Seventh framework programme
Food, Agriculture and Fisheries, and Biotechnology

Specific International Co-operation Actions
Small or medium scale focused research project

Sweet Fuel

Sweet Sorghum
an alternative energy Crop

Grant Agreement n° 227422

Deliverable 3.15:

Identification of genetic markers linked to tillering trait

Composition of the consortium

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

Our breeding objective in developing sweet sorghum cultivars is to develop lines and cultivars with reduced or no tillering to be able to control stem population in sweet sorghum production systems.

Two fertility restorer lines for cytoplasm A1, BR501R (Brandes) and BR505R (Wray), both released sweet sorghum cultivars were crossed with the objective to develop a Recombinant Inbred Line (RIL) population by single seed descent (SSD) for the purpose of identifying QTLs associated with plant tillering, total sugars in the juice and sucrose in the juice. Brandes is a high tillering sweet sorghum cultivar with low purity (low sucrose) and Wray is a non-tillering cultivar with high purity. The F1 was self pollinated to produce a large F2 population. Two hundred seventy-five $F_{2:2}$ RILs were advanced to the S_8 ($F_{2:9}$) generation. DNA was extracted for 273 RILs and the two parents and genotyping by sequencing (GBS) was completed in 2012/2013.

Our first attempt at phenotyping 223 RILs for tillering was in 2011/2012 and 2012/2013by counting the number of plants that emerged and the number of stems at maturity in the agronomic/industrial evaluation. Upon evaluation of these results, we concluded that we needed to refine the methodology for evaluating tillering.

In 2013/2014 we conducted an experiment where we evaluated BR501R, BR505, four RILs varying in tillering and two known high tillering lines with three plant densities within the row; 4, 8 and 12 plants per meter. The results reported in table 1 indicate that four plants per meter in rows with 70 cm between rows is adequate for phenotyping lines. The higher plant densities, about 10 plants per m, used in the agronomic phenotyping reduced expression of the tillering trait.

Table 1.

Tillers per plant of eight contrasting genotypes at the plant densities				
Genotype	Type of Tillering	Plants per meter of row		
		4	8	12
(BR505 * BR501)-9-1-1-1-1	Non-tillering	0.26	0.37	0.39
BR505	Non-tillering	0.62	0.35	0.56
BR501	Tillering	1.37	0.85	0.49
(BR505 * BR501)-149-1-1-1-1	Tillering	1.96	0.93	1.16
(BR505 * BR501)-2-1-1-1-1	Tillering	2.23	1.66	1.61
(BR505 * BR501)-217-1-1-1-1	Tillering	2.73	1.62	1.14
CMSXS651	Highly tillering	3.44	2.88	2.27
CMSXS652	Highly tillering	3.79	3.02	0.18

Based on these results, we plan to phenotype 273RILs of this population, and by association with genotyping data already collected, we will identify QTL associated with tillering and develop genetic markers for use in molecular breeding.