

## Title : Evolutionary history of a global invasive ant, *Paratrechina longicornis*

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### Abstract

The longhorn crazy ant, *Paratrechina longicornis*, is a ubiquitous agricultural/household pest throughout much of the tropics and subtropics. In the present study, we developed 36 polymorphic microsatellite markers for *P. longicornis*, examined worldwide mtDNA and nDNA variation in *P. longicornis* and its associated *Wolbachia* bacterial symbionts. Analyses of mtDNA sequences of 13 geographic regions reveal two highly diverged mtDNA clades that co-occur in most of the geographic regions. These two mtDNA clades are associated with different *Wolbachia* infection patterns, but are not congruent with patterns of nDNA (microsatellite) variation. Two *Wolbachia* strains, *wLonA* and *wLonF*, occur: *wLonA* appears to be primarily transmitted maternally, and its infection status are consistent with a relatively recent *Wolbachia*-induced selective sweep. On the other hand, the history of *wLonF* infections in *P. longicornis* appears to be characterized by frequent gains and losses over time. Identical *Wolbachia* strain shared between specialist ant cricket *Myrmecophilus americanus* and *P. longicornis* implies the occurrence of *Wolbachia* horizontal transmission possibly through intimate ecological associations. The estimation of nDNA variation in worldwide populations reveals a extremely high level of heterozygosity, a possible genetic consequence derived from its unusual reproductive mode where workers are produced from hybridization of divergent queen and male clones. Our study showed that this system is widespread across our studied populations of *P. longicornis* and might act as an adaptive trait linked to the invasion success of this species as it potentially relaxes the costs associated with inbreeding.

Keywords: Invasive ant, microsatellite, mtDNA, phylogeography, *Wolbachia*