Unravelling cluster root development in white lupin

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Plants show a strong level of developmental plasticity that is controlled by a complex combination of perception, integration and response. Root systems are a fantastic tool to study this plasticity since the number and position of lateral roots is deeply altered by the environment. We are trying to understand the fundamental mechanisms governing lateral root development and its control by the environment. Our research focuses on two main biological systems: the model plant *Arabidopsis thaliana* and white lupin (*Lupinus albus*). Our main project (ERC *Starting grant* LUPIN ROOTS) aims at understanding the formation of cluster roots in white lupin. These roots are specific lateral roots that are dedicated towards efficient phosphate acquisition and are produced as a response to its deficiency. From a developmental point of view, they consist in the induction of numerous rootlet primordia that will emerge to produce a "bottlebrush"-like structure. We believe that studying these extraordinary structures will help us understand plant organ formation as a response to their environment. Beyond its fantastic root development, white lupin is a model of interest because of its high protein seed content and because as a Legume it interacts with rhizobial bacteria to form nitrogen-fixing nodules but does not engage in mycorhizal associations.

In order to understand how cluster roots are formed, we described their development by classical histology approaches. We also set up "hairy root" transformation to use auxin markers and focus on auxin-realted genes (Gallardo et al., 2018). In parallel, we generated and started to screen an EMS mutagenized population. We have identified *constitutive cluster root* mutants and we are now trying to find the genes responsible for their phenotype. In 2017, we sequenced white lupin genome and generated a high-quality assembly at the chromosome level (2n=50). The genome size is 450Mb and the N50 of the final assembly is 17Mb. Also, we have performed detailed timecourse transcriptomics analysis by RNAseq that we plan to use for establishing Gene Regulatory Networks in order to find important candidates regulating cluster root formation.

Gallardo, C., Hufnagel, B., Casset, C., Alcon, C., Garcia, F., Divol, F., Marquès, L., Doumas, P., and Péret, B. (2018). Anatomical and hormonal description of rootlet primordium development along white lupin cluster root. Physiol Plant, in press