

greatest difference in FROH between CART and non-CART (0.386 vs. 0.16, respectively; $p < .0001$). Considering the different ROH lengths, FROH has been decreasing considerably in CART strain over the generations (FROH_{9g} = 0.103 to FROH_{3g} = 0.035), indicating that the large inbreeding events occurred in the past. Finally, we determined the existence of two regions in which ROH incidence was significantly increased (ROH islands) only observed in CART (30:10,120,984–10,354,052 and 30:11,756,033–15,171,027). Within them, we detected 13 candidate genes related to immune response and morphogenesis, according to gene ontology analysis. Overall, our study suggests that the Carthusian strain had a differential selection process over last 500 years which caused a marked increase in inbreeding, as well as the existence of a selected pattern in terms of homozygosity in comparison with the PRE horse, mostly related to genomic regions associated with immune response and morphogenesis.

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A conservation strategy for Italian honey bees

Maria Grazia De Iorio^a, Giulietta Minozzi^a, Gustavo Gandini^a, Stefano Biffani^b, Alessandra Stella^b, Giulio Pagnacco^b

^aDipartimento di Medicina Veterinaria (DIMEVET), University of Milan, Milano, Italy

^bCNR-IBBA Milano, CNR, Milano, Italy

Contact giulietta.minozzi@unimi.it

The presence of different breeds of *Apis mellifera* in the same area can cause progressive hybridization between genetic types and issues of conservation of genetic diversity. This is due to the fact that a virgin queen freely mates only once in her life, in flight and with many drones (10–15) of potentially different varieties/genetic types. For this reason, the introduction of mating control in beekeeping can be seen as a proper conservation approach to preserve biodiversity. In this study we propose a strategy to conserve diversity in honey bees by the use of isolated mating areas (IMA). The scheme involves the participation of numerous beekeepers who submit their best mother colonies to a test of conformity to the genetic type of interest. Secondly, batteries of sister virgins queens are obtained by each of the mother colonies that have passed the test and are then committed to the production of drones, the drone-producing queens (DPQ). It is very important that DPQs conserve the greatest possible genetic variability. Therefore, we recommend to increase the number of mother colonies instead of the number of queens, given the same number of DPQ. Subsequently, the DPQs are located in a well-defined IMA protected from the presence of other colonies of unknown variety, where interested beekeepers can bring their virgin queens for mating. From the synergy between the BEENOMIX Project (Regionally Funded project) and the AISSA association, three IMA

have been created in Italy where beekeepers can bring their own mating nucleus. The three areas are located in San Pietro Island (South West Sardinia), Ponza Island (LT) and Val Bodengo (SO), to be activated in the next few years and are guaranteed by specific local ordinances.

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Frequency assessment of casein genes variants in Tunisian dromedary (*Camelus dromedarius*) population

Neyrouz Letaief^a, Sonia Bedhiaf-Romdhani^a, Wiem Ben Salem^b, Ahmed Abdelmaged Sabah Mohammed^c, Alfredo Paucillo^c

^aLaboratoire des Productions Animales et Fourragères, National Agricultural Research Institute of Tunisia (INRAT), Ariana, Tunisia

^bOffice d'élevage et du Paturages, (OEP), Tunis, Tunisia

^cDipartimento di Scienze Agrarie, Forestali e Alimentari, University of Turin (UniTo), Grugliasco, Italy

Contact alfredo.paucillo@unito.it

Recent years have witnessed an increasing interest in camel milk and in its processing into various products due to its great nutritional and therapeutic value. This growing focus has led researchers to investigate the genetic variation of some candidate genes associated with camel milk yield and quality such as caseins, major proteins in this milk. The molecular characterization of those genes has been then studied in different camel populations and multispecies comparison of the casein gene cluster has been conducted. The aim of this study was to investigate the distribution of genetic variants c.150G > T, g.2126A > G and g.1029T > C at CSN1S1 (α S1-casein), CSN2 (β -casein) and CSN3 (κ -casein), respectively, in Tunisian camel population. Blood samples were collected from unrelated Maghrebi camels ($n = 159$) reared in different localities. Genomic DNA was extracted from 5 mL of whole blood and specific DNA fragments were amplified according to already published protocols to generate amplicons of the 903, 659 and 488 bp. Restriction Fragment Length Polymorphism (RFLP) methods, using Sml I, Hph I and Alu I endonucleases, were used for genotype identification. Allele frequencies and Hardy-Weinberg (HW) equilibrium were calculated. Distribution of genotypes for the CSN1S1 gene highlighted that the most common genotype was GG (0.87), whereas no homozygous TT was found in the investigated population. Despite that, the frequency of T allele (0.066) is very similar to that reported in previous published papers carried out on Sudanese and Nigerian