

ABSTRACT

**Low mitochondrial DNA diversity of Japanese Polled and Kuchinoshima feral cattle**

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This study aims to estimate the mitochondrial genetic diversity and structure of Japanese Polled and Kuchinoshima feral cattle, which are maintained in small populations. We determined the mitochondrial DNA (mtDNA) displacement loop (D-loop) sequences for both cattle populations and analyzed these in conjunction with previously published data from Northeast Asian cattle populations. Our findings showed that Japanese native cattle have a predominant, Asian-specific mtDNA haplogroup T4 with high frequencies (0.43-0.81). This excluded Kuchinoshima cattle (32 animals), which had only one mtDNA haplotype belonging to the haplogroup T3. Japanese Polled showed relatively lower mtDNA diversity in the average sequence divergence (0.0020) than other Wagyu breeds (0.0036-0.0047). Japanese Polled have been maintained in a limited area of Yamaguchi, and the population size is now less than 200. Therefore, low mtDNA diversity in the Japanese Polled could be explained by the decreasing population size in the last three decades. We found low mtDNA diversity in both Japanese Polled and Kuchinoshima cattle. The genetic information obtained in this study will be useful for maintaining these populations and for understanding the origin of Japanese native cattle.