

PROJECT TITLE

A high-throughput phenotyping approach for the dissection of the root structure in common bean using a population of introgression developed for the study of the domestication syndrome of pod shattering

CONSORTIUM

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SUMMARY OF THE REPORT

The project Roots *P. vulgaris* (ID:331) seeks to investigate the domestication of root traits to elucidate the genetic basis of crop adaptation. Common bean is considered a model species for evolutionary studies. As other leguminous crops, common bean recruits nitrogen-fixing bacteria from soil through the production of root exudates. Establishing a symbiosis is a cost for the plant and it is hypothesized that with the massive input of nitrogen fertilizer, modern common bean varieties could have partially lost this ability. Thus, we think that dissecting the genetic basis of common bean root structure architecture (RSA) constitute an important starting point for the understanding of its adaptative capacity. A mapping population, built for the segregation of pod shattering trait, and which parental lines showed divergent root architectures, was used. The installation Aeroponics in UC Louvain was selected to obtain measurements in a non-limiting environment for the growth of root tissues. With the responsible of the installation, Professor Xavier Draye, we discussed on strategies to conduct our experiment during the covid pandemic. A proper number of seeds for each line has been sent to UC Louvain to fully exploit the spaces available in the installation and successively Xavier defined the best suitable experimental design. We have just 2 genotypes replicated twice, 46 genotypes replicated 3 times and 203 genotypes replicated 4 times. A control line had to be included to avoid biases due to the block structure of the installation. The experiment lasted 17 days, the time expected for roots to reach 60 cm height, the maximum length supported by the installation. Finally, the team of Xavier collected plants and measured the weight of root and shoot tissues, fresh and dry. These data are already available and through a simple visualization of means and standard deviations, we observed a good variability within our population, with parental lines showing divergent behavior and with some lines having more extreme values than parentals suggesting aberrant segregation. Analysis of variance showed a significant effect of the genotype. GWAS analysis will be performed with data from the image analysis pipeline. Meanwhile we organized a single seed descent of the RIL population to collect leaf tissues for DNA extraction that will be further processed through a genotyping by sequencing (GbS) approach. Parental lines have been sequenced through whole genome sequencing (WGS), allowing chromosome-level genome de novo assemblies (generalization of the pangenome), providing a more comprehensive and complete reference for the annotation of SNPs identified in the whole population. Through this approach we hope to identify variants of interest that could have not been mapped as they could reside in the dispensable genome. We hope that our pipeline could be used in other legume crops, facilitating the exploitation of the hidden half of plants in breeding programs.