Phenotyping of pea plant on the 4PMI (Plant Phenotyping Platform for Plant and Microorganism Interaction) which allows the high throughput phenotyping (Fig. 1A-B) and automated irrigation (Fig. 1C) of pea plants (Pisum sativum L. var. Rondo). Plants were grown in sandy soil in Rhizotubes which are cylindrical-shaped-rhizotrons that enable non-invasive image acquisition of plants shoot (Fig. 1D-G) and root systems (Fig. 1H-K). WW N+ : well-watered with nitrate; WW N– : well-watered without nitrate; WS N+ : water-stressed with nitrate; WS N– : well-watered without nitrate.

Conclusions

These results provide insights on the spatial regulation of exudation at the whole plant level, a first step to build a mechanistic understanding of exudation and its trade-off with productivity and resilience. Further, the correlation of these exudation patterns with microbial community structure and activity as well as soil C-N cycling will provide means to target and drive these communities in order to promote plant productivity and soil services such as C storage and N-cycling. Understanding these ecophysiological trade-offs and rhizosphere interactions is essential to develop ideotypes that are adapted to low-input agroecosystems facing climate change.

Bibliography

- *Prudent et al. (2023). The diversity of soil microbial communities matter when legumes face drought. Plant, Cell & Environment.*
- *Tixier et al. (2023). Root exudation of carbon and nitrogen compounds varies over the day-night cycle in pea: The role of diurnal changes in internal pools. Plant, Cell & Environment.*

606/57. GENETIC VARIATION FOR DROUGHT TOLERANCE IN SOYBEAN AND SELECTION OPPORTUNITIES

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Summary:

Objectives

Soybean cultivation is steadily increasing in the EU, responding to a growing demand for feed and food purposes. The unpredictable dry spells caused by the changing climate in most European regions, and the decreasing availability of irrigation water in Southern Europe, emphasize the need of selecting drought-tolerant cultivars, but there is limited knowledge on drought tolerance variation in soybean. Genomic selection may represent an efficient selection strategy for a complex trait such as drought tolerance, as shown for pea (Annicchiarico et al., 2020).

Concise description of the work (materials & methods)

A germplasm collection mostly encompassing European cultivars was evaluated in Lodi (northern Italy) under managed drought stress and moisture-favourable conditions, to gain knowledge on the germplasm variation for drought tolerance and on phenotypic and genomic selection opportunities. Grain yield (GY) was assessed for 59 early-maturing (MG 000/0) and 77 intermediate-maturity (MG 0+/II) cultivars grown in a phenotyping platform composed of eight large (24.0 m × 1.6 m × 0.8 deep), bottomless containers under a field rainout shelter equipped with a double-rail irrigation boom, adopting

an alpha-lattice design with four replications per condition. Favourable and stress conditions implied soil moisture kept within 60-80% and 10-30% of the available water, respectively, starting from mean full flowering (R2 stage). The stress treatment received only 46% of irrigation water compared with the favourable one over the growing season. The cultivars were genotyped by the 50K Soybean array, which yielded over 19K SNP markers after filtering stages, to assess different genomic selection (GS) models for GY under both moisture regimes. A GWAS was performed concurrently.

Main Results

On average, drought stress reduced GY by 65%. Both early and intermediate-maturing groups of cultivars exhibited large genotype × environment interaction and fairly modest consistency of yield responses across conditions (as shown by genetic correlations for cultivar GY across conditions of 0.51 and 0.66 for early and intermediate groups, respectively). For both groups, cultivar genetic variation was definitely narrower under stress than under favourable conditions (16.6% vs. 22.7%, expressed as genetic coefficient of variation for GY). The GWAS suggested that GY is determined by many small-effect genes in both conditions. Genomic regions tending to association with GY showed inconsistency between stressed and favourable conditions, suggesting partly different genetic control of the trait in the two conditions. Poorer genetic variation under stress concurred to lower GS prediction ability observed for GY under drought stress relative to favourable conditions (Figure 1).
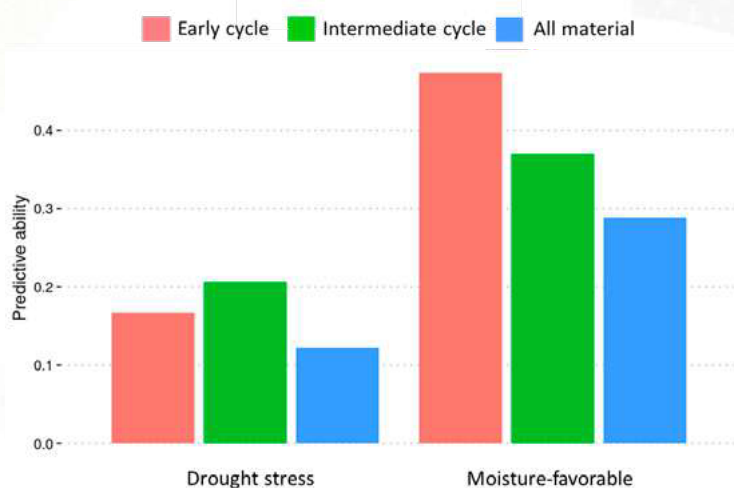

Figure 1. Predictive ability for soybean grain yield in drought stress and moisture-favourable managed environments according to the best-performing model among rrBLUP, Bayesian Lasso, Weighted GBLUP, for early-maturing (MG 000/0) and intermediate-maturity (MG 0+/II) cultivars groups and the whole set of cultivars.

Conclusions

Our results reinforce the crucial importance of specific selection for drought tolerance under stress in soybean, and the strategic importance of identifying novel genetic resources with greater drought tolerance than current cultivars.

Bibliography

● *Annicchiarico, P., Nazzicari, N., Laouar, M., Thami-Alami, I., Romani, M., Pecetti, L., 2020. Development and proof-of-concept application of genome-enabled selection for pea grain yield under severe terminal drought. Int. J. Mol. Sci. 21, 2414. https://doi.org/10.3390/ijms21072414.*

606/105. DROUGHT RESPONSE, SEED QUALITY AND YIELD OF BIOFORTIFIED COMMON BEANS IN A CONTEST OF CLIMATIC CHANGE

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