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ABSTRACT BOOK

assessment study in Thai commercial *A. mellifera* population from the last decade. We also detected no evidence of recent changes in effective population size (Tajima's $D = -0.25$, $P > 0.05$; Fu's $F_s = -3.75$, $P > 0.05$), indicating no recent major change in propagative population. Our results demonstrated that Thai's manage *A. mellifera* may heading to reduce genetic diversity. The admixture management might be considered to promote genetic diversity of the population is suggested.

[P.02.21] The Welsh Dark bee (*Apis mellifera mellifera*) is not extinct

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Due to past and present imports of *Apis mellifera ligustica* (Italian bees), *Apis mellifera carnica* (Carniolan bees) and the English Buckfast bee (a hybrid strain) across its entire natural range, *Apis mellifera mellifera* is now threatened with extinction by genetic pollution through hybridization. Whilst the status of remnant *A. m. mellifera* populations is well documented on the European mainland, few studies have been undertaken to identify surviving populations on the British Isles. A few *A. m. mellifera* stocks are thought to persist in Scotland and the southwest of England and recently, Ireland might appear to contain multiple non-hybridized *A. m. mellifera* populations. 163 young worker bees, representing 121 colonies from across Wales, were genetically screened in an attempt to identify remnant *A. m. mellifera* stocks, as part of a conservation breeding program. Recent studies have demonstrated that honey bees of local origin have significantly higher survival chances than honey bees of non-local origin due to their adaptation to their local environment, suggesting that conservation of locally adapted honey bees is a logistical and practical possibility to develop sustainable apiculture. Within this survey, we made use of a custom-tailored SNP genotype assay to estimate the extent of C lineage introgression in the ncDNA as well as sequencing of the tRNAleu-cox2 intergenic region of the mtDNA to check for the ancestry of the tested colonies.

[P.02.22] Quantifying the relationship between genome-wide colony-level genetic diversity and honey bee health and productivity

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A number of studies have investigated the relationship between social insect colony-level genetic diversity and measures of colony health and productivity. However, such studies have been conducted with small sample sizes, limited numbers of genetic markers and extreme experimental designs, such as comparing colonies headed by singly-inseminated queens to those headed by multiply-inseminated queens. Using 918 colonies situated across Canada, we investigate the relationship between genome-wide colony diversity and various phenotypic measurements, such as fall cluster size, fall weight, viral load and winter survival. Results of this study will help guide researchers and beekeepers by quantifying the importance of genetic diversity with respect to honey bee health and productivity.

[P.02.23] Efficacy of DNA barcoding for identification of female castes of *Bombus ignitus* and *B. ardens* using cytochrome oxidase I and their genetic variations

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Bumble bees are important pollinators of many wild flowers and economic crops. Among Korean bumble bees, female castes of *Bombus ignitus* and *B. ardens* are morphologically similar sharing black head and thorax and abdominal tergites 1-3 while the abdominal tergites 4-6 of both species are yellow. Drones are easily distinguishable, but foraging females are not. To test the efficacy of DNA barcoding method for identification of female castes of these species, 39 females of both species were collected in South Korea and sequenced using a 653 bp fragment of the cytochrome oxidase subunit 1 (CO1) region of mitochondrial DNA. 33 samples of *B. ignitus* were obtained from three commercial populations in Yecheon, Sangju (South Korea) and Japan, to compare the sequence variations and haplotype diversity. The result showed that DNA barcoding is an efficient method to differentiate *B. ignites* and *B. ardens*. In addition, Yecheon population with three haplotypes had the highest sequence variation in the studied populations of *B. ignites*. Sequence variations of 653 bp of CO1 gene of *B. ardens* collected in this study and 284 previously recorded sequences of Korean populations showed 13 haplotypes with pairwise nucleotide variation between 0.16 - 0.32 % while sequences variation in 448 bp of the same gene of *B. ignitus* collected in this study and 401 previously recorded sequences of Korean, Japanese, Chinese and Belgium populations showed 18 haplotypes with 0.21- 2.01% pairwise nucleotide variation.

[P.02.24] Genomic tools for tracking invasive Africanized honey bees

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The honey bee, *Apis mellifera*, is an ecologically and economically important species contributing to pollination services worldwide.