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Analysis of genetic structure of non-descript local goat populations in Sri Lanka

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The knowledge on genetic structure of organisms is important not only to understand the evolutionary processes it has undergone but also to realize the role of environment on this process. Population genetics and phylogenetic studies are important to provide opinions on effective conservation and reintroduction plans especially when the target population is under threat of extinction. Sri Lankan non-descript local goats represent a threatened population due to indiscriminate slaughter and cross breeding practices. Population genetic structure of these animals is unknown other than the fact that they were introduced by Arabian sailors. Therefore, this study was devoted to evaluate genetic structure of local goats aiming to provide information for conservation programs.

The experiment was initiated with collection of blood samples from 61 goats in northern, northwestern, eastern and southern provinces of the country and DNA extraction from blood samples, polymerase chain reaction for exon 2-3 of alpha lactalbumin (LALBA) gene and DNA sequencing were performed subsequently. Phylogenetic trees were constructed utilizing Maximum Likelihood (ML) and Bayesian Inference (BI) methods in GARLI (v.96) and MrBayes (3.2.5.) software respectively. Parsimony networks were constructed in TCS (v1.2.1.). Within and among population genetic variabilities were calculated using AMOVA while pairwise mismatch distribution and selective neutrality were estimated in Arlequin 3.5.

Both ML and BI produced the same tree topology with little genetic structure and lower bootstrap branch support while the parsimony network consists of four main clusters which were not representing the sampling locality suggesting genetically likenesses. The idea is strongly supported by AMOVA test where within population variability is greater (98.74%) than among population (1.26%) (Fst=0.012, d.f=98, P=0.18) which may be attributed to cross breeding and transportation of animals. However, observed heterozygosity is still lower than the expected value ensuing, significantly negative results in neutrality tests; Fu's Fs ($p<0/005$) and Tajima's D ($p<0.5$). This can be resulted from a resent population expansion followed by a bottleneck event. Uni-model distribution of the mismatch profile also supports the idea of expansion of population size.

Results of this study reveal that local goat population is heterogeneous and contemporary population structure is highly influenced by anthropogenic activities. Therefore, immediate actions are recommended to conserve their genetic resources.

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