incubating 0.75 g of diet with pepsin (1%; pH2) for 2 h at 39 °C; then a pancreatin solution (10%; pH 6.8) was added and incubated for 4h at 39 °C. At the end, sulpho-salicylic acid (20%) was used to precipitate the residual protein. The undigested residue was filtered in glass crucibles, dried at 103 °C and ashed at 550 °C. The mean chemical composition of the extruded diet was (% a.f.): dry matter 92.88 ± 1.05, ash 7.33 ± 0.79, crude protein 31.75 ± 3.64, ether extract 12.66 ± 2.13 and crude fibre 5.16 ± 2.26.
The determination coefficient ($r^2 = 0.7607$) suggest that the proposed *in vitro* method provided an accurate prediction of *in vivo* digestibility, even if on average OMD_iv values were lower than OMD ones. Correlating chemical composition parameters with OMD and OMD_iv values, the two methods showed similar trend. Only lipids content and structural carbohydrates significantly affected OM digestibility: crude fibre was the main factor that influenced negatively ($p<.01$) digestibility (−0.697 and −0.598 for OMD and OMD_iv, respectively), while ether extract was positively correlated with digestibility (0.493; $p<.05$ and 0.589; $p<.01$, respectively).
These preliminary results suggest the goodness of the proposed method to predict OM digestibility, even if the digestibility of other nutrients have to be studied and a larger number of different pet-food have to be tested in order to better represent the wide variation of pet-food which exists on the market and, consequently, to achieve a better adjustment of the obtained equation.

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DogBiome: the gut microbiome project for dog

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Recently, a description of the microbial population of many niches of the organism, for example, the gastrointestinal tract, is feasible thanks to the use of advanced techniques such as High-throughput DNA sequencing that allows the simultaneous analysis of microbiota. Regarding the companion animals, a growing number of studies investigated faecal microbiome in healthy or affected subjects, although the methodologies used in the different laboratories do not allow a straight comparison among results. Despite this, they still have the interest in studying microbiome in depth, also to see how diet modifications can affect this latter.
In the present study, we report data collected from several in house researches carried out in healthy dogs, with the aim to describe the variability of microbial taxa in the faeces, providing a global picture of the composition of faecal microbiota. Overall, the database contains 334 samples from 132 dogs, which were collected during dietary intervention studies, where the diet composition and nutritional supply were under experimental control. According to the experimental design of the trials, for some dogs serial faecal samples were collected to assess the response of microbiota to the diet. The procedure of samples collection, storage, DNA extraction and sequencing, bioinformatic and statistical analysis followed a defined pipeline. The relative abundances (RA) of *Firmicutes*, *Bacteroidetes* and *Fusobacteria* represented more than 90% of the phyla, with minor percentages of *Proteobacteria* and *Actinobacteria*. At a genus taxonomic level, 72 genera were found with an RA >0.001%, although 20 of these genera accounted for more than 90% of the total RA. The genera with a threshold of RA >5% were *Clostridium*, *Blautia*, *Fusobacterium* and *Bacteroides*. Alpha and beta biodiversity were relevant complementary information to underpin faecal microbiome.
This DOGBIOME database represents a unique archive of dog faecal microbiota, which can form the basis for the identification of reference values, if any, of microbial community. The same data can also be used as a diagnostic tool to screen subject for gastrointestinal conditions. Nevertheless, the implementation of this archive will also help researchers to design diets and to investigate the effect of nutrients on gut functions.

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ANIMAL BREEDING AND GENOMICS – GENOMIC EDITING

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Unveiling the Biodiversity of the Italian honeybees by next generation sequencing

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Among the domestic animals, the honey bee (Apis mellifera) has an extremely important role both for the production of honey, wax, pollen and royal jelly, but above all for the pollination

of arboreal and herbaceous species fundamental for human nutrition. Nevertheless, the genetic management of this species both at a selective and biodiversity conservation level has been proven to be difficult. One of the main reasons lies on the fact that the reproductive moment escapes possible human control as the virgin queen (VQ) is fertilised in flight by a variable number of drones present in the environment. Furthermore, free coupling opens the way to the genetic erosion of local varieties by different genetic subtypes. The Apis mellifera, in fact, presents over 30 subtypes described in detail in the '80s by Friedrich Ruttner on a morphometric basis and by Father Adam (Karl Kehrle) of Buckfast Abbey based on the production and behavioural traits. In this scenario, it becomes urgent to provide protection of the local varieties from the phenomena of genetic erosion.

To implement a correct genetic conservation plan it is necessary to describe the biodiversity present today in a robust manner. The availability of the Honeybee genome allows using next-generation sequencing methods to define subtypes/subpopulations more precisely.

In this context, we analysed patterns of genetic variation of several populations of Honeybees sampled in Italy. In detail, whole genome sequencing has been performed on 125 bee samples by Illumina technology. Sequences have been mapped to the reference genome obtaining a mean coverage of 18.6X (minimum coverage 7.33X and maximum coverage 29.75X). In total, after quality check, 4,095,663 SNPs have been identified. The SNP dataset has been pruned based on linkage disequilibrium (LD) and principal component analysis (PCA) has been performed. The resulting pruned dataset contains 1,032,587 SNP. Results of the PCA analysis of the 125 honeybees allowed to identify and subgroup bees according to their subtype. The SNP collection can be mined to create a SNP panel for subtype testing.

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O161

The illumina® greater good initiative. A further step toward inclusion of camels in the 'agrigenomic revolution'

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Camels represent a key livestock resource in several low-income countries where they can positively impact food security and resilience. Unlike the other livestock species, the genomic revolution is still in its early infancy for camels. Notwithstanding, a growing world-wide demand for innovation exists, as attested by (i) the recent establishment of the International Camel Consortium for Genetic Improvement and Conservation (ICC-GIC), now counting over than 80 members from various countries; (ii) the ongoing work to establish the organisation of the camel genome at the chromosome level; (iii) the publication of various dromedary transcriptomes. Here, we describe the project, supported by the Illumina Greater Good Initiative Grant, aiming at developing an Illumina Camel Genotyping BeadChip. Implementation of a selection of SNP loci in a SNP genotyping platform may allow rapid and cost-effective genotyping of hundreds of thousands markers in large numbers of animals, thus boosting downstream applications such as genome-wide association studies for production traits and genome-based selective breeding. As the risk of the 'SNP ascertainment bias' phenomenon has been shown to be one of the major drawbacks in SNP array design, the project will preliminary perform a whole-genome camel diversity study across the whole geographic range of camel distribution. Using the core collection of DNA samples available from the ICC-GIC members, a total amount of 20 terabases of Illumina NovaSeq sequencing data will be produced, partly using the 10X Genomics Linked-Read sequencing approach. This strategy will allow to obtain a deep insight on the genomic variation at a large geographic scale (over 400 animals will be whole-genome sequenced), provide better resolution of haplotypes, detect and characterise structural variants, improve the currently available reference genomes, deepen understanding of evolutionary processes (domestication, inter-specific hybridisation, dispersal and selection) that shaped the camel genomes, and possibly decipher the molecular basis of the peculiar physiological adaptation traits of camels. Also, in line with the mission of ICC-GIC, this initiative will allow to strengthen the relationships among the camel scientific community. Finally, the availability of a camel SNP genotyping platform may, in the mid-term, boosts national governments investments in country-based breeding programmes based on systematic phenotype and genealogical recording.