

# Cattle Biodiversity in Past and Present in South to East Asia

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## **Abstract**

Cattle have had an important but incompletely understood association with early human civilization and expansion. The study of their origins and diversity may enlighten on hitherto unknown aspects of prehistory. All modern cattle have been considered to be domesticated from captured aurochs at the primary domestication centres of Anatolia and the Fertile Crescent, however, this is an opinion that may be an artifact of the history of archaeology. Recent molecular studies using mitochondrial DNA (mtDNA) reveal molecular evidence for a predomestic divergence between zebu, or humped cattle (*Bos indicus*), and taurine, or humpless cattle (*Bos taurus*). Subsequent mtDNA studies for the origin and genetic diversity of Asian *Bos taurus* cattle revealed five major types of mtDNA haplogroups, T (auroch type), T1 (African type), T2 (Middle East type), T3 (European type) and T4 (Asian type) in cattle. The *Bos taurus* mtDNA sequences fall into several geographically distributed haplogroups. Mongolian cattle showed higher genetic diversity due to genetic admixture through ancient trade. Detailed examination of *Bos indicus* mtDNA sequence diversity also reveals a separation of sequences into discrete haplogroups. The analysis clearly coalesces to two moderately divergent predominant haplogroups, termed I1 and I2. Higher nucleotide diversity in Indian than anywhere across Asia for both the two observed mitochondrial lineages (I1, I2), indicates India as the centre of origin for all *Bos indicus* cattle. In addition, the nucleotide diversity supports this region as the origin of I1, which this mitochondrial lineage is the main one observed across East and Southeast Asia. For I2, more complex pattern of diversity was detected. The result indicates difficulty for pinpointing of a single region for the origin of the I2 haplogroup.

**Keywords:** biodiversity; cattle; domestication; mitochondrial DNA; nucleotide sequence; origin