PLANT & ANIMAL GENOME XXII
The Largest Ag-Genomics Meeting in the World.
January 11-15, 2014
San Diego, CA
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Improving Phosphorus Efficiency in Sorghum by the Identification and Validation of Sorghum Homologs for *Pstol1*, a Rice Gene Responsible for a Major Phosphorous Uptake QTL (*Pup1*)

Date: Monday, January 13, 2014
Room: Grand Exhibit Hall

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Low availability of P in the soil is one of the main constraints for plant development and crop production in tropical regions. The rice gene *Pstol1*, which encodes a protein kinase that enhances early root growth and P acquisition, was recently cloned and characterized. We employed comparative genomics to identify sorghum *Pstol1* homologs and then validated them as bona fide genes underlying tolerance to P deficiency in sorghum. A sorghum association panel was phenotyped for agronomic performance under low P in the field and well as for root morphology traits; also SNPs within sorghum Pstol1 homologs were identified. Our data suggests that SNPs within sorghum *Pstol1* homologs are associated both with changes in root morphology/root system architecture, as well as with P acquisition traits. Gene validation was conducted via phenotyping members of a large sorghum recombinant inbred line population that was genotyped by sequencing (GBS). The results indicate that some *Pstol1* homologs co-localize with QTLs controlling root morphology traits and shoot dry weight. Association analysis was also conducted in a sorghum landrace panel adapted to West Africa that was phenotyped in pots for yield traits on low P soils. From this study we found that SNPs within *Pup1* homologs were significantly associated with traits related to P uptake and yield under low P conditions. Furthermore, consistent allelic effects were observed in both panels. The same alleles increased P uptake in Brazil and Africa, indicating that multiple *Pup1* homologs play a role in P uptake and efficiency in sorghum. Our results indicate that *Pup1* homologs in sorghum have the ability to enhance P uptake and crop performance on low P soils by a mechanism related to early root growth enhancement, similar to *Pup1* in rice.

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