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Detailed expression analysis of maize Pstol1 homologs in contrasting genotypes for phosphorus efficiency

(submitted by Sylvia M de Sousa <sylvia.sousa@embrapa.br>)
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Maize is generally considered to have a high fertility soil requirement, so the development of phosphorus-efficient maize genotypes would be beneficial in low-input agroecosystems and would improve the sustainability of high-input agroecosystems. Plants developed several mechanisms to adapt to low phosphorus (P) conditions, indicating that this is a complex trait. The main mechanism that has been implicated with increased P acquisition efficiency involves changes in root morphology. In this context, Phosphorus-starvation tolerance 1 (Pstol1) was identified as the gene underlying the Pup1 locus, which is responsible for enhanced early root growth, P uptake and grain yield in rice and sorghum. Recently, we performed comprehensive QTL mapping in maize recombinant inbred line population (RIL) in nutrient solution under low-P conditions and pointed out candidate genes as maize homologs (ZmPSTOL1, ZmPSTOL4, e ZmPSTOL6) to the rice PSTOL1 (OsPSTOL1) based on QTL co-localization with root and P efficiency traits. In the present study, we aimed to verify the spatial and temporal gene expression of these maize Pstol1 homologs in two P contrasting maize genotypes (L3 – efficient and L22 – inefficient). First, the temporal expression revealed that all genes start to express, in nutrient solution, at 7 days after germination (DAG) and had their peak of expression at 17 DAG. Expression profile of the candidate genes was assessed in different maize tissues (tassel, leaves, stem, seeds and roots) that were harvest during flowering, revealing that ZmPSTOL1 and ZmPSTOL6 were more expressed in roots and tassel of the inefficient line (L22) while ZmPSTOL4 was more expressed in these same tissues but of the efficient line (L3). We also harvested different root parts (primary, lateral, non-embryonic seminal, embryonic seminal, crown) of L3 and L22 grown in nutrient solution at 17 DAG. These results showed that ZmPSTOL1 and ZmPSTOL6 were more expressed in all root types of L22 line and ZmPSTOL4 was more expressed in L3 primary root, especially at the differentiation zone. Finally we correlated gene expression from contrasting lines with root morphology traits. These results shed a light on the illusive Pstol1 pathway; however, further functional studies are required to comprehend the actual pathway leading to root system modulation by Pstol1.

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Determining Heat Tolerance via Chlorophyll Readings and Electrolyte Leakage

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With global climate change predicted to cause increases in temperatures in many parts of the world, it has become increasingly important to study the effects of heat stress on plants. Excessive heat, along with other abiotic stresses, is known to be detrimental to crop yields which could endanger future food security. We have initiated a project to study heat stress in maize with the eventual goal of developing heat tolerant maize germplasm for the developing world. We have done field trials for the NAM founders in India to determine heat tolerance of the various lines and found B97, Mo17, and CML 322 to be among the most heat tolerant while B73 is most susceptible. Based on a literature search and availability of transposon insertions, we have selected certain maize mutants potentially involved in heat stress tolerance. We have measured chlorophyll readings for these mutants in a growth chamber under heat stress as well as taken electrolyte leakage data. We found that three mutants: lipid transfer protein, carbohydrate transporter, and fatty acid desaturase had consistently lower chlorophyll readings than W22, their wild type counterpart. We also found that the electrolyte leakage data for B97, Mo17, and CML322 matches well with the field phenotypes thus potentially providing an accurate, simple assay to test for heat tolerance.

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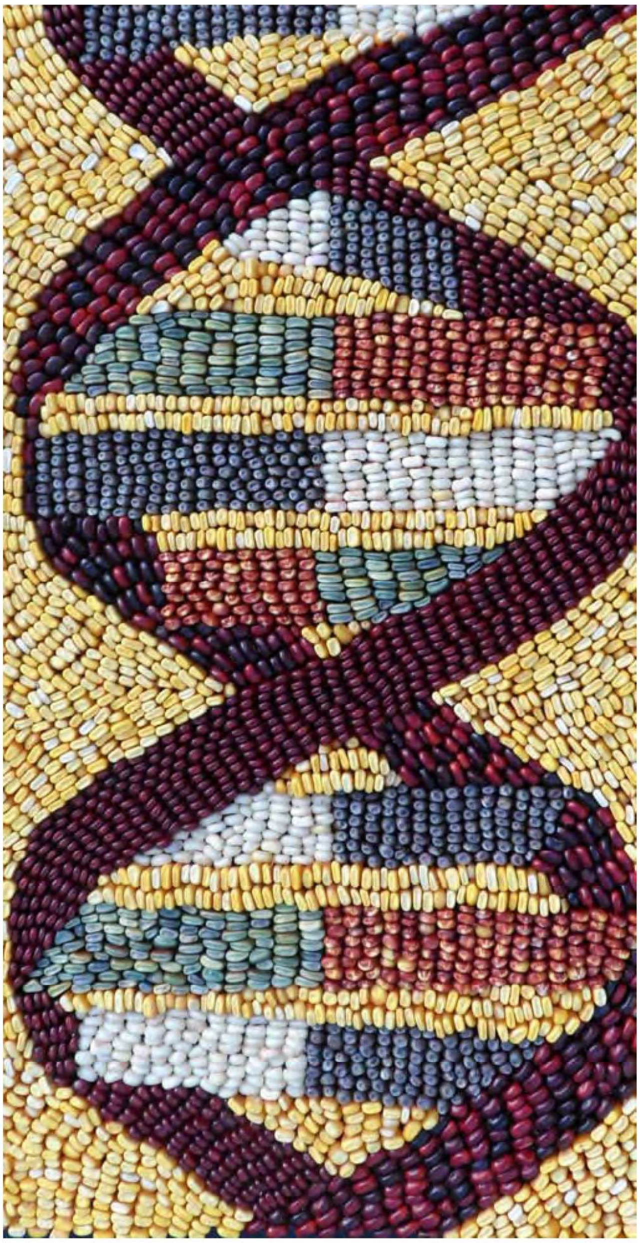
Program and Abstracts



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P73	**Robert Augustine** <raugustine@wisc.edu>	*Defining the SUMOylation System in Zea mays and its Roles in Stress Protection*
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