

# **55<sup>th</sup> Annual Maize Genetics Conference**

Program and Abstracts



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**P301**

### **Production of biofuel from cellulosic biomass**

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Increasing world population and limited resources is necessarily synonymous with energy crisis. Fossil fuel has been exploited since industrial revolution and have contributed to polluting the earth to nearlethal limits. In this situation fuel from biological organisms (Biofuel ) is very promising in meeting the global energy demands and also restoring balance in the ecosystem. It is renewable and clean sourceof energy. Biofuel though produced from various sources is not yet commercially viable due to its high cost in production. In our lab we are focusing on cellulosic biofuel production from sorghum stalks.

Sorghum is a very promising energy crop as it can grow in relatively hostile conditions with low input in terms of fertilizer and water, also has a high biomass (measured by its height and maturity). This unique character of sorghum can silence the bioethical issues that are inherent to biofuel production as it can be grown on land considered marginal for growing food crops. High biomass along with high saccharification yield (conversion of cellulosic biomass to fermentable sugars like xylose and glucose) will ensure a more cost effective biofuel. To improve saccharification yield, our lab is trying to identify candidate genes especially involved in cell wall synthesis that affects the process of saccharification. Genotyping and association mapping are in progress using genetic markers with bioinformatics tools like TASSEL and GAPIT.

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**P302**

### **QTL mapping for P efficiency and root traits under low phosphorus availability in maize and identification of putative PSTOL1 homologues**

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Phosphorus (P) is one of the most limiting mineral nutrient for plants and crucial to the productivity of several crops, including maize. However, the low P is a primary constrain for maize productivity. One strategy adopted by plants under P starvation is the modification of their root morphology. In rice, a QTL (Pup1) was associated with P efficiency and increased root growth under low P. Recently, a gene underlying Pup1 locus was identified and denominated Phosphorus-starvation tolerance 1 (PSTOL1). This gene enhances root growth when overexpressed, improving P uptake and consequently grain yield. In maize, several QTLs for root traits were identified under P contrasting levels in nutrient solution and field conditions. Nevertheless, the relationship between root architecture and P efficiency remain unknown and candidate genes to these traits have not been identified yet. Thus, this work aimed to analyze the relationship between root morphology and P efficiency as well as the genetic basis underlying these traits in maize. We performed QTL analyzes to search for a functional homologue of OsPSTOL1. Based on rice PSTOL1 amino acid sequence we searched several maize sequence databases. We selected 12 predicted proteins with more than 50% identity with rice and Arabidopsis protein kinases. These proteins clustered in three major subfamilies. We found four predicted genes with more than 65% identity with OsPSTOL1, which were located on chromosomes 3, 4 and 8. We identified three to four QTLs for each trait, explaining 23.5 to 45.3% of the total genotypic variance. The QTLs for the analyzed phenotypic traits were concentrated in few genomic regions, mainly on chromosomes 1, 8 and 10. We observed the co-localization of Zm1\_PSTOL1 with QTLs clusters, including root morphology traits, total plant dry weight and P acquisition efficiency, on chromosome 8. We also observed that Zm1\_PSTOL1 expression occurred only in the parental line that was the donor for these QTLs. These results represent the first evidence that the gene Zm1\_PSTOL1 can be related to P acquisition efficiency. However, additional studies are needed to validate this gene as Pup1 functional homologue in maize.

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