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Introduction

High yielding crop varieties with improved water use efficiency (WUE) and drought tolerance are needed for a sustainable agriculture facing climate change. Using near isogenic lines (NILs), we showed that a single genomic segment on chr 7 affects several drought-related traits in maize, i.e. WUE, carbon isotope discrimination ($\Delta^{13}\text{C}$), leaf growth sensitivity to drought, stomatal conductance, stomatal density and leaf abscisic acid (ABA) concentration. Such a genetic co-localization of multiple traits may be due to pleiotropic effects of the same gene(s) and/or tight linkage of causal genes.

To understand the genetic basis of the investigated traits, their interplay and trade-offs and to define their causal gene(s), we generated recombinants based on the NILs. The well-characterized genetic material carries overlapping segments of the target region, which enables the genetic dissection of traits in this segment. We performed extensive phenotyping of the recombinants and combined physiological (WUE, stomatal characteristics) and metabolic (e.g. ABA and ABA catabolites) measurements, which allowed us to narrow down the target segment. We selected potential causal genes that may underlie the observed phenotypes and characterized them molecularly.

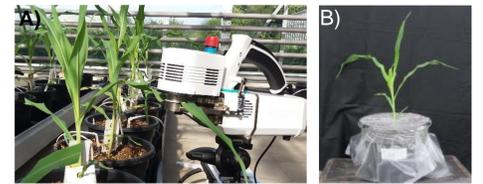
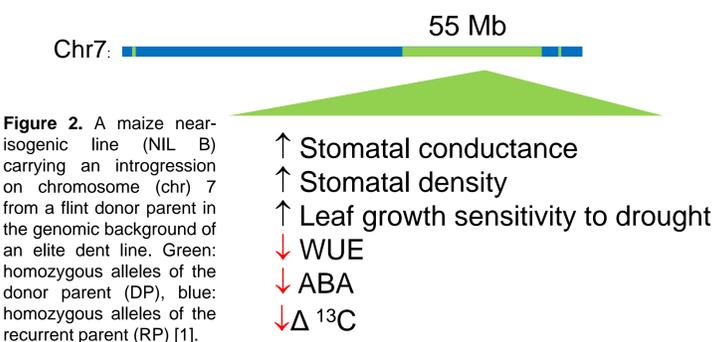


Figure 1. Phenotyping experiments in the greenhouse. A) Gas-exchange measurements of CO_2 assimilation and stomatal conductance with infrared gas analyser (IRGA) LI-6800 Portable Photosynthesis System. B) Whole plant water use efficiency ($\text{WUE}_{\text{plant}}$) experiment.

Results

Genetic material



Pleiotropy or linkage- one genomic segment controls multiple drought-related traits

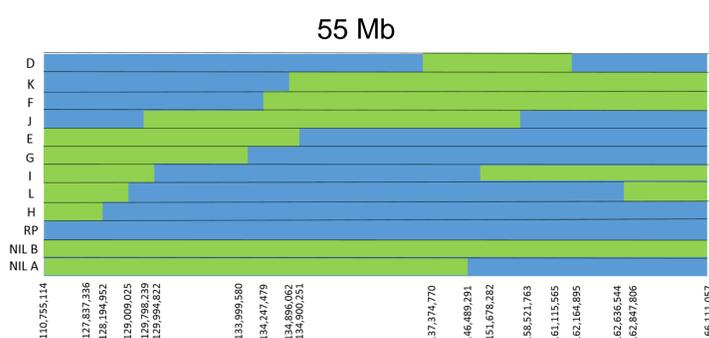
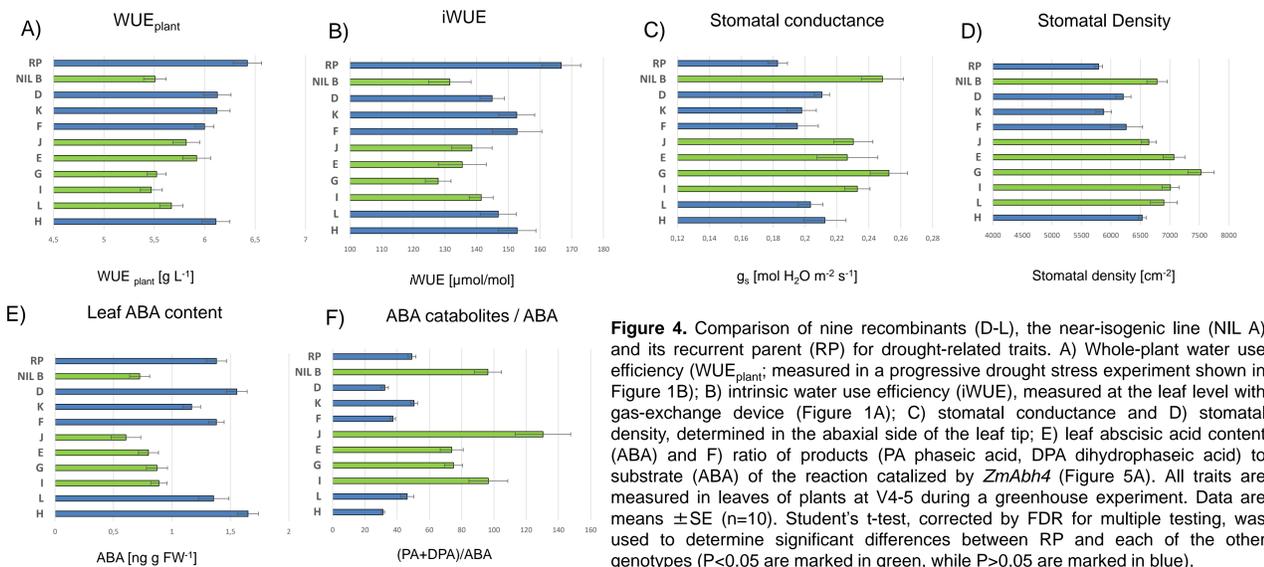
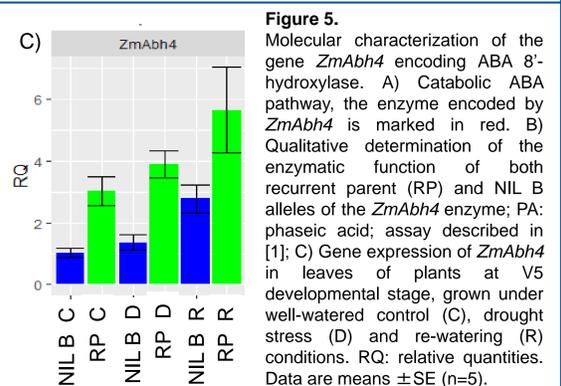
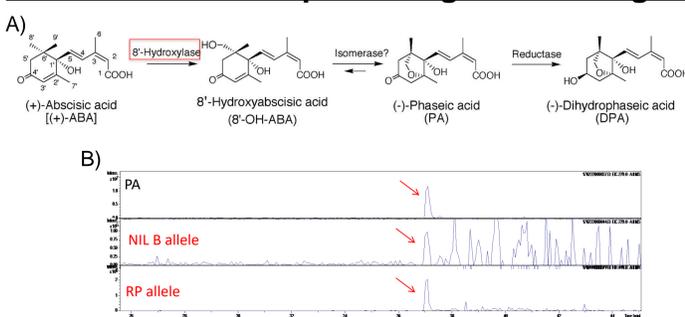


Figure 3. Recombinants with overlapping segments in the chr 7 region carried by NIL B. Recombinants (backcrosses NIL B x RP) are marked with capital letters. Numbers below indicate genomic coordinates according to B73_RefGen_v4. Green: homozygous alleles of the donor parent (DP), blue: homozygous alleles of the recurrent parent (RP).

Phenotyping



ZmAbh4: the most promising candidate gene



Conclusions

- High ABA concentrations and high stomatal conductance is most probably the main reason for the observed lower WUE and $\Delta^{13}\text{C}$.
- *ZmAbh4* is the most prominent candidate gene for the observed phenotype.
- The observed phenotype is probably caused by the differences in expression of one main gene, involved in ABA catabolism, but it is possibly enhanced by a cumulative effect with other genes linked in the same genomic region.

Outlook

Characterization of knockout mutants for all 5 *ZmAbh* genes, expressed in different organs of the maize plant will give the opportunity to separate elevated WUE from germination-related trade-offs.



References and acknowledgements

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