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 (DPO). It is very important that DPOs 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 DPO. Subsequently, the DPOs 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**

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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 (αS1-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 SmI 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...