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23. Y-chromosomal haplotypes in domestic and wild goats reveal ancient paternal bottlenecks and recent introgressions

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By its paternal transmission, Y-chromosomal haplotypes are sensitive markers of population history and male-mediated introgression. Previous studies have identified in domestic goats four major Y-chromosomal haplotypes Y1A, Y1B, Y2A and Y2B with a marked geographic differentiation and several regional variants. In this study we combine whole-genome sequences (WGSs) of 392 male goats from 64 modern breeds and 7 wild goat species generated by the Vargoats goat genome project, 136 entries in the Short-Read Archive and genotypes of diagnostic SNPs of several modern and ancient samples. We identified single-copy male-specific SNPs in four scaffolds, containing *SRY*, *ZFY*, *DBY* with *SSX3Y* and *UTY*, and *USP9Y* with *UMN2001*, respectively. Phylogenetic analyses indicated haplogroups corresponding to Y1B, Y2A and Y2B, respectively, but Y1A is split into Y1AA and Y1AB. All these haplogroups were detected in ancient DNA samples from southeast Europe. In different branches of the tree, the haplotypes from domestic goats, Iranian bezoars and Anatolian bezoars, respectively, have separate positions. Notably, the Anatolian haplotypes are near the roots of the tree or of subtrees, suggesting that the Iranian bezoars are closer to the wild ancestors of domestic sheep. Haplogroup distributions for 150 domestic breeds indicates on all three continents ancient paternal population bottlenecks, especially during the migration into northern Europe. In addition, sharing of haplogroups reveals male-mediated introgression of Boer goat into Uganda, Kenya, Tanzania, Malawi and Zimbabwe, and of European goats into the native Korean goat population. This study illustrates the power of the Y-chromosomal variation for the reconstructing the history of mammalian species with a wide geographic range.