



## Genetic tailoring for the most important dairy cattle breed

The world's most important dairy breed, the black Holstein, is subject to the highest demands: It should not only produce a lot of milk, but also be as healthy and long-lived as possible. To achieve these goals, modern animal breeding relies on molecular data. The Research Institute for Farm Animal Biology in Dummerstorf (FBN), with the support of northern Germany's dairy cattle breeders, the „Förderverein Bioökonomieforschung e.V. (FBF)“ and the „Vereinigte Informationssystemen Tierhaltung w.V. (VIT)“ succeeded in developing a genetic map for 44,000 molecular markers. For this purpose, data from more than 367,000 Holstein cattle were evaluated, which guarantees a very high accuracy of the map.

In Germany, with more than 1.8 million registered animals, Holstein cattle have been bred for a wide variety of traits since the end of the 19th century. However, the success of breeding depends on how strongly a trait expression is hereditary. For example, the longevity of a cow, as opposed to the amount of milk produced, has a low heritability, making improvement in useful life through traditional breeding a lengthy process. For more than a decade, molecular markers have now become indispensable in animal breeding. In modern animal breeding through genomic selection, parental animals are selected for breeding based on their expression at molecular markers. This has influenced breeding strategies and greatly accelerated breeding success. For genomic selection, it is necessary to record the state of molecular markers across the entire genome and for as many animals as possible. This provides about 50,000 pieces of information per animal.

Over the years, enormous amounts of data have thus accumulated. Scientists at the FBN, with the support of northern Germany's dairy cattle breeders, the „Förderverein Bioökonomieforschung e.V., Bonn“, and the largest IT service provider for animal husbandry and breeding, "Vereinigte Informationssysteme Tierhaltung w.V. (VIT)" in Verden, Germany, compiled and evaluated these data in a uniform manner. The dairy cattle population consists of large, paternal half-sib families, which is a result of intensive artificial insemination. These family structures provide valuable information on how the standardly recorded markers are related to each other. Scientists inside the FBN Institute of Genetics and Biometrics have summarized these findings as a genetic map.

"A genetic map indicates how far apart molecular markers are - not in a physical unit of measurement like a ruler, but in a genetic unit. This genetic unit of measurement is important for breeders because it is related to the likelihood that molecular variants will be transmitted together from parent to offspring," explained study leader Dr. Dörte Wittenburg.

"Our results can now be used to advance the development of novel methods for genomic selection," said Dr. Dörte Wittenburg. "Not only at FBN, but worldwide, methods are being researched to be able to identify the 'top sires'. We are looking for the parent animals that have an exceptionally high chance of producing offspring with extremely good trait expression - for the calculation, we need the genetic distances between the molecular markers. That's the only way we can successfully drive traits like longevity."

The study results were published in the online journal *Genetics Selection Evolution\**, which focuses on genetic issues in domestic and farm animals. The three-year research project is funded by the German Federal Ministry of Education and Research.

*In the department "Statistical Methods in Genomics", mathematical methods are developed for the evaluation of performance or health traits in which hereditary influence has been shown to play a role. Genetic markers distributed across all chromosomes play a key role in this process. They are easily measurable with biotechnological methods and effectively applicable with mathematical methods.*

### **\*Original publication**

#### **Genetics Selection Evolution**

Saber Qanbari & Dörte Wittenburg, Published: 14 December 2020:

Male recombination map of the autosomal genome in German Holstein. *Genet. Sel. Evol.*, 52, 73.

<https://doi.org/10.1186/s12711-020-00593-z>

#### **Further Information:**

[www.fbf-forschung.de](http://www.fbf-forschung.de)

[www.vit.de](http://www.vit.de)

#### ***Picture: FBN, Ronald Grahl***

*Dr Dörte Wittenburg heads the department "Statistical Methods in Genomics" at the FBN.*

*Together with PD Dr Saber Qanbari, she has created the first genetic map for German Holstein cattle. The map is available to all breeders worldwide.*

#### ***Picture: FBN, Dörte Wittenburg***

*The breeding value of an animal is the benchmark for whether an animal is selected for breeding (green range). The aim of novel methods is to find top candidates from the rare, orange range.*

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