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Translational genomics approaches to increase sorghum yield on acid soils

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Widespread worldwide, acid soils are prevalent in tropical and sub-tropical regions where food security is still a challenge. Two important constraints for crop production in those areas are aluminum (Al) toxicity and phosphorus (P) deficiency due to P fixation into soil clays reducing availability. Al toxicity restricts root development into highly acidic sub-soil layers, enhancing the deleterious effects of drought stress on crop production. Our program seeks to identify the molecular determinants of sorghum adaptation to acid soils and to deploy those into molecular breeding strategies. For example, a single allele of the Al-activated citrate transporter, SbMATE, has been recently shown to increase grain yield by ~0.5 ton ha-1 for sorghum lines and hybrids cultivated on an acid, Al toxic soil. SbMATE detoxifies Al by promoting the exclusion of its ionic forms from sensitive sites in the root apex, via formation of stable Al-citrate complexes. Using association mapping we developed gene-specific markers useful for high-throughput allele mining approaches, bridging gene discovery and pre-breeding. SbMATE is however prone to genetic background effects. Our recent advances in this area led to the identification of two interacting transcription factors via genome wide association mapping (GWAS). We have recently shown that sorghum homologs of a serine/threonine receptor kinase, which was previously identified by other groups in rice, enhance phosphorus uptake and sorghum yield on a low-P soil. This is likely a result from enhanced root surface area favoring P diffusion and uptake, which is also being explored in maize transgenics. Our program on P efficiency includes a GWAS framework including multiple traits related to sorghum performance on low-P soils and root system architecture. In this talk, we will give an overview of our efforts towards the development of a molecular breeding pipeline to achieve overall sorghum adaptation to acid soils.