



On 30 November WUR hosted the bi-annual Breed4Food seminar, entitled “Broadening the scope”. In total 65 people participated in person, and another 18 participated online. “Broadening the scope” referred to the importance of increasing societal and ethical awareness of the Breed4Food community and to the recently funded additional Public Private Partnership Breed4Food-BRIGHT. In addition to providing an update for Breed4Food work packages (WP) 1-5, the four Breed4Food-BRIGHT projects were pitched during the seminar.

Breed4Food-BRIGHT

Renzo Bonifazi pitched his project aiming to reduce data dimensions to increase efficiency of large-scale genomic prediction, while not losing useful information. Jeremie Vandenplas pitched his project that aims to implement and test a neural network kernel in MiXBLUP to enable the partners to validate and apply this kind of machine learning models to large scale datasets. Yvonne Wientjes pitched her project on modelling the expected change of genetic correlations under selection. Finally, Henk Bovenhuis pitched the project of Martijn Derks that aims to measure the viruses present in an animal (the so-called “virome”) from whole genome sequence data derived from blood.

Core engine for genomic prediction - WP1

WP1 aims to deliver state of the art, fast and efficient software for very large genomic evaluations. Matias Schrauf illustrated the efficiency of MiXBLUP for solving large single-step genomic evaluations through its application on a 6-trait dataset provided by the Irish Cattle Breeding Federation (ICBF; Ireland). This dataset included 26 million animals, of which 2.6 million animals were genotyped. MiXBLUP solved this genomic evaluation in less than three hours when running on the latest processors optimized for parallel computing (Nvidia GPU H100). This result demonstrates that MiXBLUP is able to handle future routine single-step genomic evaluations of the Breed4Food partners. Additionally, the first results for the task ‘Multi-breed multi-trait genomic evaluations’ were presented, which suggest that some traits indeed may benefit from information of other breeds. Finally, Marco Bink, WP1 co-leader, highlighted that all these achievements greatly benefitted from pro-active collaborations with external partners, such as ICBF, Luke (Finland), Delft University of Technology, and University of Mannheim (Germany).

DNA informed breeding - WP2

Novel sequencing techniques using long reads or low pass sequencing are becoming very accessible in general, and WP2 presented two use cases. Torsten Pook presented results on low pass sequencing. Low pass sequencing is becoming cost-effective, and imputation of SNPs is accurate enough to replace current SNP array data. Aniek Bouwman showed that with long read sequence data a breed-specific reference genome can be created, which slightly increases overall imputation accuracy, and especially in regions with structural variation. Coming year Work Package 2 will look further into this.

Phenotyping interface - WP3

Currently used and future technologies can measure information and traits more real-time and in a more objective way. In order to make sure this kind of multidimensional data can be used for breeding program purposes, WP3 develops strategies on how to deal with this data. Istvan Fodor and Torsten Pook shared ideas on methodology and imputation of multidimensional data based on examples like fatty acid and climate data. Torsten Pook showed how predictions of fatty acid content in milk based on high-dimensional midinfrared data can be improved by fine-tuning the data curation and the model used. Based on analysis of temperature data, Istvan Fodor showed that heat stress can be an issue indoors as well as outdoors, and that deviations of the expected production curve can be used to measure the impact of heat stress. Going forward WP3 will continue to work on methodology and incorporation of multidimensional data. A blueprint is created that contains step-by-step guidance on how to deal with different types of data, and what kind of analysis and scripts can be useful for specific data types.

Genomic breeding program optimisation - WP4

WP4 focusses on how to optimize breeding programs, making best use of breeding values and other information on the breeding population. The simulation software MoBPS, developed by Torsten Pook, has been adopted and is being further developed as breeding program optimization tool by WP4. Torsten presented the comparison of several selection strategies. He showed that including average relationship to the breeding population in the selection index increases long-term genetic gain, and that this allows to increase selection intensity, such that both short-term gain and the rate of inbreeding are not affected. Tobias Niehoff presented his developments on the use of Mendelian Sampling variance, which extends selection criteria to additionally include the expected genetic variation among grandoffspring of selected candidates. Higher variation implies that in the future more of the grandoffspring of selected candidates will be selected. With this approach, more genetic gain can be achieved while realizing a somewhat lower rate of inbreeding and retaining more genetic variance.

Ethics & Society - WP5

In 2023, WP5 mainly focused on ethics in animal breeding. As a desk study, the scientific literature was analysed to identify explicit ethic analyses of breeding activities. In the seminar, Karel de Greef highlighted two other activities. A major activity in 2023 was the ethics course, in which about 25 employees of the Breed4Food partners participated. In two sessions, three topics were introduced, explained and combined: Ethical concepts, Moral intuitions and Cultural attitudes towards animals. In one session, breeding issues were discussed among participants, and the final session explored how breeding companies can deal with ethical issues. An important development concerns the Dutch governmental policy towards 'Dierwaardige Veehouderij' (humane livestock farming). This is currently focused on husbandry conditions, but it is expected that breeding activities will also be addressed in the near future. It is noteworthy that similar developments are seen in European policy (EFSA and European parliament), albeit that the European route is rather focused on directives (rules), whereas the Dutch development targets covenants between chain partners, NGO's and the government. In 2024, WP5 will explore breeding aspects of Dierwaardige veehouderij and EFSA-views on breeding.

