

Systems biological analysis of drought tolerance in oilseed rape

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Vigour performance under abiotic stresses such as drought is important for efficient plant production. The aim of this project is to identify regulatory gene expression networks responsible for good germination performance under different abiotic stress conditions of extreme vigour genotypes from segregating *Brassica napus* populations and a diversity set. This is useful for marker identification to be used for subsequent marker assisted selection in breeding of stable high-vigour genotypes.

Selection of high and low vigour extremes

High-vigour and low-vigour winter oilseed rape were selected based on digital high-throughput seedling phenotype data for *time required to reach 50% of germination (T50)*, *mean germination time (MGT)* and *total germination rate (GR)*. 36 lines were selected with very good or poor germination:

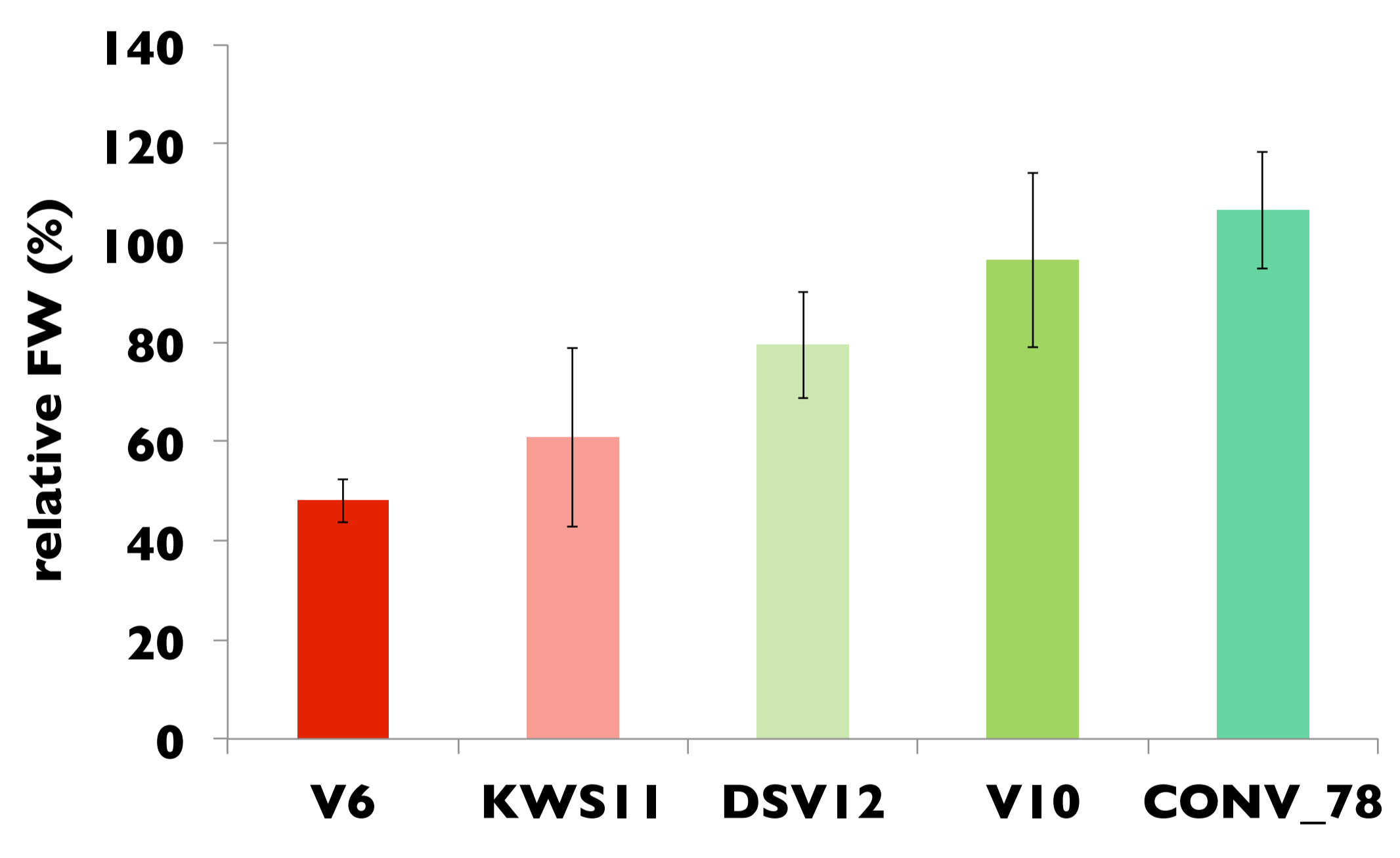
- ✿ 18 high-vigour genotypes
- ✿ 18 low-vigour genotypes

Treatment and sampling for transcriptome study

- ✿ Hydroponic culture for 30 days in climate chamber:
 - ✿ *In vitro* drought stress simulation from day 24 with 5% PEG vs. control (MS medium)
 - ✿ Roots and shoots from 6 homozygous plants per genotype and treatment were collection for RNA extraction
 - ✿ Fresh weight measurements were used for preliminary characterization of drought stress responses



Differential drought stress responses



- ✿ The selected genotypes showed significantly different responses in terms of relative fresh weight under drought stress:
 - ✿ Drought-sensitive genotypes had fresh weight reductions of up to 50 %, while fresh weight of drought-resistant genotypes was not affected

- ✿ FW correlated positively with the seed parameters T50 ($r=0.44$) and MGT $r=0.30$
- ✿ There was no significant correlation between seed vigour and the relative fresh weight
- ✿ Factors other than seedling vigour seem to be involved in stress resistance

Systems biological analysis

- ✿ Sequencing-based expression profiling is currently being performed for root and shoot samples
- ✿ 100 bp paired-end 3'-EST tag sequencing is being performed on the Illumina HiSeq 2000 platform for quantification of global gene expression
- ✿ Transcript annotation will be performed to the *B. napus* draft genome sequence
- ✿ In parallel, sample aliquots are being subjected to a general metabolite profiling by mass spectrometry
- ✿ Systems biological analysis will be performed using phenotype, genotype, transcriptome and metabolite data



Long term aims

- ✿ Phenotypic, genetic and metabolic networks identified by the systems analysis will be used to identify promising indicator traits, genetic markers and biomarkers for selection towards improved drought tolerance and vigour in winter rapeseed