

Biocomputing Platforms to provide data management platform for the European-wide LUPA dog genetics project

Biocomputing Platforms has been selected as the provider of the genotype data management system for the EU-funded LUPA project. The 16 million euro LUPA project is being conducted by a consortium of 20 research groups at European veterinary schools and universities. Researching canine genetics, the LUPA project's work will have applications for advancing the study of human disease genetics. The BC|SNPmax system will be utilized for the project data management and genetic analysis.

Helping people through canine genetic research

Dogs share many of the same diseases and environmental risk factors as humans, and they also have highly distinctive breeds with distinct disease predispositions. Some breeds have been essentially inbred for hundreds of generations. Most purebred dogs come with generations of known pedigrees. Within each dog breed, the genetic variation is small, which is a great benefit when using methods of statistical genetics to locate disease-causing genes.

DNA samples and clinical data from 10,000 dogs for a genome-wide association study, fine-mapping and molecular level studies

The LUPA project will collect 10,000 DNA samples from purebred dogs, which are either healthy or affected with a specific disease. The samples will be genotyped in a centralized, high-throughput SNP genotyping facility. The SNP genotypes will then be stored in a central database, and made available to all of the participating research groups. After the project completes a genome-wide association study, a later-stage fine-mapping of the candidate genes will be done. The results will be examined on the molecular level by expert animal and human genomics centers.

A common data warehouse and management system for 20 European research groups

All research data is collected to and stored in the secure BC|SNPmax database, developed by Biocomputing Platforms. The collaborating researchers can access the shared LUPA database through a secure web-browser interface. The BC/SNPmax system provides the researchers easy-to-use interfaces for a large number of genetic analysis programs used in statistical analysis of the data, as well as an automated result delivery system.

NOTES TO EDITORS:

The list of participant institutions and more information about the LUPA project can be found at www.eurolupa.org.

For more information on BC|SNPmax system or other products and services of Biocomputing Platforms, contact:

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