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Right	<p>許諾条件により本文は2021-02-01に公開; 1. Tseng, Shu-Ping, et al. "Genetic diversity and Wolbachia infection patterns in a globally distributed invasive ant." <i>Frontiers in genetics</i> 10 (2019): 838. doi: 10.3389/fgene.2019.00838 (The final publication is available at Frontier in genetics via https://www.frontiersin.org/article/10.3389/fgene.2019.00838/full) 2. Tseng, Shu-Ping, et al. "Isolation and characterization of novel microsatellite markers for a globally distributed invasive ant <i>Paratrechina longicornis</i> (Hymenoptera: Formicidae)." <i>European Journal of Entomology</i> 116 (2019): 253-257. doi: 10.14411/eje.2019.029 (The final publication is available at European Journal of Entomology via https://www.eje.cz/artkey/eje-201901-0029_isolation_and_characterization_of_novel_microsatellite_markers_for_a_globally_distributed_invasive_ant_paratrec.php)</p>
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(続紙 1)

京都大学	博士 (農 学)	氏名	Shu-Ping Tseng
論文題目	Evolutionary history of a global invasive ant, <i>Paratrechina longicornis</i> (侵略的外来種ヒゲナガアメイロアリ (<i>Paratrechina longicornis</i>) の進化史)		
(論文内容の要旨)			
<p>One of successful management strategies to mitigate the negative impacts of invasive species relies on reconstructing the invasion history, which traces patterns of ongoing invasion pathways and accordingly prioritizes quarantine resources to those of high invasion risk. The longhorn crazy ant, <i>Paratrechina longicornis</i>, is regarded as a significant invasive species due to its ecological impacts. Although <i>P. longicornis</i> has been reported worldwide for more than a century, the origin and invasion history of this species remain controversial. Examining the global genetic pattern of <i>P. longicornis</i> may provide insight into the invasion history of this species. To date, the global genetic structure of <i>P. longicornis</i> has not yet been extensively studied, partially because of the limited number of genetic markers currently available. In this thesis, the author developed 36 polymorphic microsatellite markers for <i>P. longicornis</i>, examined worldwide mtDNA and nDNA variation in <i>P. longicornis</i> and its associated <i>Wolbachia</i> bacterial symbionts. The present study aims to elaborate the evolutionary biology of <i>P. longicornis</i>, focuses on the invasion history of the longhorn crazy ant and its symbionts, to address questions through the lens of bioinvasion and evolutionary genetics.</p> <p>In this thesis, Chapter 1 contains a general introduction of <i>P. longicornis</i>. This chapter is focused on the current understanding about the invasive history and reproductive biology of this species. The prevalence of <i>Wolbachia</i> infections across the ant species also been introduced in this chapter.</p> <p>In Chapter 2, the author developed 36 polymorphic microsatellite markers for <i>P. longicornis</i> and characterized these markers by genotyping <i>P. longicornis</i> workers from 74 colonies in East and Southeast Asia. The results from this chapter show that the new microsatellite markers serve as a practical tool to reconstruct routes of invasion and assess the population genetics of this invasive ant.</p> <p>In Chapter 3, the author examined worldwide genetic variation in <i>P. longicornis</i> and its associated <i>Wolbachia</i> bacterial symbionts. Analyses of mtDNA sequences of 248 <i>P. longicornis</i> workers from 13 geographic regions reveal two highly diverged mtDNA clades that co-occur in most of the geographic regions. The finding that numerous mtDNA haplotypes are shared among regions implies that</p>			

inadvertent long-distance movement through human commerce is common in *P. longicornis* and has shaped the genetic structure of this invasive ant worldwide. Multilocus sequence typing reveals two distinct *Wolbachia* strains in *P. longicornis*, namely, *wLonA* and *wLonF*. The evolutionary histories of these two strains differ; *wLonA* appears to be primarily transmitted maternally, and patterns of mtDNA and nDNA variation and *wLonA* infection status are consistent with a relatively recent *Wolbachia*-induced selective sweep. In contrast, the observed patterns of mtDNA variation and *wLonF* infections suggest frequent horizontal transfer and losses of *wLonF* infections.

In Chapter 4, the author attempted to elucidate sources of *wLonF* by surveying *Wolbachia* infections in various ant guests. While *Wolbachia* is primarily transmitted maternally in arthropods, horizontal transmission between species has been commonly documented. The results from this chapter indicate that *P. longicornis* and a specialist ant cricket *Myrmecophilus americanus* shared an identical *Wolbachia* strain, implying the occurrence of *Wolbachia* horizontal transmission between ant and its specialist ant guest. Besides this, the author identified other two cases of *Wolbachia* transfer among ant and ant crickets, elucidating the role of intimate ecological associations in successful *Wolbachia* horizontal transmission.

In Chapter 5, the author employed 36 novel microsatellite markers to assess the population genetic structure, and the composition of male and queen founders and the dispersal patterns of *P. longicornis*. The results from this chapter suggested that all colonies from the studied regions follow a double-clonal reproduction system, whereby queens and males are produced asexually and workers are produced by sexual reproduction. Remarkably, queens and males from the studied regions belong to two separate non-recombining gene pools. Several widespread paternal and maternal multilocus lineages were identified suggesting that *P. longicornis* populations are most likely resulted from multiple introductions involving genetically distinct propagules. The lack of detectable spatial pattern within studied regions suggests that the spread of *P. longicornis* by colony budding alone seems unlikely and leads us to conclude that human-mediated long distance dispersal may have played a major role in shaping the current distribution and population genetic structure of *P. longicornis*.

注) 論文内容の要旨と論文審査の結果の要旨は1頁を38字×36行で作成し、合わせて、3,000字を標準とすること。

論文内容の要旨を英語で記入する場合は、400～1,100 wordsで作成し
審査結果の要旨は日本語500～2,000字程度で作成すること。

(続紙 2)

(論文審査の結果の要旨)

ヒゲナガアメイロアリ (*Paratrechina longicornis*) は世界のほとんどの熱帯、亜熱帯地域でその侵入が確認されている重要な侵略的外来種である。しかしながら、世界的な分布の拡大と移入先における生態系への影響が懸念されているにもかかわらず、その管理の基盤となる基礎的な生物学的知見には乏しいのが現状である。本論文は、世界全体の広範囲なサンプリングと多数の遺伝子マーカーの開発により、ヒゲナガアメイロアリの原産地の推定を行うとともにその生殖様式について詳細な解析を行い、さらには集団の遺伝子構造に関する細胞内共生細菌 *Wolbachia* の役割について新しい観点からの検討を加えたものであり、特に評価すべき点として以下の4点を挙げるができる。

1. 侵略的外来種の進化史の理解には、その分布拡大の様式を遺伝子レベルで解析することが不可欠である。36個のマイクロサテライトマーカーを新たに開発し、広範囲なサンプリングをもとにヒゲナガアメイロアリの侵略史を推定するとともに、その分布拡大における人間活動の重要性を明らかにした。
2. 種々の地域の個体群におけるミトコンドリア遺伝子の多様性について、細胞内共生細菌である *Wolbachia* による選択的一掃が重要な役割を果たしていることを初めて明らかにした。
3. 本種が、女王と王を無性生殖で産生し、一方職蟻を有性生殖で産生するという **double-clonal reproduction system** を有することを見出した。この特異な生殖様式と *Wolbachia* の垂直伝搬という事実は、*Wolbachia* による生物的防除の可能性を示唆している。
4. これまでアリ類では報告されていなかった *Wolbachia* タイプ F による本種の感染例を初めて発見した。その感染源について広範囲な好蟻性生物に関する調査を行った結果、好蟻性コオロギ *Myrmecophilus americanus* からの水平伝搬の可能性を示すことに成功した。

以上のように、本論文は侵略的外来種ヒゲナガアメイロアリの進化史について、広範囲なサンプリングと最新の遺伝子的解析をもとにその原産地を推定するとともに、集団の遺伝子構造に関する細胞内共生細菌との相互作用を明らかにしたものであり、侵略生物学、保全生物学、社会生物学、害虫管理学の発展に寄与するところが大きい。

よって、本論文は博士（農学）の学位論文として価値あるものと認める。

なお、令和2年1月18日、論文並びにそれに関連した分野にわたり試問した結果、博士（農学）の学位を授与される学力が十分あるものと認めた。

注) 論文内容の要旨、審査の結果の要旨及び学位論文は、本学学術情報リポジトリに掲載し、公表とする。

ただし、特許申請、雑誌掲載等の関係により、要旨を学位授与後即日公表することに支障がある場合は、以下に公表可能とする日付を記入すること。

要旨公開可能日： 年 月 日以降 (学位授与日から3ヶ月以内)