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**Population Genetic Structure of Swallows within the Pacific Clade****Thakshila T.<sup>1\*</sup>, Scordato E.<sup>2</sup>, Seneviratne S.<sup>1</sup>**<sup>1</sup>*University of Colombo, Colombo 03, Sri Lanka*<sup>2</sup>*California State Polytechnic University, Pomona, United States**\*thilini.thakshila.tt@gmail.com***Abstract**

Swallows are amongst the best-known families of birds to man in terms of their behaviour and ecology. They belong to family Hirundinidae in the genus *Hirundo*. Swallows have relatively conserved morphology due to their aerial insectivorous lifestyle. Therefore, fine morphological characters and genetic markers are needed to objectively evaluate the phylogenetic status of this group. We constructed both morphometric and phylogenetic analysis to determine the population sub structuring of Swallows in the Oriental region (commonly known as Pacific Swallows). Two mitochondrial gene regions; NADH dehydrogenase 2 (ND2) and cytochrome b (Cyt b) were considered separately and concatenated manner using PopArt (version 1.7). For each analysis 18 Sri Lankan Hill Swallow (*Hirundo javanica domicola*) sequences from six locations and 18 sequences from *H.j. javanica* (Western Malaysia, Japan, Borneo), *H.j. tahitica* (Papua New Guinea) and *H.j. neoxena* (Australia and New Zealand) were used. All haplotypes were mapped using median joining network algorithm with epsilon ( $\epsilon$ ) value of 0. Based on the haplotype network five main clusters could be identified. Higher number of single nucleotide polymorphic sites (SNPs) were present between those five clusters. Low level of gene flow between those clusters were identified, possibly due to geographical isolation. Results obtained from phenotypic and phylogenetic analysis further supported the obtained haplotype network indicating greater degree of isolation, hence limited gene flow. Three haplotypes within Sri Lanka, two haplotypes within Australia and New Zealand, one haplotype within Tahiti Island, two haplotypes within Fiji Islands, and six haplotypes within Borneo and Japan were obtained. Most parsimonious explanation to this would be higher level of gene flow within islands and low level of gene flow between distant geographic locations.

**Keywords:** Haplotype network, Phylogenetic status, Geographical isolation