

## RESEARCH ARTICLE SUMMARY

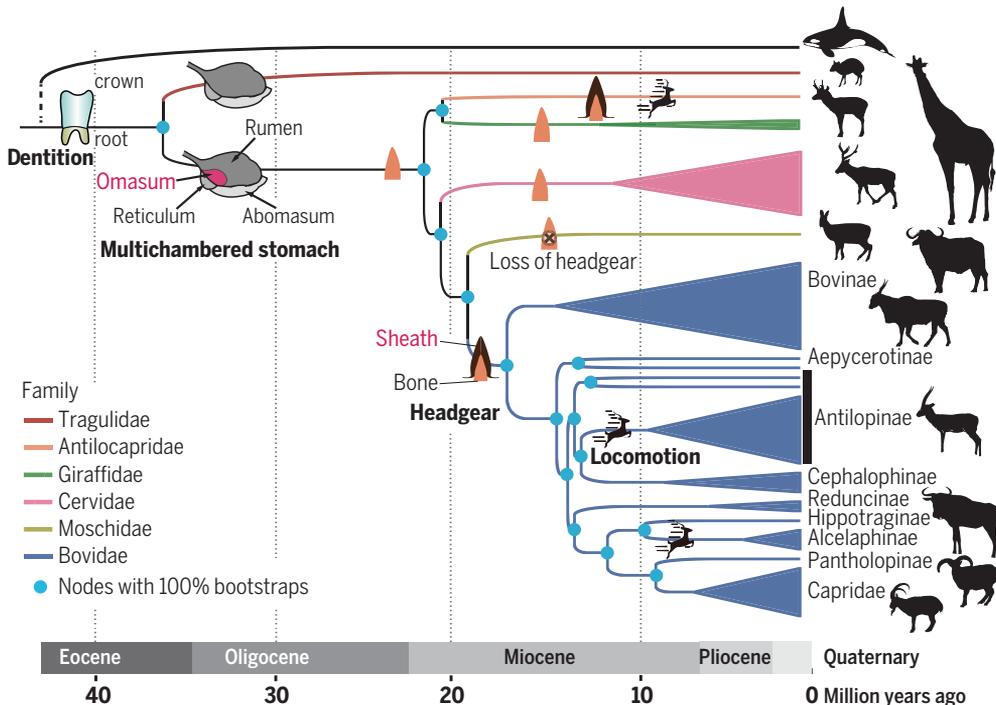
## RUMINANT GENOMES

# Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits

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**INTRODUCTION:** The ruminants are one of the most successful mammalian lineages, exhibiting extensive morphological and ecological diversity and containing several key livestock species, such as cattle, buffalo, yak, sheep, and goat. Ruminants have evolved several distinct characteristics such as a multichambered stomach, cranial appendages (headgear), special-

ized dentition, a highly cursorial locomotion, and a wide range of body size variations. Despite their biological prominence and value to human societies, the evolutionary history of ruminants has not been fully resolved, and the molecular mechanisms underlying their particular characteristics remains largely unknown.



**Phylogeny and trait evolution of ruminants.** The phylogenetic tree of ruminants is presented with the species within same families and subfamilies collapsed. The ruminants have many textbook examples of distinct traits. The four-chambered stomach with omasum chamber is a key innovation evolved in pecoran ruminants. Headgear keratinous sheath only appear in Bovidae and Antilocapridae lineages. Many ruminants have evolved high-crowned or hypsodont teeth. The Antilocapridae and two bovid lineages are among the mammals with highest cursorial locomotion ability.

**RATIONALE:** We seek to resolve the controversies in the ruminant phylogeny and reveal the genetic basis underpinning the evolutionary innovations in ruminants. Here, we report the newly sequenced genomes of 44 ruminant species, covering about half the genera and all six extant Ruminantia families. We included seven published ruminant genomes (five bovids and two cervids) to reconstruct the phylogenetic tree by using improved time calibrations. We also reconstructed the Pleistocene demographic histories of these ruminant species using whole-

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genome heterozygosity information. Together with transcriptomic data of 516 samples from 68 tissues of four species, we conducted comparative genomic analyses to reveal candidate genes and regulatory elements that might have contributed to the evolution of the distinct ruminant characteristics.

**RESULTS:** Using whole-genome orthologous sequences obtained from 51 ruminants, we have produced a new well-supported ruminant phylogenetic tree. The new tree resolves previous controversies over the deep branches of ruminant families, as well as the highly radiated Bovidae family. We estimated the emergence of crown Ruminantia to the late Oligocene (39.1 million to 32.3 million years ago) and that

of Pecora to the Neocene (23.3 million to 20.8 million years ago). Investigations of demographic history revealed massive population decline events that occurred in most ruminant species, starting from ~100,000 to 50,000 years ago, which was temporally and spatially concurrent with the increased human activities on different continents during this period. We further identified many genomic changes that associate with important evolutionary innovations, such as the multichambered stomach, headgear, body size variation, cursorial locomotion, and dentition.

**CONCLUSION:** Our results demonstrate the power of using comparative phylogenomic approaches in resolving the deep branches of phylogeny that result from rapid radiations. The data and results presented in this study provide valuable resources and insights into the evolution of ruminant and mammalian biology. ■

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Cite this article as L. Chen *et al.*, *Science* **364**, eaav6202 (2019). DOI: 10.1126/science.aav6202