

GENOME-WIDE ASSOCIATION OF OIL YIELD PLASTICITY TO DROUGHT, NITROGEN AND CHILLING STRESSES IN SUNFLOWER

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ABSTRACT

To face the climate change, the plasticity of genome is a great advantage that plant breeders could build on in order to adapt varieties to new environments. A way to accelerate the adaptation is by the discovery of new alleles involved in the plasticity responses and their introgression in elite varieties. So we conducted a genome wide association study (GWAS) in plasticity responses face to multiple abiotic stresses. We characterized 14 environments by their levels face to four abiotic stresses: nitrogen, drought, chilling and heat, thanks to the SUNFLO crop model. Three known varieties, used as controls and observed in the 14 environments, allowed computing the stress felt during key periods of the growth development. Among the 56 stress indices computed by SUNFLO, the best model to fit the oil yield, regarding the AIC criteria averaged on the three above control varieties, contained only three stresses: the nitrogen during the whole growth period, the drought from sowing to filling and the chilling before flowering. The observed oil yield of a panel of 371 sunflower lines was regressed by linear norm reaction model with the three stress indices of the best model. The slope of each stress norm reaction was used as plasticity phenotypes. Association mapping was based on a set of 65,534 SNPs with MAF >0.05 using the usual mixed model of association, including the maintainer or restorer status as fixed effect and the Alike in State relatedness matrix for the polygenic random term. A forward approach was performed to detect multiple associated SNPs. Homology study of detected SNPs with the annotated genes of Arabidopsis completed the analyses. The results concerning the plasticity face to chilling will be detailed in this talk

Key Words : Plasticity, multi-stress, abiotic, GWAS