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Modelling as a tool for identifying root architecture traits defining root systems adapted to a nitrogen-limited environment

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Background:

Optimization of the root system architecture (RSA) is a promising lever to increase nitrogen use efficiency, which is a major issue to preserve yields while reducing nitrogen (N) fertilizer inputs, as required by the emerging new agricultural context. This is particularly relevant for winter oilseed rape, which has high nitrogen requirements.

Objective:

Using a modelling approach, we aimed to (i) rank the impact of various traits describing root architecture on the root system development and (ii) define combinations of root architecture traits shaping root morphotypes more or less adapted to a low nitrogen environment.

Methods:

Using the ArchiSimple model, we implemented and simulated five output variables, that were not accessible through experimentation, to describe root system development: root total biomass (g), length of the primary root (mm), volume of explored soil (mm^2), proportion of thin roots, and colonization efficiency, considered as the ratio between volume of explored soil and total root biomass.

A sensitivity analysis was performed to quantify the impact of nine of the ArchiSimple parameters, which have biological significance and correspond to root architecture traits. The range of variation was defined to represent the genetic diversity and plasticity to nitrogen availability observed in previous experimentations on rapeseed.

Then, we simulated 20,000 genotypes differing in RSA, through the variation of five parameters emerging from the sensitivity analysis. The values of these parameters were randomly chosen within a range defined from previous experimentations. The five outputs variables were computed for each genotype and clusters were then generated to group genotypes in a three-dimension space described by thin root proportion, volume of explored soil and colonization efficiency.

Results:

The sensitivity analysis highlighted five of the nine parameters studied as having a significant impact on total biomass, length of primary root, volume of explored soil, colonization efficiency and the proportion of thin roots.

Five clusters emerged from in silico genotype simulations, characterized by contrasting values of thin root proportion, volume of explored soil and colonization efficiency. For each cluster, we found close correlations between mean values of root architecture traits of the genotypes composing the cluster and the output variables characterizing the cluster. Thus, genotypes with the smallest colonization efficiency were characterized by the highest values of root elongation rate (EL), diameter ratio between mother versus daughter roots (DlDm) and maximal root diameter (Dmax), and by the lowest values of delay before root elongation (DelBEl) and inter-branching distance (IBD). Genotypes with RSA traits specific of N limited plants were mainly found in three of the five clusters and were characterized by small values of EL, DlDm, Dmax and high values of DelBEl, IBD.

Conclusions:

Our study shows that modelling is an integrated tool, useful to overcome experimental constraints and prospect a wide number of virtual combinations. It allowed us to identify the main RSA traits driving root system development and to suggest combination of RSA traits leading to root system architectures differentially adapted to contrasting soil nutritional environments. It opens promising perspectives for rapeseed breeding.