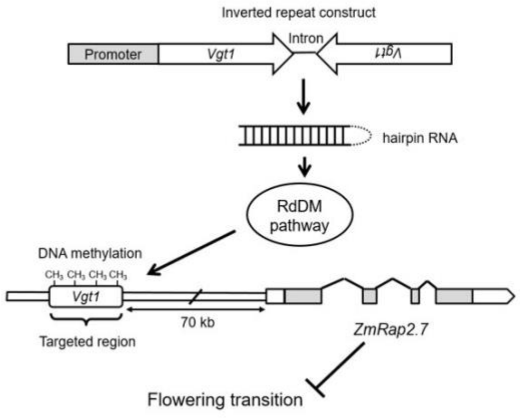
Session 3: Free communications

The first talk of the session was given by **Muhammad Khan** on the topic “Genetic control of awn roughness in barley (*Hordeum vulgare L.*)”

Vgt1 acts as a cis-regulatory element that regulates flowering time and growth speed in maize - Dr. Johan Zicola

Although maize is a major crop species and genetic model, few *cis*-regulatory elements have been characterized. Transcriptional enhancers, a subclass of *cis*-regulatory elements, participate in the differentiation of cells and tissues in all multicellular organisms. We focused on the putative enhancer *Vgt1*, which was initially identified as a major QTL for flowering time in maize and aimed to clarify its function. We show that *Vgt1* is enriched for enhancer-associated chromatin features. For further characterization, we generated transgenic lines with artificially-induced DNA methylation at *Vgt1* to epigenetically silence the activity of this candidate enhancer. Transgenic plants showed early flowering and accelerated growth speed during early developmental stages. *Vgt1* epigenetic silencing is also associated with a slight downregulation of the expression *ZmRap2.7*, a homolog of the floral repressor *APETALA2* in Arabidopsis. Overall, our data show that *Vgt1* is involved in flowering time and growth speed in maize and that it possibly acts as an enhancer of the downstream gene *ZmRap2.7*.

[Text based on the abstract provided by the speaker]



Wild type Transgenic IR-*Vgt1*

Genome-wide association study for frost tolerance in winter faba bean (*Vicia faba* L.) - Alex Windhorst

Europe has a substantial deficit in plant protein production which is mainly balanced by large-scale soy imports. Moreover, the European agricultural system relies mainly on cereal-based crop production and therefore requires heavy input of mineral fertilizer to sustain the targeted yield volumes. As an autochthone, Old-World pulse crop and with its high average seed protein content of 29 %, faba bean (*Vicia faba* L.) could substantially contribute to the increase of local plant protein production and lessen the energy input into agriculture.

In fact, the interest in faba bean and its cultivation started to increase again in the past decade. However, mainly spring faba bean cultivars are grown despite the superior yield potential of winter type faba beans. The existing winter faba bean cultivars do have an insufficient winter hardiness and thus the risk of winterkill prevents their cultivation in Central, Northern and Eastern EU countries. The current European winter faba bean production is limited to the UK and southern and costal parts of France, regions with mild winter temperatures. Hence, breeding of winter faba bean cultivars with an improved winter hardiness would not only promote their cultivation in Europe but simultaneously increase the production of domestic vegetal protein and thus decrease the environmental impact of EU's agriculture.

To genetically improve winter hardiness, we aim to analyze one of its major contributors, the frost tolerance. We tested a set of 189 winter bean inbred lines under controlled climate chamber conditions. The inbred lines are derived from the famous Göttinger Winter Bean population and referred to as Association-Set (A-Set). The A-Set was tested in 10 separate frost experiments with two replicates each (Ali et al., 2016). The respective frost tolerance of the lines was assessed by scoring the frost damages in leaves and stems as 'loss of color' and 'loss of turgidity' visually. In addition, the lines' ability to survive the frost tests was measured by monitoring the plants survival and vigor during a 30-day period. The repeatability of these traits was $0.637 < h^2 < 0.947$.

We found a significant genetic variation for all traits among the A-Set lines. Furthermore, some of the lines show significantly higher frost tolerance than the old French winter bean landrace Côte d'Or, which is widely known for its outstanding winter hardiness and frost tolerance. We recently assessed the population structure of the A-Set based on 24,151 genetically mapped Single Nucleotide Polymorphisms (SNPs) and carried out a Genome-wide Association Study (GWAS) to identify SNPs significantly associated with frost damage and with survival of the frost test. The identified putative QTLs have to be validated in the next step, using climate chamber data of an independent set of 64 winter bean inbred lines, the Validation-Set (V-Set), as well as multi-year multi-site field data for both the A- and the V-Set.

[Text based on the abstract provided by the speaker]

Genotype imputation and putative lethal variants in horses - Paula Reich

Publicly available whole-genome sequence data from 317 horses of various breeds was analysed in order to identify embryonic lethal mutations. Thereby, a considerable number of high-impact variants showing missing homozygosity were detected in various essential genes, potentially representing deleterious mutations in horses. In order to increase the available number of horses with sequence-level data and thereby improve the identification of lethal variants, an optimised strategy for genotype imputation in German warmblood horses was developed using the same dataset of 317 horses. Different factors were investigated and showed an influence on the accuracy of imputation, namely the size and composition of the reference panel, the imputation software and the marker density of the genotyping array. The strategy of imputation resulting in the highest accuracy of imputation can be used to obtain imputed sequence-level genotypes for a large number of horses and boost the power of downstream analyses in future studies.

[Text based on the abstract provided by the speaker]