

Phenotyping root architectural traits of a tropical japonica rice panel in view of association mapping

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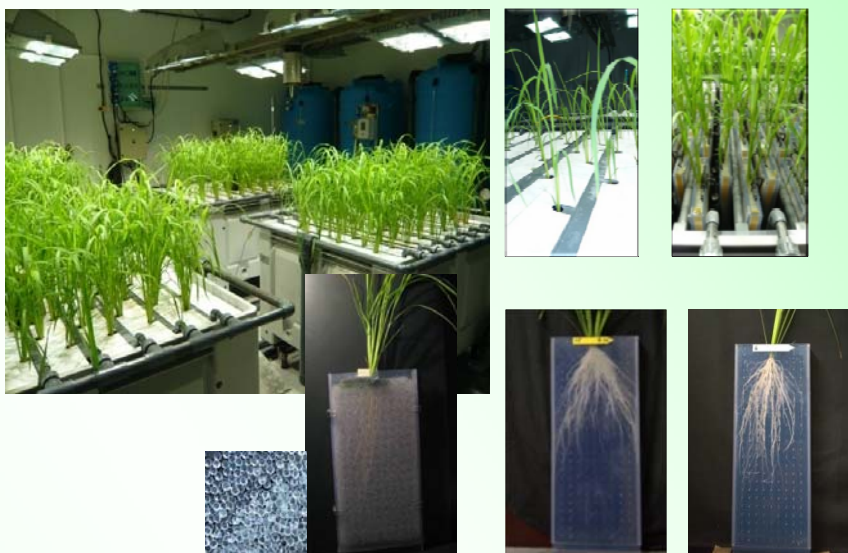
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Objective: In a climate change context, breeding for a better root architecture is a promising approach to improve drought resistance in cereals. A deep and thick root system in place when a drought spell occurs is a strategy efficient for rainfed rice in most agronomical situations. The aim of the work is to understand the genetic bases of root architectural traits in rice through association study and identify promising alleles for marker-aided selection

Material and methods:

The study was conducted with an association panel of 170 tropical japonica rice lines. The panel had already been characterized with 25 SSR markers and is presently being genotyped with 1 million SNP markers. The phenotyping system, set in a growth chamber, relied on transparent 50 cm x 20 cm x 2 cm plexiglas sandwiches with a grid of regularly spaced mails. The sandwiches were filled with glass beads that simulated soil mechanical impedance and could easily be removed at the end of the experiment. Plates were distributed in 4 independent tanks with a circulating nutrient solution and automatic pH control.

The experimental design was an alpha lattice with 2 replications. Plants were grown up to 35 das.



Results:

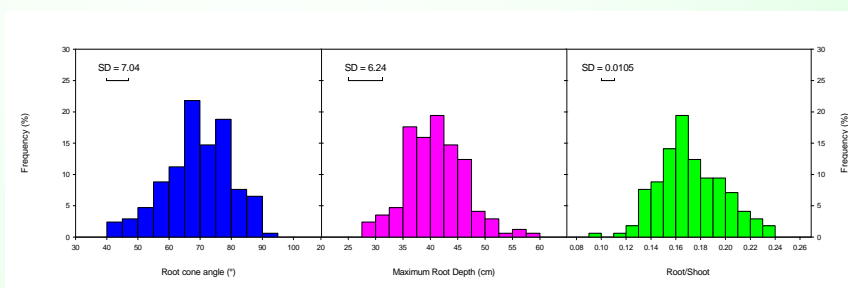
- A large and significant genotypic variability was observed for maximal root depth, number of crown roots below 30 cm, root cone angle, root dry mass in different layers and root/shoot ratio.

- Brazilian upland varieties, bulus from Indonesia and varieties from Taiwan showed the best performances in terms of root depth.

- The correlation between root cone angle and root depth was weak but positive for this population in this system, which was unexpected.

- A principal component analysis was conducted on the data. The two first axes explained 71% of the variability. The first axis was determined by biomass and the second by root depth parameters

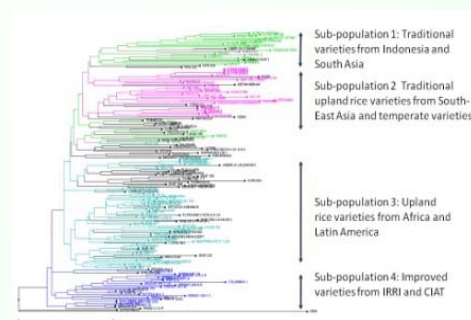
- We used passport information and genetic data to see whether these parameters were explaining the trait distributions. The sub-continent of origin and the type of the variety (traditional versus improved) had a significant effect on root depth but the genetic groups as defined by Structure did not.



Conclusion:

The variability of the panel and the absence of strong link between phenotype and genetic structure show the panel is adapted for association studies and future breeding program for root development.

The panel has also been characterized in parallel for other traits contributing to drought resistance. Once the genotypic data from the 1 million SNP chip are available, this work will be used for genomic selection for drought resistance.



NJ tree of the japonica panel with projection of the 4 sub-populations defined by the software Structure (different colors)