

# Transnational Access Report

## 1. General Information

Project Acronym (ID):	Iselect
Project Title	Identification of genomic regions influencing sensitivity to soil water deficit and evaporative demand in an elite dent by flint introgression library of maize.
Installation used	Phenodyn
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## 2. Duration of access

Begin of the project	End of the project
First day the installation was used	Last day the installation was used
03.03.2014	09.04.2014

## 3. Project summary (max. 250 words)

The goal of the study is to fine map and functionally characterize genomic regions in maize contributing to sensitivity to soil water deficit and evaporative demand. An introgression library (IL) derived from a cross between an elite European dent line (recurrent parent, RP) known to exhibit high yield stability under water limited conditions and an elite flint line (donor parent, DP) was available at the beginning of the project. The IL had been screened under well-watered and drought stress conditions in previous field, rain out shelter and greenhouse trials. A set of 12 near isogenic lines (NILs) was selected from the IL for the experiment at Phenodyn. Additionally seven sub-IL lines carrying smaller genome fragments of candidate NILs complemented the experimental set together with the parents of the NILs. NILs were selected which showed contrasting phenotypes compared to RP and carried candidate genomic regions for the traits anthesis-silking interval, carbon isotope discrimination, plant height and leaf elongation rate. The genome of each NIL has been structurally characterized with SNP markers in high resolution.

Objectives of the project are (i) to assess the genetic variability for sensitivity to evaporative demand and soil water deficit in the selected NILs, (ii) to identify NILs and individual genomic regions with contrasting sensitivity to evaporative demand and soil water deficit, (iii) to identify NILs and genomic regions with contrasting recovery potential after a phase of drought stress, and (iv) to relate results from controlled phenotyping conditions to yield stability under water limited conditions in the field.

## 4. Main achievements (max. 250 words)

The screening of the 21 genotypes was successfully conducted during the experiment at INRA Montpellier. Phenotypic data for the traits germination rate, phenological development, leaf length, final leaf area, fresh weight biomass, leaf elongation rate and transpiration rate were successfully collected under well-watered and drought stress conditions. For the traits leaf elongation rate and daily water loss data points were automatically collected at high resolution. Substantial variation was observed for plant growth and leaf area although introgression lines had been preselected for similar developmental trajectories. Already under well-watered conditions a high variability in the maximum leaf elongation rate was visible. The gradual reduction of soil water potential was directly reflected by a decreased leaf elongation rate. Distinct

differences in leaf elongation rates were observed in reaction to evaporative demand, indicating genotypic differences in either stomatal control or plant hydraulic conductivity. Introgression lines predicted to show differences in stomatal conductance based on earlier field and greenhouse trials showed clear differences to the RP in terms of their daily water loss in Phenodyn. For estimating daily transpiration conditional on plant transpiring surface, the development of a calibration function to describe the relationship between plant development and leaf area is currently under development. When the experiment was finished, soil samples from each pot were taken to capture the trait root DNA density (RDD). RDD was investigated to quantitatively measure root viability and below ground biomass in the examined genotypes. Analysis of the soil samples is finished, the trait showed significant genotypic variation and high heritability. In summary it can be said that the experiment was very successful and has yielded promising results for the identification of genomic regions contributing to sensitivity to soil water deficit and evaporative demand.

#### **4. Publications related to the access granted, acknowledging the support by EC**

Data analyses are still in progress. The highly complex multilayered data structure requires a sophisticated analysis pipeline which is currently developed together with the project partners from INRA. A publication of results is planned in the near future.