

第 23 回 昆虫学格致セミナー

日時:2016 年 7 月 15 日(金) 午後 13 時 30 分～15 時 30 分

場所:京都大学農学部 1 階 E-103 号室

タイトル: Invasion genetics and *Wolbachia* infection of globally widespread ants

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Molecular genetic markers, along with advent of analytical approaches, have been utilized to reconstruct the histories of biological invasions. Such combination is so powerful not only facilitating the understanding of detailed information for invasion dynamics but also bridging contemporary evolution and invasion success during biological invasion. In this seminar, using two globally widespread invasive ants as the model system, the usefulness of the application of genetic techniques to investigate biological invasions is demonstrated. Genetic assessment at a diverse set of molecular markers revealed that at least nine separate introductions of red imported fire ant *Solenopsis invicta* have occurred into newly invaded areas and that virtually all recent introductions could be consistently traced back to the US. This invasion pattern follows a bridgehead invasion scenario where a particular invasive population (the US in this case), instead of native range, serves as the major source for all subsequent incursions. Nevertheless, the story for the other invasive ant, longhorn crazy ants (*Paratrechina longicornis*), seems completely different. All *P. longicornis* workers collected worldwide belong to one of the two deeply-divided mtDNA clades, and no concordance between geographic distribution and genetic structure is observed. The finding of a clade-specific host-*Wolbachia* association perfectly explains such genetic structuring and coincides with the *Wolbachia* nature as a common manipulator of host mtDNA genome, especially those of arthropods. Despite limited phylogeographic resolution due to linkage disequilibrium with the maternally inherited symbiont, identifying mechanisms underlying co-evolutionary interactions between invasive ants and *Wolbachia* (e.g., horizontal transmission or selective advantage) may further shed light on potential for developing a novel pest management strategy on invasive ants using this bacterium.