IOWA STATE UNIVERSITY
Department of Agronomy

Association Mapping for Plant Architecture Traits Related to Brassinosteroids in a Diverse *Sorghum bicolor* Collection

María B. Mantilla Pérez*, Jing Zhao, Yanhai Yin and Maria G. Salas Fernandez
*mantilla@iastate.edu

INTRODUCTION

Sorghum has received attention as a bioenergy crop because of its water use efficiency and yield biomass potential. It has become necessary to understand the genetics that control plant architecture traits that increase biomass production. Brassinosteroids (BRs) are steroid hormones that control different aspects of plant growth, development, and have effects over plant architecture traits. Association mapping analysis is a method used to identify associations between markers that can be linked to causal polymorphisms and specific phenotypes.

OBJECTIVE

To test associations between plant architecture phenotypes and allelic variations in BR candidate genes found in a diverse sorghum collection.

MATERIALS AND METHODS

315 accessions were used to measure eight traits of interest: leaf angle, flowering time, plant height, panicle length, panicle exsertion, number of internodes, number of tillers, and stem circumference. BLUPs were used to predict phenotypic values and correlations between traits were calculated (Tab.1). 701 genome-wide SNPs were used to determine population structure and coefficient of co-ancestry using STRUCTURE2.2.3 and SPAGeDI1.4 respectively. 256 SNPs present in 29 BR signaling and biosynthesis genes were used for marker-trait association analysis using TASSEL 3.0. False discovery rate was used to determine significance level.

Correlation	Plant Height	Panicle length	Panicle Exertion	Stem circum	No. of Tiller	No. of Internode	Flowering time	Leaf angle
Plant Height	–							
Panicle length	0.14*	–						
Panicle Exertion	0.47***	0.11	–					
Stem circumfere	-0.31***	0.12*	-0.21***	–				
No. of Tiller	-0.02	0.03	0.05	-0.42***	–			
No. of Internode	0.18**	0.04	-0.09	0.56***	-0.46***	–		
Flowering time	0.15*	0.18**	-0.07	0.46***	-0.30***	0.77***	–	
Leaf angle	0.30***	-0.08	0.04	-0.22***	0.05	-0.12*	-0.20**	–

*significant at the probability of 0.05 level
**significant at the probability of 0.01 level
***significant at the probability of 0.001 level

Table 1. Correlations between the phenotypes of interest.

RESULTS

5 subpopulations were identified using STRUCTURE and PCA (Fig.1).

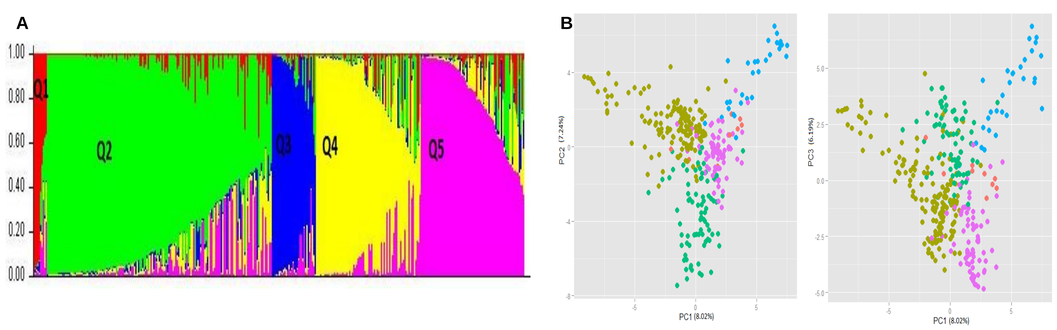

Figure 1. A) Population Structure. Q1, Guinea-Bicolor; Q2, Caudatum; Q3, Guinea-Caudatum (West Africa); Q4, Kafir; Q5, Durra. **B)** Principal component analysis was consistent with population structure. Red:Guinea-Bicolor. Light Green: Caudatum. Bue:Guinea Caudatum (West Africa). Purple: Kafir . Dark Green:Durra.

80 markers were found associated with 7 traits of interest: leaf angle, plant height, panicle length, panicle exsertion, number of tillers, flowering time, and stem circumference. 9 BR signaling and 10 BR biosynthesis candidate genes were found associated (Fig. 2).

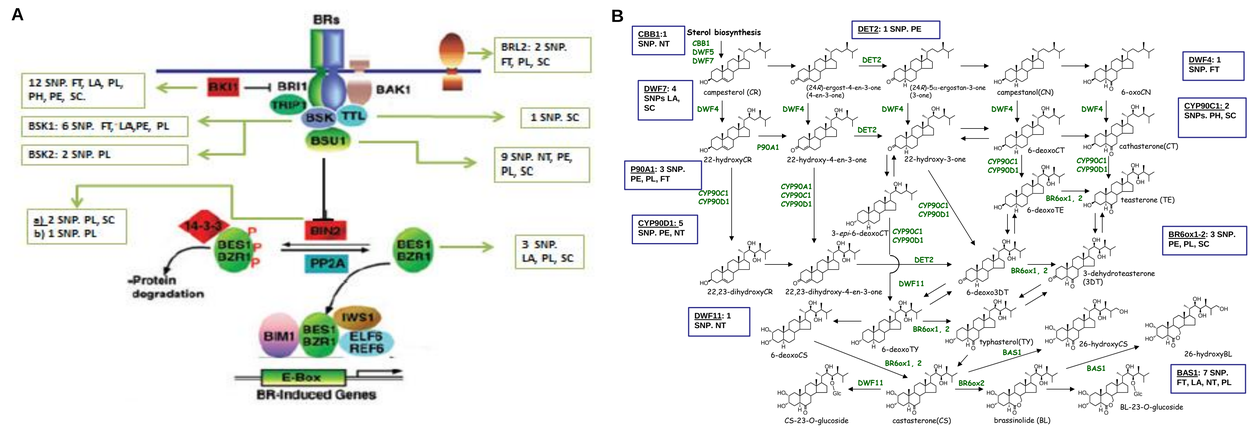

Figure 2. A) BR signaling pathway (Ye et al., 2011) and **B)** BR biosynthesis pathway (Taiz, and Zeiger , 2010). In both figures there is a detail of the candidate genes and number of markers found to be associated with phenotypes. FT: flowering time. LA: leaf angle. NT: number of tillers. PE: panicle exsertion .PL: panicle length. PH: plant height. SC: stem circumference.

16 markers were found associated with more than one phenotype and, although the percentage of variation explained is less than 5%, the phenotypic effect of the markers is consistent with phenotypic correlations between traits (Tab. 2).

Gene/Path	Phenotype	Marker	p-value	q-value	R2	SNP	Effect
BKI1 Signaling	Exser	S2_61882507	9.27E-04	0.15	4.8%	A	-4.66
						T	0.00
	Panlenght	S2_61882507	3.58E-03	0.13	4.2%	A	-2.72
						T	0.00
	Flower	S2_61882507	7.82E-03	0.18	2.7%	A	-1.86
						T	0.00
	Flower	S2_61884862	5.95E-03	0.18	2.8%	A	-1.98
						C	0.00
	Stemcir	S2_61884862	3.47E-03	0.11	3.2%	A	-0.40
						C	0.00
	Flower	S2_61886473	2.01E-02	0.25	1.9%	G	-1.69
						T	0.00
	Stemcir	S2_61886473	8.71E-03	0.12	2.4%	G	-0.37
						T	0.00
	Flower	S2_61887636	1.67E-02	0.23	2.2%	G	-1.77
						C	0.00
	Panlenght	S2_61887636	2.90E-02	0.25	1.7%	G	-2.13
						C	0.00
	Stemcir	S2_61887636	7.21E-03	0.12	2.8%	G	-0.38
						C	0.00
	Flower	S2_61888021	1.48E-02	0.22	2.3%	A	-1.75
						T	0.00
	Stemcir	S2_61888021	4.07E-03	0.11	3.0%	A	-0.39
						T	0.00
BSK1 Signaling	Exser	S1_52588681	1.09E-02	0.17	2.9%	G	-2.93
						C	0.00
	Flower	S1_52588681	7.48E-03	0.18	3.0%	G	1.58
						C	0.00
	Panlenght	S1_52588681	6.62E-03	0.20	2.8%	G	2.17
						C	0.00
	Exser	S1_52590019	1.22E-02	0.17	3.1%	T	3.09
						G	0.00
	Flower	S1_52590019	8.03E-03	0.18	3.3%	T	-1.67
						G	0.00
	Leaf	S1_52589217	4.50E-03	0.17	4.2%	G	-7.69
						T	0.00
	Panlenght	S1_52589217	1.33E-02	0.25	3.1%	G	2.75
						T	0.00
BES1 Signaling	Panlenght	S2_71773005	3.18E-02	0.25	1.7%	G	-2.08
						T	0.00
	Leaf	S2_71773005	1.25E-02	0.23	2.7%	G	5.87
						T	0.00
	Stemcir	S2_71773005	4.57E-03	0.11	3.3%	G	-0.40
						T	0.00
BRL 2 Signaling	Flower	S1_46097621	3.65E-03	0.18	4.2%	G	-2.23
						T	0.00
	Stemcir	S1_46097621	6.92E-03	0.12	3.4%	G	-0.41
						T	0.00
BSU1 Signaling	Panlenght	S8_53600913	1.51E-02	0.25	3.5%	G	-3.64
						A	0.00
	Stemcir	S8_53600913	2.26E-02	0.16	3.0%	G	-0.49
						A	0.00
BIN2 Signaling	Panlenght	S3_13870895	1.47E-02	0.25	3.0%	A	-3.78
						G	0.00
	Stemcir	S3_13870895	1.25E-02	0.14	3.2%	A	-0.56
						G	0.00
CP450 /CYP90D1 Biosynthesis	Exser	S2_69324927	9.08E-03	0.17	2.5%	T	2.58
						A	0.00
	Tiller	S2_69324927	3.12E-03	0.17	3.1%	T	-0.20
						A	0.00
DWF7 Biosynthesis	Leaf	S3_7222075	7.47E-03	0.23	3.6%	C	-7.61
						A	0.00
	Stemcir	S3_7222075	1.56E-02	0.16	2.6%	C	0.41
						A	0.00
CPD Biosynthesis	Flower	S5_2712388	4.86E-03	0.18	5.7%	G	1.93
						A	0.00
	Panlenght	S5_2712388	1.78E-02	0.25	4.6%	G	2.21
						A	0.00
ROT / 3 CYP90C1 Biosynthesis	Ht	S5_1250575	4.27E-03	0.27	3.7%	G	34.50
						A	0.00
	Stemcir	S5_1250575	2.12E-02	0.16	2.9%	G	-0.37
						A	0.00

Table 2. Markers associated with more than one phenotype of interest, the p-value, q-value and their effect on the phenotype. Effects on green are in accordance with significantly correlated phenotypes.

CONCLUSIONS

This study is the first association analysis between plant architecture traits and brassinosteroids in sorghum. Population structure results and marker-trait results are consistent with previous studies[1,3,4]. The presence of multiple markers, from different genes, associated with one phenotype of interest provides robustness to the results. The identification of markers that have an effect on different phenotypes has biological sense. The agreement between marker-trait associations with phenotypic correlations supports the future use of identified markers in sorghum breeding programs.

REFERENCES

1. Casa, A.M., G. Pressoira, P.J. Brown, S.E. Mitchell, W.L. Rooney, M.R. Tuinstrac, C.D. Franks, and S. Kresovicha. 2008. Community resources and strategies for association mapping in sorghum. Crop Sci. 48:30–40.
2. Morris, G.P, P. Ramu, S. P. Deshpande, C. T. Hash, T. Shah, H. D. Upadhyaya, O. Riera-Lizarazu, P. J. Brown, C. B. Acharya, S. E. Mitchell, J. Harriman, J. C. Glaubitz, E. S. Buckler, and S. Kresovich,Population genomis and genome-wide association studies of agroclimatic traits in sorghum. PNAS 2:453-548.
3. Sukumaran, S., W. Xiang, S. R. Bean, J. F. Pedersen, S. Kresovich, M. R. Tuinstra, T. T. Tesso, M. T. Hamblin, and J. Yu. 2012. Association Mapping for Grain Quality in a Diverse Sorghum Collection. The Plant Genome 5:126–135.
4. Taiz, L. and Zeiger, E., 2010. Plant Physiology. Fifth edition. Sinauer Associates, Inc., Sunderland, Massachussets.
5. Ye H., Li L., Yin Y. 2011. Recent advances in the regulation of brassinosteroid signaling and biosynthesis pathways. *J. Integr. Plant Biol.* 53, 455–468.
6. Yu, J. and E.S. Buckler. 2006. Genetic association mapping and genome organization of maize. Curr. Opin. Biotechnol. 17:155–160.