

Stories in the DNA

Genetic tools can help uncover evolutionary histories, migration patterns and admixture events of domesticated animals and their wild ancestors. The genetic window into the past can help shape breeding strategies and inform animal agricultural practices that should lead to a more resilient and sustainable future.

Interesting agricultural origin stories abound, and sophisticated genomic analyses can now help to unravel how the different genomes of ancestral agricultural species have mixed and mingled throughout history to produce extant crops and livestock. Last month, we highlighted [exciting areas in plant genomics](#); here, we wish to give some attention to animal genomics, specifically in relation to how population genetics analyses can provide fascinating insights into not only the evolution of particular animal species but also our own human histories.

The complex interplay among animal husbandry, human lifestyle and the environment has been adapting and developing for millennia. These three elements influence and shape one another, and genetic analysis can supply integral information for the reconstruction of previous events as well as guidance in how to best adapt to changes in the future. Importantly, the integration of genomic information with archeological data and local knowledge from farmers and pastoralists paints a more comprehensive picture of animal domestication events and agricultural developments.

In this issue, the International Livestock Research Institute and collaborators [analyze whole-genome sequences](#) from 172 African cattle from 16 breeds, to reconstruct the migration and admixture events of these important pastoral species. African cattle are highly phenotypically diverse, and most have *Bos taurus* (humpless taurine cattle) and *Bos indicus* (humped indicine cattle) ancestries, which in turn derived from domestication of the *Bos primigenius* subspecies. *B. taurus* cattle were introduced through North Africa and later (around 4,000–3,000 years ago) spread through the continent. *B. indicus* arrived through the Red Sea and Indian Ocean coastal regions around 700 CE. In this study, the authors aimed to estimate taurine × indicine admixture events to obtain a more accurate history of domesticated African cattle and relate it to the development of African pastoralism, specifically in the Horn of Africa.

Selective pressure stemming from weather, environment and disease also leaves ‘footprints’ in the DNA and contributes to the majestic diversity of African cattle, as highlighted in the Ankole cattle picture featured on the cover of this issue (adapted from T. Dessie and O. Mwai (eds) [The Story of Cattle in Africa: Why Diversity Matters](#);

2019). Admixture of species resulted in new combinations of advantageous traits that aided in the adaptation to new and specific environments. Heat tolerance, disease resistance and drought adaptations all provide various levels of selective advantage, depending on geography, exposure and genetic background. Population genetics analysis is a lens to past migration and admixture events, and it allows for the identification of genes and genetic loci that contribute to the success of African cattle pastoralism across a wide range of environments.

The identification of these genes can help inform strategies for improving animal productivity and food security, which become increasingly crucial in circumstances in which population growth and climate change together increase the pressure on current food and agricultural systems. Keeping a global perspective and appreciating and learning from the vast resources of knowledge and expertise that can be found throughout the world are important, particularly among those who are closest to the crops and livestock that sustain us. □

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