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Mitochondrial DNA (mtDNA) has been widely used to study population-genetic relationship between members of a species. mtDNA is found to be haploid and maternally inherited, and it evolves much faster than nuclear DNA, and therefore is ideal for such studies. The NADH dehydrogenase subunit 5 gene (ND5) of the mitochondrial genome has been identified as a gene exhibiting a high degree of intra-specific sequence divergence.

The objective of the present study was to determine the genetic diversity of the Sri Lankan elephant, *Elephas maximus maximus*, using ND5 as a molecular marker. A 550 bp region of the ND5 gene was amplified by Polymerase Chain Reaction using the primers L13525 and H14127, and the sequence determined by automated DNA sequence analyzer (ABI Prism). A total 16 samples were analysed, and the sequence determined for both strands. A total of nine polymorphic sites were observed, giving rise to five different mtDNA haplotypes. Fifty percent of the sample (n=8) belonged to one haplotype. The number of first, second and third codon position transitions observed were 1, 1, and 6 respectively. The only transversion occurred at a third codon position. All third codon transitions were silent mutations, while the other three mutations were amino acid replacements. Two replacements were Phe-Leu, while the third was Leu-Ser. This is the first report of the sequence analysis of the mitochondrial ND5 gene of *Elephas maximus*.