9.16 Molecular Analysis of *Tamarixia radiata* from America Uncovers Extensive Haplotype Variation: Multiple Groups?


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A phylogeographic analysis was performed on field-collected populations of *Tamarixia radiata* from South (Argentina, Brazil, Paraguay, and Uruguay) and North (Florida, Texas, and México) America along with laboratory strains from Asia (Pakistan, Southern China, and Northern Vietnam) by sequencing the mitochondrial cytochrome oxidase subunit 1 gene (COI) (518-bp). Two colonies of the same strain from Pakistan were analyzed that were maintained at two different locations (Pak-1 and Pak-2). Our ongoing goal is to determine whether *T. radiata* could exist as a cryptic species complex or to determine whether groups can be uncovered and distinguished. Extensive haplotype (hp) variation was uncovered with a total of 52 haplotypes out of 91 individuals, indicating that 57% of individuals carried a different haplotype. Four haplotypes were shared among countries and continents: hp2 in Florida, China, and Vietnam; hp8 in Texas, México, Argentina, Brazil, and Pak-2; hp16 in Brazil and Pak-1; and hp21 in Uruguay and Pak-1. Interestingly, no sharing of haplotypes was seen between the Pak-1 and Pak-2 stains. A NeighborNet phylogenetic network clustered the haplotypes into four groups: Group 1 (Florida, China, and Vietnam), Group 2 (Uruguay and Pak-1), Group 3 (Argentina, Brazil, Uruguay, Pak-1, and Vietnam), and Group 4 (Texas, México, Brazil, Paraguay, and Pak-2). Each of these haplotypes was positioned at a specific node in the network, implicitly suggesting that each may be an ancestral haplotype. Similar results were seen with a 95% confidence statistical parsimony network. Are these groups reproductively compatible? Accurate identifications are crucial to the success of biological control programs.