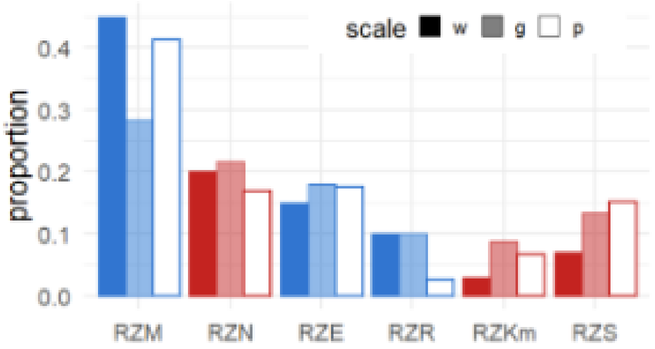
Session 4: Breeding programs and free communications

The fourth session on Friday morning was a mixture of breeding programs as well as plant, animal and insect related topics. Chair of this session was **Dr. Christian Reimer** who is as well as the key note speaker from the animal breeding and genetics group of the University of Göttingen.

Key note: How index weights translate into genetic progress (and *vice versa*) - Prof. Henner Simianer



In the key note talk **Prof. Simianer** pointed out that breeding always aims at the simultaneous improvement of a whole set of traits, and this is implemented by defining a complex breeding goal, which is basically a weighted combination of different traits. But do these assigned weights translate in the same composition of genetic and phenotypic trend, and do these expected trends match with the observed ones? In his contribution he presented a methodological framework based on selection index theory that provides the links between those different scales and illustrated it with an example from dairy cattle breeding. It is shown that the composition of genetic trend differs substantially between the scales, and that especially for functional traits with low heritability the phenotypic trend falls short of the assigned weight. It also is shown that farmers seem to apply other effective weights than the ones defined by the breeding organisations, in that they put more emphasis on type and reproduction, while longevity, udder health and maternal calving behaviour are weighted much less in practical breeding decisions. The suggested methodological framework provides a basis for a more transparent development of appropriately balanced breeding goals.

[Text based on the abstract provided by the speaker]

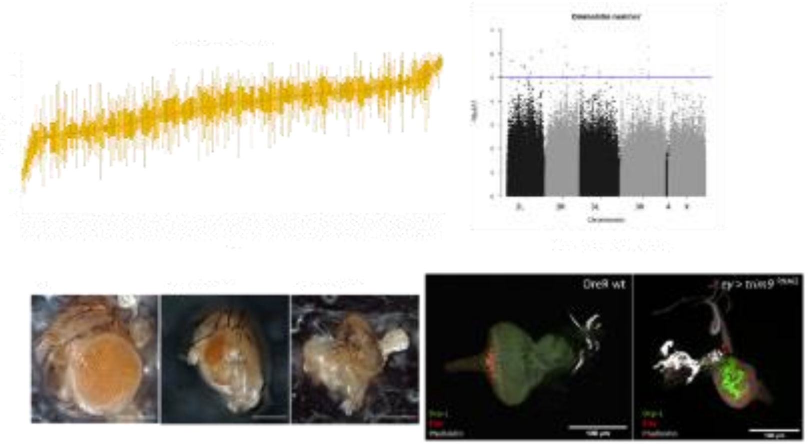
Potential of shortening the generation interval by the use of genomic selection in a layer breeding program – Lisa Büttgen

Next **Lisa Büttgen**, also from the of the group of animal breeding and genetics, presented the results from a simulation study, using the software MoBPSweb, to analyse the potential of shortening the generation interval in laying hen breeding programs. In the simulations halving the generation interval for males and females, while using genomic selection and having no phenotypes of the hens of the actual generation available and halving the generation interval only for males by dividing the population into two time shifted subpopulation, were compared with a breeding program with common generation interval for males and females. The simulations have shown that shortening the generation interval only for males, genotyping them selecting the females to select them based on genomic breeding values while selecting the females phenotypically has shown to have no advantage for the genetic progress, whereas it led to a higher genetic gain, when genotyping also all female selection candidates and also selecting them based on genomic breeding value estimation. Halving the generation interval for males and females has shown to be highly advantageous in terms of genetic progress when considering the same individual numbers, which leads due to the timespan the hens were kept to get further performance measurements, to a higher need of stable capacity. When keeping the stable capacity constant shortening the generation interval for males and females has shown to be not advantageous.

[Text based on the abstract provided by the speaker

Dissecting intraspecific variation in compound eyes size in Drosophila melanogaster - Amel Chitioui

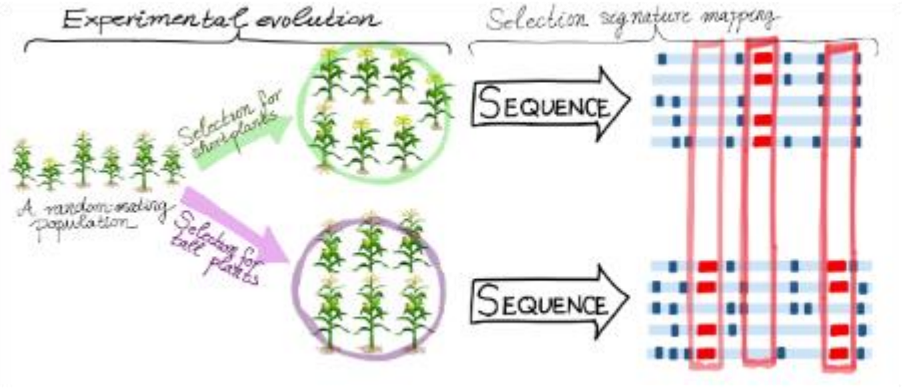
In the subsequent talk given by **Amel Chitioui** of the group of animal breeding and genetics and the department of developmental biology of the University of Göttingen the topic switched to “Dissecting intraspecific variation in compound eye size in *Drosophila Melanogaster*”. She pointed out that understanding the evolution of complex morphological traits is still one of the main challenges in evolutionary biology. This requires the identification of the causative genomic regions and the molecular changes responsible for phenotypic differences. Natural variation in compound eye size is pervasive in insects. To study eye size variation, *Drosophila melanogaster* is a great model to reveal the developmental and molecular mechanisms underlying complex trait evolution using a micro-evo-devo approach. In this study, they employ the *Drosophila melanogaster* Genetic Reference Panel (DGRP) to genetically dissect the intraspecific variation in eye size. A tremendous variation in ommatidia number between 162 DGRP strains was observed. To establish a link between phenotypic divergence and genetic changes, they performed genome wide association studies (GWAS). A functional validation screen of the three genes containing most associated single nucleotide polymorphisms (mbl, trim9, CG15498) confirmed a potential involvement in eye size regulation. To better understand the cellular and developmental processes regulated by these genes, we analyzed trim9 in more detail. This gene encodes for a RING domain E3 ubiquitin ligase. Knockdown of this gene in the eye-antennal imaginal disc (EAD) resulted in an increase of apoptotic cells and a severe reduction or the entire absence of compound eyes. The data suggests that Trim9 may be a negative regulator of apoptosis during eye development. The role of apoptosis in ommatidia number variation in Drosophila has not been observed yet, making this study an exciting start for upcoming research on morphological evolution. In ongoing experiments, they test, whether variation in trim9 expression and thus differences in apoptosis underlies natural variation in eye size among DGRP lines.



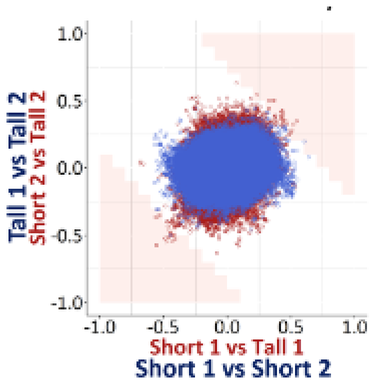
[Text based on the abstract provided by the speaker]

Experimental evolution identifies height-associated SNPs in maize – Mila Tost

The last talk of this session by **Mila Tost** from the division of plant breeding methodology of the University of Göttingen focused on an "Experimental evolution identifies height-associated SNPs in maize".



For this they selected two subpopulations for short plant height and two subpopulations for tall plant height. These were scanned for patterns of selection on a genome-level to study the impact of selection and to identify selected sites which are associated with plant height. This procedure is referred as "Evolve & Resequence" approach, which was previously only implemented on model species. So that they are the first group, who implemented this approach on a crop species with an extremely large population size under real field conditions. They selected only for three generations, which is relatively short in comparison to other studies, but still they were able to receive highly divergent subpopulations. To derive significance thresholds, they calculated the false discovery rate of selection. This is done by dividing the number of markers diverged between the subpopulations selected in the same direction by the number of markers diverged between the subpopulation selected in opposite directions. Previous studies on experimentally evolved subpopulations without replicated selection used significance thresholds based on the empiric distribution, which are prone to either miss true positives or to include false positives.



They proved that the significance thresholds based on the false discovery rate were more reliable than the significance thresholds based on the empiric distribution, since they apparently included less false positive observations. Overall, they found markers close to candidate genes associated with plant height. Markers in close location to these candidate genes were also found in a single-plant GWAS conducted on the same population but only after one generation of selection, and other studies implemented on inbred panels. But the markers they found, were much closer to the candidate genes.

[Text based on the abstract provided by the speaker]