

Differentiation of native goat breeds of Jordan on the basis of morphostructural characteristics

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Abstract

A total of 493 does from 50 herds were measured to identify the different Jordanian goat breeds based on morphostructural characteristics. Different discriminant analysis methods (simple, cluster, canonical, stepwise) were applied on 20 metrical variables to discriminate among different genetic groups. Results identified four genetic groups: Damascus, Mountain, Dhawi and Desert in addition to a population of crossbred goats. Distribution of Mountain and Damascus breeds and the crossbred population was over the five clusters with varying frequencies. Dhawi and Desert breeds showed similar distribution of their populations over the clusters. All pair-wise Mahalanobis distances were significant ($P < 0.001$). Mountain goat breed tends to have the closest distance to all other native goats in Jordan. The largest distance was that between Dhawi and Damascus breeds (22.23). The dendrogram showed two large clusters: cluster one included Damascus breed as a large group and two sub clusters of Mountain breed and crossbred goats. Cluster two included Desert and Dhawi breeds. The canonical discriminant analysis and the stepwise discriminant analysis revealed that nose shape was the most discriminating variable among different pair-wise breeds' comparisons, followed by withers height (WH) then body weight, ear type, color and teat placement. Chest width (CW), withers depth (WD), rump width showed small discriminatory power. Crossbred goats have been found to be derived mainly from Damascus and Mountain breeds, with more relation to the latter.

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1. Introduction

Goats have received little attention by researchers in Jordan compared to other livestock species. It is believed that the goat population in Jordan belongs to several breeds and crosses involving these breeds.

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Jordanian breeds vary in color, body weight, size, morphostructural characteristics, shape of horns and presence or absence of horns and wattles. Also, differences can be observed among goats of different geographical parts of the country. These differences were not previously investigated and knowledge of such diversity is important especially when there is a strong tendency to mix these breeds with exotic genotypes introduced recently to the country.

Morphological characters provide useful information to detect genetic relationships of breeds in different domestic species (Herrera et al., 1996; Jordana et al., 1993, 1995). Genetic diversity and similarity among or within breeds, was studied using morphostructural differences (Herrera et al., 1996; Rey et al., 1995). In an attempt to distinguish between brown and gray Bengal goats, body length (BL) and chest circumference showed significant differences between these breeds (Mukeherjee et al., 1979). Similarly, Herrera et al. (1996) successfully used some body measurements such as, shin circumference (SC), chest girth, chest depth, rump length (RL) and width, and shoulder height to discriminate between five goat breeds in Spain. Because variation in mature body weight is considerable even among breeds with similar withers height (WH), it was used to estimate phylogenetic relationship between some Spanish goat breeds (Jordana et al., 1993). According to Al-Khoury (1997) no such studies have been made on the genetic differentiation of Jordanian goat breeds by analysis of morphological characters. Therefore, the objective of this study was to identify the different native goat breeds in Jordan based on morphostructural characteristics.

2. Materials and methods

2.1. Data collection

A survey was conducted to study goat breeds in all 12 governorates of Jordan. Some governorates were combined as one unit due to their small surface area and because their herds were being intermixed. Jerash and Ajlun governorates were grouped as one unit, likewise Karak and Tafilah. Each of the following governorates was treated as an individual area: Amman, Zarqa, Madaba, Irbid, Ma'an, Aqaba, Balqa and Mafraq. Five herds per sampling area were surveyed and 10 adult does

of 3 years or older were measured from each herd (493 does).

Measurements taken by researcher for each doe were nose shape (straight, slightly convex, convex, largely convex or very largely convex), ear shape (large wide, large narrow, medium, medium bent, small or trace), presence or absence of horns and wattles, color (black, white, brown, gray or mix), body weight, head length (HL), head width (HW), chest width (CW), heart girth (HG), withers depth (WD), WH, foreleg height (FH), SC, BL, RL, rump width (RW), rump height (RH), rare leg height (RH), udder shape (well formed or not) and teat placement (forward, backward, inner or outer) (Herrera et al., 1996). During body measurements, does were standing upright and restrained in such a way that their heads, necks, and barrels were stretched almost in a straight line. Body weight was measured by pocket balance. Herd owners were asked to determine the local name of does breed.

2.2. Statistical analysis

Since data had different units of measurements, they were standardized to zero mean and a unit standard deviation. Statistical Analysis System (SAS, 1994) was utilized for the analysis. Preliminary testing of data was carried out to determine outliers to be discarded before further analysis, resulting in the exclusion of two goats.

No previous knowledge was available about the presence of specific breeds in specific areas and farmers' answers were not dependable in this respect since when asked about the breed most the time, their answer was Balady (local) breed of goat. After further asking some times they revealed a specific name. Therefore, initial assumption was made that each herd is a different genotypes. However, the local names given by farmers in each governorate were matched with these 50 clusters using SAS FREQ to determine the optimal number of clusters (groups) that are reliable to resume other analysis. SAS FASTCLUS and CANDISC procedures were utilized to form clusters and calculate the canonical variables (CAN) which were used to match breed-governorate groups until reached the satisfactory number of clusters (genetic groups).

The simple discriminant analysis was used to calculate the probabilities of including an animal in its actual breed and to determine assignment errors that are made during classification of the populations utilizing

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