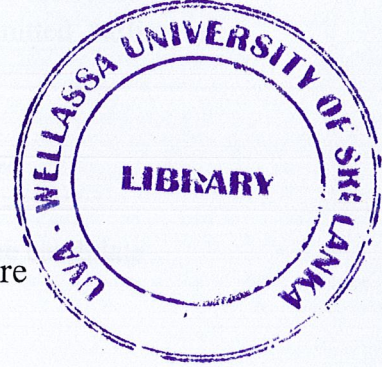


**PHYLOGENETIC CHARACTERIZATION OF THE
NON - DESCRIPTIVE LOCAL CATTLE
POPULATION IN THE NORTHERN PROVINCE OF
SRI LANKA**



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by

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ABSTRACT

Sri Lankan agriculture is based on a symbiotic relationship between crop and animal production, with cattle serving as the basis. But the population of indigenous cattle is declining with the modern production systems and needs immediate scientific management. Genetic characterization and phylogenetic analysis are the initial steps in the development of proper management strategies for preserving genetic diversity and preventing undesirable loss of alleles. Thus, in this study we majorly investigated genetic diversity and phylogenetic relationship of local non-descriptive cattle population in Northern Province of Sri Lanka using mitochondrial cytochrome *b* (mtDNA *cyt b*) gene sequences. The analysis of autosomal DNA was performed on 34 cattle sequences which exhibited sufficient genetic diversity across all the species of genus *Bos*. The aligned sequences of the mtDNA *cyt b* gene regions of the 34 animals were 816 base pairs long. The mtDNA *cyt b* region base percentages had a strong bias towards A + T according to the mean percentages of four nitrogen bases. Tamura-Nei evolutionary divergence over sequence pairs between groups ranged from 0.0016 to 0.0859. The phylogenetic analysis assigned the local non-descriptive Northern cattle population in to distinct lineages of *Bos indicus* ancestry. With the closest relationship to Indian *Bos indicus* breeds, it can assume that the subsequent introgression of Indian indicine may have influenced the matrilineal origin of the studied Northern cattle population. A close genetic distance was observed between local non-descriptive cattle population in Northern Province and the other studied local cattle populations in Sri Lanka.

Key Words: Northern cattle, Phylogenetic Analysis, mtDNA *cyt b* gene