

Molecular Marker Analysis of Progeny Origins in Sibling-mating and Crossing in Lowland Switchgrass (*P. virgatum* L.)



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Introduction

Switchgrass (*Panicum virgatum* L.) has been targeted for development as a bioenergy crop, however no breeding method for developing economically viable hybrid cultivars exists.

Objective

To assess the viability of generating inbred lines to be crossed under field conditions for hybrid cultivar production.

Materials and Methods

Plant Materials

Inbred progeny of ‘NL94 LYE 16x13’ (NL94) and ‘SL93 7x15’ (SL93) were planted into ten plots (Table 1 below and Fig. 1) at the OSU Agronomy Farm and seed was collected from selected plants in these plots and germinated in the greenhouse (Fig. 2). Tissue samples were then collected from parents and progeny for DNA isolation and PCR analysis.

Marker Selection and Progeny Analysis

Sixty-Four SSR primer pairs were selected using a linkage map by Liu et al. (2012). These markers were tested for polymorphisms with DNA extracted from one NL94 and one SL93 inbred progeny. From this analysis 5 monomorphic and 5 polymorphic markers were selected for genotyping the selected parents and their progeny.



Fig. 1. Plot 7 NL94XSL93 Crossing Plot



Fig. 2. Progeny seedlings prepared for tissue sampling

Results

Differences were seen in the parental origins of progeny between mating types, genotypes, and inbreeding levels (see Table 1).

Table 1. Progeny Origins by Plot

Plot	Mating Type	Number of Progeny	Selfed Progeny	Sibling-mating Progeny	Outcrossed Progeny
1	SL93 S3	34	55.9%	44.1%	0.0%
2	SL93 S1	47	4.3%	95.7%	0.0%
4	SL93 S3 x NL94 S3	44	25.0%	0.0%	75.0%
5	SL93 S3 x NL94 S3	52	21.2%	5.8%	73.1%
6	SL93 S3 x NL94 S3	17	5.9%	17.6%	76.5%
7	SL93 S1 x NL94 S1	78	0.0%	11.5%	88.5%
8	NL94 S1	46	2.2%	97.8%	0.0%
9	NL94 S2	22	18.2%	81.8%	0.0%
10	NL94 S3	1	0.0%	100.0%	0.0%

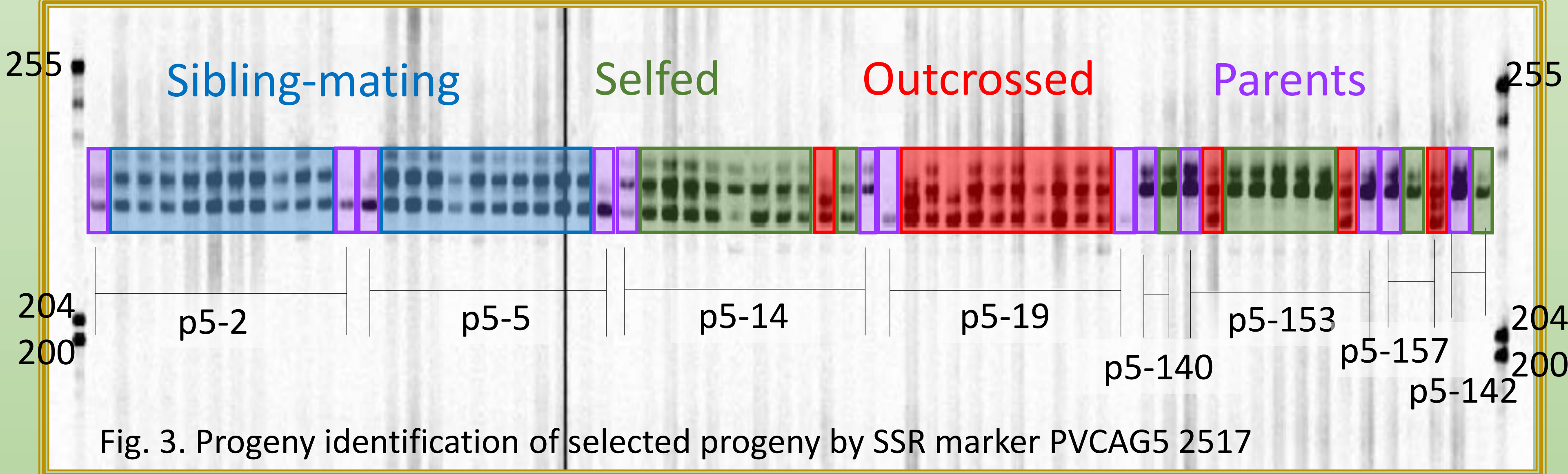


Fig. 3. Progeny identification of selected progeny by SSR marker PVCAG5 2517

Future Prospects

Currently in progress is the collection of a second year of genotyping data. Information from this study will give insight on the effect that multiple generations of inbreeding have on seed origins, and will help breeders assess the viability of producing hybrids using inbred lines grown from seed under field conditions.

Acknowledgements

Thanks to T. Fang, G. Williams, and P. Feng for their assistance and the Oklahoma Agricultural Experiment Station for funding the project.

Reference

Liu et al. 2012. A high-density simple sequence repeat-based genetic linkage map of switchgrass. G3. 2: 357.

