



47th APIMONDIA

International Apicultural Congress

August 24 - 28, 2022
ISTANBUL, TÜRKİYE
www.apimondia2021.com

ABSTRACT BOOK

and the removal of homozygous individuals. In this work, we demonstrate the use of SIMplyBee by exploring relationships and inbreeding within and between honeybee populations and subspecies. We simulated 10 years of closed mating within two purebred populations, *A. m. carnica* and *A. m. mellifera*, and hybridisation between them. The latter served to inspect the effect of importing genetic material on relationships and inbreeding. After simulation, we examined whole-genome relationship coefficients based on three sources of information: i) expected identity by descent by recording the pedigree of each honeybee, ii) realised identity by descent by recording recombinations of chromosomes within a pedigree of each honeybee, and iii) identity by state by recording alleles of each honeybee. We observed relationships between i) workers within colonies, ii) queens within subspecies, and iii) queens between subspecies. In addition, we monitored inbreeding at the *csd* locus and the effect it has on the observed and realized whole-genome relationships. We observed a major impact of the *csd* on the relationship coefficients, as the expected pedigree relationship exceeded the realised genomic relationship coefficients, due to pedigree theory not accommodating for strong selection at the *csd* locus. With this, we demonstrated that SIMplyBee is a powerful hypothesis testing tool for honeybee management and breeding.

[OP-150 \[Bee Biology\]](#)

Morphological Characterization of Selected Honey Bees (*Apis mellifera* L.) Originated from Western and Central Black Sea

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There are many races and their ecotypes adapted to different climatic and geographical conditions in Turkey. Genetic pollution has emerged in the region's bees due to migratory beekeeping activities and queen bee sales across the country. The supply of qualified breeding material to beekeepers will make significant contributions to the increase in yield.

In the study, 200 colonies obtained from the non-migratory beekeeping areas of the Western and Central Black Sea Region were selected between the years 2014-2022. Queen bee was raised and artificial insemination was done every two years. During artificial insemination, was taken not to inseminate queen bees with their relatives. Artificially inseminated queen bees were given all colonies and the population was completed to 200 again. Worker bee samples were taken during the swarming period from 50 selected colonies that completed the third generation, and morphometric measurements were made from 10 worker bees and 41 characters in each sample. Thus, it was provided to reveal the possibilities of comparison in terms of morphological characters with the Caucasian Bee (*Apis mellifera* caucasia), Anatolian Bee (*Apis mellifera* anatolica), Hatay Bee (*Apis mellifera* syrica) and Yğılca ecotype of Anatolian Bee. Linear discriminant analysis was used for this comparison.

According to the function values, three different clustering areas were formed in the coordinate system. The first area is to cover the Hatay Bee (*Apis mellifera* srica) and Anatolian Bee (*Apis mellifera* anatolica). The second area is to include Düzce-Yğılca genotype and breeding material. The third area is only having the Caucasian Bee (*Apis mellifera* caucasia) bee race.

Hatay Bee (*Apis mellifera* srica) samples were distributed in its own group at 100%. Anatolian Bee (*Apis mellifera* anatolica) 97%, Düzce-Yğılca Genotype 98%, Caucasian Bee (*Apis mellifera* caucasia) 100%, and 100% of our breeding material was distributed to its own group.

With the selection studies, quality breeding material with high yield level, good development and high wintering ability has been obtained. The morphological characteristics of the breeding material were determined. It is important to protect, produce and deliver this important material to producers.

[OP-151 \[Bee Biology\]](#)

Predicting distribution modeling of *Apis florea* F. in the world

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Climate change will markedly impact biology, population ecology and spatial distribution patterns of pollinator because of the influence of future greenhouse effect on insect development and population dynamics. The dwarf honey bee (*Apis florea* F.) is one of the most important pollinator species of tropical and arid regions of Iran and other countries. Considering the

importance of dwarf honey bee as an important pollinator in the world, the current study was carried out to the model spatial distribution and future distribution of dwarf honey bee in 2070 and to assess the effect of environmental factors on this species. For this purpose, 75 occurrence records and documented available were used for the modeling. Potential distribution map was created using maximum entropy (Maxent) model based on recorded data and eight different climate variables. The results of this study showed that the maximum distribution probability was that of the Palearctic region. Southern regions of Iran, Saudi Arabia, India and south eastern regions of Asia were found as the best regions for the presence of the species. According to the Jackknife test, the variables mean temperature of warmest quarter, precipitation seasonality and temperature seasonality showed the maximum contribution in the species distribution modeling. The results indicated that under climate change scenario (CCCMA, CSIRO), suitable habitats for *Apis florea* will increase towards 2070. Based on our results, it can be concluded that suitable places for distribution of dwarf honey bee will be increased in the future.

[OP-152 \[Bee Biology\]](#)

Morphometric Characterization of Cypriot Honeybee *Apis mellifera cypriaca* and Its Venom Cytotoxic Effectiveness against Cancer Cells

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Bee venom is a valuable bee product that has an important place in the health and cosmetics sector. Studies conducted in recent years showed that the composition of bee venom varies according to seasonal conditions, regional differences and pollen sources. For this reason, it is very important to determine the bee venom content in different geographical conditions and flora. With its productive characteristics, the Cypriot bee is a bee race whose characteristics are on the verge of disappearing with the hybridizations made over the years because of its aggressive character. For this reason, this study will provide basic information for obtaining data of Cypriot honeybee venom, standardizing bee venom and making it an apiceutical product. In the present study, venom samples were collected from different 2 apiaries of Cyprus (Mallidag (Magosa) Village and Lefkosa Center). The samples were kept in absolute ethanol. Additionally, venom samples were collected from each apiary with electroshock method. Venoms obtained after drying on the glass surface of venom collector by scraping. All samples lyophilized, stored in dry condition at +4 °C in amber bottles. Classification of bee races made by geometrical morphometry method. The venom samples of determined races and ecotypes compared with biochemical analyzes and with way, Cypriot honeybee venom profile tried to be defined. Venom protein contents were determined by BCA protein assay. A panel of cancerous (prostate, glioblastoma, cervix, lung, colon, breast, pancreas cells) and non-cancerous (healthy lung fibroblast cells) cells were screened for determining cytotoxic potential by MTT assay in order to carry out apitherapeutic application. The protein content estimated at 676.35 ± 26.09 µg/ml for Mallidag (Magosa) Village sample and 577.60 ± 73.25 µg/ml for the Lefkosa Center sample in 1 mg/ml lyophilized crude venom. IC50 values of the cells treated with Mallidag (Magosa) Village venom varied between 3.83 ± 0.55 µg/ml and 23.97 ± 0.53 µg/ml, while cells treated with Lefkosa venom had IC50 values approximately between 6.73 ± 1.38 µg/ml and 18.80 ± 3.09 µg/ml. Data obtained from the experiments proved that venom samples from Cyprus showed high potential against cancerous cells. Further experiments will lead the way in Cyprus for increasing the apitherapeutic applications with venoms that can easily found throughout the country and make a contribution to Cyprus economy.

[OP-153 \[Bee Biology\]](#)

A mobile phone application to survey and monitor the wild colonies of *Apis mellifera*

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Although *Apiss mellifera* have been reared by humans for millennia, it remains a wild animal as reported by ancient authors and modern beekeepers and researchers. Until a few decades ago, wild colonies of *Apiss mellifera* were largely common. However, since the early 1980s there has been a rapid and underestimated rarefaction of the «wild» colonies due to a parasite, the fearsome Varroa destructor mite. The effect of the Varroa mite on unmanaged colonies was so strong that today in Europe most of the survived honey bees live in hives managed by beekeepers. Indeed, for many years it has even been thought that in Europe wild honey bees were disappeared. Rather surprisingly, there are no scientific studies on this phenomenon and the only available information deals with the number and distribution of honey bees colonies owned by beekeepers. In recent years, reports and interest in wild honey bee colonies have increased significantly and today we can say that even in many areas of Europe these colonies are still there. The app BeeWild intends to survey and monitor these wild colonies through a typical citizen science action.