ABSTRACT

Genetic diversity of 7 Thai indigenous chicken lines were evaluated on the basis of microsatellite DNA polymorphisms. Thai indigenous chicken lines were Luenghangkhoa, Praduhangdam, Chee, Bantam, Betong, Naked Neck and Frizzle. Commercial broiler hybrid line (Arbor Acres), commercial layer hybrid line (Isa Brown) and Red Jungle Fowl (Gallus gallus gallus) were also included in this study. The genomic DNA were extracted from individual chicken blood. Twenty microsatellite DNA markers were used to amplify the extracted genomic DNA by polymerase chain reaction. DNA bands were separated and detected. Genetic diversity within and between populations were analyzed by POPGENE version 1.32. All the microsatellite loci were found to be polymorphic. The number of alleles was varying from 3 to 15 per locus, and the mean number of alleles per locus was 7.7. The mean observed and expected heterozygosity of Thai indigenous chicken ranged from 0.400 (Bantam) to 0.510 (Chee) and 0.531 (Frizzle) to 0.638 (Chee), respectively. From the 10 populations evaluated, the lowest genetic distance was between Luenghangkhoa and Praduhangdam (0.1120) and the highest was between Bantam and Isa Brown (0.4316). Among the 7 Thai indigenous chicken lines, the genetic distance ranged from 0.1120 to 0.3593. A phylogenetic tree was constructed based on Nei’s genetic distance by UPGMGA method. The lines were grouped into three clusters as following; the first group Thai indigenous chicken lines and Red Jungle Fowl, the second group Bantam and the third group Arbor Acres and Isa Brown.