

Genetic Structure of Four Bovine Populations in the Philippines Using Microsatellites

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Abstract : This study evaluated polymorphism of 11 microsatellite markers in four local genetic groups of cattle. Batanes cattle which has never been studied using microsatellites is evaluated for its genetic distance from the Ilocos cattle while Brahman and Holstein-Sahiwal are also included as there were insemination programs by the government using these two breeds. PCR products that were genotyped for each marker were analyzed using POPGENEv32. Results showed that 55% ($F_{st}=0.5501$) of the genetic variation is due to the differences between populations while the remaining 45% is due to individual variation. The F_{st} value also indicates that there were very great differences from population to population using the range proposed by Sewall and Wright. The constructed phylogenetic tree based on Nei's genetic distance using the modified neighbor joining procedure of PHYLIPv3.5 showed the admixture of Brahman and Holstein-Sahiwal having them grouped in the same clade. Batanes and Ilocos cattle were grouped in a different cluster showing that they have descended from a single parental population. This would presumably address the claim that Batanes and Ilocos cattle are genetically distant from other groups and still exist despite the artificial insemination program of the government using Brahman and other imported breeds. The knowledge about the genetic structure of this population supports the development of conservation programs for the smallholder farmers.

Keywords : microsatellites, cattle, Philippines, populations, genetic structure

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