
 ABSTRACTS (PH D THESIS)

Evolutionary history of a global invasive ant, *Paratrechina longicornis*

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One successful management strategy to mitigate the negative impacts of invasive species relies on reconstructing the invasion history, which traces the patterns of ongoing invasion pathways and prioritizes quarantine resources accordingly to areas at high risk of invasion. The longhorn crazy ant, *Paratrechina longicornis*, is considered to be a significant invasive species due to its ecological impacts. Although *P. longicornis* has been reported worldwide for more than a century, its origin and invasion history remain controversial. Examining the global genetic pattern of *P. longicornis* may provide insight into the invasion history of this species. The present study aims to elaborate the evolutionary biology of *P. longicornis*, the longhorn crazy ant, focusing on the invasion history of this species and its symbionts to address questions through the lens of bioinvasion and evolutionary genetics.

The global genetic structure of *P. longicornis* has not yet been extensively studied, partially because of the limited number of genetic markers currently available. In the present study, we developed 36 polymorphic microsatellite markers for *P. longicornis* and characterized these markers by genotyping *P. longicornis* workers from 74 colonies in East and Southeast Asia. The results show that these new microsatellite markers are effective as a practical tool for reconstructing routes of invasion and assessing the population genetics of this invasive ant.

Analyses of mtDNA sequences of *P. longicornis* from 13 geographic regions reveal two highly diverged mtDNA clades that co-occur in most of the regions studied. The finding that numerous mtDNA haplotypes are shared among regions implies that inadvertent long-distance movement through human commerce is common in *P. longicornis* and has shaped the genetic structure of this invasive ant worldwide. In addition, our results indicate that the two highly diverged 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 is consistent with a relatively recent *Wolbachia*-induced selective sweep, while the history of *wLonF* infections in *P. longicornis* appears to be characterized by frequent gains and losses over time.

Table 1. Prevalence of *Wolbachia wLonA* and *wLonF* infections in *Paratrechina longicornis*

No. nests (percentage)	<i>wLonA</i>	<i>wLonAF</i>	<i>wLonF</i>	Uninfected
Clade I	42 (33%)	56 (44%)	8 (6%)	21 (17%)
Clade II	0 (0%)	0 (0%)	47 (39%)	74 (61%)
Total	42 (17%)	56 (23%)	55 (22%)	95 (38%)

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We further elucidated the sources of *wLonF* by surveying *Wolbachia* infection in various ant guests. Although *Wolbachia* is primarily transmitted maternally in arthropods, horizontal transmission between species has been commonly documented [1-3]. Our present results indicate that *P. longicornis* and a specialist ant cricket *Myrmecophilus americanus* share an identical *Wolbachia* strain, implying the occurrence of horizontal *Wolbachia* transmission between the ant and its specialist ant guest. We also identified two additional cases of *Wolbachia* transfer among ants and ant crickets, elucidating the role of intimate ecological associations in successful horizontal *Wolbachia* transmission.

The estimation of nDNA variation in worldwide populations reveals an extremely high level of heterozygosity in *P. longicornis*, a possible genetic consequence of its unusual reproductive mode in which workers are produced from the hybridization of a 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 given that it potentially relaxes the costs associated with inbreeding.

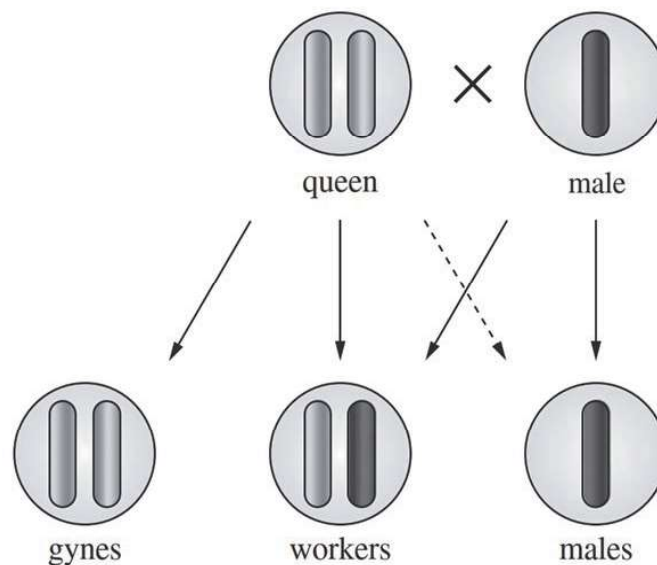


Figure 1. Clonal reproduction in queens and males of *P. longicornis*. This figure was adopted from Pearcy *et al.* (2011)[4]. Maternal (light) and paternal (dark) chromosomes are displayed. Contribution to the genome of the offspring is indicated by arrows (the dashed arrow represents the mother laying haploid eggs with no actual contribution to the genome).

References

- [1] Baldo, L., Ayoub, N.A., Hayashi, C.Y., Russell, J.A., Stahlhut, J.K., and Werren, J.H. "Insight into the routes of *Wolbachia* invasion: high levels of horizontal transfer in the spider genus *Agelenopsis* revealed by *Wolbachia* strain and mitochondrial DNA diversity," *Mol. Ecol.* vol. 17, no. 2, pp. 557–569, 2008.
- [2] Raychoudhury, R., Baldo, L., Oliveira, D.C.S.G., and Werren, J.H. "Modes of acquisition of *Wolbachia*: horizontal transfer; hybrid introgression; and codivergence in the *Nasonia* species complex," *Evolution* vol. 63, no. 1, pp. 165–183, 2009.
- [3] Ahmed, M.Z., Breinholt, J.W., and Kawahara, A.Y. "Evidence for common horizontal transmission of *Wolbachia* among butterflies and moths," *BMC Evol. Biol.* vol. 6, no. 1, pp. 118, 2016.
- [4] Pearcy, M., Goodisman, M.A.D., and Keller, L. "Sib mating without inbreeding in the longhorn crazy ant," *Proc. R. Soc. Lond., B, Biol. Sci.* vol. 278, no. 1718, pp. 2677-2681, 2011.