Special Issue

Population Genetics of Honeybees

Message from the Guest Editor

Honeybee is an important bioresource and model organism for eusociality. With the recent development of genome sequencing technology, the use of large-scale genetic information is becoming the mainstream of diversity studies. Approaches using mitochondrial genomes are increasing, and this leads to reexaminations of phylogenetic classification at the inter-specific level. In intra-specific level analyses, whole-genome SNPs provide insight into population history and adaptation mechanisms mainly in the western honeybee (*A. mellifera*) and eastern honeybee (*A. cerana*). Honeybee has wide-range distributions on a global scale, and the knowledge of local populations is essential for the development of the related research fields. Especially, research on the honeybee from Asian countries is lacking compared to that of the western honeybee, *A. mellifera*. We hence welcome submissions of articles focusing on the population genetics of honeybee species from Asia using complete mitochondrial genome sequences, whole-genome SNPs (e.g., RAD, MIG-seq or Re-seq), and multiplex microsatellite markers (more than eight locus).

Guest Editor

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

Arthropods are a diverse and abundant group of animals that are important to a variety of research dictates. For example, hexapods act as bio-indicators of ecosystem function and pest status and serve as model systems for questions concerning physiology, embryology, genetics, and social interaction. The editorial board and staff at Insects is committed to providing contributors an open access forum to showcase objective and innovative research as well as succinct review articles. Our journal is dedicated to providing timely and thorough review of qualified submissions and we welcome you to submit a contribution.

Editor-in-Chief

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