

Transnational Access Report

1. General Information

Project Acronym (ID):	Tomato root QTLs
Project Title	QTL-mapping for root system architecture traits in tomato
Installation used	FZJ, SCREEN Root SP
Name of Group Leader	Harro Bouwmeester
Name of organization	Wageningen University

2. Duration of access

Begin of the project	End of the project
First day the installation was used	Last day the installation was used
February 3, 2014	April 4, 2014

3. Access to the Installation

SCREEN Root SP

4. Project summary (max. 250 words)

In a preliminary experiment we revealed a large variation in primary and secondary metabolite composition of root exudates from ten wild and commercial tomato genotypes. In a different preliminary experiment, we observed clear differences in Root System Architecture (RSA) within the same tomato diversity panel. During repeated attempts using various methods we were not able to translate these morphological differences into objective quantitative parameters. Lateral root length, lateral root density and primary root length are examples of traits for which large phenotypic differences could be observed by the naked eye. Quantification of such parameters is the biggest challenge in phenotyping for root morphology. Bottlenecks are entanglement of roots growing in a 3D-conformation or detangling of these same roots without causing damage. Technical limitations have hampered visualizing and analysing of RSA in soil. It is probably these limitations that explain why high-throughput phenotyping of root traits in breeding populations has not taken flight yet. In this project lateral root number has our special interest when phenotyping for root morphology because organic acid exudation mainly occurs behind the root meristem. The goal of the described experiment was to find QTLs for RSA traits in the tomato genome. In a later phase, this data will be used to relate quantitative trait loci (QTL) for root exudation and RSA and to find candidate genes for RSA by meta-analysis.

5. Main achievements (max. 250 words)

We found significant differences between lines of the IL-population for the traits total lateral root length, lateral root number and root system width ($P < 0.05$). The standard deviation for these traits was 12%, 8% and 9% of the average respectively, implicating that the variance due to experimental error was relatively small and the used experimental procedure was accurate. The differences for these traits between the highest and lowest scoring lines were 405%, 246% and 228% respectively, proving that the phenotypic variance for these traits is large. However for these traits there were no single lines that stood out from the rest of the population and the differences between lines were subtle. This means that the studied traits behave in a rather quantitative way, implicating they are probably controlled by a lot of minor genes

instead of few major genes. Still, genotypes scoring high for these traits are likely to contain one or several of these minor genes.

The average length of one lateral root and the total root length were not significantly different ($P=0.070$ and $P=0.079$) but could have been with a little bit more statistical power. There were no significant differences in tertiary root length and branching angle.

This was the first time that a breeding population was screened for RSA and that genetic differences within such a population were revealed with such a high-throughput platform. Despite the absence of really distinctive lines we will still try to find candidate genes in the introgressed genomic regions of lines scoring highest or lowest for RSA traits. This will be done using genomic information in combination with known RSA genes in other plant species.

6. Publications related to the access granted, acknowledging the support by EC.

Please specify the type of publication or presentation (scientific journal, book, patent, abstract, proceedings, article) and provide the full reference or link.

Expected December 2014