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ABSTRACT BOOK



5. PARALLEL SESSION 1.2 – PLANT BREEDING

PS-1.2-01

A QTL Based Model to Quantify the Water Used of 200 Barley (*Hordeum Vulgare* L.) Genotypes Under Drought Stress.

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Abstract: Water scarcity is one of the largest yield-limiting factor in southern countries of the world, and most climate change scenario predict an increase in surface area subject to drought stress in many parts of the world. Research and breeding programs are therefore looking for candidate genes that can be used as a basis to increase the drought tolerance of future crops such as Barley (*Hordeum vulgare* L.).

Using ecophysiological models, it is now possible to simulate the water use of a couple of genotypes under different environments. A genetic model also allows to quantify the contribution of each genome regions of a crop species under a single environment. The combination of physiological models and quantitative trait loci (QTL) analysis of some plants phenes might help to predict the performance of all genotypes of a plant species under all environments and allows the genetic variability of a physiological drought response to be analyzed.

From 2012 to 2015, a multi-year project to characterize the physiological diversity of drought reactions in the shoot organs of various spring barley genotypes was performed at Leibniz Universität Hannover. The influence of drought stress on leaf growth and water use at different growing stage of 200 diverse Barley genotypes, adapted to Central European growing conditions was quantified. A model to predict the water used of each of the genotype was developed and a genome wide association studies was performed for each measured quantitative trait under drought stress. These parameters were calculated as a function of soil water and estimated for these parameters QTLs, which are incorporated as a genetic component in the ecophysiological model to build the QTL-based model.

A high diversity in the response to drought stress was observed amount all the 200 genotypes and the model successfully reproduced the expected effect of drought stress on water used for all genotypes. Some QTLs that are responsible of the variability in water related parameters of the 200 Barley genotypes were found and their contributions were quantified.

Keywords: Drought stress, Barley, QTL-based model, Water use, Transpiration

PS-1.2-02

Effect of Temperature and Daylength on Phenology for Contrasted Soybean Genotypes Grown in Europe

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Abstract: European Union (EU-28) needs to import about 40 million tons of soybean (seed equivalent.year-1) to feed livestock and population to a lesser extent. Since a few years, soybean production in Europe has largely increased but remains still insufficient. In a context of climate change, southern areas tend to face more drought and heat waves while northern ones will benefit from higher temperatures in late season. Three other cropping strategies could be considered to grow soybean

under these conditions: early sowing to escape drought, northward expansion of the crop, or double cropping. This will change deeply the photoperiod and temperature conditions during the crop season. As soybean is a tropical short-day plant, it is important to understand the temperature-photoperiod interactions on phenology for current genotypes grown in Europe (under long daylengths and contrasted temperatures). For that, a study was conducted in INRA Toulouse (SW France), combining fine phenotyping on an outdoor platform and in controlled conditions.

In 2017, two experiments were carried out using 10 contrasted genotypes from maturity groups 000 to II : 1- A pot experiment on the Heliaphen platform in natural climatic conditions where germinated plants were transplanted at 6 dates (17-march, 6-april, 16-may, 26-june, 24-july, 1st-september). Pots were fully fertilized and irrigated during all the experiment. Development stages were recorded once or twice a week (BBCH scale). 2- A germination experiment in cold chamber/incubator. 100 seeds by genotype were incubated at 10 temperatures (from 4 to 43°C) in Petri dishes on moist paper. The germinating seeds were counted twice a day.

Germination results were used to calculate the base temperature of each genotype (Tb from 4.6 to 6.7°C). This information was essential for the relevant calculation of the onset of each development stage and the duration of phases expressed in growing degree days (GDD). For most stages, ANOVA analysis pointed out a highly significant effect of genotype by planting date interaction on GDD accumulation. The results showed that GDD accumulation from cotyledon stage to maturity (BBCH stage 10 to 80) was impacted more by planting date (cv = 16 %, p < 0,001) than by genotype (cv = 10 %, p < 0,001). In addition, the difference across genotypes steadily decreased when daylength was reduced by later sowing dates (from 14.5 to 12.5 h).

These results will be used first to calibrate phenological models then different crop growth models. These models will be necessary to test a wider range of “genotype x environment x management” combinations with the perspective of designing suitable cropping areas and ideotypes for soybean in France and Europe.

Keywords: Photoperiod, *Glycine max*, genotype by environment interaction, crop development, planting date

PS-1.2-03

Identification of Favorable Genomic Regions Associated to Drought Response Traits of 50 Tomato (*Solanum pennellii* x M82) Introgression Lines

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Abstract: Drought is one of the progressive abiotic constraints for crop productivity. Plants try to adapt the drought stress through the avoidance and/or tolerance of tissue water deficits depending on genotypic diversity. The cultivated tomato *Solanum lycopersicum* contains only a small fraction of the genetic variation present in its wild relatives. Wild germplasms confer the favorable QTLs or genomic regions associated to favorable quantitative traits. A genome library of the wild species *Solanum pennellii* (LA0716) (Sp) in the cultivated recurrent (*Solanum lycopersicum* cv. M82) background comprises of 50 first generation introgression lines (ILs), each containing a single introgression segment from the green fruited donor species and all together covering