Understanding invasion history: the recent range expansion and population genetics of the Argentine ant in Japan

Maki Inoue[a], Koichi Goka[a], and Fuminori Ito[b]
[a] National Institute for Environmental Studies, JAPAN
[b] Kagawa University, JAPAN

The Argentine ant, *Linepithema humile*, has been spreading via human activities from its native range in South America across much of the globe for more than a century. Its successful worldwide expansion is attributed to a social structure, namely supercoloniality, whereby individuals from separate nests cooperate. In the species' introduced range, *L. humile* is characterized by the formation of large supercolonies across tens to thousands of kilometers, whereas colony size is generally smaller in the native ranges. *Linepithema humile*, first noted in 1993, is now found in several regions of Japan. To prevent further range expansion of *L. humile* in Japan, early detection, rapid response systems, and control measures are required. A fundamental component of such prevention is identifying the pathways of introduction and movement of introduced populations into and across Japan. Here, we used mitochondrial DNA to examine the genetic structure of introduced *L. humile* populations in Japan and how they relate to other introduced and native populations to understand the species' invasion history in Japan. Sequencing revealed six haplotypes distributed across its introduced ranges, of which five were present in Japan. The first haplotype was shared by the dominant Japanese, European, North American, Australian, and New Zealand supercolonies; the second by the Kobe C supercolony and a Florida population; and the third by the Kobe B and secondary Californian supercolonies and North Carolina colonies. The remaining three haplotypes were each restricted to the Kobe A, Tokyo, and Catalonian supercolonies, respectively. Each of the five mutually antagonistic supercolonies in Japan was fixed for one of the five haplotypes, and multiple supercolonies were found within a small area. The large number of haplotypes found in Japan likely reflects the strong propagule pressure resulting from the fact that Japan is one of the top five importers of trade commodities in the world. The short invasion history of *L. humile* in Japan could explain the maintenance of genetic diversity of each independently introduction. In addition, sampling in Japan mostly occurred at major international shipping ports that are likely to be primary sites of introduction. The several recently established *L. humile* populations within a small area in Japan provide an opportunity to identify the sources of introduction and the local patterns of spread.

Corresponding Author:
Dr. Maki Inoue
National Institute for Environmental Studies
16-2 Onogawa, Tsukuba-shi, Ibaraki 305-8506, JAPAN
E-mail address: inoue.maki@nies.go.jp