



Genetic diversity of Y-short tandem repeats in chinese native cattle breeds

Y.P. Xin¹, L.S. Zan¹, Y.F. Liu², W.Q. Tian³, H.B. Wang¹, G. Cheng¹,
A.N. Li¹ and W.C. Yang¹

¹College of Animal Science and Technology, Northwest A&F University,
Yangling, Shaanxi, China

²College of Food Engineering and Nutritional Science,
Shaanxi Normal University, Xi'an, Shaanxi, China

³Yangling Vocational Technical College, Yangling, Shaanxi, China

Corresponding author: L.S. Zan
E-mail: zanls@yahoo.com.cn

Genet. Mol. Res. 13 (4): 9578-9587 (2014)

Received June 21, 2013

Accepted September 22, 2014

Published November 14, 2014

DOI <http://dx.doi.org/10.4238/2014.November.14.1>

ABSTRACT. The aim of this study is to use Y-chromosome gene polymorphism method to investigate regional differences in genetic variation and population evolution history of the Chinese native cattle breeds. Six Y-chromosome short tandem repeat (Y-STR) loci (*UMN0929*, *UMN0108*, *UMN0920*, *INRA124*, *UMN2404*, and *UMN0103*) were analyzed using 1016 healthy and heterogenetic males and 90 females of 9 native cattle breeds (Qinchuan, Jinnan, Zaosheng, Luxi, Nanyang, Jiaxian, Dabieshan, Yanbian, and Menggu) in China. Allele frequency and gene diversity were calculated for the various populations. The results indicated that Y-STRs in the 6 loci have polymorphisms and genetic diversity in Chinese cattle populations. The genetic diversity analysis revealed that the Chinese cattle populations have a close genetic relationship. The analysis of *INRA124*, *UMN2404*, and *UMN0103* loci revealed the original history of Chinese cattle because of which cattle belonging to *Bos taurus* or *Bos indicus* could be determined. Interestingly, a declining zebu introgression was displayed

from South to North and from East to West in the Chinese geographical distribution, which implied that cattle population from various regions of China had been subjected to somewhat different evolutionary history. This conclusion supported other evidences such as earlier archaeological, historical research, and blood protein polymorphism analysis.

Key words: Cattle; Y-chromosome; Polymorphism; Haplotype; Short tandem repeat