

MEDIA INFORMATION

Leibniz Institute for Farm Animal Biology

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LEIBNIZ INSTITUTE
FOR FARM ANIMAL BIOLOGY

Advanced biomathematics improves the planning of animal experiments

Dummerstorf scientists want to plan the search for useful variants in animal genomes more efficiently

Scientists at the Leibniz Institute for Farm Animal Biology Dummerstorf have succeeded in significantly optimizing the experimental design of association studies. A group of researchers from the FBN Institute of Genetics and Biometry, in cooperation with the FBN Institute of Genome Biology, has now published* the groundbreaking results of the study funded by the German Research Foundation (DFG) and made a software package available. This specifically involves the design of experiments for the fine mapping of genomic regions with influence on quantitative traits in farm animals.

"A farm animal breed is characterized by a variety of traits. Not only performance traits such as milk quantity and meat quality, but also health attributes are of great interest," explained project leader Dr. Dörte Wittenburg (Photo). In cattle, for example, these are the number of certain (somatic) cells in the udder, which are an important measure of udder health, or in pigs the cortisol concentration in the blood of an animal as an indicator of stress. "In order to better select animals for breeding, the genes that influence such traits must be researched. Knowing which favourable and unfavourable traits are inherited together can improve the welfare and performance of farm animals in the future".

DNA markers linked to a trait gene are found in so-called association studies, in which the relationship between DNA marker variants and trait expression is statistically tested. These studies can be used to make specific variants in the genome responsible, e.g. for disease resistance. Because there is a close relationship between DNA markers in the neighbourhood, the challenge is to actually find the DNA marker variant coupled to the trait. For such association studies, many animals have to be tested in order to enable a reliable statistical analysis.

"Until now, it has not been possible to take into account the strong link between DNA markers when planning experiments. In our approach we look more closely at the neighbourhood of a presumably causative variant and the pedigree of the animals. This enables us to optimise the design of a study and determine the necessary number of animals to be tested in order to narrow down the causal variant more precisely or to find out whether several variants might have a joint influence on the feature under investigation," said the biomathematician. "Using computer-simulated data, we were able to show that, compared to conventional methods, the number of animals required is

approximately 15 to 40 % lower, depending on the trait, without reducing the quality of an association study.”

As a result, a software package was made available to the scientific community, which allows a substantial improvement of the experimental design. With this program, experiments in different areas of animal and plant breeding can be planned more efficiently.

In the division "Statistical Methods in Genomics" at FBN, mathematical methods are developed for the evaluation of performance or health characteristics in which hereditary influence has been shown to play a role. Genetic markers, which are distributed over all chromosomes, play a key role here. They can be easily measured with biotechnological methods and effectively applied with mathematical methods.

*Publications

BMC Genetics, 2020

Design of Experiments for Fine-Mapping Quantitative Trait Loci in Livestock Populations

<https://bmcbgenet.biomedcentral.com/articles/10.1186/s12863-020-00871-1>

DOI 10.1186/s12863-020-00871-1

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Bonk S, Reichelt M, Teuscher F, Segelke D, Reinsch N. Mendelian sampling covariability of marker effects and genetic values. *Genet Sel Evol.* 2016; 48(1):36.

Wittenburg D, Teuscher F, Klosa J, Reinsch N. Covariance between genotypic effects and its use for genomic inference in half-sib families. *G3 Genes Genom Genet.* 2016; 6:2761–72.

Photo: FBN

Dr. Dörte Wittenburg is the head of the department "Statistical Methods in Genomics" at FBN.

The Leibniz Association

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