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Dr. Boris Parent graduated from INSA Toulouse in 2005 (French engineer school), and obtained a PhD in plant ecophysiology at the LEPSE-INRA laboratory (Montpellier, France) in 2008, with a thesis on leaf development in rice and maize in response to temperature and water deficit. After four years of Post Doctoral Fellowship at ACPFG, (Adelaide, Australia), where he worked on the development of systematic analyses of plant responses to drought and high temperature in wheat and barley, Dr. Parent rejoined the LEPSE-INRA laboratory with a permanent position in 2013. He now focuses on the analysis of the intra- and inter-specific diversity of plant responses to drought and high temperatures, and the modelling of its effect on plant performances in various environmental scenarios. The main idea of Dr. Parent's research project is that genotype by environment interactions (GEI) are emergent properties of simple biological processes which all respond differently to the plant micro-environment. He uses phenotyping platforms, allowing the analysis of responses traits, independent from the environment, on hundreds of genotypes and species. Dr. Parent develops ecophysiological models for several plant processes which are parametrized with platform results. The integration of such ecophysiological models and sets of parameter values in crop models allows testing the comparative advantages of any combination of trait / allele values in hundreds of environments over Europe.

Genetic variability of plant responses to evaporative demand and water deficit, a forward integration from phenotyping to simulation of plant performances in the field

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Crop improvement for drought is based on the selection of alleles that increase yield in dry or hot conditions. The Genotype by Environment Interactions (GxE) is typically high in these environments, with alleles conferring either positive or negative effects, depending on drought scenarios (Tardieu, 2012). Rather than trying to over-simplify GxE, for instance, in managed drought experiments, we propose an integrative approach using genome wide association studies (GWAS), phenotyping and modelling. It aims at predicting in which drought scenarios a combination of trait/allele could confer advantages (Parent and Tardieu, 2015). Indeed, (i) we phenotype the intra- and inter-specific variability of development and growth responses to temperature, evaporative demand and water deficit with phenotyping platforms. (ii) We develop ecophysiological models with parameters which can be directly extracted from measurements in platforms and in the field. (iii) We carry out GWAS at different scales, from -omic to plant scale in platform, and to yield components in network of field experiments to identify QTLs linked to conditional allelic effects depending on environmental conditions, and to values of model parameters. (iv) We use either direct measurements or the allelic compositions at target QTLs to determine the phenotypic profiles (set of parameter values) of real or virtual genotypes. (v) We simulate genotypic performance and the contribution of genomic regions under current and future stress situations over Europe via modelling. Results are compared to the observed genetic variability in networks of field experiments and are used as feedbacks for improving our phenotyping routines and ecophysiological models.