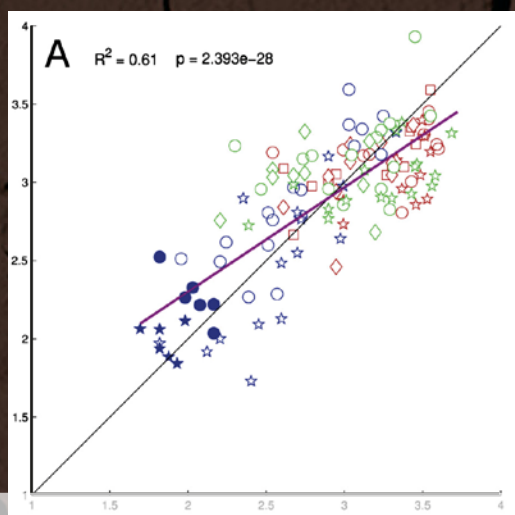# A biomarker based on gene expression indicates plant water status in controlled and natural environments

Correlations between pre-dawn leaf water potential measured in the field and predicted by the water status biomarker plotted as $\ln(-\Psi_{PD})$, where Ψ_{PD} is expressed in bar. Field data samples harvested between 11:00 and 12:30 without correction for harvest time represent three different trials. The three-gene model, represented by the regression line in violet, produced better predictions (n=142 plants).

Plant or soil water status is required in many scientific fields to understand plant responses to drought. Because the transcriptomic response to abiotic conditions, such as water deficit, reflects plant water status, genomic tools could be used to develop a new type of molecular biomarker.

Using the sunflower (*Helianthus annuus L.*) as a model species to study the transcriptomic response to water deficit both in greenhouse and field conditions, we specifically identified three genes that showed an expression pattern highly correlated to plant water status as estimated by the pre-dawn leaf water potential, fraction of transpirable soil water, soil water content or fraction of total soil water in controlled conditions. We developed a generalized linear model to estimate these classical water status indicators from the expression levels of the three selected genes under controlled conditions. This estimation was independent of the four tested genotypes and the stage (pre- or post-flowering) of the plant. We further validated this gene expression biomarker under field conditions for four genotypes in three different trials, over a large range of water status, and we were able to correct their expression values for a large diurnal sampling period.

Conception : G.Esteve - Crédit photo : N.Langlade (image de fond)