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Abstract Title: Genetic diversity analysis of lowland switchgrass (*Panicum virgatum* L.) using SSR (Simple Sequence Repeats) markers

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Abstract (250 words or less): Switchgrass is a warm-season, perennial, C4 grass used for forage, soil conservation, and biofuel production. Its polyploidy, outcrossing behavior, and self-incompatibility has resulted into significant genetic diversity among and within switchgrass populations. An understanding of extent of genetic variation among and within different population sources is important for their efficient use in cultivar development. Twenty three populations of lowland switchgrass including 13 Plant Introduction accessions obtained from USDA Germplasm Resource Information Network (USDA-GRIN) and 10 improved cultivars and breeding lines are being phenotyped at the University of Tennessee, East Tennessee Research and Education Center (ETREC) Plant Science Unit. Each population in the evaluation is represented by 15 genotypes. Young leaf tissue samples were collected from field-grown plants, and DNA samples were extracted from each individual using the CTAB method. Touch down PCR was done using 384-well thermal cyclers. Upland 'Cave-in-rock' and 'Summer' were also included for comparison. A total of 27 SSR markers developed in Noble Foundation were used for PCR amplification. Samples were then genotyped using an ABI 3730 capillary sequencer at the Plant Biology Department of Noble Foundation. All genotypes were manually checked and cleaned using Genemapper. Base pair scores were converted to binary scores with the presence of a PCR product scored as 1 and 0 for its absence. Preliminary result using principal component analysis grouped the switchgrass accessions according to the different populations. Further data analyses are in progress.