

T16 

Enhancing phosphorus efficiency in maize and sorghum

(submitted by Sylvia Morais de Sousa <sylvia.sousa@embrapa.br>)

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Phosphorus (P) is an essential nutrient to plants and is acquired as inorganic phosphate from the rhizosphere solution. P is one of the least available nutrients particularly in highly weathered, tropical soils, limiting substantially plant growth. Our work aimed to study root traits involved with P acquisition efficiency and to identify and validate maize and sorghum homologs to Phosphorus Starvation Tolerance 1 (PSTOL1), a gene responsible for enhanced early root growth, P uptake and grain yield in rice. Association mapping was undertaken in two sorghum association panels phenotyped for P uptake, root system morphology and architecture in hydroponics and grain yield and biomass accumulation under low-P conditions. SbPSTOL1 alleles reducing root diameter were associated with enhanced P uptake under low P in hydroponics, whereas other alleles increasing root surface area also increase grain yield in low-P soil. SbPSTOL1 genes colocalized with QTLs for traits underlying root morphology and dry weight accumulation under low P-soil. For maize, two multiple interval models were used to map QTLs related to root traits, biomass accumulation and P content in a maize RIL population cultivated in nutrient solution. Multiple interval mapping models for single and multiple traits were combined and revealed 13 genomic regions significantly associated with the target traits in a complementary way. Some of these quantitative trait loci (QTLs) were coincident with QTLs for root morphology traits and grain yield previously mapped, whereas others harbored ZmPSTOL1 candidate genes. OsPstol1 and its maize and sorghum homologs were cloned in the pMCG1005 vector and tobacco Petit Havana plants were genetically transformed via *Agrobacterium tumefaciens*. Several events presented one copy of the transgene and those that also showed high transgene expression were selected for phenotypic evaluation under low P conditions. The transgenic plants, T1 and T2 generations, were grown for ~60 days in ½ MS medium with low P under controlled conditions. When compared with the control, plants transformed with pMCG1005 (empty vector) the PSTOL1 transgenic plants presented higher vegetative growth and root surface area under low P. Our results indicated that PSTOL1 homologs have a similar role as osPSTOL1 gene in rice plants and have potential to enhance P acquisition and yield in different species.

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Program and Abstracts



March 22 – March 25, 2018

Palais du Grand Large
Saint-Malo, France

Saturday, March 24

8:30 AM – 10:30 AM	SESSION 6 – INTERACTIONS WITH THE ENVIRONMENT Chair: Natalia de Leon	Talks 16-21. Pages 39-44.
8:30 AM	ANNOUNCEMENTS	(Chateaubriand)
8:40 AM	Sylvia Morais de Sousa, Embrapa Milho e Sorgo <i>Enhancing phosphorus efficiency in maize and sorghum</i>	[T16]
9:00 AM	Laurie Maistriaux, Université catholique de Louvain <i>Regulation of aquaporin expression in maize: proximal and distal eQTLs</i>	[T17]
9:20 AM	Justin Blancon, BIOGEMMA <i>Innovative and high-throughput field phenotyping method provides leaf traits for breeding of drought tolerance - From Leaf Area Index dynamics to its physiological components</i>	[T18]
9:40 AM	Joerg Degenhardt, Martin Luther University Halle <i>Characterization of biosynthetic pathways and regulatory elements for the production of the volatile homoterpenes DMNT and TMTT in Zea mays</i>	[T19]
10:00 AM	Marcel Bucher, University of Cologne <i>Mycorrhizal phosphate uptake affects maize root-associated microbiota</i>	[T20]
10:20 AM	Katherine Murphy, University of California - Davis <i>Discovery of dolabralexins, previously unrecognized terpenoid defense compounds in maize (Zea mays).</i>	[T21]
10:40 AM	BREAK	
11:15 AM – 12:55 PM	SESSION 7 – EXPRESSING THE GENOME Chair: Andrea Eveland	Talks 22-26. Pages 45-49.
11:15 AM	Jacob Washburn, Cornell University <i>Predicting across the central dogma of molecular biology: DNA to mRNA abundance</i>	[T22]
11:35 AM	Bradlee Nelms, Stanford University <i>Mapping the archesporial cell to meiocyte progression using single-cell RNA-Seq</i>	[T23]
11:55 AM	Jutta Baldauf, University of Bonn <i>Single parent expression is a general mechanism driving extensive complementation of non-syntenic genes in maize hybrids</i>	[T24]
12:15 PM	Edoardo Bertolini, Donald Danforth Plant Science Center <i>The regulatory landscape of developing maize inflorescences: linking phenotypic variation to the functional non-coding genome</i>	[T25]