

OR090*Unique reproduction system of invasive ants avoids genetic bottlenecks***Misato Miyakawa**, Alexander Mikheyev

In the Hymenoptera, sex is usually determined by a single locus. Heterozygotes are female and hemizygotes are male. Inbreeding leads to homozygosity at the sex determining and the production of diploid males, which are typically sterile, and act as a major burden for the colony. Hymenoptera employ a range of strategies such as outbreeding, or gender-specific reproduction to avoid diploid male production. Recently, an extraordinary reproduction system has been reported in the ants *Wasmannia auropunctata*, *Vollenhovia emeryi*, and *Paratrechina longicornis*. In this system queens and males are produced clonally, receiving only maternal and paternal genomes, respectively. Workers are produced sexually, but are sterile. Thus, gene pools are separated between sexes. Because all three of these species employing this strategy are invasive, it may have some strategic advantage, namely to avoid inbreeding during low population sizes at the start of an invasion (Pearcy et al. 2011, Proc. R. Soc. B). However, the existence of clonal males has never been documented in these species, so the extent to which inbreeding will affect their production remains unknown. Using the facultatively clonal species *V. emeryi*, we crossed sexually produced queens (with both parental genomes) with their brothers, with which the queens shared half their genomes. 25 to 30% of the resulting offspring were diploid males. Ordinarily, haploid males are produced only in autumn in nature and lab. By contrast, we observed continuous diploid male production from March to December, suggesting a high cost of inbreeding in this species. The significant deviation from a 50:50 Mendelian ratio it is clear that at least two loci underlie sexual development. Using FASSST ddRAD tagging, we compared genomes of diploid males and their full sisters in order to identify regions containing gender-determining elements. These data should help to narrow the field of candidate genes related to sex determination.