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Morphological and Genetic Diversity of Domestic Yak (*Bos grunniens*) at High Altitude Rangelands of Gilgit Baltistan, Pakistan

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Abstract

In the mountain range of Hindukush and Karakoram at northern Pakistan, yak is an important farm animal for providing milk, meat and other domestic and agricultural needs. However, the genetic studies on this farm animal are rare since it is a neglected animal species in the region. In this study, we examined the morphological and genetic diversity of yak populations involving 120 yaks from six different populations (20 from each; 14 females and 6 males). Body measurements and hair samples were taken in 2018. Thirteen microsatellite loci were used to determine the morphological difference and the level of genetic variation and relationship within and between populations. Heart girth, height at withers, body length, height at rump, horn length, muzzle circumference, tail and hair length, backline and head profile, as well as coat and horn colour differed significantly ($p < 0.01$) between sex and across different populations, while ear length and the distance between ends of horn were similar. The mean value of observed heterozygosity was 0.652 ± 0.02 , whereas the mean expected heterozygosity (H_e) was 0.645 ± 0.01 . Average genetic diversity was highest in Chipurson population ($H_e = 0.667$) and lowest in Khaplu population ($H_e = 0.610$). The results of genetic distance indicated the distance between Shimshal and Khaplu yak population was the most and the least between the populations of Phander and Hoper, the values were 0.2441 and 0.0722 respectively. Besides, three distinct genetic clusters were found. Overall, lower F_{is} value (-0.026 ± 0.02) indicated individuals in the populations were less related than expected under a model of random mating. Furthermore, highest genetic variation (94 %) was observed within individuals across populations, 2 % of the total genetic variation was among individuals within populations, and only 4 % was among populations, resulting in a relatively low F_{st} of 0.052. Our work underlines the importance of yak genetic diversity not only to obtain better understanding of the current domestic yak status but also to illustrate the importance for the development of biological genetic conservation strategies and specific breeding programs in yaks to enhance livelihood opportunities for subsistence level agro-pastorals in Gilgit Baltistan region.

Keywords: Genetic diversity, Gilgit Baltistan, microsatellite, yak

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