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The domestic dog (*Canis familiaris*) was the first species to be domesticated. Today, the 'Fédération Cynologique Internationale' distinguishes and recognises 360 canine breeds, classified in 10 ethnological groups. Group 5 'Spitz and primitive type' is subdivided into 7 sections. The Kelb tal Fenech (KTF) is allocated in section 6, while section 7 includes the Italian breed Cirneco dell'Etna (CIE) and different breeds (Valenciano, Ibicenco, Canario, Andaluz) of the Spanish Podenco (POD).

The KTF is Malta's national dog, esteemed for rabbit hunting. Some scholars suggest that it descended from the Ancient Egyptian Tesem. Two more canine breeds were well-regarded for rabbit hunting: the CIE, a Mediterranean breed from Sicily, and the POD originated in the Canary Islands.

All these breeds are morphologically quite similar, and it is tempting to assume that they are genetically related. Besides their common hunting utilisation, the genetic diversities and relationship within and among these dog breeds were investigated using STR markers. The genetic analysis was conducted using blood samples from each breed as source of DNA. Following the DNA extraction, multiplex PCRs were carried out using a panel of 17 ISAG suggested microsatellites. One breed (German Shepherd) was included as an outgroup. The following parameters were analysed: genetic variation, genetic distance, genetic structure and admixture.

An average of 6.30 alleles per locus were observed in the six studied breeds. The mean number of observed alleles ranged from 4.44 (KTF) to 7.88 (POD Valenciano). The highest observed heterozygosity (0.73) was detected in POD Andaluz, whereas the lowest (0.56) in KTF. The inbreeding coefficient estimated ranged from -0.0296 in POD Canario to 0.0670 in POD Valenciano. The Reynolds weighted genetic distance revealed three distinct clusters; the first cluster included the four POD populations, the second had CIE, while the last cluster consisted of KTF. The structure analysis results ascertained that some level of genetic admixture is reported especially in POD populations. KTF and CIE seem to have a clear genetic identity even if some genetic admixture with POD is highlighted for CIE.

The findings strongly suggest that the KTF and the POD Ibicenco seem to have a distinct genetic identity probably due to its geographic isolation. A genetic introgression of POD populations in

CIE is appreciable. Moreover, a certain degree of genetic admixture in POD populations is detected.

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Metigree: a genomic tool to enhance the well-being of Italian mongrel dogs

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Mongrels and mixed-breed dogs are animals that do not belong to any of the officially recognised breeds. Figures vary, but one recent paper reported that 75% of the 1 billion dogs worldwide are free-ranging and breeding. Applying the same percentage to the current 7 million dogs in Italy would amount to 5 million mongrels, of which about 4 million have owners, 0.2 million are in pounds, and 0.8 million are strays.

Our research aimed at determining the ancestry of mongrel dogs to further promote, protect and safeguard their well-being. Saliva samples from 20 mongrels collected according to European rules were genotyped using the canine 230K SNP chip.

Using a combination of ranked supervised admixture and haplotype sharing, we compared our results with a database of 183 breeds and populations (including 24 Italian breeds and populations, wild dogs and wolves).

By comparing the percentages of genomic background associated with one or more breeds, we obtained 3 types of results when assigning membership breeds to each of our 20 dogs:

- 'real mongrels': the first breed accounts for less 10% of their genomic background with no phenotype consistent for any breed of reference, with the exception of the size;
- 'mixed breeds': the first breed accounts for 11 to 74% of their genomic variance with phenotype resemblance ranging from mild to high;
- 'purebred dogs' without official pedigree: the first breed accounts for 75% or more of their genomic background.

We propose coining the word METIGREE, deriving from the Italian 'METIccio' (mongrel) and 'pediGREE', to reconstruct ancestral line for mongrels by using genomic analysis.

This scientific identification of mongrels would increase their chances of adoption and further our knowledge of their temperament and health issues, thus reducing medical costs while promoting the dogs' and their owners' happiness.

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