Genetic diversity and relationships among flowering traits in a line panel from BS39 maize population grown under tropical environments in Brazil

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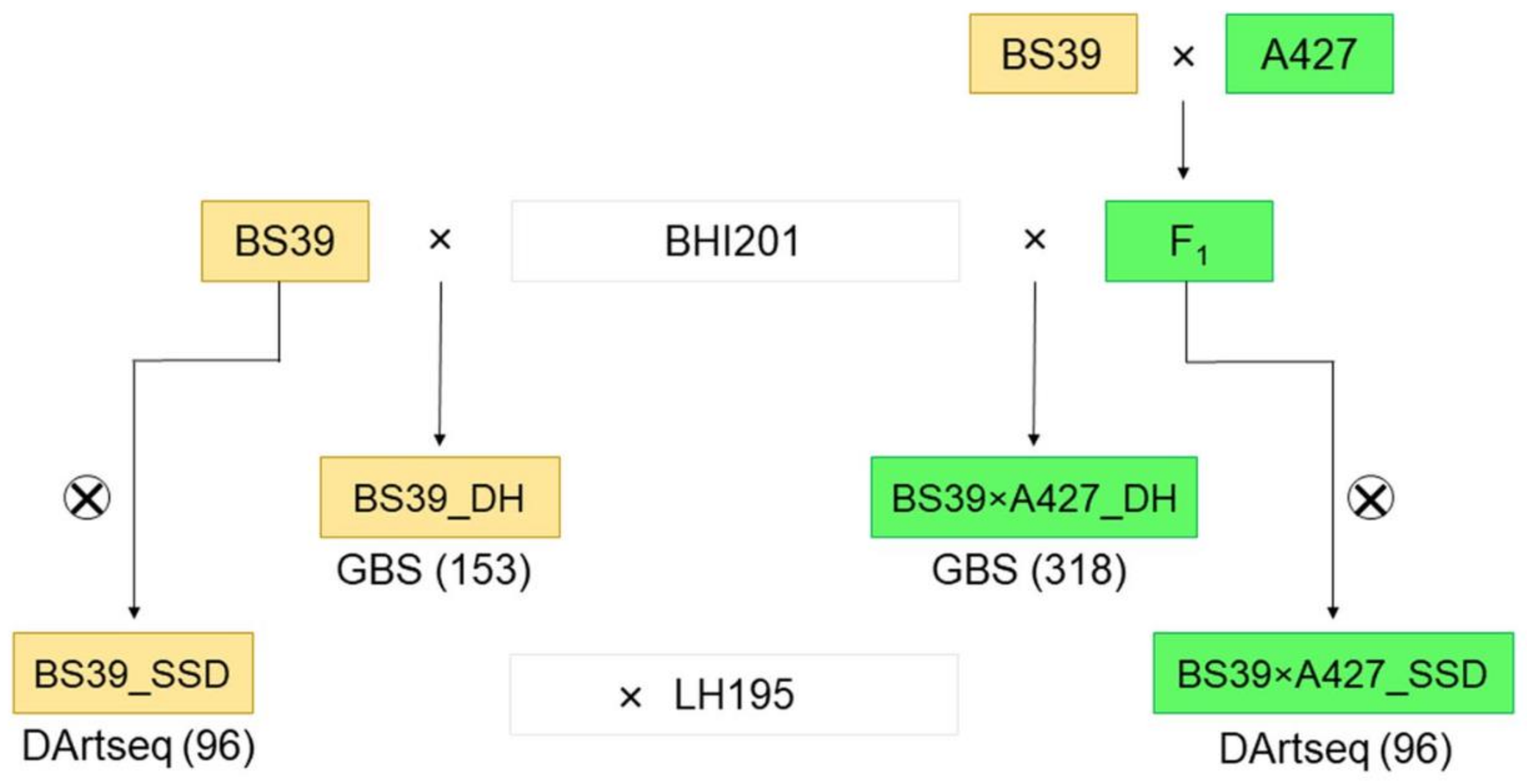
BACKGROUND



BS39 × A427

BS39 × BHI201 × F$_1$

⊗ BS39_DH GBS (153) BS39×A427_DH GBS (318) ⊗

BS39_SSD DArtseq (96) × LH195 BS39×A427_SSD DArtseq (96)

Goal: to access the genotypic variation and genetic diversity among BS39 lines for lines for days to pollen (DTP) and days to silking (DTS) evaluated in tropical environments in Brazil.

METHODS

Site: The evaluation was carried out Viçosa and Coimbra, state of Minas Gerais, Brazil.

Number of genotypes: 186 inbred lines;

Phenotypic data: days to pollen shedding (DTP and days to silking (DTS);

Genotypic data: 97,345 SNPs markers;

Statistical analyses: variance component analyses, Roger's modified distance, genome wide association study (GWAS -FarmCPU).

RESULTS

Table 1: Variance components due to BS39 lines for days to pollen (DTP) and days to silking (DTS) evaluated in tropical environments in Brazil

Trait	Mean	$\hat{\sigma}^2_g$/1	$\hat{\sigma}^2_{ge}$	Φ^2_e	$\hat{h}^2$	CV(%)
DTP	65.26	7.95*	0.85*	643.15*	0.70	3.69
DTS	66.78	17.56*	1.06*	852.18*	0.85	3.40

/1 $\hat{\sigma}^2_g$: variance componente due to inbred lines; $\hat{\sigma}^2_{ge}$: variance componente due to inbred x local; $\hat{h}^2$: broad sense heritability; CV: variance coeficiente; *: significant at 1% probability by the Likehood Ratio Test (LRT);

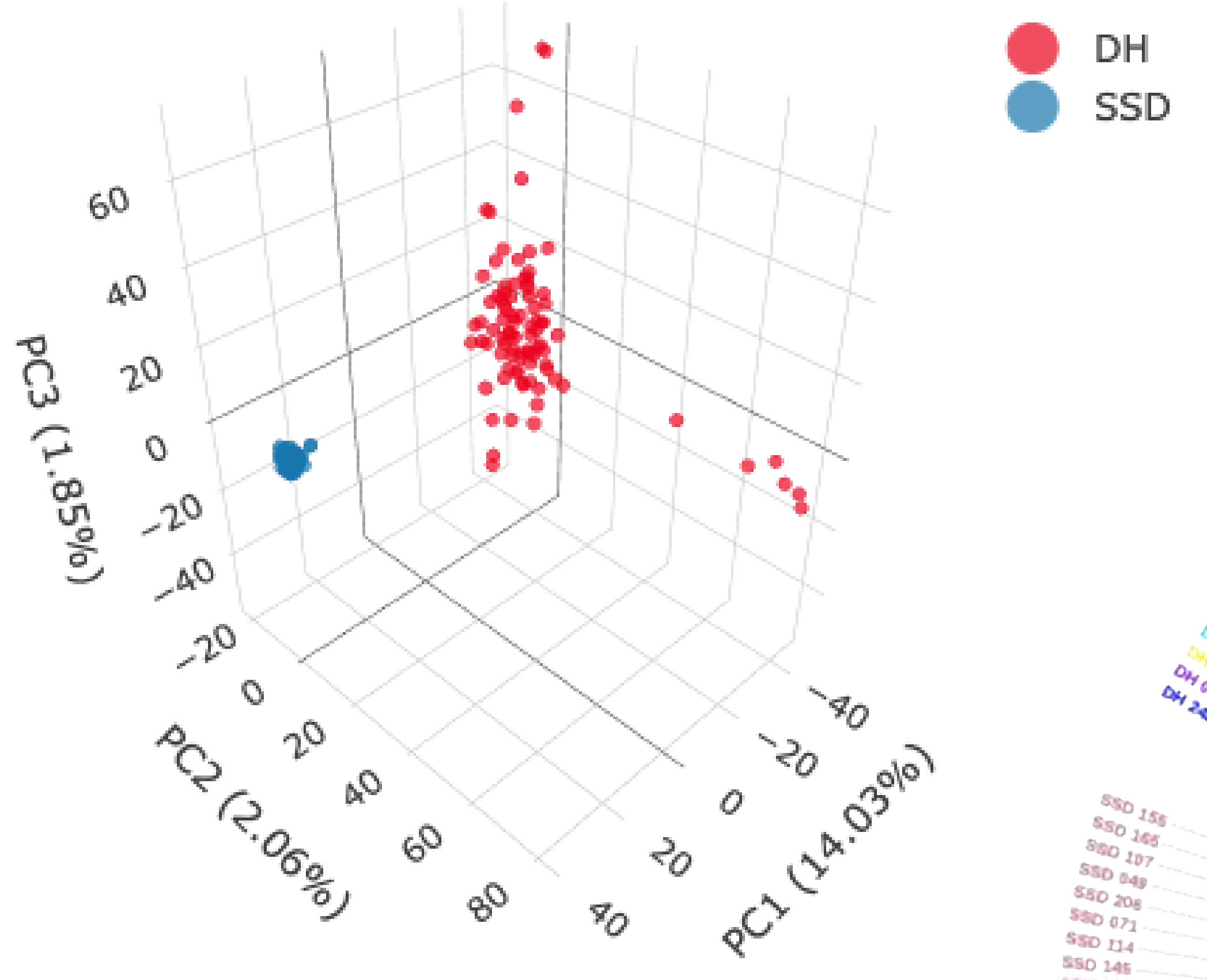


Figure 1: Plot of principal component analysis (PCA) estimated with 97,345 SNP markers of 186 inbred lines

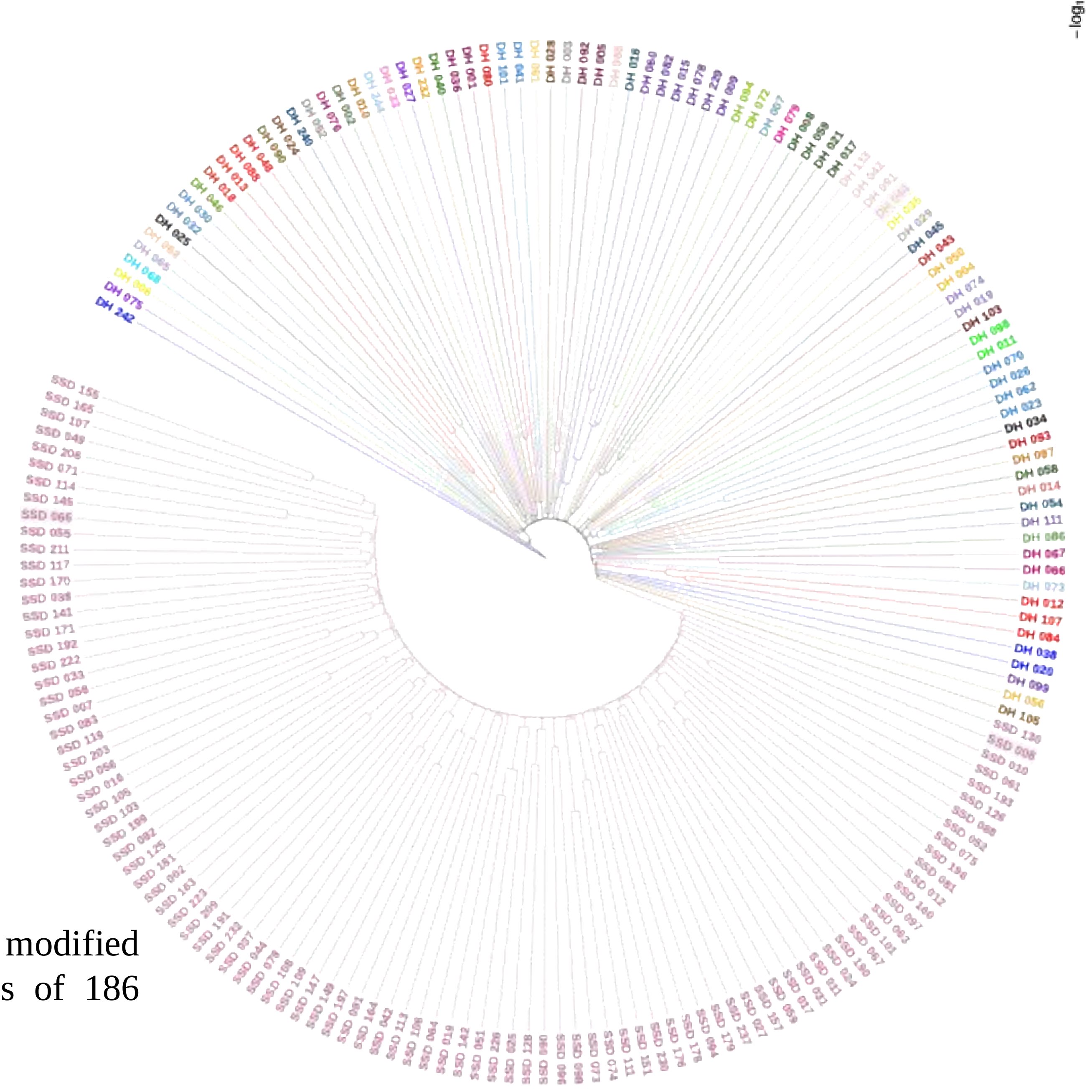


Figure 2: Dendogram based on Roger's modified distance estimated with 97,345 SNP markers of 186 inbred lines

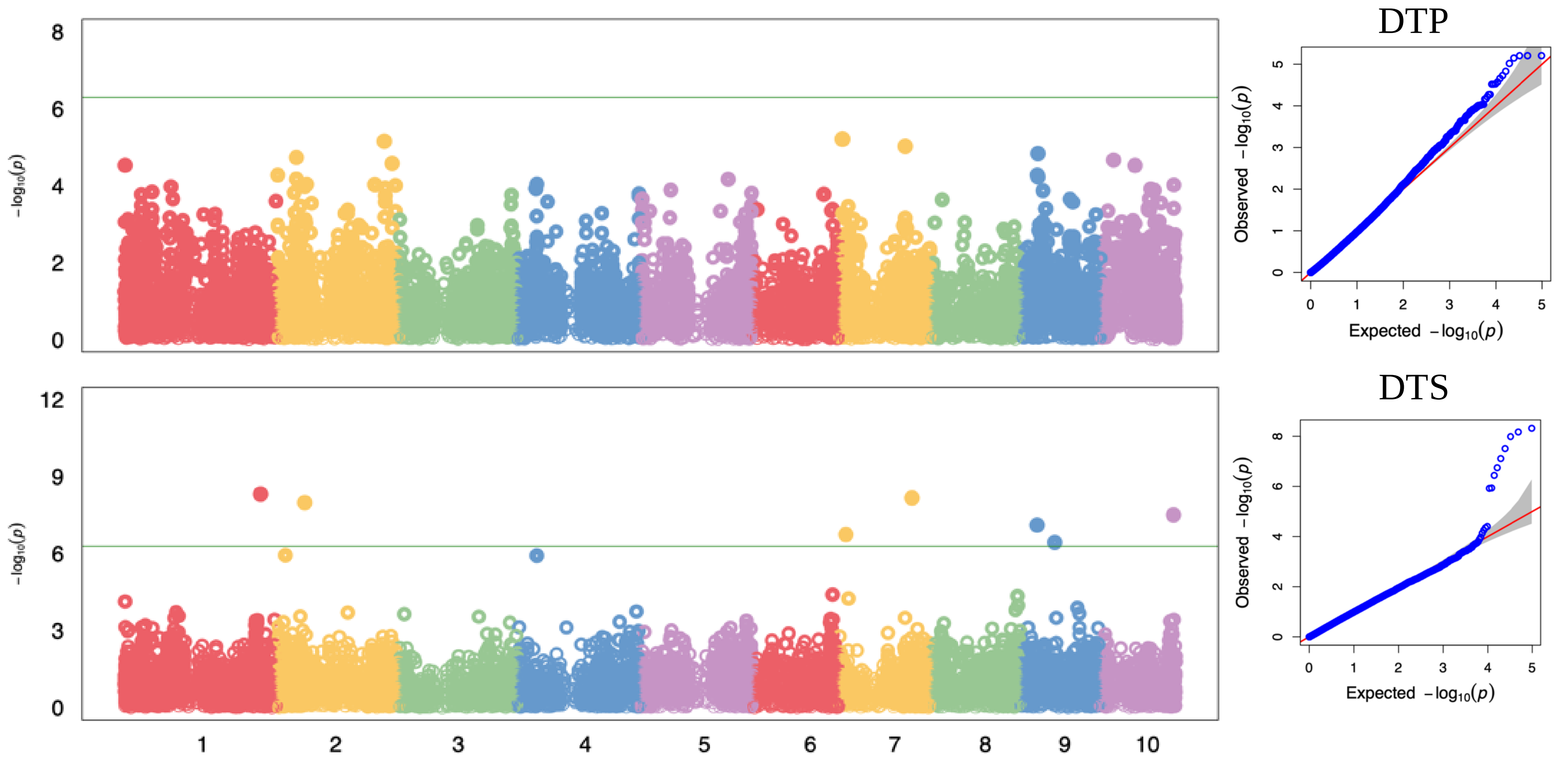


Figure 3: Manhattan and QQ plots plot of GWAS for flowering-related traits in maize. In the Manhattan plot, different colors represent different chromosomes. In the QQ plots, red lines represent that the expected −log10(p) is equal to the observed served −log10(p)

Table 2: Signifficant SNPs associated with days to silking

SNP	Chr	Pos	P.value	Trait	Effect
S1_268877694	1	273,608,129	4.80E-09	DTS	-1.58
S2_53103396	2	55,136,432	1.03E-08	DTS	-2.23
S7_13393160	7	13,393,160	1.79E-07	DTS	1.14
S7_145450320	7	145,450,320	6.74E-09	DTS	-1.67
S9_106627325	9	32,542,168	7.74E-08	DTS	1.79
S9_67881478	9	67,881,478	3.63E-07	DTS	-2.06
S10_144919716	10	145,640,125	3.10E-08	DTS	-1.53

Chr: chromosome; Pos: SNP position; R2 (%): the phenotypic variance explained by each SNP

Table 3: Putative candidate genes for days to silking

Trait	SNP	B73 Gene ID	Zm Gene ID	Function Annotation
DTS	S2_53103396	GRMZM2G014651	Zm00001eb083110	Protein 4-coumarate--CoA ligase 2
DTS	S7_13393160	GRMZM2G354335	Zm00001eb302080	Protein maternally expressed gene 1
DTS	S10_144919716	GRMZM2G448051	Zm00001eb431400	Protein peroxidase 1

CONCLUSION

We concluded that there is genetic variability and diversity in panel of BS39 lines, and three of the significant SNP's encode genes that could be related to flowering traits.

Funding agencies: