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

Asif Hameed[1], Eva Schlecht[1], Muhammad Tariq[2], Andreas Buerkert[3], Carsten Scheper[4], Sven Koenig[4], Regina Roessler[1,5]

[1]University of Kassel/University of Göttingen, Animal Husbandry in the Tropics and Subtropics, Germany
[2]University of Agriculture, Dept. of Livestock Management, Toba Tek Singh, Pakistan
[3]University of Kassel, Organic Plant Production and Agroecosystems Research in the Tropics and Subtropics, Germany
[4]Justus-Liebig-University of Gießen, Institute of Animal Breeding and Genetics, Gießen, Germany
[5]University of Kassel, Animal Breeding, Germany

Introduction

- Yaks provide domestic and agricultural needs in high harsh mountain regions of northern Pakistan.

- Genetic studies are rare as animals are a neglected species in the region.

- We examined the morphological and genetic diversity of yak populations in Gilgit-Baltistan.

Fig. 1: Study area (a) and yaks in Khaplu and Chipurson valley (b, c)

Fig. 2: Average values (cm) of body measurements of yaks across the six populations (valleys).

Material and Methods

- Selection of 6 valleys within Gilgit-Baltistan (Fig. 1a).

- Body measurements and hair samples were taken from 120 yaks (14 cows and 6 bulls per valley).

- Thirteen microsatellite loci were used for genetic characterisation.

Conclusions

- High phenotypic and genetic diversity identified.

- Populations less related than expected under a model of random mating.

- Genetic conservation strategies and specific breeding programs should enhance local livelihoods.

Results

- Heart girth, height at withers, body length, horn length and muzzle circumference differ (p<0.01) between populations (Fig. 2).

- Six distinctive coat colors (black, blue, brown, grey white, yellow) and two patterns (plain and patchy) determined (Fig. 1 b,c).
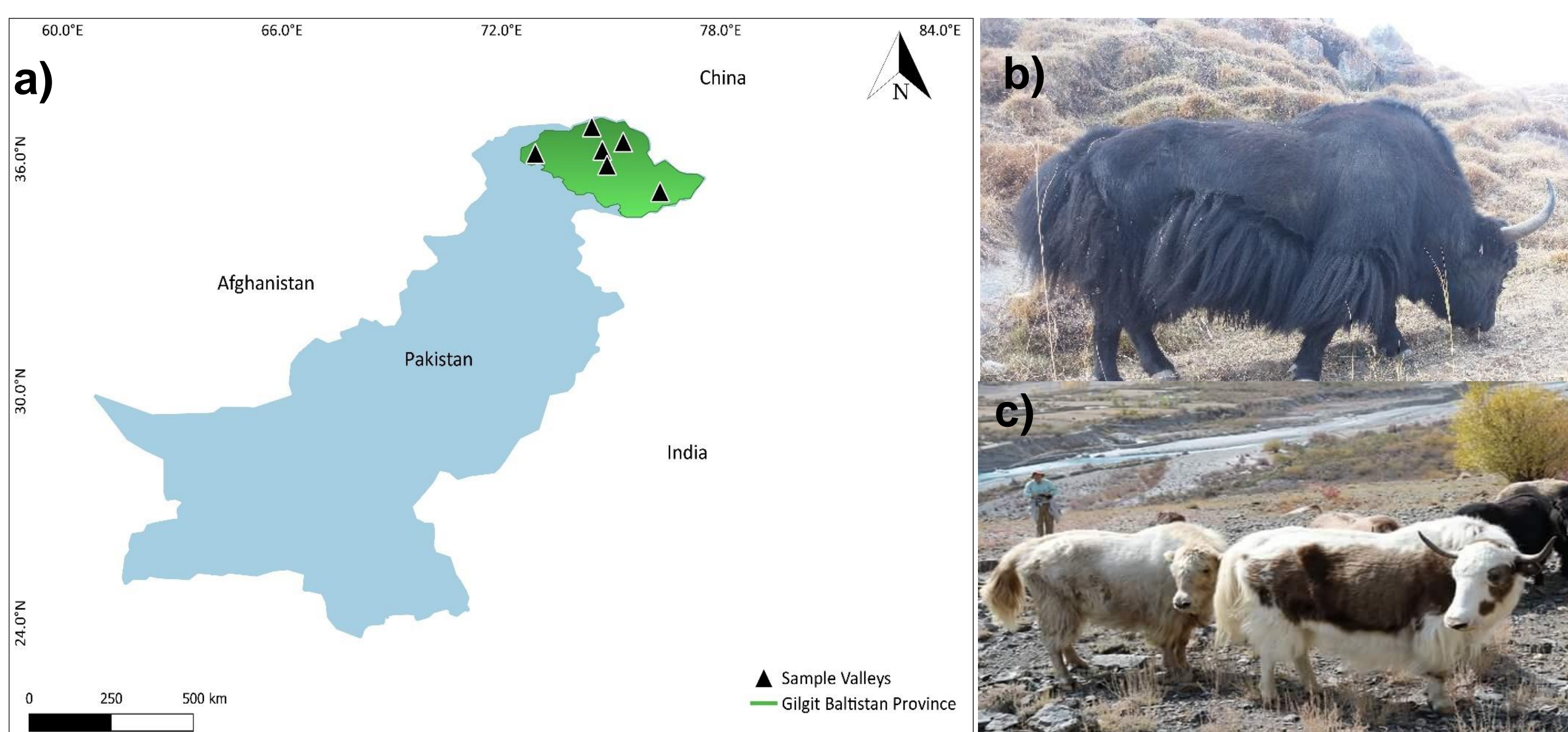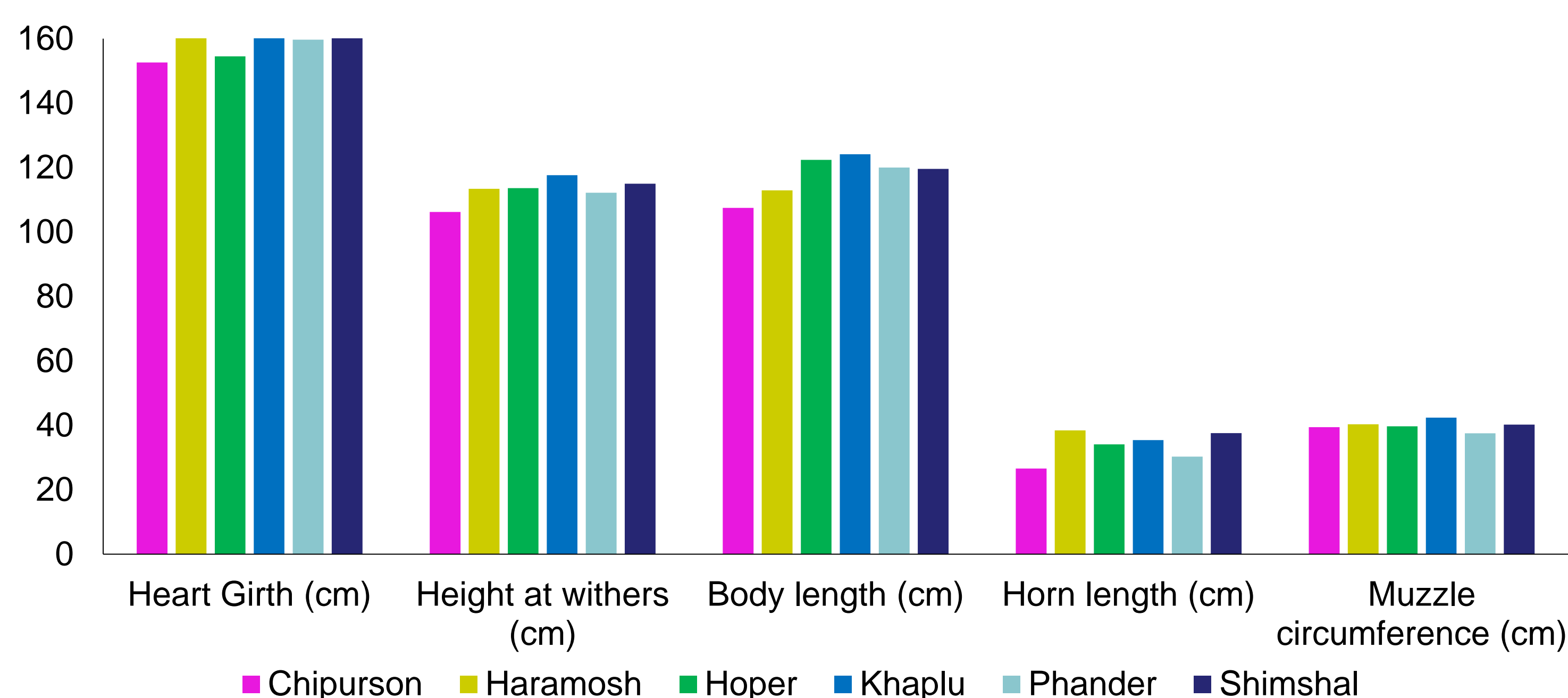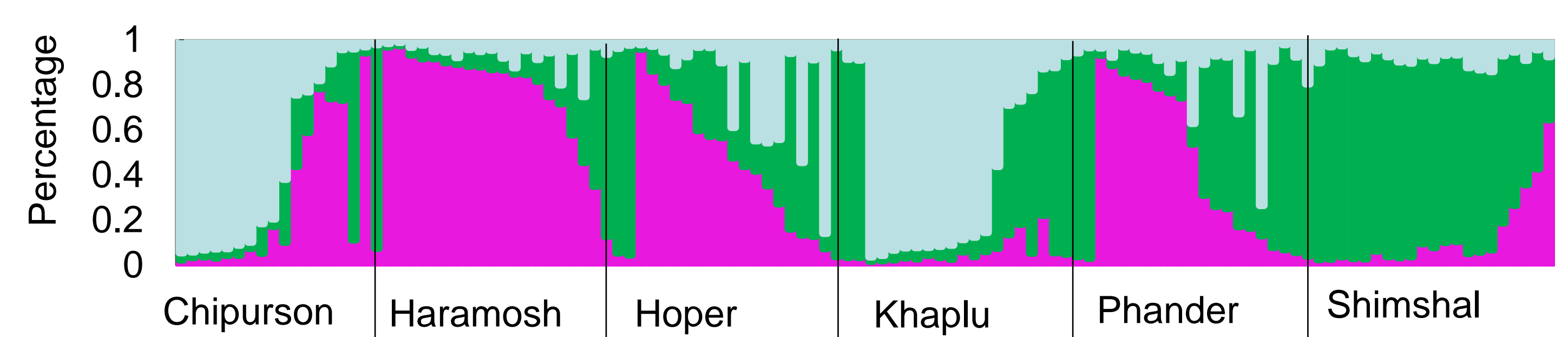
- Shinny hair and medium tail length observed.

Fig. 3: Bayesian inference of most likely clusters (K = 3) of yak populations sampled in Gilgit Baltistan, Pakistan.

- Mean observed (Ho) and expected heterozygosity (He) is 0.652 and 0.645, respectively.

- Average genetic diversity highest in Chipurson (He= 0.667) and lowest in Khaplu population (He= 0.610).

- Genetic distance greatest between Shimshal and Khaplu (0.2441) and smallest between Phander and Hoper (0.0722) populations.

- Low inbreeding coefficient value (Fis value, -0.026).

- Three distinct genetic clusters present (Fig. 3).