

Contribution of tomato rootstock on biomass production under nitrogen deficiency

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Our research group

Plant roots play crucial roles in crop performance. They affect major biological functions like water and nutrient uptake, anchorage and carbohydrate storage. Failure to fulfill these functions leads to significant yield losses throughout the world. The goal of our research is to contribute to the manipulation of crop plant morphology (roots in particular) to sustain agronomic performance in harsh or suboptimal environments, using genetics and breeding. Our activities combine genetic analysis of root development, management of soil-plant interactions and 4D modeling of the soil-plant system



Context

The EU project RootOPower aims to develop a multidisciplinary suite of new tools targeted to the root system to enhance agronomic stability and sustainability of dicotyledonous crops under multiple and combined abiotic stresses: salinity, water stress, soil compaction and low fertilizer (N, P, K) input. In this project, our team is responsible for the genetic dissection of the root system architecture of a large collection of tomato rootstock under nitrogen deficiency and its effect on on biomass production.

Originality



Figure 1 : Tomato rootstock
(Picture of M.E. Ghanem)

The choice of tomato as model species is motivated by the ease of manipulating the root and shoot independently through grafting (Figure 1). This technique will be exploited to assess of the effect of root traits on crop performance by using a segregating population of rootstocks combined with a unique scion.

Genetic analysis

The first step in the project is the replicated massive phenotyping of the root growth and architecture of the segregating population, under control and nitrogen deficient conditions.

The population is a set of 140 recombinant inbred lines (RILs) from a cross between *Solanum lycopersicum* var. cerasiforme and *S. pimpinellifolium* (used as rootstocks).

Phenotyping will be conducted in an aeroponics platform that allows the time-lapse imaging of shoot and root growth during ca. 10 days with a time resolution of two hours (Figure 2).

In addition, we will quantify the hormone (ABA, ACC, auxin, cytokinins, jasmonic acid, salicylic acid) and element (cations and anions, C, N, O) composition of the xylem sap collected from de-topped root stumps.

QTL analysis will be used to dissect the genetic variation of all traits and biomass production under control and nitrogen deficient conditions in order to identify the underlying traits contributing to low N resistance.

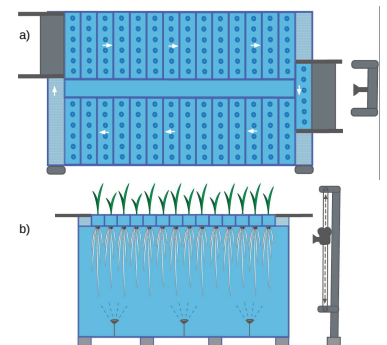


Figure 2 : Schematic representation of the aeroponic box (Ligeza A. and al., 2011. Aeroponics as a tool for high throughput phenotyping. "plant phenotyping workshop", Juelich, Germany). a) Top view. White arrows represent the robotized displacement of plant-holding strips. b) Side view. Roots are sprayed with the solution from the bottom of the box. Root images are captured when each plant is positioned in front of the camera.

Modelling

The second step of the project will be to incorporate the effects of QTLs for all traits and conditions considered in the RootOPower project into a mathematical root architecture model in order to make predictions of biomass production under combinations of abiotic stresses. These predictions will be made under various hypotheses re. the shoot-root relationships. This *in silico* work will lead to the definition of critical experiments that will be made to test those hypotheses.