

# **Whole genome sequence data identifies admixture and selection in wild members of the *Bos* genus**

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## **Abstract**

The genus *Bos*, which includes domestic cattle and its wild bovid relatives is a clade with rich evolutionary history intrinsically linked with anthropogenic forces. The cosmopolitan distribution of different members of this group either naturally or after human introduction has been the result of millions of years of evolutionary events such as migration, radiation, bottlenecks, adaptation, domestication, and hybridization. Unweaving the worldwide signatures of these events within the genomes of modern animals has previously lacked a comprehensive enough approach, either failing to have enough diversity, depth, or overall sample size. We use 1810 resequenced genomes from over 200 breeds of wild and domestic animals from the genus *Bos* and utilizing the latest demographic methods which proved highly effective and scalable in human studies, estimate a genealogy for *Bos* species across over a thousand individuals of diverse origins, the relative time scale of coalescent events, ancestral allele frequencies, and mutation rates following introgression. We leverage this globally diverse cohort to formally test theories of foundational introgression and hybrid origin for wild and domestic members of this clade. One hypothesis we present is that Bison originated as a hybrid species between the ancestors of modern Yaks and Gaurs or Bantengs, before migrating to and colonizing North America. Exploratory analyses with TreeMix admixture networks suggested this relationship, and  $f_4$  statistics and qpGraph networks more explicitly tested this hypothesis. We further explore this data for evidence of selection which has differentiated these species. These data highlight the complex nature of species formation.