

Applying ecophysiological knowledge and methods to unravel the genetical basis for tolerance of leaf growth to water deficit in sunflower

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ABSTRACT

- Water stress is the major limitation to sunflower yields worldwide. Possible global climate change scenarios suggest a future increase in the risk of drought. Increasing the tolerance of sunflower hybrids to water deficit is, therefore, of great importance. To attain this goal it is necessary to identify genes and genomic regions conferring improved tolerance. The objectives of this paper are i) to describe how stable markers associated with the maintenance of leaf growth (a key ecophysiological trait highly correlated with plant yield and transpiration) during the water deficit period were identified by applying ecophysiological knowledge and methods, and ii) to propose future research aimed at more rapid obtainance of sunflower genotypes with improved tolerance to water deficits.
- A method was established which allows reproducible soil-water deficit treatments to be applied to different sunflower genotypes. This method was automated by developing a low-cost, flexible, automatic platform for high-throughput measurement of plant water use and growth. By applying the established method, the genetic variability of the response of leaf growth to water deficit was assessed among 18 sunflower inbred lines representing a broad range of genetic diversity. Lines with contrasting responses of leaf expansion rate and of leaf growth duration were selected for further analysis. They were physiologically and genetically characterized. They were crossed to obtain two segregating populations (F2 plants+ F2:3 families and an independent F8 RILs.). Single marker analysis was performed associating genotype data from F2 individuals and phenotype data from F2 individuals and F2:3 families and genotype data and phenotype data from F8 RILs. Molecular markers associated with the response of leaf growth to water deficit and with recovery of leaf growth after re-watering were identified. A same molecular marker was found to be associated with leaf growth maintenance during the water deficit period in the two populations and in experiments performed in growth chambers or the greenhouse. These results provide evidence of the stability of this region of the genome associated to the response of leaf expansion to water deficit in sunflower.
- Results presented here suggest that applying ecophysiological based methods and robust models could be helpful to fill the current gap between genotype and phenotype, specially for complex traits such (e.g. the responses leaf area growth to water deficits) and could be helpful to identify genes and genomic regions associated with higher tolerance independently from environmental conditions during the experiments. As phenotyping has become a bottleneck for understanding the genetic basis of complex traits, low- cost automatic platform for high-throughput measurement of plant water use and growth could be helpful in sunflower studies tolerance to water deficit. Physical phenotyping is however not enough for rapidly obtention of tolerant sunflower hybrids. Biochemical and molecular phenotyping could be necessary to identify key regulatory genes with a positive phenotypic impact under drought conditions and could enable high throughput screening for advantageous phenotypes at the earliest possible stage in the breeding process. Together with QTLs studies (as described here for leaf growth tolerance to water deficit), this will enable new varieties to be brought to market in a much shorter time than is currently feasible. To attain this goal, it is suggested that collaborative efforts are necessary among groups with different expertise, probably integrating an international research network.

Key words: Phenotyping, QTLs, leaf growth recovery, molecular markers.