

## Introduction

Switchgrass (*Panicum virgatum*) is developed as a promising cellulosic bioenergy crop due to its multiple agronomic advantages. Reproductive stage is a key developmental process, consequently affecting biomass production in the crop. **Accordingly, the objective of this study was to identify genomic regions responsible for reproductive stages in lowland switchgrass.**

## Materials and Methods

A hybrid population consisting of 179 progeny genotypes derived from a cross between parents NL94 (♀) × SL93 (♂) and a self-pollinated population of 277 progeny from first generation (S1) selfing of NL94, were tested in this study. Two locations were used for phenotypic screening experiment, in each location, a randomized complete block design with three replicates was used. A numerical scale ranging from 1 to 7 was used to evaluate maturity stages of the two populations. A total of 175 simple sequence repeat (SSR) markers were genotyped in the hybrid population. Genotypic data of more than 500 SSR markers in the S1 population collected in two previous experiments were used as well. Marker linkage analysis and QTL analysis were performed using JoinMap 4 and MapQTL 6, respectively.



Fig. 1. Mapping pop. planted in 2011 (A), and data collected 2012-13 (B & C) at Stillwater, OK

## Results

There was a substantial amount of variation in the two populations. Two major QTLs were identified on linkage group 2b and 8b in the hybrid population, while in the selfed population, two major QTL regions occurred on linkage group 2b and 7a (Fig. 2). Besides, several other QTLs were observed sporadically at different time points. Among all of these QTL regions, the one on linkage group 2b (between marker **nfsg-125** and **nfsg-09**) has a consistent effect across two populations and different time points (Table 1).

## Results cont.

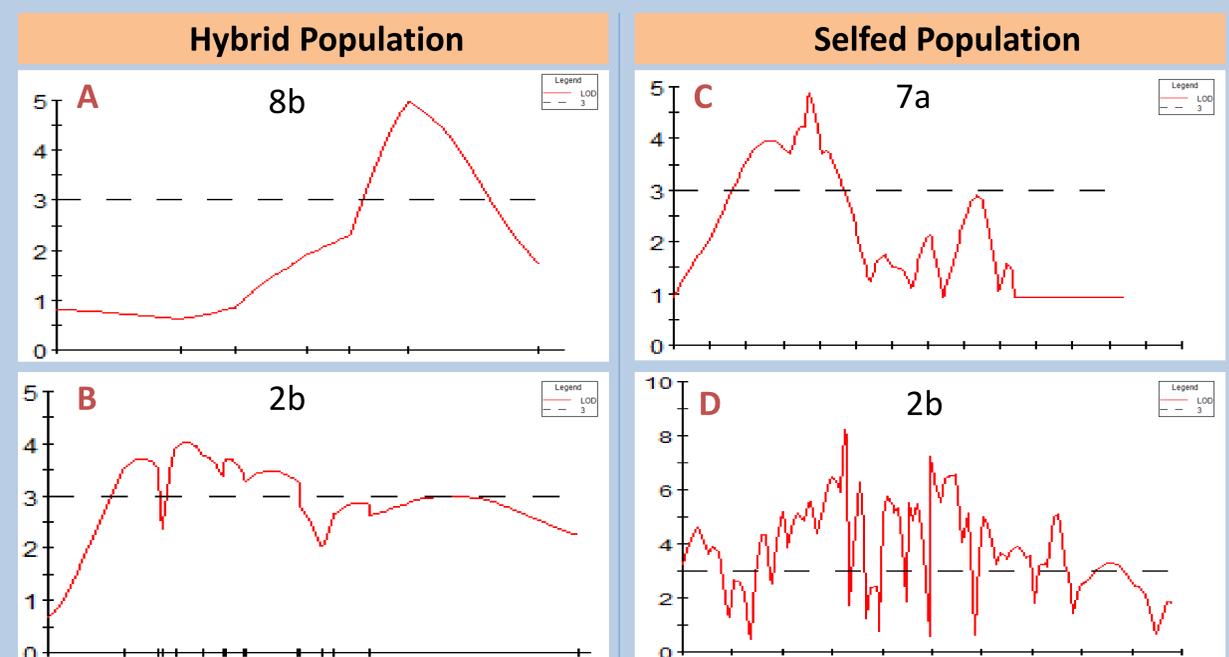


Fig. 2. QTL LOD profiles (A-D) and major QTL identified on linkage group 8b (A) and 2b (B) in the hybrid population, and on linkage group 7a (C) and 2b (D) in the selfed population

Table 1. Major QTLs identified in two populations, yellow color highlighted region is the common QTL identified in two populations on linkage group 2b

Hybrid Pop.	LG	1a	2b	3a	3b	8b
	Marker	PVGA-1253	nfsg-125	PVCA-55	sww-1761	PVGA-1149
Region	sww-606	nfsg-09	PVAAG-2857	sww-1643	PVGA-1275	
% Expl. Var.	12.4	12.5	11.0	13.0	15.5	
Selfed Pop.	LG	2b	2b	2b	7a	9a
	Marker	PVCA-65	nfsg-125	PVCAG-2352	PVAAG-3051	PVE-49/50
Region	PVCA-269	PVE-1143	nfsg-135	sww-2532	nfsg-137	
% Expl. Var.	13.6	23.3	11.6	11.5	11.4	

## Reference

Liu, L.L., Y.Q. Wu, Y.W. Wang, and T. Samuels. 2012. A high-density simple sequence repeated-based genetic linkage map of switchgrass. *G3* 2:357-370.

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