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THE DEVELOPMENT OF A FELINE BIO-BANK TO PROVIDE NEW INSIGHTS INTO THE CONTROL OF GENETIC DISEASES AND POPULATION GENETIC VARIABILITY

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The aim of the present work is to describe the development of a feline Bio-Bank to provide samples, genealogy and clinical descriptions of cat (*Felis catus*) specimens from different breeds to supply useful and effective support in the study of the genetic diseases and the population structure of the domestic cat. The Bio-Bank collects from the Faculty of Veterinary Medicine (Milan), from the “Osservatorio Veterinario Italiano Cardiopatie del cane e del gatto” and from VETogene. Data were analysed using the PROC FREQ (SAS® statistic package) for the calculation of frequencies. 2394 cats have been collected since 2003. The most represented sample type is blood (95%) followed by buccal cotton (2.51%) and brush swab (1.75%). 25 pure breeds are collected in the Bio-Bank, the highest number of samples are from Maine Coons (981;40.98%), Persians (458;19.13%), Ragdolls (237;9.90%), Exotic Shorthairs (180;7.52%) and Siberians (109;4.55%). 64 samples are from housecat subjects, the 97.33% have a recognised pedigree (FIFe, WCF, TICA). All the 4 categories of the FIFe classification are present in the Bio-Bank: CategoryII Semi-long hair is the most represented (60%), the least represented category is the Oriental breed one (0.75%). Sex ratio is 0.66:1 M:F. 20.18% of the collected cats are Ultrasound analysed for HCM (according to the guidelines of the Osservatorio); 25.89% are Maine Coons; >50% of Bengals, Housecats, Norwegian Forest cats and Siberians have also Ultrasound analysis. A clear positive trend in the number of samples stored/year has been recorded with a linear angular coefficient 85.1 and a determination coefficient R²=0.89. A precise biological sample collection completed with a regular population data record (pedigree data, microchip) and clinical reliable description of the subjects samples collected is a successful way to create a bio bank able to supply effective tools in the study of genetic disorders and population genetic variability