

**P738****Development of a Globally Representative SSR Marker Kit for Sweetpotato (*Ipomoea batatas*)***Date: Monday, January 13, 2014**Room: Grand Exhibit Hall*

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Sweetpotato is the fifth most important global crop. The largest comprehensive collection of sweetpotato plants is held in trust at the International Potato Center (CIP). To analyze genetic similarity, group germplasm, to complement phenotypic characterization and evaluation data, we developed a single sequence repeat (SSR) marker kit for sweetpotato. To capture the germplasm diversity in CIPs genebank of approximately 8000 sweetpotato accessions a composite genotype set (CGS) was developed comprising 395 accessions. Selection criteria for this set included geographic range, nutrient content and resistances to abiotic and biotic stresses. We compiled a database of SSR marker candidates with 500 primers based on a literature review and previous unpublished work at CIP. Out of these primers we selected 46 SSR markers based on screening results, ease of use in the laboratory (amplification and visualization), PIC (polymorphism information content) and PD (power of discrimination) values. Observed PIC values ranged from 0.575 (IBL42) to 0.954 (IBL169). The marker set has a discriminatory power (PD) of 0.945x10⁻⁶⁶. 94% of the CGS genotypes can be discriminated using this kit. The kit is currently being used to characterize the remaining CIP sweetpotato collection. In total, 1029 alleles were identified, from a minimum of 5 alleles (IBL42 and IBS15) to a maximum of 23 alleles (IBS199), averaging 11.5 alleles per marker. As positive controls for internal use and between laboratories comparison purposes, we also identified a minimal set of 96 accessions that represent all amplifiable alleles for the kit.

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January 10 - 15, 2014

Where:

San Diego, CA