

Whole genome sequence data elucidates signatures of cattle domestication and global bovid migration patterns

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Abstract

Domesticated cattle and its wild bovid relatives are a clade with rich evolutionary history intrinsically linked with anthropogenic forces. Of particular interest to the fields of population genetics, anthropology and evolutionary biology, is the process of domestication. While directional-selection on the complex of traits encompassed in ‘domestication syndrome’ has been previously identified with soft-sweeps, it remains unclear whether this polygenic selection was gradual, or a confluence of related molecular events allowed this compounded phenotype to arise relatively quickly. Additionally, the classical view that domestication resulted from a bottleneck event with persistent isolation has been questioned due to the high pervasiveness of gene flow between wild and non-wild animals. Past efforts in cattle and other domestic mammalian species either lacked samples with enough diversity, quality or overall size to uncover many of the genetic signatures of selection or accurately map admixture worldwide. 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 for in human studies, estimate a genealogy for domestic cattle across thousands of individuals of diverse origins, the relative time scale of coalescent events, ancestral allele frequencies, and mutation rates following introgression. This will allow us to detect evolutionary forces that were present during domestication, such as selective pressure on polygenic traits, and the impacts of wild species interbreeding to better elucidate the genetics behind domestication in the context of human history and biogeographical space and time.