

## ABSTRACT

### **Phylogenetic Relationships of Northeast Asian Cattle to Other Cattle Populations Determined Using Mitochondrial DNA D-Loop Sequence Polymorphism**

*Kyu-Il Kim, Jun-Heon Lee, Sung-Soo Lee & Young-Hoon Yang*

Phylogenetic relationships of Northeast Asian cattle to various other cattle breeds including *Bos taurus*, *Bos indicus*, and *Bison bison* were assessed using mtDNA D-loop sequences. A neighbor-joining tree was constructed using sequences determined for 4 Cheju Black, 4 Cheju Yellow, 4 Korean Yellow cattle (*Bos taurus*), and 2 American Brahman cattle (*Bos indicus*), and also published sequences for 31 Japanese Black cattle, 45 European breed cattle, 6 African zebus, 2 African taurines, and 6 Indian zebus. Five American bisons (*Bison bison*) were used as an outgroup. The neighbor-joining tree showed that American bisons and Indian zebus are clearly separate from other cattle breeds, respectively, and African cattle clustered together, although with a low bootstrap probability (<50%). Results indicate that cattle in Northeast Asia, Europe, and Africa are closely related to each other—suggesting their recent divergence, but are separate from Indian zebus.