ROOT ARCHITECTURE PHENOTYPING IN AEROPONICS: A CRITICAL REVIEW

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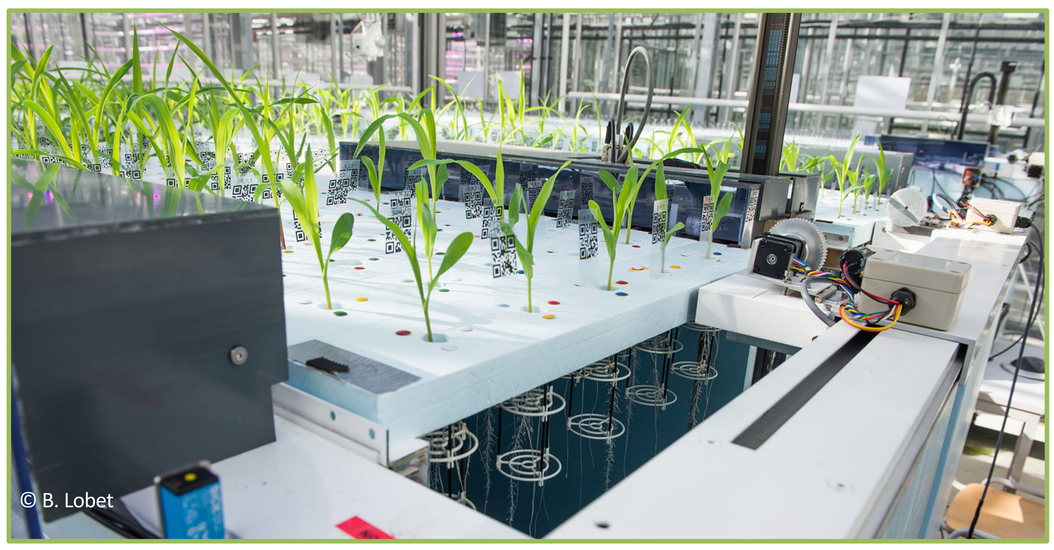
CONTEXT



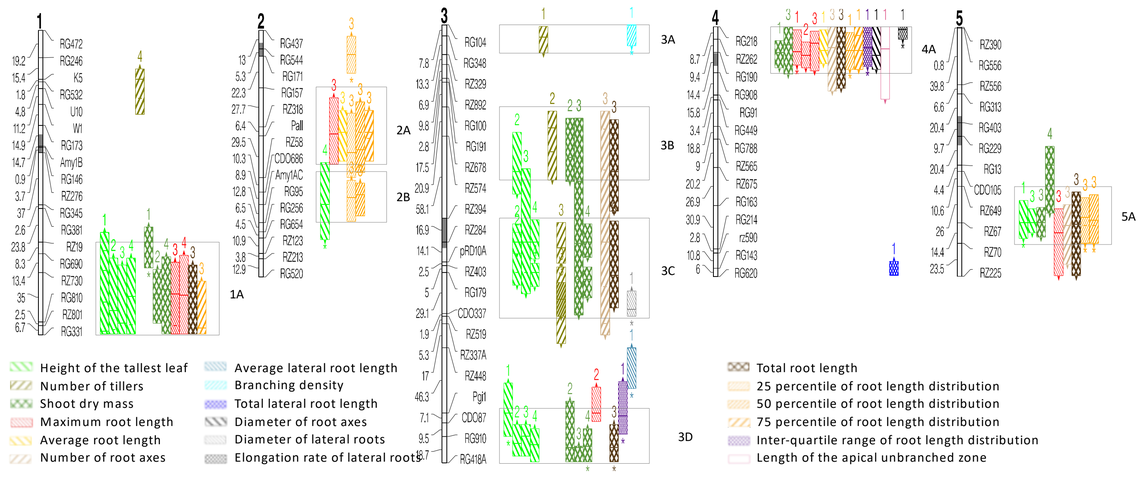
- Phenotyping root dynamics in aeroponics has proven to be an **affordable**, **non-invasive** and **high throughput** technique suitable for quantitative genetic analysis.
- However, root systems grown in aeroponics could be **poor surrogates** of field-grown root systems, largely because mechanical impedance is lacking.
- This poster assesses what we have learnt from 10 years of **QTL analyses** of the root system architecture **dynamics** of cereals in aeroponics.

EXPERIMENTS

①

- In rice (*Oryza sativa*), we performed a deep phenotyping (15 traits) at **advanced flowering stage** with a DH population (IR64xAzucena, 126 lines) and four repetitions in time. 80 QTLs were detected (interval mapping).
- The range of heritabilities was large: between 19 and 63% (higher values for stem size and maximum root length).
- We found that root traits are controlled by a **suite of small-effects** and often **pleiotropic loci** with important V_E and **GxE interactions**.
- Half of these QTLs **co-localize** with other field studies (de Dorlodot, 2007).

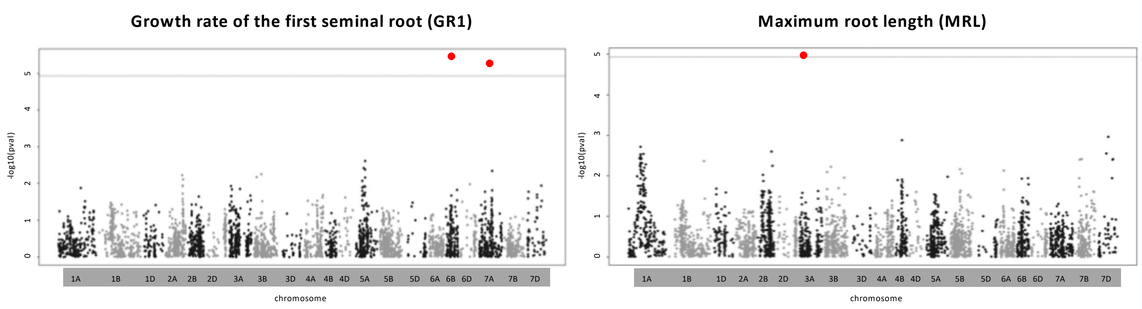
Linkage map of the majority of the QTLs found. Numbers 1 to 4 at the top of each support interval = 4 replicates in time. The direction of the arrow indicates the additive effect of the QTL (upward = positive effect from the Azucena allele; downward = positive effect from the IR64 allele) (de Dorlodot, 2007).



②

- In wheat (*Triticum aestivum*), we analyzed a **large diversity panel (450 lines)**, until the 3rd leaf stage, with a 2-hr temporal resolution and two reps in time. Only three QTLS were found (GWAS).
- The range of heritabilities was narrow (between 26 and 33%).
- V_E was important. The correlation between root apical diameter and growth rate was surprisingly low.

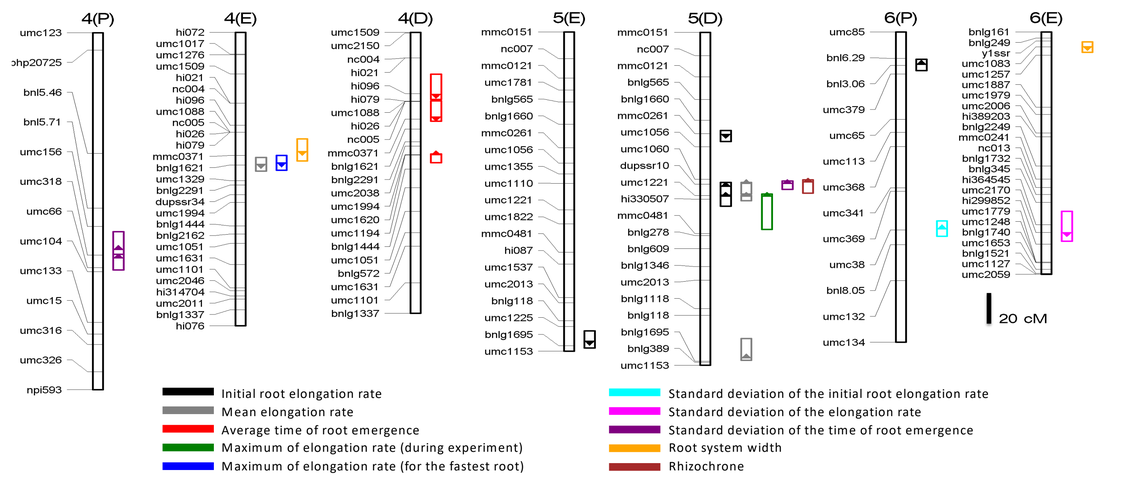
Manhattan plot of the growth rate (GR1) and the maximum root length (MRL) of the first seminal root. 2 QTLs for GR1 and 1 QTL for MRL were detected with a score above the Bonferroni-corrected threshold (Thaon, 2017).



③

- In maize (*Zea mays*), we phenotyped (10 root traits) **three RILs populations (100 lines each)**, until the 4th leaf stage, with a 2-hr temporal resolution. 38 QTLs were found (interval mapping).
- The range of heritabilities was large (between 10 and 66%), with highest values for root elongation rate.
- Several QTLs were confirmed in two or in the three populations, and 16 QTLs **overlapped** with QTLs found by Welcker et al (2011).
- No correlation was found between elongation rate and seed weight.

Excerpt of the QTL map for the root traits phenotyped in the three mapping populations (CMLP1 x CMLP2, P; FV2 x Io, D; FV2 x FV252, E). The direction of the arrow indicates the additive effect of the QTL (upward: positive effect contributed by the first parent) (Civava, 2016).



OUTCOME

- High resolution in aeroponics allows to detect **small-effect QTLs**

  Such QTLs might be missed with lower resolution.
- A **minority** of the QTLs detected in aeroponics have **large effects**

  This is intriguing. Would field QTLs result largely from GxE ?
- **Late phenotyping** has yielded the largest number of QTLs

  This may reveal age-specific QTLs or QTLs whose effects cumulate with time and would be un-noticed at early stages.
- Root traits in aeroponics can be affected by **large V_E**

  We need to understand these E effects, as some of them may be surrogates for aspects of the soil E and provide useful insights for GxE.
- **Contrasted** populations, selected for water deficit study, display larger number of QTLs than large diversity panels
- Many QTLs in aeroponics **co-localize** with other studies and populations. Many also **coincide** with QTLs for **related traits**: root system width *vs* LER response to WD (Welcker et al, 2011), number of root axes *vs* number of tillers (de Dorlodot, 2007), root length distribution *vs* earliness (de Dorlodot, 2007).

  These results suggest that the artificial aeroponics environment does not invalidate the technique in a wider context.

Currently, we investigate **lateral root growth** variability and we try to dissect **V_E**. As of today, aeroponics seems a **promising platform** to dissect the variability of root growth dynamics.

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