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Program and Abstracts

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## Optimizing Tissue Culture Parameters for Callus Induction and Regeneration of Transgenic Sorghum Lines.

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Sorghum [Sorghum bicolor (L.) Moench] is a C4 grass of African origin. It belongs to Poaceae family and is widely cultivated in diverse climates around the world for food and forage. Sorghum is one of the most important cereals in the world after rice, maize, wheat and barley. Its high genetic diversity can be utilized to improve economically important traits to meet the challenge of climate change and ever increasing food demands across globe. It has significant genetic homology with sugarcane and maize and is an attractive candidate for energy crop due to its high biomass, yield and sugar content. It is highly stress tolerant and has high water use efficiency due to its deep root system and reduced transpiration rate thus can grow on marginal soil with low nutrient and water inputs.
Candidate genes related to economically important traits like height, biomass, maturity, tiller number, kernel weight, saccharification has been mapped by QTL mapping and association mapping using SNP and SSR markers. Mini-core collection developed at International crop research institute for semi arid tropics were used for the mapping purpose. The functional validation of the genes remains a challenge due to recalcitrant nature of sorghum genetic transformation. However, it is achievable by both biolistic (Casas et al. 1993) and Agrobacterium (Zhao et al. 2000) methods. We are using Agrobacterium mediated transformation protocols to optimize our tissue culture media for callus formation and regeneration of plants. Several explants like immature embryo, seeds, apical meristem, and leaf were used. several genotypes are tested along with different media and hormone concentration. MS based media with 2 mg per L 2,4-D and 0.2 mg per L kinetin have shown better results in callus formation. However it is too early to confirm the right media and genotype combination as several are on test.

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## Overexpression of rice Phosphorus Starvation Tolerance 1 gene and its sorghum and maize homologs in transgenic tobacco

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Low phosphorus (P) availability in soil is a major constraint for crop production in tropical regions. Phosphorus-Starvation Tolerance1 (OsPstol1) is a protein kinase that enhances root surface, P acquisition and grain yield in rice under P deficiency. Sorghum homologs of OsPstol1 were identified by association mapping 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, in Brazil and/or in Mali. Maize and sorghum candidate genes co-localized with quantitative trait loci (QTL) for traits underlying root morphology and dry weight accumulation under low P via QTL mapping. In order to validate the function of these genes, rice OsPstol1 (control) and its maize (ZmPSTOL3.06, ZmPSTOL8.02 and ZmPSTOL8.05_1) and sorghum (Sb07g002840, Sb03g031690 and Sb03g006765) homologs were cloned downstream of ubiquitin promoter in pMCG1005 vector, using bar gene as a selective marker. Tobacco Petit havana plants were genetically transformed via Agrobacterium tumefaciens EHA101 strain and regenerated from selected callus in shooting and rooting medium supplemented with 100 mg/ml of Tioxin and 1 mg/L of Phosphinothricin. PCR with gene specific (~700 bp) and bar (~400 bp) primers confirmed the presence of Pstol1 genes in tobacco plants. Most plants presented one copy number and overexpressed the transgene correctly. Moreover, the overexpression of Pstol1 genes significantly enhanced root surface area under low P. Currently these transgenic tobacco plants harboring the seven different genetic cassettes are being tested the enhancement of P acquisition and grain yield under low P conditions.

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