

# Mapping of QTL Underlying Biomass Yield and Related Traits in Switchgrass

Desalegn D. Serba<sup>1</sup>, Guillaume Daverdin<sup>2</sup>, E. Charles Brummer<sup>1</sup>, Joseph H. Bouton<sup>1</sup>, Katrien H. Devos<sup>2</sup> and Malay C. Saha<sup>1</sup>

<sup>1</sup>Forage Improvement Division, The Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401;  
<sup>2</sup>University of Georgia, College of Agricultural and Environmental Sciences, 3111 Miller Plant Sciences Building, Athens, GA 30602

## Abstract

Switchgrass is a warm-season perennial grass identified as a promising dedicated bioenergy crop. Improvement of biomass yield and cell wall composition traits is paramount to meet the production target. Application of molecular markers in breeding programs increases the selection efficiency and gain. With the aim of developing marker-assisted selection (MAS) in switchgrass, quantitative trait loci (QTL) analysis was conducted for biomass yield and related traits using data obtained from several environments on ♀AP13 × ♂VS16 a mapping population. The parental linkage maps were constructed using SSR and STS markers. The population showed significant variations in all the traits studied including transgressive segregations. Based on composite interval mapping, a total of 35 main-effects QTL were identified for each of biomass yield and plant height. The phenotypic variability explained (PVE) by individual QTL ranged from 4.5-24.0% for biomass yield and from 4.6-30.6% for plant height. A total of 20, 39 and 41 main-effect QTL were detected for regrowth, heading dates and vegetative growth length, respectively. The PVE ranged from 4.8-23.2, 5.0-51.8 and 4.1-50.3% for regrowth, heading date and vegetative growth length, respectively. QTL with pleiotropic effects that may enable indirect selection for biomass yield via contributing traits were identified. Ten genomic regions were found important in controlling biomass yield and related traits. The markers anchoring the QTL can be used in MAS breeding to maximize selection gain for biomass yield in switchgrass.

## Introduction

Switchgrass (*Panicum virgatum* L.) is one of the herbaceous species mandated as a dedicated feedstock for next-generation bioenergy production. Biomass yield improvement is one of the priority research areas in bioenergy feedstock development programs. To facilitate the breeding program using marker-assisted selection (MAS), identification of quantitative trait loci (QTL) underlying the traits is of paramount importance. Thus, QTL analysis was conducted for yield and developmental traits on parental linkage maps of AP13 x VS16 a mapping population. The objectives of this project were to identify genomic regions responsible for increased biomass yield, plant height, early regrowth and late heading, and to identify molecular markers that can be used as an aid for indirect selection of desirable genotypes for these traits.

## Materials and Methods

The QTL analysis was conducted using parental linkage maps of AP13 and VS16 constructed with SSR and STS markers. The map used for the QTL analysis excluded the DArT markers used in the map reported as the data were available for 135 genotypes (Serba et al., 2013). Each of the parental maps had 18 linkage groups. Least square means of 188 progeny phenotypic data from two to three locations over three to four years were used for the analysis. QTL analysis was conducted using WinQTL Cartographer version 2.5 (Wang et al., 2006) with backcross model. A LOD threshold of 2.5 ( $p < 0.05$ ) was used to claim a putative QTL for each trait. Map regions with LOD scores greater than the threshold were presented as putative QTL and the nearest markers to the QTL positions were selected.

## References

Serba, D., Wu, L., Daverdin, G., Bahri, B.A., Wang, X., Kilian, A., Bouton, J.H., Brummer, E.C., Saha, M.C. and Devos, K.M., 2013. Linkage maps of lowland and upland tetraploid switchgrass ecotypes. *Bioenergy Research* DOI 10.1007/s12155-013-9315-6  
Wang, S., Basten, C.J., Zeng, Z.-B. 2006. Windows QTL Cartographer 2.5. Department of Statistics, North Carolina State University, Raleigh, NC.

## Results

- The population had significant variations for all the traits across environments.
- A total of 35 main-effects QTL were identified for biomass yield and plant height. Ten genomic regions presumed important in controlling biomass yield and/or plant height in switchgrass (i.e., Fig. 2) were mapped.
- The percent of phenotypic variance explained (PVE) by individual QTL ranged from 4.53-23.99% for biomass yield and from 4.55-30.55% for plant height.
- Several QTL were found consistently across environments (Table 1, Fig. 2). QTL mapped in four genomic regions had significant QTL × environment interactions.
- Five QTL with pleiotropic effects on both traits were identified that may enable indirect selection for biomass yield via selection for plant height.

Table 1. Major QTL detected for biomass yield and plant height across environments

QTL name	LG	Position (cM)	LOD (A)	PVE (%)	Additive effect
by3a-m.09b	IIIa-m	17.7	5.1	23.99	0.37
by4b-m.09b	IVb-m	46.4	3.0	10.29	0.25
by5a-f.09g	Va-f	95.6	3.2	12.90	0.07
by9b-f.10b	IXb-f	45.2	4.7	11.93	0.33
by4b-m.10b	IVb-m	31.5	3.4	14.56	0.33
by3a-m.10g	IIIa-m	20.7	3.2	12.22	0.14
by9a-m.10g	IXa-m	33.6	3.9	11.38	0.14
by2b-f.11a	IIb-f	53.0	2.5	10.50	0.11
by9a-m.11g	IXa-m	79.1	4.8	13.08	0.10
by9b-f.BLUP	IXb-f	45.2	4.4	11.31	0.13
by4b-m.BLUP	IVb-m	46.4	2.8	10.42	0.12
ph5a-m.09a	Va-m	41.9	4.6	8.08	5.52
ph9a-f.09g	IXa-f	24.8	2.9	15.75	7.43
ph4a-m.09g	IVa-m	34.7	3.3	9.90	-5.96
ph5b-m.09g	Vb-m	25.5	2.6	12.85	6.71
ph1b-f.10a	Ib-f	25.9	3.2	6.16	5.14
ph9a-m.10a	IXa-m	30.6	3.8	30.55	11.36
ph1a-f.11b	Ia-f	53.7	3.0	6.25	6.20
ph2a-f.BLUP	IIa-f	55.3	2.4	6.54	3.01
ph4a-m.BLUP	IVa-m	78.3	6.3	12.85	-4.22

- Totals of 20 and 39 additive main-effect QTL were detected for regrowth and heading, respectively (i.e., Table 2, Fig. 3).
- The PVE by individual QTL ranged from 5.15-34.64% for regrowth and 3.81-50.03% for heading.
- Eight genomic regions that contained clusters of loci that control vegetative growth in switchgrass were identified.
- Thirteen pleiotropic QTL influencing regrowth and heading date were mapped.

Table 2. Major QTL detected for regrowth and heading date across environments

QTL Name	LG	Position (cM)	LOD (A)	PVE (%)	Additive effect
drg5a-m.09A	Va-m	3.30	4.7	11.25	-1.1
drg3b-f.09A	IIIb-f	58.04	2.7	22.69	-2.1
drg4a-m.09A	IVa-m	53.92	2.5	15.73	-1.7
drg8a-f.11A	VIIIa-f	70.77	3.9	16.67	-1.5
drg3b-m.11B	IIIb-m	46.02	3.3	34.64	-3.1
drg4a-mf.BLUP	IVa-m	53.92	2.7	17.30	-1.0
dhd5b-f.08A	Vb-f	46.2	10.8	27.45	5.1
dhd2b-m.08A	IIb-m	54.6	10.6	15.12	3.8
dhd8b-f.09B	VIIIb-f	20.8	3.0	23.45	13.0
dhd8b-f.09B	VIIIb-f	55.0	2.7	15.45	10.6
dhd7b-f.11A	VIIb-f	66.1	4.1	12.86	3.0
dhd2b-m.11A	IIb-m	75.6	3.0	13.21	3.1
Dhd2b-m.BLUP	IIb-m	75.6	4.3	18.39	3.5

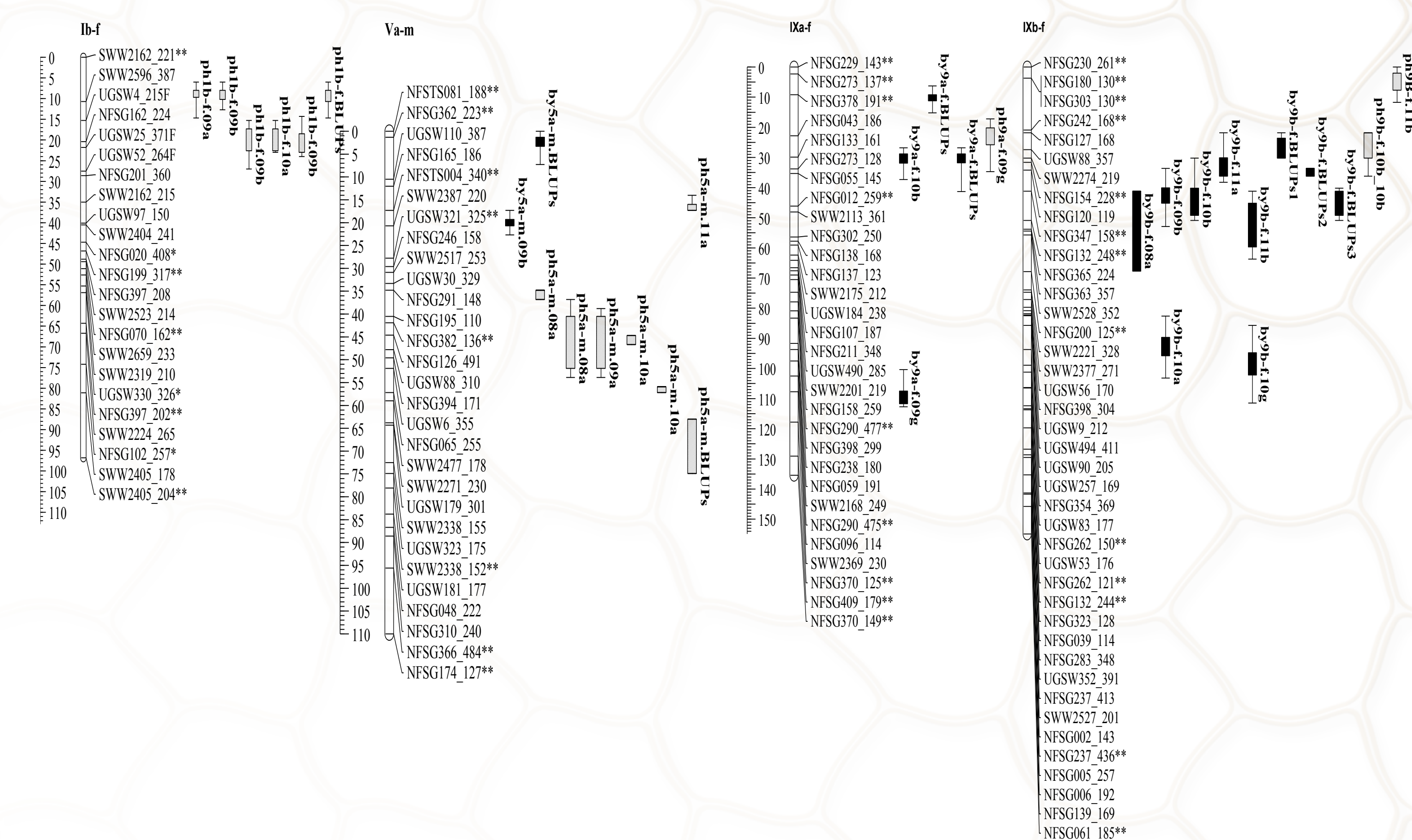


Figure 2. Major QTL detected for biomass yield and plant height detected on parental maps

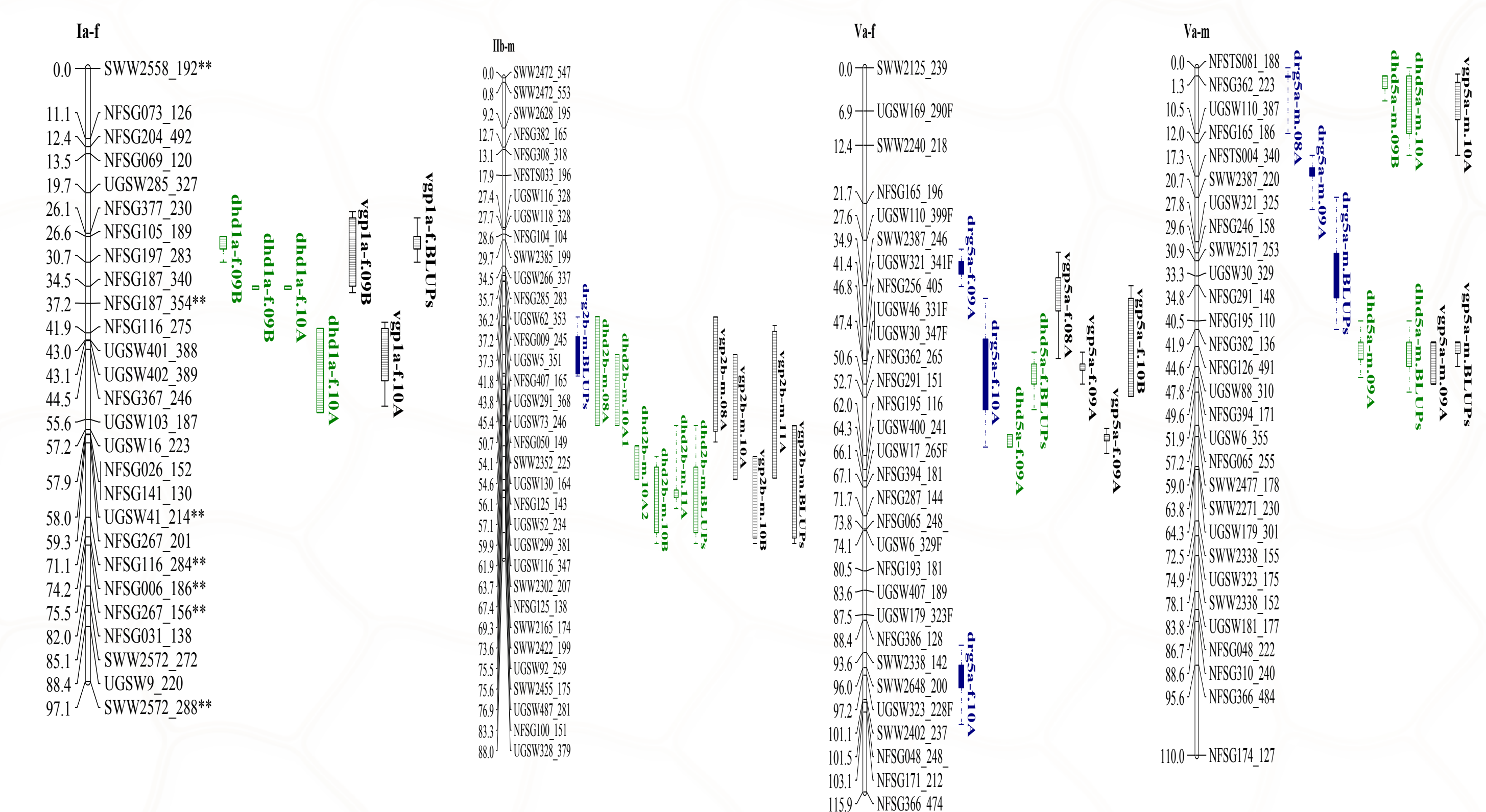


Figure 3. Major QTL detected for days to regrowth and heading on AP13 and VS16 parental maps

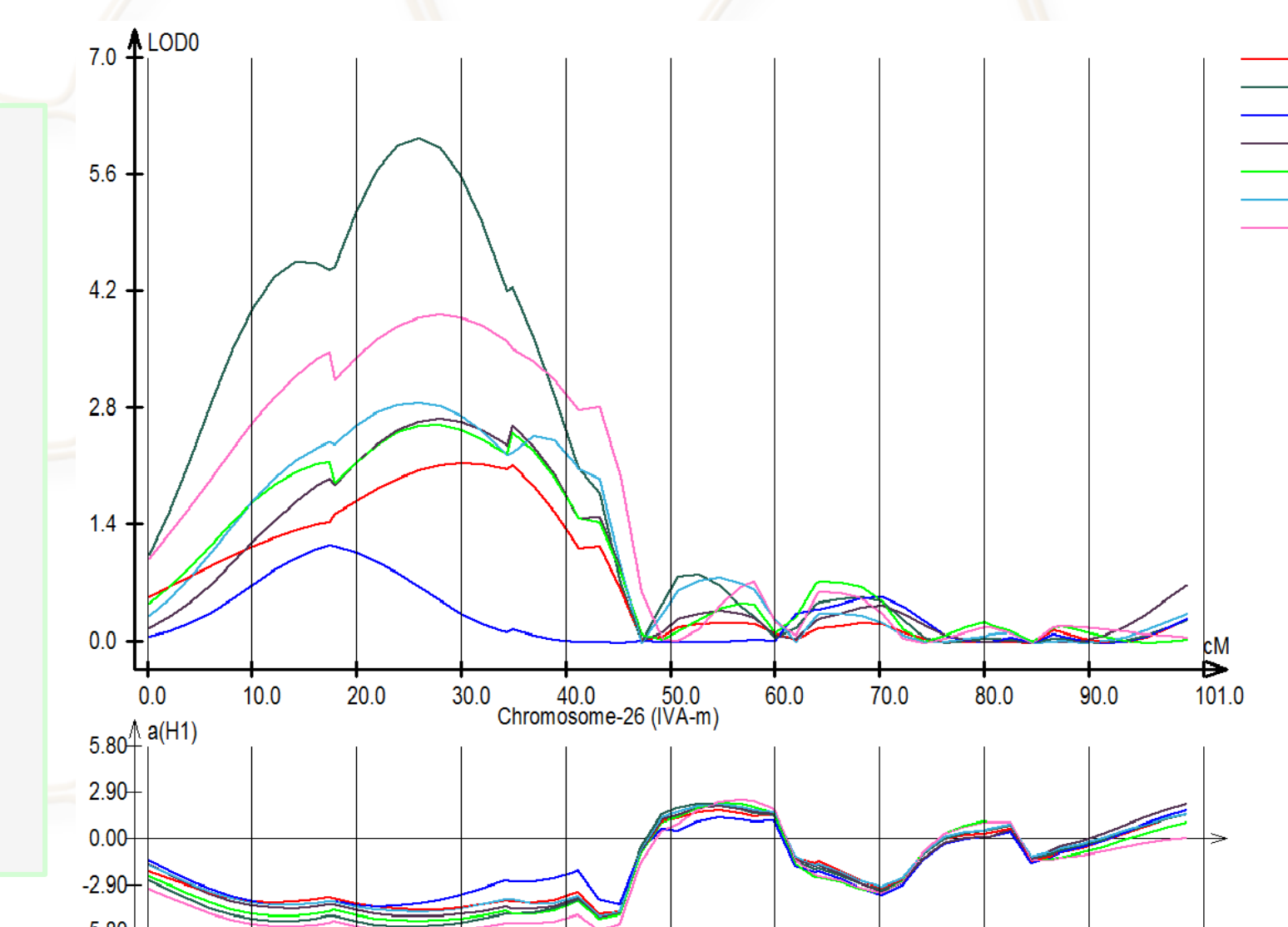


Figure 1. Plant height QTL on LG Va-m detected across environments

