



Genotypes of the red velvet mite, *Balaustium murorum* (Trombidiformes, Erythraeidae) in the Northern Hemisphere and estimation of the migration process to Japan*

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Balaustium murorum is considered to be widely distributed in the western part of the Palearctic region of Eurasia and has recently been reported for redescription and ecological information (e.g., Wohltmann 2000; Małkol 2010). Since *B. murorum* has been widely reported in Japan since the 1980s, it has been considered to be an introduced species from Europe (M. Shiba, personal communication). However, Hiruta *et al.* (2018) reported that the Japanese population had unique haplotypes for both 18s rRNA and COI genes not found in the European population, making it difficult to conclude that the Japanese population was formed from European individuals with the introduction of the modern period by the frequent movement of people. In the present study, we attempted to clarify the diversity of *B. murorum* by topotypes (Germany) and intensive sampling from several countries in Europe, Japan, and a few countries in Eurasia. The evolutionary history of the expansion of *B. murorum* into Japan was estimated by COI sequences, including BOLD open barcoding sequences (<https://www.boldsystems.org/>) from the samples of North America, and genome-wide analysis using MIG-seq by samples of the Palearctic region of Eurasia (Suyama *et al.* 2015). Based on the COI sequences, individuals of *B. murorum* were found in Japan, a few countries in Eurasia, Europe, and North America by comparison with topotype sequence. Therefore, this species seems to be widely distributed in the Holarctic region. These populations are closely related in that the pairwise genetic distances among the *B. murorum* are within 1.2% (K2P) and share a major haplotype in all of the sites. From the genome-wide analysis, the Japanese population had low genetic diversity than the European one and was presumed to have been formed from a small number of individuals. The period of immigration event may be as much older than recent urbanization in Japan, and at least several thousand years have passed since the evolutionary event.

Keywords: Eurasia, genotyping, MIG-seq, Palearctic region, population genetics

References

- Małkol, J. (2010) A redescription of *Balaustium murorum* (Hermann, 1804) (Acari: Prostigmata: Erythraeidae) with notes on related taxa. *Annales Zoologici*, 60 (3), 439–454.
<https://doi.org/10.3161/000345410X535424>
- Wohltmann, A. (2000) The evolution of life histories in Parasitengona (Acari: Prostigmata). *Acarologia*, 41 (1/2), 145–204.
- Hiruta, S. F., Shimano, S. & Shiba, M. (2018) A preliminary molecular phylogeny shows Japanese and Austrian populations of the red mite *Balaustium murorum* (Acari: Trombidiformes: Erythraeidae) to be closely related. *Experimental and Applied Acarology*, 74 (3), 225–238.
<https://doi.org/10.1007/s10493-018-0228-0>
- Suyama, Y. & Matsuki, Y. (2015) MIG-seq: an effective PCR-based method for genome-wide single-nucleotide polymorphism genotyping using the next-generation sequencing platform. *Scientific Reports*, 5 (1), 1–12.
<https://doi.org/10.1038/srep16963>