workers. The queen is the only fertile female of the colony that mates with 10 to 20 drones just once, and stores a life lasting reserve of sperm cells in her spermatheca. Drones are haploid and their gametes are clones of their genotype. Furthermore, drones die right after mating, which means they mate just once in their lifetime.

Restricted Maximum Likelihood (REML) and Best Linear Unbiased Prediction (BLUP) are important methodologies in livestock breeding for estimating variance components and predicting breeding values, respectively. These methods require information on the genetic relationship among tested individuals in order to estimate the individual additive genetic merit for a phenotypic trait. Ordinary rules for the estimation of genetic relationship are not applicable to honeybees due to queen's multiple mating and haploid males. The aim of the work was to develop a numerator relationship matrix adapted to honeybee peculiarities, in order to estimate breeding value, variance components and genetic parameters for honey yield. Tested colonies ($n = 120$) derived from 8 parental lines have been distributed in 4 apiaries nearby Lodi (Lombardy). Honey was harvested twice during spring 2016. A modified R function was used to compute the inverse of numerator relationship matrix, which is required for the estimation of variance components and the prediction of breeding values. The fitted mixed model included fixed effects of apiary, strength of the colony and production, and both genetic additive and permanent environment random effects. Preliminary results show heritability and repeatability of honey production of 0.33 and 0.54, respectively. These results are in agreement with parameters estimated through different methods reported in literature.

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Genomic landscape and biodiversity of Italian dogs

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The availability of genomic tools, such as SNP chip and whole genome sequencing technologies, have given researchers the opportunity to understand the relationships between, and genetic background of, dog populations. However, such international studies have included few Italian populations. This project aims to highlight the uniqueness of Italian dog populations and deepen our understanding of the genetic relationships that exists between them.

Almost 300 dogs from 18 important Italian breeds and ecotypes (17 ± 4 average number $\pm$ SD of animals per breed, breeds list: http://www.enci.it/libro-genealogico/razze-italiane) were considered for this study. Within each population, dogs were selected for analysis if they were unrelated at the second generation. Biological samples were collected according to the European regulations on animal welfare. All samples were genotyped with the Illumina 170K HD SNP chip. Data were checked for missing genotypes, minor allele frequencies, cryptic relatedness and duplicate individuals. Genotype phasing used individual pairwise identity by descend estimations. Distances were estimated as shared alleles identity by state between individuals, whereas populations distances were estimated as Reynolds distances. Both distances were then used to assemble a Neighbor-joining phylogenetic tree using the PHYLIP software. Finally, the genetic background of populations was defined using ADMIXTURE software. Those results provide the first deep insight into the genomic landscape of Italian dog breeds and ecotypes, highlighting their phylogenetic relationships. Our findings confirm most of the known history of the breed analyzed, grouping by their working ability and show an average inbreeding ($\pm$ SD) of 0.15 ($\pm$ 0.11).

Genomic data analysis has proven to be an important tool for revealing relationships within and across populations. These data can be used to define individual relationships, such as parentage and inbreeding, or those between populations, estimating genetic distances and phylogenetic relatedness. These studies will provide the Italian Kennel Club (ENCI) with new tools that, together with classic management instruments, can improve genealogical registration quality, selection strategies for breeding, as well as understanding of genetic makeup and breed composition, all leading to improved health and welfare for Italian breeds.