

Karyotypic and mtDNA based characterization of Malaysian water buffalo

ABSTRACT

Background: In Malaysia, the domestic water buffaloes (*Bubalus bubalis*) are classified into the swamp and the murreh buffaloes. Identification of these buffaloes is usually made via their phenotypic appearances. This study characterizes the subspecies of water buffaloes using karyotype, molecular and phylogenetic analyses. Blood of 105 buffaloes, phenotypically identified as swamp, murreh and crossbred buffaloes were cultured, terminated and harvested using conventional karyotype protocol to determine the number of chromosomes. Then, the D-loop of mitochondrial DNA of 10 swamp, 6 crossbred and 4 murreh buffaloes which were identified earlier by karyotyping were used to construct a phylogenetic tree was constructed. Results Karyotypic analysis confirmed that all 93 animals phenotypically identified as swamp buffaloes with 48 chromosomes, all 7 as crossbreds with 49 chromosomes, and all 5 as murreh buffaloes with 50 chromosomes. The D-loop of mitochondrial DNA analysis showed that 10 haplotypes were observed with haplotype diversity of 0.8000 ± 0.089 . Sequence characterization revealed 72 variable sites in which 67 were parsimony informative sites with sequence diversity of 0.01906. The swamp and murreh buffaloes clearly formed 2 different clades in the phylogenetic tree, indicating clear maternal divergence from each other. The crossbreds were grouped within the swamp buffalo clade, indicating the dominant maternal swamp buffalo gene in the crossbreds. Conclusion: Thus, the karyotyping could be used to differentiate the water buffaloes while genotypic analysis could be used to characterize the water buffaloes and their crossbreds.

Keyword: Karyotyping; Mitochondrial DNA; Phylogenetic; Water buffaloes