A PCR-Based Method for Quantifying Apomixis in Buffelgrass. (C01-burson151355-Oral)

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Abstract:

Molecular studies of apomixis are hindered by difficulties in determining plant reproductive behavior. Cytological examinations and progeny tests are costly, resulting in smaller mapping populations and fewer phenotype evaluations. Markers linked to apomixis have oversimplified the trait by failing to address the range of reproductive phenotypes in apomicts. We have identified markers equivalent to a gene pair (Aa) segregating 1:1 in a buffelgrass population. The heterozygote status (A/- or a/-) was determined for each hybrid. More than 200 progeny from hybrids (1 obligate sexual, 1 obligate apomict, and 5 facultative apomicts) were screened. Markers in the obligate sexual segregated 1:1 and were transmitted to 50% of the progeny. Markers in the obligate apomict segregated 1:0 and were transmitted to 100% of the progeny. Markers in the facultative apomicts were transmitted to 50% of sexually-derived progeny and 100% of apomicticly-derived progeny. Each percent in excess of 50% corresponded to a 2% expression of apomixis. Results were compared to cytological and progeny test data for each hybrid. The utility of our PCR method for QTL mapping of apomixis will be discussed.

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