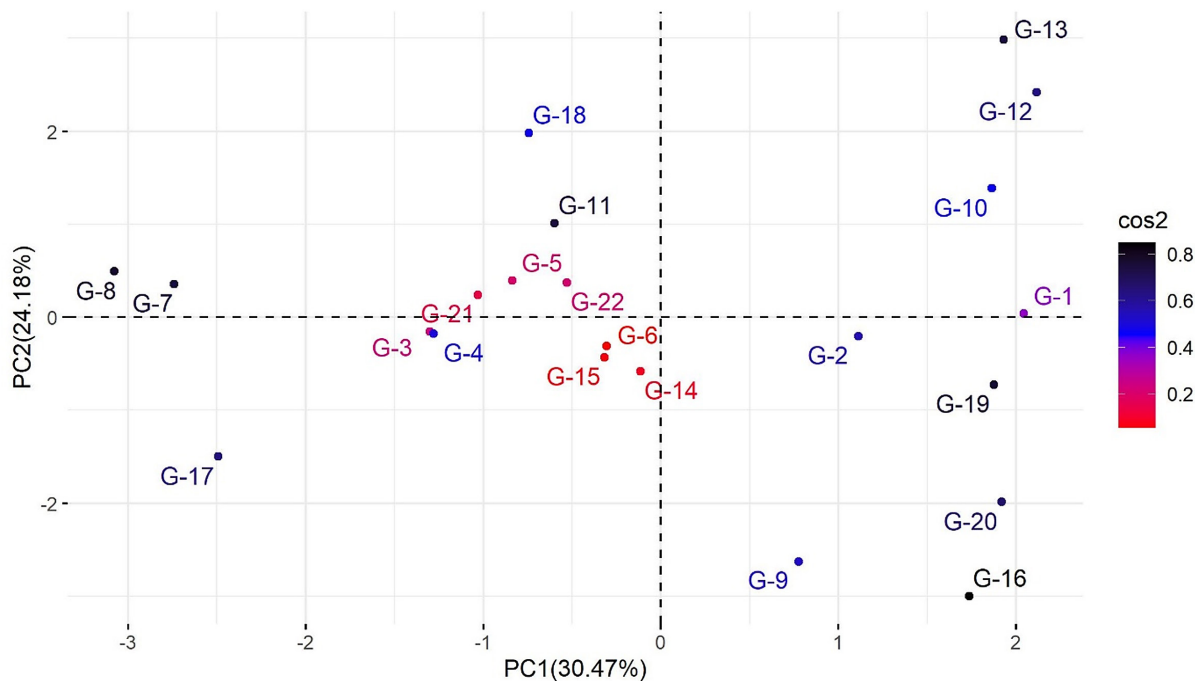

Fig. 4. PCA biplot representing the distribution of sheep breeds based on the presence of variability among them for the studied traits

Source: Authors' own elaboration

explained 18.13% and 5.84% of variations, respectively, according to da Silva et al. (2015), which is partially consistent with the results of the current investigation.

Hierarchical cluster analysis

Average linkage was used to create a hierarchical cluster dendrogram (Fig. 5) between groups. According to Kantardzic (2003), variables were normalized to range from 0 to 1. To ensure that large numerical values do not alter distance determinations, the variables had to be normalized first before the hierarchical cluster analysis could begin. After this is finished, a dendrogram can be constructed using hierarchical cluster analysis to synthesize large datasets into understandable groupings that illustrate relationships between the measured parameters. Using the data generated for the study, hierarchical cluster analysis was conducted in this investigation. The average group linkage method was used to create the dendrogram. During the clustering process, the two clusters that had the shortest linkage distance were connected at each subsequent phase. The dendrogram's horizontal axis indicates the distance between groups. After the dendrogram is evaluated, four groups of behaviors are identified based on various attributes (groups I–IV). As denoted by Groups I, II, III, and IV, the hierarchical cluster analysis enabled the division of behaviors into four distinct categories. The dendrogram's four branches were separated, as seen by the colored line. Group the color blue denoted me, while groups II, III, and IV were designated by the colors indigo, yellow, and red, respectively. Group IV had fewer entities, while Group III had a relatively higher number of individuals. This dendrogram illustrates the relationships between the genetic diversity of sheep that have been researched. The cluster analysis provided a comprehensive picture of the variation among the studied sheep breeds.

Group I contained genotypes G-1, G-2, G-9, G-16, G-19, and G-20. Among the genotypes in group I, the G-2 and G-19 genotypes exhibited the most resemblance to each other. This branch was divided into two groups, which split at a distance of 4.0. One group was divided into two subgroups at a similarity matrix of 3.5. Additionally, one group was divided into two subgroups at a distance of 3.0. Again, this group split into two subgroups at a distance of 1.5. This subgroup contained G-2 and G-19 genotypes. The closest relationship was found in this group because there was minimal distance. The indigo color denoted cluster group II, which contained G-3, G-4, G-14, G-15, and G-17. Genotypes G-14 and G-15 exhibited greater similarity than the other groups, and they were divided at a 0.025 similarity matrix. Groups III and IV were almost similar. They were divided at 1.5 distance. Genotypes G-14, G-15, and G-3, G-4 belonged to the same cluster. Between groups, their variability was less, and similarity was more than at the other branch. The yellow color denoted cluster group III, which contained the genotypes G-5, G-6, G-7, G-8, G-11, G-18, G-21, and G-22. Between groups, their variability was less, and similarity was more than at the other branch. Red color indicated cluster IV containing the G-10, G-12, and G-13 genotypes. This branch was divided into two groups based on a similarity matrix of 4.5, characterized by different traits. One group was further divided into two subgroups, which were then split at a distance of 3.0.
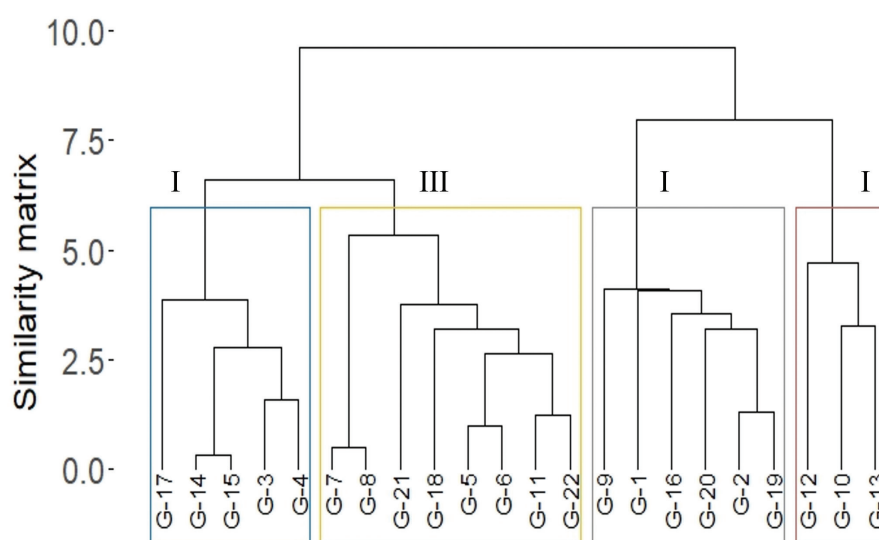

Fig 5. Distribution of sheep genotypes according to cluster analysis
Source: Authors' own elaboration

The distribution pattern revealed that cluster III had the highest number of genotypes (8), while cluster IV had the lowest number (3). Three groups were identified in a study by Serrano et al. (2021), with cluster I showing the highest number of genotypes that differed from the results of the current investigation. Sa'adi et al. (2021) reported four clusters, and Oliveira et al. (2018) found four clusters for Santa Ines meat sheep, as well as Salman (2020) observed four clusters for breeding goat. The current study supports the findings of Oliveira et al. (2018), Sa'adi et al. (2021), and Salman (2020).

Cluster number, percent, and name of genotypes in different clusters of sheep

Twenty-two genotypes were divided into four clusters based on the diversity limit (Table 3). The distribution pattern expressed a maximum (8) number of genotypes (G-5, 6, 7, 8, 11, 18, 21, 22) in cluster III. It comprised 36.36% of the total genotypes, where cluster IV contained only three genotypes (G-10, 12, 13), and it covered 13.64% of the total genotypes. The significant correlation between most variables in this study and their duplication effect may have contributed to the small number of genotypes in the clusters. Cluster I and II included 6 (G-1, 2, 9, 16, 19, 20) and 5 (G-3, 4, 14, 15, 17) genotypes, respectively. Cluster I covered 27.27% and cluster II covered 22.72% of the total genotypes.

Intra and inter-cluster distance in 22 sheep genotypes

Table 4 shows the distances between and within clusters. The diagonally displayed intra-cluster distances were relatively small. In every instance, the inter-cluster distances were larger than the intra-cluster distances, indicating that there is more variety among the genotypes within a single group than there is among the genotypes of distinct groups.

The highest intra-cluster distance was observed in cluster IV (3.99), with intra-cluster distances ranging from 2.34 to 3.99. The range of the inter-cluster distance was 3.6 to 5.06. Clusters II and IV had the maximum inter-cluster distance (5.06). The least inter-cluster distance (3.36) was found between clusters II and III, indicating that the genotypes within these clusters were comparatively close to one another when compared to genotypes grouped in other clusters. This indicated that these clusters were genetically more divergent from each other than any other pairs of clusters.

To retain a relatively broad genetic basis, it is advisable to avoid selecting parents from genetically homogeneous clusters when crossing genotypes from those clusters, as this may not yield a greater heterotic value. Genetic distance is the primary factor influencing the degree of heterosis. According to Sarker et al. (2013), in order to maximize variability in the ensuing generations, parents for hybridization should be chosen from two clusters with larger inter-cluster distances. Significantly different genotypes would result in a wide range of diversity in the offspring generation, allowing for additional selection and advancement. This made selection crucial for sheep breeding programs. Therefore, hybridization between genotypes from clusters II and IV was observed to result in a high level of expression of heterotic vigor and a greater number of desirable transgression segregations (producing hybrid progeny phenotypes that exceed the parental phenotypes) in this study. These results are consistent with the findings of the current study.

Cluster means for nine traits of 22 sheep genotypes

Table 5 displays the mean performance of the various clusters for the various morphological features that were computed. The components were divided into four clusters, considering nine traits: maturity age, maturity weight, first

Table 3. Name, percentage, and cluster number of each genotype in each cluster

Cluster	Number of genotypes	Percent (%)	Name of genotypes
I	6	27.27	1, 2, 9, 16, 19, 20
II	5	22.72	3, 4, 14, 15, 17
III	8	36.36	5, 6, 7, 8, 11, 18, 21, 22
IV	3	13.64	10, 12, 13

Source: Authors' own elaboration

Table 4. Intra- (diagonal) and inter-cluster distances in 22 sheep genotypes

Cluster	I	II	III	IV
I	3.33			
II	4.38	2.34		
III	4.48	3.36	2.84	
IV	4.98	5.06	4.92	3.99

Source: Authors' own elaboration

lambing weight, gain between maturity and first lambing, gestation period, birth weight of lambs, weaning age, and gain between birth and weaning periods. Cluster I had the most significant value for the gestation period (162.89 days). It had the second-highest value in gain between maturity and first lambing (1.12 kg), weaning age (156.33 days), weaning weight (4.57 kg), and gain between birth and weaning period (3.47 kg). In comparison to the other clusters, most genotypes in this cluster exhibited the lowest performance in the majority of the characteristics. It performed the worst in terms of weight at first lambing (11.33 kg) and weight at maturity (10.22 kg). Cluster II showed that the two highest values belonged to weaning weight (9.06 kg) and gain between the birth and weaning periods (7.43 kg). It had the second-highest values in age at maturity (170 days), weight (11.11 kg), weight at first lambing (11.95 kg), gestation period (160.33 days), and birth weight of lambs (1.62 kg), ranking next to cluster III, cluster IV, and cluster I, respectively.

In comparison to the other clusters, most genotypes in this cluster exhibited moderate performance for the majority of the characteristics. Weight at maturity (13.66 kg), weight at first lambing (14.34 kg), and lamb birth weight (1.80 kg) were the three highest values in Cluster III. Cluster IV showed the three highest values: age at maturity (187.5 days), gain between maturity and first lambing (1.14 kg), and weaning age (168.0 days).

For age at maturity, 161.78 days were found in Cluster I. Similarly, 170 days, 156.67 days, and 187.5 days were found in cluster II, cluster III, and cluster IV, respectively. Among them, cluster IV showed the highest value (187.5 days) and cluster III showed the lowest value (156.67 days). In terms of weight at maturity, weights of 10.22 kg, 11.11 kg, 13.66 kg, and 10.25 kg were found in cluster I, cluster II, cluster III, and cluster IV, respectively. Among them, cluster III displayed the highest value, at 13.66 kg, and cluster I displayed the lowest value, at 10.22 kg. For the first lambing weight,

clusters I, II, III, and IV were 11.33 kg, 11.95 kg, 14.34 kg, and 11.40 kg, respectively. Here, cluster III showed the highest value (14.34 kg) and cluster I displayed the lowest value (11.33 kg). The gain between maturity and first lambing was found to be 1.12 kg, 0.84 kg, 0.68 kg, and 1.14 kg in clusters I, II, III, and IV, respectively. Cluster IV represented the highest value (1.14 kg) and cluster III represented the lowest value (0.68 kg). In clusters I, II, III, and IV, the gestation period was determined to be 162.89 days, 160.33 days, 156.33 days, and 158.75 days, respectively. Cluster I denoted the maximum duration of 162.89 days, while Cluster III indicated the minimum duration of 156.33 days. The lambs' birth weights were 1.10 kg, 1.62 kg, 1.80 kg, and 1.09 kg for clusters I, II, III, and IV, respectively. The maximum value (1.80 kg) was represented by cluster III, and the lowest value (1.09 kg) by cluster IV. The weaning ages of clusters I, II, III, and IV were obtained at 156.33 days, 151.66 days, 147.33 days, and 168.0 days, respectively. Cluster IV denoted the maximum duration of 168 days, while Cluster III indicated the minimum duration of 147.33 days. Cluster I, Cluster II, Cluster III, and Cluster IV showed weaning weight of 4.57 kg, 9.06 kg, 4.32 kg, and 3.57 kg, respectively.

For cluster I, cluster II, cluster III, and cluster IV, the gain between birth and weaning period was 3.47 kg, 7.43 kg, 2.51 kg, and 2.48 kg, respectively. Cluster II denoted the maximum weight of 7.43 kg, while Cluster III showed the minimum weight of 2.51 kg. Individuals should be chosen from the cluster with the best positive reaction for the most significant number of attributes, according to the mean value of the cluster analysis. The genotypes that performed the best for the traits under investigation in this study were found in cluster III. Serrano et al. (2021) carried out a similar experiment. Out of the three clusters they discovered, cluster III had the best performance. The prospect of directly picking one genotype for immediate usage was ruled out when it was observed that no cluster included at least one genotype with

Table 5. Cluster means of reproductive traits for 22 sheep genotypes

Trait	Cluster I	Cluster II	Cluster III	Cluster IV
Age at maturity (days)	161.78	170.00	156.67	187.5*
Weight at maturity (kg)	10.22	11.11	13.66*	10.25
Weight at first lambing (kg)	11.33	11.95	14.34*	11.40
Gain between maturity & first lambing (kg)	1.12	0.84	0.68	1.14*
Gestation period (days)	162.89*	160.33	156.33	158.75
Birth weight of lamb (kg)	1.10	1.62	1.80*	1.09
Weaning age (day)	156.33	151.66	147.33	168.0*
Weaning weight (kg)	4.57	9.06*	4.32	3.57
Gain between birth & weaning period (kg)	3.47	7.43*	2.51	2.48
*=highest value among the clusters				

Source: Authors' own elaboration

all the desired features. To carefully integrate all the desired features, it is necessary to cross the genotypes chosen from different clusters.

Conclusions

The purpose of this study was to analyze the morphological, reproductive, and production capabilities of Bangladeshi cross-bred sheep through performance analysis. Out of the overall number, male lambs accounted for 54.55%, while female lambs contributed 45.45%. Four significant components were identified by Principal Component Analysis (PCA), accounting for 81.84% of the total variations. Four clusters were identified based on the genotype distribution, with cluster III having the highest number of genotypes (eight out of twenty-two) and contributing 36.36% of the overall genotype distribution, along with three positive features (weight at maturity, weight at first lambing, and lamb's birth weight). The majority of the quantitative characteristics of the sheep under study showed significant genetic variations. Cluster III's features were characterized by better genotypes, which contributed to breeding success. The maximum cluster distance between clusters II and IV was discovered. According to the study's findings, parental lines from clusters II and IV can be obtained for hybridization purposes to produce progeny with high birth weights. In contrast, the genotypes of cluster III may be employed for potential commercialization.

Conflict of Interest

The authors attest that the publishing of this article does not present any conflicts of interest.

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