

PROJECT TITLE

Uncovering molecular mechanisms and impact of xerobanching

CONSORTIUM

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SUMMARY OF THE REPORT

Root branching is a major root-shape trait that governs soil foraging capacity [1, 2]. Our recent research has revealed that root branching can be regulated by soil moisture at much finer spatial scales than previously realised [3, 4]. Using X-ray Computed Tomography, we demonstrated that when roots grow across a zone of low water availability in soil (e.g. air-filled gap), branching is completely suppressed [4]. This novel adaptive response observed under transient water stress is termed as xerobanching and was found to be conserved in many crop species (Figure 1). Given the agronomic importance of root branching in determining water and nutrient uptake efficiency of plants, studying xerobanching can play a pivotal role in improving root foraging capacity.

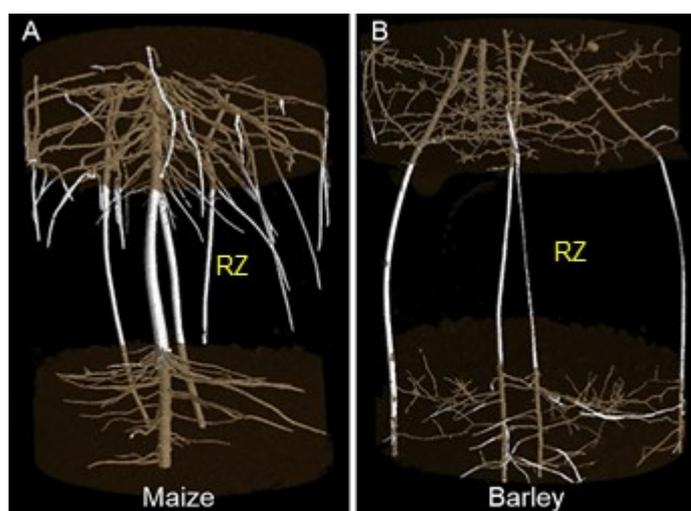


Figure 1

Initial studies reveal that xerobanching is dependent on abscisic acid and auxin. However, the underlying molecular mechanisms involved in regulation of this novel adaptive response remain to be elucidated. Therefore, to uncover the molecular mechanism(s) underpinning xerobanching and assess its impact on crop performance, a diversity population of foxtail millet (*Setaria italica*) was screened to score the natural variations in their xerobanching response.

To address the key questions, we used the aeroponics platform (RootPhAir) at Universite catholique de Louvain for high throughput root phenotyping of 309 *Setaria* accessions. Very uniform germination of *Setaria* accessions was successfully accomplished in RootPhAir (Figure 2).



Figure 2

Plants were grown under optimum physiological conditions for one month. 64 genotypes were replicated twice, 232 genotypes were replicated 3 times and 13 genotypes were replicated 12 times. Primary roots and nodal roots were exposed to transient water-deficit stress followed by normal watering. Images were captured to estimate lateral root density and other root parameters (Figure 3).



Figure 3

Data about variation in several root traits of different *Setaria* genotypes was successfully acquired through RootPhAir. The generated phenotypic datasets will be utilized to perform GWAS analysis to discover the underlying candidate genes/alleles involved in regulation of xerobanching as well as other root traits in *Setaria*. The project has generated wealth of information about phenotypic variation in several root traits of *Setaria*. This would serve as a critical information in identifying genetic loci regulating root traits through GWAS. Additionally, the project outputs will serve the basis of several follow-up experiments that will ultimately help to develop new *Setaria* varieties with improved performance in resource poor soils.