Microsatellites to Detect Effects of Reciprocal Recurrent Selection in Maize Populations. (C01-hinze085153-Poster)

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Abstract:

Genetic parameters were estimated for two maize populations (BSSS and BSCB1) undergoing reciprocal recurrent selection. This is cyclical selection program with the goal of increasing the frequency of favorable alleles within a population without losing genetic variability. To investigate this, we used simple sequence repeat (SSR) markers to genotype 30 individuals from seven cycles of selection in both populations. Each population's progenitor lines have also been genotyped to serve as a reference point for identifying alleles that were initially available for entry into the populations. A preliminary analysis of nine polymorphic SSR loci shows the total number of alleles range from three to seven per locus with the average number of alleles equal to 5.56. Each set of cycles and progenitors from both populations was highly differentiated; the proportion of the total variation attributable to differences among sets was 0.221. Nei's genetic distance between BSSS and BSCB1 tended to increase with subsequent cycles and was greatest (D=0.607) when comparing C12 of each population. Observed heterozygosity for all loci (Hobs=0.327) was less than expected heterozygosity (Hexp=0.503).

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