

## Aberystwyth University

### *Water saving traits co-map with a major terminal drought tolerance quantitative trait locus in pearl millet [*Pennisetum glaucum* (L.) R. Br.]*

Kholova, Jana; Nepolean, T.; Hash, C. T.; Supriya, A.; Rajaram, Vengaldas; Senthilvel, S.; Kakker, Aparna; Yadav, R. S.; Vadez, Vincent

*Published in:*  
Molecular Breeding

*DOI:*  
[10.1007/s11032-012-9720-0](https://doi.org/10.1007/s11032-012-9720-0)

*Publication date:*  
2012

*Citation for published version (APA):*

Kholova, J., Nepolean, T., Hash, C. T., Supriya, A., Rajaram, V., Senthilvel, S., Kakker, A., Yadav, R. S., & Vadez, V. (2012). Water saving traits co-map with a major terminal drought tolerance quantitative trait locus in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Molecular Breeding*, 30(3), 1337-1353.  
<https://doi.org/10.1007/s11032-012-9720-0>

#### **Document License** CC BY

#### **General rights**

Copyright and moral rights for the publications made accessible in the Aberystwyth Research Portal (the Institutional Repository) are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the Aberystwyth Research Portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the Aberystwyth Research Portal

#### **Take down policy**

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

tel: +44 1970 62 2400  
email: [is@aber.ac.uk](mailto:is@aber.ac.uk)

Water saving traits co-map with a major terminal drought tolerance quantitative trait loci in pearl millet (*Pennisetum glaucum* (L.) R. Br.).

**Jana Kholová<sup>1</sup>, T. Nepolean<sup>2</sup>, C. Tom Hash<sup>1</sup>, A. Supriya<sup>1,4</sup>, S. Senthilvel<sup>1</sup>, Aparna Kakkera<sup>1</sup>, Rattan Yadav<sup>3</sup> and Vincent Vadez<sup>1\*</sup>**

**Supplementary Table 1.** Average minimum and maximum temperature (Tmin, Tmax), humidity (RHmin, RHmax) and VPD of distinct experimental sets 14 days prior to assessment of physiological traits

Set Number	Tmin	RHmin	Tmax	RHmax	VPDmin	VPDmax
set 1	15.69	32.33	35.84	94.16	0.10	3.93
set 2	16.02	31.71	35.81	92.69	0.13	3.96
set 3	15.74	30.78	35.76	91.71	0.15	4.01
set 4	14.93	29.28	35.70	91.67	0.15	4.10
set 5	15.06	30.90	35.11	93.50	0.11	3.88

**Supplementary Table 2.** The variation within and between experimental RIL sets approximated by the set average, standard deviation (SD), minimum and maximum range of trait values and differences between parental genotypes across experimental sets. Below the trait values, the results of ANOVA showing the significance of variation across sets, genotypes and genotype x set interactions at the levels of significance;  $p < 0.001$  (\*\*\*) ;  $p < 0.01$  (\*\*);  $p < 0.05$  (\*); “ns” stands for non-significant variation and MS for mean square. The LSD of means is visualized as letters next to trait/parent average where different letters indicate significant difference of means and *vice versa*.

These traits are; leaf dry weight (LDW [g]), root dry weight (RDW [g]), shoot dry weight (ShDW[g]), stem dry weight (StDW[g]), biomass dry weight (BDW[g]), leaf area (LA [cm<sup>2</sup>]) specific leaf weight (SLW [g cm<sup>-2</sup>]), transpiration rate (Tr [g water cm<sup>-2</sup> leaf area h<sup>-1</sup>]) and absolute transpiration (T [g]). The measurements between 7:30-10:30 a.m. are indicated with suffix M and 10:30 a.m.-2:30 p.m. with suffix A and particular set’s suffix indicates the date of measurement in December 2009.

trait-set	average	SD	Range	H77/833-2	PRLT2/89-33
BDW 23	7.47(c)	1.89	4.05-11.81	6.47	7.44
BDW 28	10.49(a)	1.77	6.09-14.03	9.5	10.86
BDW 31	9.00(b)	1.99	4.85-13.29	9.38	12.77
variation source	set	genotype	genotype x set	<b>8.45±0.99(a)</b>	<b>10.36±1.56(a)</b>
Significance	***	***	***		
LA 18	467.04(d)	112.61	206.75-766.25	285.69	-
LA 21	1072.49(b)	222.16	615.89-1604.31	995.45	1269.54
LA 23	898.30(c)	230.17	419.99-1402.59	547.46	965.94
LA 28	1198.35(a)	217.5	657.86-1749.9	1215.89	1303.97
LA 31	1052.60(b)	221.54	582.54-1649.22	916.85	1770.99
variation source	set	genotype	genotype x set	<b>792.3±166.25(b)</b>	<b>1327.6±166.16(a)</b>
Significance	***	***	***		
LDW 18	3.07(d)	0.59	1.68-4.34	2.19	-
LDW 21	4.00(c)	0.77	1.76-5.42	3.64	5.1
LDW 23	3.95(c)	0.98	2.24-7.06	3.2	3.6
LDW 28	5.10(a)	0.79	3.12-6.98	5.5	4.85
LDW 31	4.38(b)	0.89	2.51-6.76	3.61	5.86
variation source	set	genotype	genotype x set	<b>3.63±0.54(a)</b>	<b>4.86±0.47(a)</b>
Significance	***	***	***		
RDW 23	1.69(c)	0.65	0.58-3.22	1.97	1.93
RDW 28	2.92(a)	0.91	1.07-5.36	2.48	4.02
RDW 31	2.35(b)	0.72	1.2-4.5	4.36	4.25
variation source	set	genotype	genotype x set	<b>2.93±0.73(a)</b>	<b>3.4±0.74(a)</b>
MS	***	ns	***		
ShDW 18	4.34(d)	0.87	2.36-6.34	3.18	-
ShDW 21	5.78(c)	1.1	2.98-8.08	5.26	6.82
ShDW 23	5.75(c)	1.37	3.23-9.36	4.5	5.51
ShDW 28	7.51(a)	1.22	4.69-9.7	7.02	6.84
ShDW 31	6.65(b)	1.41	3.55-10.07	5.02	8.52
variation source	set	genotype	genotype x set	<b>5±0.62(a)</b>	<b>6.9±0.62(a)</b>
Significance	***	***	***		
SLW 18	0.0067(a)	0.001	0.0046-0.0109	0.0077	-
SLW 21	0.0038(d)	0.0009	0.0021-0.006	0.0037	0.004
SLW 23	0.0045(b)	0.0006	0.0032-0.0063	0.0058	0.0037
SLW 28	0.0043(bc)	0.0004	0.0035-0.0055	0.0045	0.0037
SLW 31	0.0042(c)	0.0005	0.0035-0.006	0.0039	0.0033
variation source	set	genotype	genotype x set	<b>0.0051±0.0007(a)</b>	<b>0.0037±0.0001(a)</b>
Significance	***	***	***		
StDW 18	1.24(d)	0.36	0.08-2.02	0.99	-
StDW 21	1.76(c)	0.49	0.59-2.96	1.62	1.72
StDW 23	1.78(c)	0.5	0.54-3.04	1.3	1.91
StDW 28	2.40(a)	0.57	0.88-3.78	1.52	1.99
StDW 31	2.24(b)	0.58	1.04-3.59	1.41	2.66
variation source	set	genotype	genotype x set	<b>1.37±0.11(a)</b>	<b>2.07±0.2(a)</b>
Significance	***	***	***		

TA 18	19.72(g)	3.3	8.03-28.28	16	-	
TA 19	21.30(f)	3.85	8.78-31.1	15.2	-	
TA 21	23.36(e)	3.88	10.8-32.78	21.97		26.03
TA 22	33.76(a)	5.53	10.98-45.15	33.8		36.88
TA 23	28.45(c)	6.09	14.18-40.18	20.8		31.27
TA 24	31.81(b)	6.83	16.22-48.15	24.9		36.02
TA 28	28.27(c)	4.61	19.1-39.77	30.4		28.15
TA 29	16.71(h)	2.4	11.52-21.88	19.3		18.58
TA 31	26.24(d)	4.49	18.4-37.85	21.35		36.55
variation source	set	genotype	genotype x set	<b>22.64±2.06(b)</b>		<b>30.5±2.56(a)</b>
Significance	***	***	ns			
TM 18	11.55(d)	2.11	4.9-18.17	9.43	-	
TM 19	7.91(e)	1.35	3.7-10.97	6.2	-	
TM 21	10.38(c)	1.68	5.57-14.17	9.7		11.17
TM 22	14.09(a)	2.44	7.33-19.33	14.73		16.57
TM 23	11.26(b)	2.7	5-18.9	10.5		13.8
TM 24	13.40(a)	2.89	7.2-20.23	11.43		14.87
TM 28	9.58(d)	1.26	5.93-12.07	10.9		9.8
TM 29	9.97(cd)	1.47	7.03-13.73	10.97		10.97
TM 31	10.11(cd)	1.69	6.83-14.47	8.2		13.5
variation source	set	genotype	genotype x set	<b>10.23±0.78(b)</b>		<b>12.95±0.91(a)</b>
Significance	***	***	**			
Tr A 18	0.0442(a)	0.0075	0.0323-0.0659	0.056	-	
Tr A 19	0.0477(b)	0.0082	0.0356-0.0752	0.0532	-	
Tr A 21	0.0227(f)	0.0036	0.0146-0.0311	0.0221		0.0205
Tr A 22	0.0331(d)	0.0061	0.0221-0.0485	0.034		0.029
Tr A 23	0.0328(e)	0.0043	0.0242-0.0423	0.038		0.0324
Tr A 24	0.0367(c)	0.0051	0.0245-0.0518	0.0455		0.0373
Tr A 28	0.0239(g)	0.0031	0.0176-0.0331	0.025		0.0216
Tr A 29	0.0141(g)	0.0018	0.0108-0.0188	0.0159		0.0142
Tr A 31	0.0258(f)	0.0034	0.0199-0.0357	0.0233		0.0206
variation source	set	genotype	genotype x set	<b>0.035±0.0048(a)</b>		<b>0.025±0.003(b)</b>
Significance	***	***	***			
Tr M 18	0.0259(a)	0.0052	0.017-0.0447	0.033	-	
Tr M 19	0.0178(b)	0.0035	0.0117-0.0299	0.0217	-	
Tr M 21	0.0101(g)	0.0019	0.0072-0.0152	0.0097		0.0088
Tr M 22	0.0138(d)	0.0031	0.0096-0.0221	0.0148		0.013
Tr M 23	0.0130(d)	0.0023	0.0078-0.0194	0.0192		0.0143
Tr M 24	0.0155(c)	0.0028	0.0079-0.0234	0.0209		0.0154
Tr M 28	0.0082(f)	0.0012	0.0057-0.0118	0.009		0.0075
Tr M 29	0.0084(h)	0.0011	0.0058-0.0111	0.009		0.0084
Tr M 31	0.0100(e)	0.0016	0.0069-0.0146	0.0089		0.0076
variation source	set	genotype	genotype x set	<b>0.016±0.0027(a)</b>		<b>0.011±0.0013(b)</b>
Significance	***	***	***			





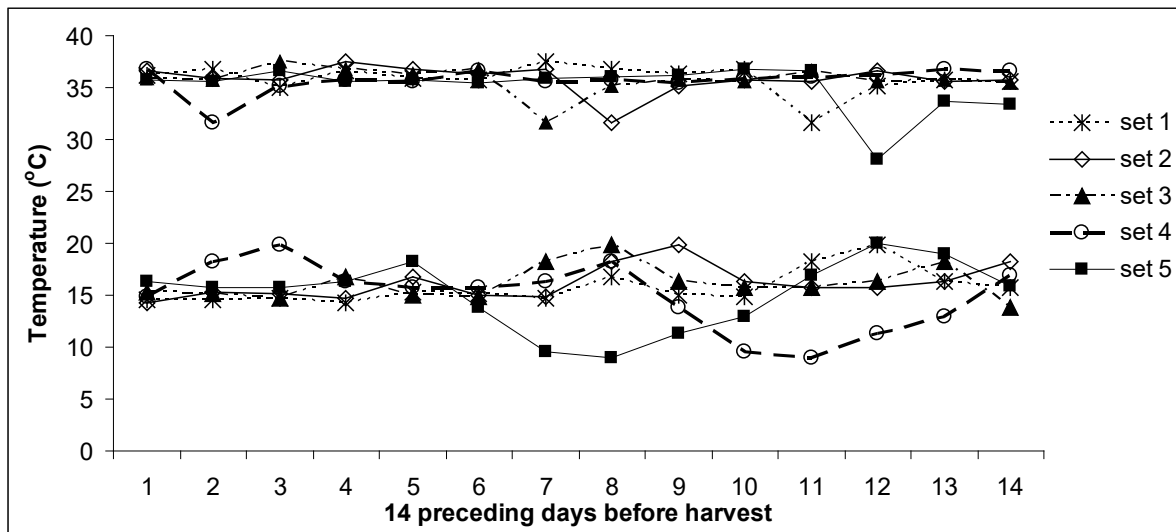


**Supplementary Table 6** Numerical output of principal component analysis (PCA) based on BLUP means of investigated traits, i.e. transpiration rate (Tr), absolute transpiration (T), leaf dry weight (LDW), root dry weight (RDW), shoot dry weight (ShDW), stem dry weight (StDW), biomass dry weight (BDW), leaf area (LA) specific leaf weight (SLW). Traits with suffix M were measured during 7:30-10:30 a.m. and traits with suffix A were measured during 10:30 a.m.-2:30 p.m. In the top part of the table the standard deviation (SD), proportion of phenotypic variance (PV) and cumulative PV for three major principal components (PC1, 2, 3) is shown. Bottom part of the table shows the values of traits loadings in particular PC

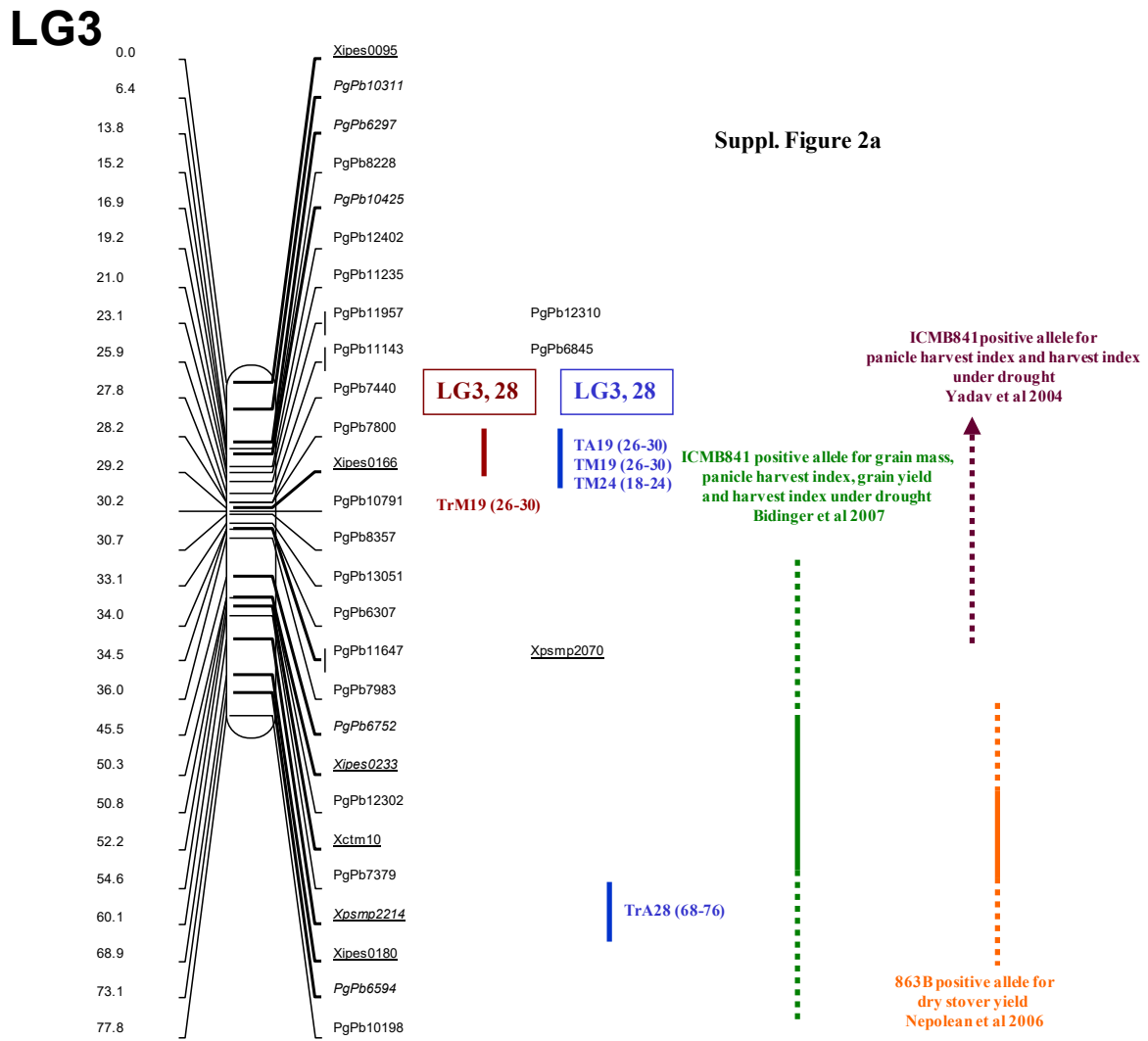
Statistics	PC 1	PC 2	PC 3
SD	2.565	1.481	0.813
PV	0.598	0.199	0.060
Cumulative PV	0.598	0.797	0.858
Loadings:			
Trait name	PC 1	PC 2	PC 3
TrM	-0.249	-0.479	negligible
TrA	-0.233	-0.455	negligible
LDW	0.351	-0.132	negligible
StDW	0.334	negligible	negligible
ShDW	0.366	-0.112	negligible
LA	0.362	0.153	negligible
SLW	-0.169	-0.518	negligible
RDW	0.254	-0.276	-0.632
BDW	0.347	-0.171	-0.386
TA	0.319	-0.161	0.37
TM	0.261	-0.329	0.544



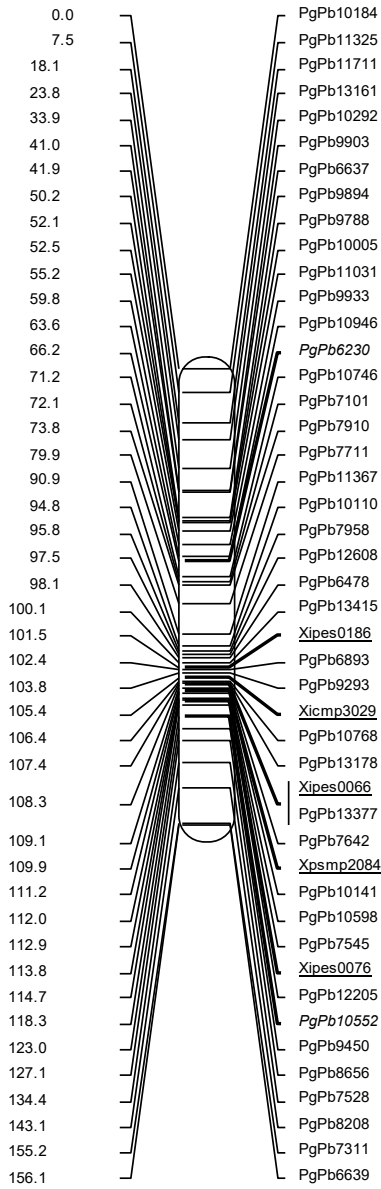
**Supplementary Fig. 1.** Maximum and minimum temperature to which the different experimental sets were exposed during 14 days prior to their assessment for Tr and related traits.



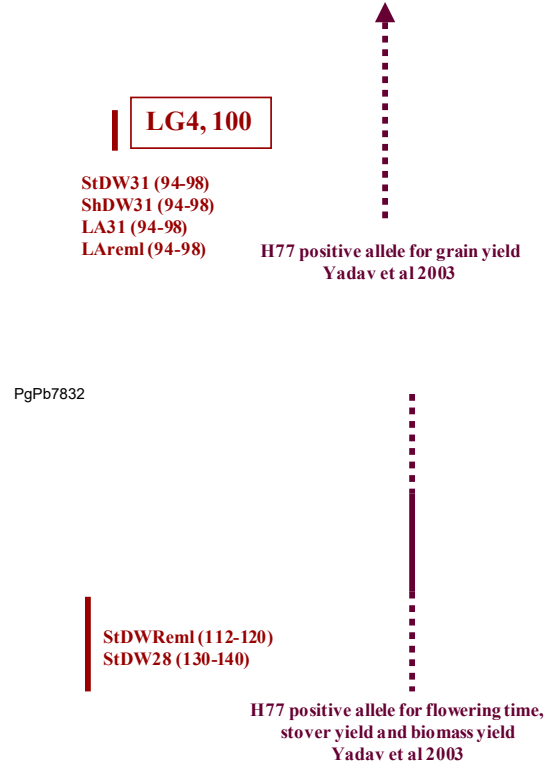
**Supplementary Fig.2.** Visualization of approximate QTLs positions within the linkage groups of minor importance (LG; chromosomes 3, 4, 5, and 6, letter a to d) consisting of SSR and DArT markers and their positions in cM.



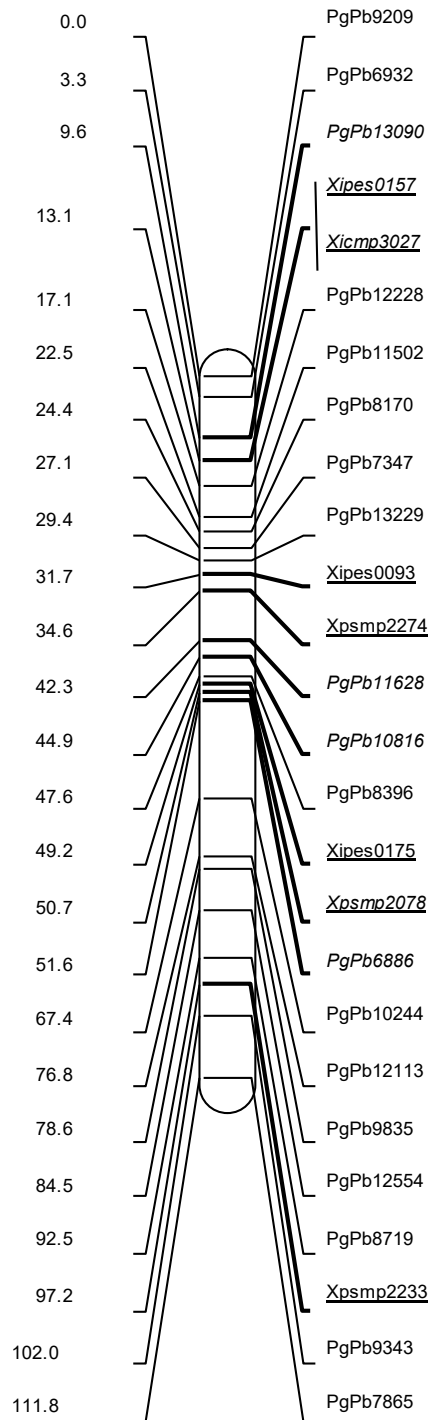
# LG4



Suppl. Figure 2b



# LG5



## Suppl. Figure 2c

*PgPb7494*

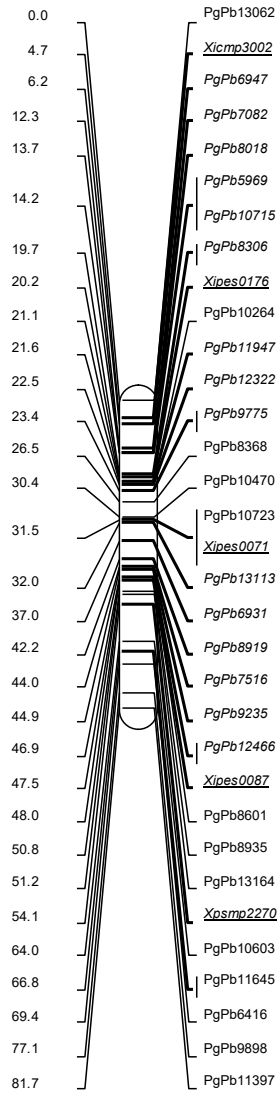
*PgPb12052*



**ICMB841 positive allele for  
dry stover yield  
Nepolean et al 2006**

**863 B positive alleles for  
grain yield, harvest index  
ICMB 841 positive allele for  
stover yield under drought  
Yadav et al 2004**

# LG6



Suppl. Figure 2d

