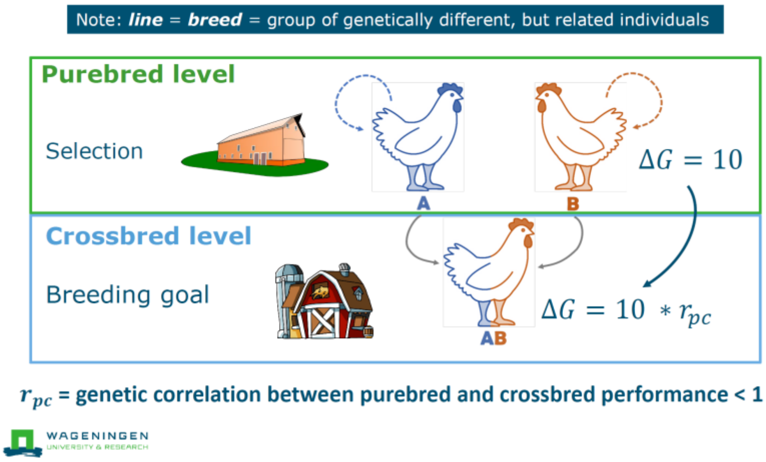
Session 5: Hybrid Breeding and free communications

The 5th session took place Friday and was the final session of the Cibreed workshop and was led by **Dr. Stefanie Griebel** from the division of plant breeding methodology from the University of Goettingen. This session was hosted under the topic “Hybrid breeding and free communication” and started with a key note by Dr. Pascal Duenk from the University of Wageningen from the group of animal breeding and genetics.

Key note: Genomic prediction for the improvement of crossbred performance – Dr. Pascal Duenk

Dr. Duenk talked in his key note about “Genomic prediction for the improvement of crossbred performance”. Crossbreeding is a practice commonly used in poultry and pig breeding programs, which allows to exploit the phenomenon of heterosis, as well as breed complementary for different traits. As P. Duenk pointed out, the general aim of these breeding programs is to improve crossbred (CB) performance, suggesting the possible need for collecting CB data. Different factors can affect prediction accuracy and response to selection, among which the genetic correlation between purebred (PB) and CB performance (r_{PC}), and the size of PB and CB reference populations.

As P. Duenk emphasized, for traits with very high r_{PC} , the collection of CB data might not be necessary. However, the use of a dominance model with a PB reference population, instead of an additive genomic prediction model, may still improve prediction accuracies. For traits with medium to low r_{PC}, and associated with important genotype-by-environment interactions, it can be beneficial to test PB animals in a CB environment and include these animals in the reference population. The disadvantage of this strategy is that the selection intensity is decreased, which may lead to a decreased response to selection.



Genotyping and collecting phenotypes from CB animals can be especially valuable for traits with a medium to low r_{PC} , caused by both genotype-by-environment interaction and non-additive genetic effects (dominance and epistasis). Nonetheless, it should also not be forgotten that the degree of relationship between a CB reference population and the selection candidates might be less strong than between a PB reference and selection candidates, which can also affect genomic prediction accuracy.

Related publications:

https://academic.oup.com/g3journal/article/7/10/3405/6027475?login=true

https://gsejournal.biomedcentral.com/articles/10.1186/s12711-019-0481-7

https://academic.oup.com/g3journal/article/10/2/783/6026314?login=true

https://academic.oup.com/jas/article/99/8/skab205/6315223

https://www.wur.nl/en/Value-Creation-Cooperation/Animal-Breeding-and-Genomics/Show-ABGC/How-can-genomic-selection-be-optimized-for-crossbreeding.htm

[Talk summarized by CiBreed Communications Team]

The subsequent talks were all held by PhD students from the University of Goettingen.

The first talk was held by **Yang Wang** from the division of crop. Yang Wang talked about "Analysis of transcriptional and small RNA variation in relation to heterosis for total root growth rate in Brassica napus L.".

Dual-purpose potential of crossbreds of two local chicken breeds and a commercial genotype – Tanja Nolte

Afterwards **Tanja Nolte** from the group of animal breeding and genetics from the University of Goettingen talked about "Dual-purpose potential of crossbreds of two local chicken breeds and a commercial genotype". In their study, they investigated the performance levels of crossbreds of two local breeds regarding their potential for dual-purpose use. The local breeds were the Vorwerkhuhn (VH) and the Bresse Gauloise (BG). The commercial layer parent hen White Rock (WR) was chosen as partner for crossbreeding and the following crosses were considered in the study: BG cock x WR hen (BWR), VH cock x BG hen (VBG), VH cock x WR hen (VWR).
Of the crossbred cockerels, the BWR and the VBG showed a similar daily weight gain. The VWR reached the target weight approximately two weeks later. With regard to laying performance and egg weights, the BWR hens performed significantly better than VWR and VBG. Taking both sexes into account, the BWR showed the highest dual-purpose potential, as their laying and fattening performance was superior to that of VBG and VWR. However, also the VBG showed improved performance levels compared to purebred VH for both sexes.

Related publications:
https://www.mdpi.com/2076-2615/10/4/702
https://www.mdpi.com/2076-2615/10/9/1480
https://www.mdpi.com/2076-2615/11/7/1947

[Text based on the abstract provided by the speaker]

Usage of a greenhouse bio test for analysing the resistance levels of genotypes of *Beta vulgaris* L. against rhizomania – Thomas M. Lange

The last talk of the workshop was given by **Thomas M. Lange** from the group of breeding informatics, who is conducting his research in collaboration together with KWS SAAT SE & Co. KGaA. Thomas M. Lange talked about “Usage of a greenhouse bio test for analysing the resistance levels of genotypes of *Beta vulgaris* L. against rhizomania”. Thomas M. Lange talked about the conduction of greenhouse bio tests, which are an important breeding strategy in sugar beet breeding, in these tests sugar beet genotypes are grown, infested with BNYVV, and then analysed after a few weeks by using double-antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) which returns optical density (OD) values.

Usually, a cutoff method is used to differentiate between resistant and susceptible genotypes where the mean of OD values per sample is compared to a threshold. Thomas M. Lange and his group used Bayes factors instead of the cutoff method, which led to higher true positive rates (TPR) and smaller false positive rates (FPR) especially for small sample sizes.

Moreover, they have analyzed the relationship between virus concentration and the OD values. To this end, they used a sample with a high virus concentration and used it to produce a serial dilution. Next, they have developed a logistic regression model with three parameters (3PL model) that can accurately describe the relationship between the measured OD values and the corresponding virus concentration. They found that the measured OD values are not normally distributed, but the estimated virus concentrations themselves are normally distributed, what gave them the opportunity to use parametric statistics such as ANOVA for data analysis.

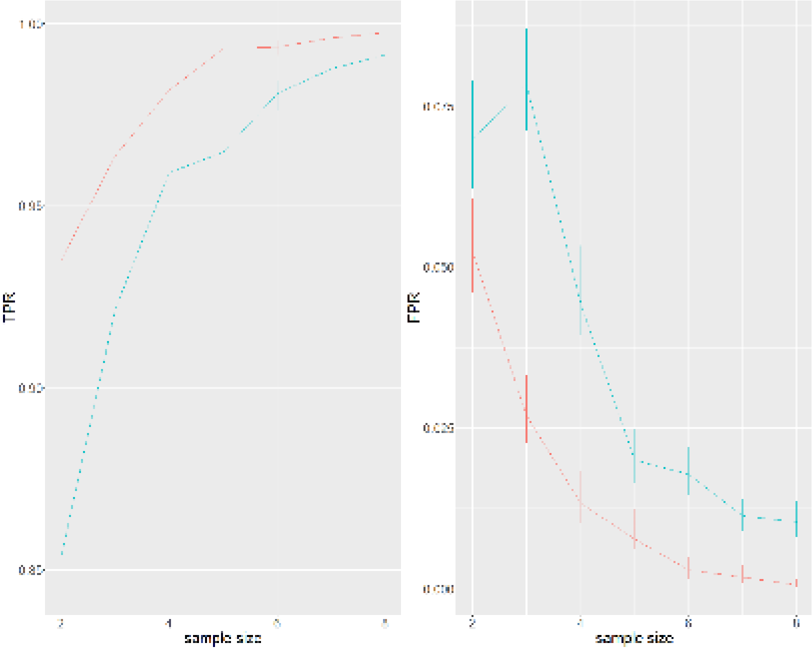


Figure 1: TPR and FPR for sample sizes from 2 to 8 for Bayes factor (red line) and cutoff method (green line)

[Text based on the abstract provided by the speaker]