Master thesis in:

Comparative transcriptome analysis in Maize root heterosis

Crop Functional Genomics

Starting date: Anytime from May 2023

Project description:

Heterosis is the phenomenon, that cross-pollinated F_1-hybrids are more vigorous than their parents. Hybrids produce more biomass, have a faster development and greater fertility. Maize, due to its cross-pollinating nature, shows this effect to an exceptional degree. As a result, the majority of the global corn production is based on hybrids. The phenotypic variation is often accompanied by transcriptomic variance. In our project we want to get a better understanding of how this variance in gene expression is regulated and how it causes the heterosis effects.

We have already created a large-scale dataset of transcriptomic and root phenotypic data, that you will help analyse. You will learn to apply bioinformatic tools for transcriptome analysis and work on high-performance-computing clusters while learning and identifying the genetic regulatory mechanisms.

In more detail, we grew 112 different lines of the maize intermated B73×Mo17 recombinant inbred line (IBM-RIL) population as parental lines and IBM-RIL lines outcrossed to the inbred lines B73 and Mo17 as F_1-hybrids. You will align the identified transcripts of the different parent and hybrid lines to the genome of Mo17 and quantify the expression of genes. Further, you will identify Single-Nucleotide-Polymorphisms (SNPs) between the Mo17 reference and our B73 lines and quantify, which allele is present in all our parent and hybrid samples. Those are then used to identify, whether a hybrid expressed the maternal or paternal allele. We have already run the analysis based on the B73 genome. Thus, the final goal, will be a comparative study of the results of the two methods: Identify differences and possibly retrieve information otherwise lost in one method. Further, it will be possible to reuse and improve existing scripts.

If you are interested in the project, please write an E-mail.

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