



Sweet Sorghum an alternative energy Crop

Grant Agreement n° 227422

WP3

Deliverable 3.18:

*Identification of the genetic markers
linked to the juicy stem and juicy*



Composition of the consortium

CIRAD
ICRISAT
EMBRAPA
KWS
IFEU
UniBO
UCSC
ARC-GCI
UANL
WIP

QTL mapping was performed using 90 RILs of 102 lines previously genotyped derived from the parents BR007 (juice stem) and SC2823 (dry stem). Two QTLs were mapped both on chromosome 6 using a composite interval mapping methodology (significance of test = 0.01) (see summary of QTL analysis below). These preliminary results provide significant evidence that the genetic control for absence or presence of juice in the stem is underlain by chromosome 6, since a high peak of $\log_{10}(p)$ was observed for one of the QTLs mapped on it. This strongly indicates a high probability that this QTL is related with the absence or presence of juice. This analysis will be redone using a larger population (400 RILs) with GBS genotyping in 2013 which will be extremely important to confirm these results.

Summary of QTL analysis

List of QTLs

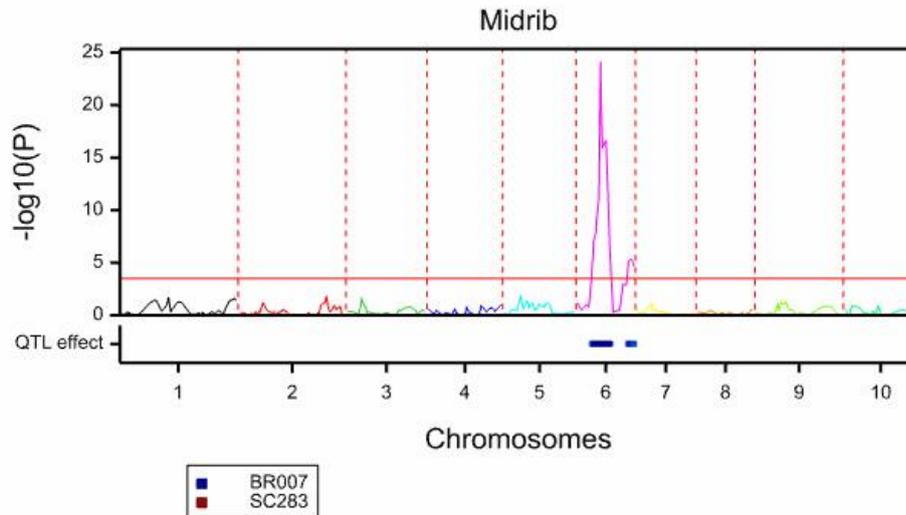
Locus no.	Locus name	Linkage group	Position	$-\log_{10}(P)$
261	sPb3372	6	60.60	15.217
272	sPb3962	6	141.70	4.743

QTL effects

Locus no.	Locus name	%Expl. Var.	Add.High value eff.	s.e. allele
261	sPb3372	53.074	0.367 BR007	0.036
272	sPb3962	10.821	0.166 BR007	0.036

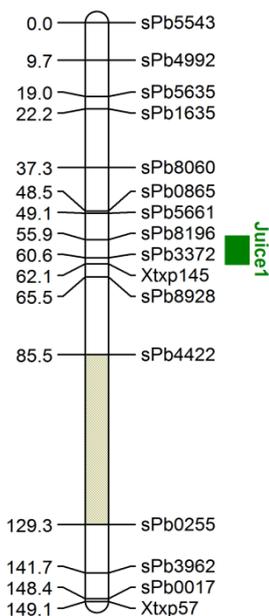
Estimated lower and upper bounds of QTL positions

Locus no.	Locus name	Lower bound	Position	Upper bound
261	sPb3372	54.991	60.600	66.209
272	sPb3962	35.524	141.700	149.100



Graphical display of the QTLs detected for midrib color (high correlated to presence or absence of juice stem in sorghum) evaluated after 50 days after sowing. The associated tail probability of the Wald statistics, P , is expressed as $-\log_{10}(P)$, analogous to the usual LOD score profile. The red horizontal line indicates significant threshold ($T=3.5$) obtained from Li and Ji (2005) correction considering $\alpha = 5\%$. Color code for p-values of QTL effects: red / yellow means positive effect of SC283 allele; dark / light blue means positive effect of BR007 allele.

Chr 06



Graph display of sorghum chromosome 6 extracted from the linkage map developed using the RIL population of the cross BR007xSC283 (Sabadin et al. 2012). Chromosome (Chr) designations were assigned according the integrated map described by Feltus et al. (2006). Cross-hatched squares depict regions with genetic distances exceeding 30cM. The markers beginning with M and sPb are DArT markers developed from MITE and PstI libraries, respectively. The positions for QTL affecting midrib color (high correlated to presence and absence of stem juice (Juice1, in green) as estimated by single environment analysis. Only the QTL showing high peak for $\log_{10}(P)$ was considered in this graph display.