

#025

Genetic diversity of oilseed rape root morphology in response to nitrogen supply

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Mineral nitrogen (N) is the quantitatively most important nutrient in cropping systems. However, a considerable N fraction is lost through runoffs with detrimental consequences for the environment and human health. One way to reduce N fertilizer input is to breed for crops with better Nitrogen Use Efficiency (NUE). Increasing the plant N uptake by optimizing the degree of root branching for exploring a larger soil volume in search of the mobile nitrate resource may contribute to that purpose. Rapeseed (*Brassica napus* L.) is a major oil crop showing a poor NUE, which makes its production highly dependent on N fertilization. Our aim is to understand the genetic control of root system architecture and how it is impacted by N nutrition. We are identifying genomic regions associated to root morphological traits by performing association mapping with a large diversity panel of inbred lines and linkage mapping with experimental populations issued from biparental crosses. That information is complemented with root transcriptome sequencing data which will allow detecting gene copies differentially expressed between accessions and between N nutrition conditions. Our aim is to identify biological mechanisms but also to deliver technological tools contributing to the creation of rapeseed varieties which yield more with fewer resources. A measurable outcome in the mid-term will be to provide genetic markers for selecting new genotypes with greater root morphological features.

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