

Synbreed Research

Synbreed Consortium[§]

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BACKGROUND

The gap between supply and demand for agricultural products is steadily increasing. Future productivity gains will depend to a large extent on the genetic improvement of crops and livestock. Therefore, research and development in breeding must fully exploit the potential of next generation technologies and integrate them into the breeding process. To meet the challenges of the future, the network Synbreed will focus on

- functional analysis of native biodiversity
- genetic analysis of complex traits
- development of optimal breeding strategies

in maize, chicken and cattle (Fig. 1).



Figure 1: Maize, chicken and cattle are important species in agriculture.

DATA GENERATION

Sequencing

Next generation sequencing technologies allow sequencing of complex genomes in manageable periods of time and at lower costs than conventional sequencing technologies. The methodology allows the identification of single nucleotide polymorphisms (SNPs) as well as copy number variants (CNVs). The scheduled sequencing of DNA-pools and individuals from chicken, cattle and maize forms the basis for the identification of sequence polymorphisms to create SNP arrays. In addition, they contribute to the integration of the existing genome sequences of chicken, cattle and maize (Fig. 2) and generate the data for the population genomics projects.



Figure 2: The sequenced genomes of chicken, cattle and maize provide the foundation for re-sequencing efforts in Synbreed.

Genotyping

SNPs resulting from next generation sequencing are used for development of genotyping arrays: For maize and chicken a 60k array will be produced, for cattle a 500k array is anticipated. These arrays will be utilized for high-throughput genotyping of thousands of individuals of cattle (N>2000), chicken (N>3000), and maize (N>4000). The genotyping data will be managed and processed with innovative bioinformatic tools and delivered to the receiving partners in the Synbreed project in an analysis-ready state.

Metabolic Profiling

Elucidating the genetic basis of natural variation of metabolites in genetically segregating populations is highly relevant for knowledge-based breeding. The metabolic profiling platform within Synbreed will provide insight into the regulatory mechanisms of primary and

secondary metabolism (Fig. 3). Metabolites of maize, chicken, and cattle will be analyzed and correlated with quantitative traits to use them as biomarkers.

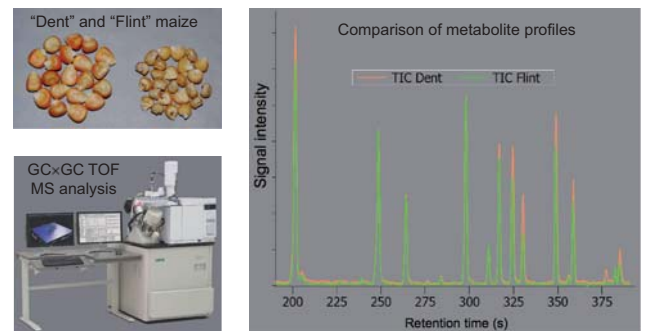


Figure 3: Metabolic profiling of "Dent" and "Flint" maize samples.

Phenotyping

For genomic selection and prediction large experimental training data sets need to be genotyped and phenotyped. Based on these data genomic breeding values will be derived and validated on experimental data from independent samples. Thus, multi-trait phenotyping is an essential component of the Synbreed project and will be performed on a large scale by the academic institutions as well as by the partners from private industry.

DATA MANAGEMENT & ANALYSIS

The development of new and efficient methods for handling and analysis of massive data is an integral part of Synbreed. In the course of the project, systems for storage, distribution, visualisation and automated analysis of data will be developed. Parametric and non-parametric statistical procedures for genomic selection and breeding value estimation (Fig. 4) will be adapted to the specific needs for chicken, cattle and maize. Methods and tools of population genomics will be developed to be used under the specific conditions of selected agricultural populations. In more advanced stages of the project the results on genome and population structure, functional polymorphisms and genomic breeding values will be integrated.

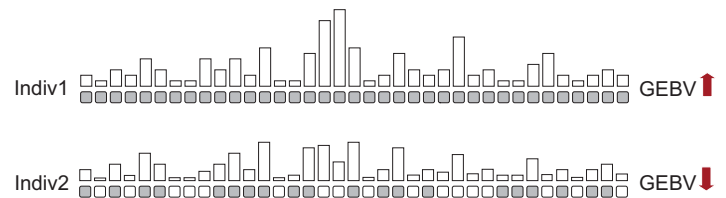


Figure 4: Genomic selection is based on the comparison of genomic breeding values (GEBV) between individuals. The GEBV is the sum of the genetic effects (bar heights) of the alleles. Some alleles in Individ2 (open squares) differ from those in Individ1, having lower genetic effects. Individ2's GEBV is therefore lower.

OUTLOOK

Wide ranging synergies will be generated by Synbreed through the joint development of theoretical concepts as well as simulation and analysis tools. Data integration across disciplines and species will provide a basis for more efficient approaches towards genome-based breeding of plants and animals.