SSR Analysis of Inheritance Mode in *Cynodon dactylon* var. *dactylon* (L.) Pers.

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Introduction

Common bermudagrass [*C. dactylon* var. *dactylon* (L.) Pers.] is the most popular and economically important member among *Cynodon* species because of its wide and multiple use for turf, forage and soil erosion control in the world (Taliaferro, 1995). However, information regarding the inheritance of common bermudagrass chromosomes is limited. **Accordingly, the objective of this experiment was to investigate the inheritance mode (disomic, tetrasomic or intermediate) in the taxon.**

Materials and Methods

Two tetraploid (2n=4x=36) first-generation selfed populations: 228 inbreds of 'Zebra', and 273 inbreds of A12359 were used in segregation analysis with simple sequence repeat (SSR) markers. Experimental procedures are given below.

Seed Germination → Sample Grinding → DNA Quantification → DNA Amplification → Gel Electrophoresis

Results and Discussions

Two gel images exhibiting SSR marker segregation patterns of Zebra population are presented in Fig. 1 and of A12359 population in Fig. 2.

Of 21 SSR markers examined in the Zebra progeny population, every SSR marker amplified two alleles and segregated in the progeny population as shown in Fig. 1. Segregation of two markers was consistent with a "1:2:1" ratio while one SSR amplified a segregation pattern of "1:3". The other 18 markers amplified band patterns different from "1:2:1" of disomic inheritance or "1:34:1" of tetrasomic inheritance.

The second population was genotyped with 13 SSR markers, and 12 SSRs each amplified two alleles. Although one SSR amplified four alleles but the four alleles segregated independently in two pairs indicating disomic inheritance and exclusion of tetrasomic inheritance. Segregation of seven SSRs was in agreement with the Mendelian segregation ratio of "1:2:1", and segregation patterns of five other markers were distorted from the ratio.

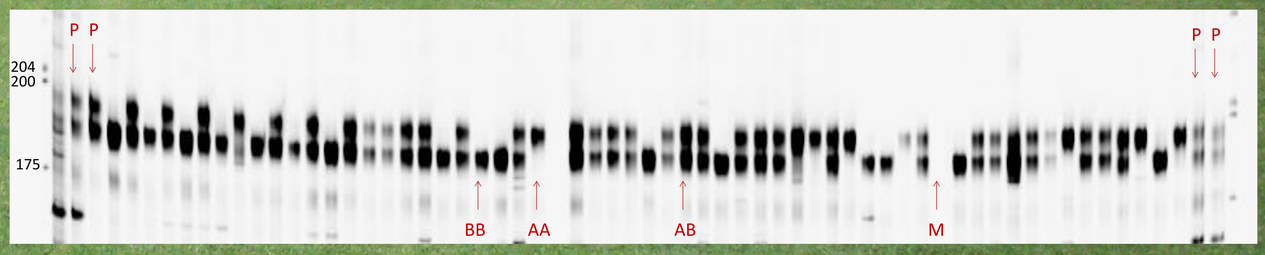

Fig. 1 Gel image of Zebra and 60 progeny amplified with an SSR marker CDGA8-1765/1766. Zebra parent (P) was coded as AB, and progenies had three types of bands: AA, AB, and BB. Missing was label as 'M'.

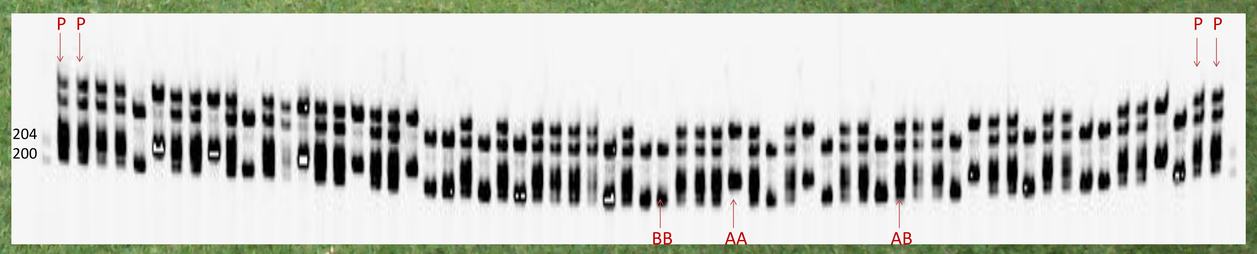

Fig. 2 Gel image of A12359 and 60 progeny amplified with an SSR marker CDAAC5-2523/2524.

In summary, segregation patterns of A12359 were disomic with certain distortions while the segregation of Zebra was disomic with severe distortions. The inheritance knowledge from this study is useful in linkage analysis, construction of genetic maps, breeding, and selection in the species.

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Reference

Taliaferro, C. M. 1995. Diversity and vulnerability of Bermuda turfgrass species. Crop Sci. 35: 327-332.