

Genetic Diversity and Variation of Nigerian Pigeon (*Columba livia domestica*) Populations Based on the Mitochondrial Coi Gene

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Abstract : The domesticated pigeon, *Columba livia domestica*, has many valuable characteristics, including high nutritional value and fast growth rate. There is a lack of information on its genetic diversity in Nigeria; thus, the genetic variability in mitochondrial cytochrome oxidase subunit I (COI) sequences of 150 domestic pigeons from four different locations was examined. Three haplotypes (HT) were identified in Nigerian populations; the most common haplotype, HT1, was shared with wild and domestic pigeons from Europe, America, and Asia, while HT2 and HT3 were unique to Nigeria. The overall haplotype diversity was 0.052 ± 0.025 , and nucleotide diversity was 0.026 ± 0.068 across the four investigated populations. The phylogenetic tree showed significant clustering and genetic relationship of Nigerian domestic pigeons with other global pigeons. The median-joining network showed a star-like pattern suggesting population expansion. AMOVA results indicated that genetic variations in Nigerian pigeons mainly occurred within populations (99.93%), while the Neutrality tests results suggested that the Nigerian domestic pigeons' population experienced recent expansion. This study showed a low genetic diversity and population differentiation among Nigerian domestic pigeons consistent with a relatively conservative COI sequence with few polymorphic sites. Furthermore, the COI gene could serve as a candidate molecular marker to investigate the genetic diversity and origin of pigeon species. The current data is insufficient for further conclusions; therefore, more research evidence from multiple molecular markers is required.

Keywords : Nigeria pigeon, COI, genetic diversity, genetic variation, conservation

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