

# Identification and validation of QTLs for Striga resistance in maize.

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## Introduction

Maize (*Zea mays* L.) is the most important staple food crop in sub-Saharan Africa (SSA). The parasitic weed, *Striga hermonthica* poses a major threat to maize production in the sub-region and can cause up to 100% yield loss. *Striga* siphons water and nutrients from the maize plant. During the past two decades, the IITA Maize Improvement Program has used conventional breeding methods, improved artificial field infestation with *S. hermonthica*, and introgression of genes for *Striga* resistance from wild maize as strategies to develop maize inbred lines and hybrids with good levels of resistance to *S. hermonthica* (Badu-Apraku and Fakorede, 2017). Molecular markers are crucial for breeding for *Striga* resistance because selection for *Striga*-resistant indicator traits is difficult as they have low heritability and are expressed during the later stages of plant growth and development. Efforts to improve maize using standard plant breeding approaches are limited and time-consuming and need to be complemented with modern molecular breeding. Therefore, IITA maize breeders have during the past decade spent considerable resources and adopted various complementary molecular approaches in plant breeding to accelerate genetic gains from selection for enhanced resistance to *Striga*. The studies were conducted to identify quantitative trait loci (QTLs) for *Striga* resistance adaptive traits including grain yield, *Striga* damage, *Striga* emergence count, and number of ears per plant, and to validate the QTLs identified for marker-assisted selection (MAS) to accelerate breeding for *Striga* resistance in maize.

## Materials and Methods

Four mapping populations and one association mapping panel were phenotyped under artificial *Striga* infestation at two locations in Nigeria, 2017 – 2020 (Table 1). The populations were also genotyped using the DArTseq markers distributed across the 10 maize chromosomes. QTLs mapping for each and across environments was carried out for four *Striga* adaptive traits using the R/qtl package with the composite interval mapping (CIM) algorithms and phenotypic BLUE values across environments were used to reduce the variation effects of the environments. Putative candidate genes were searched using the Maize GDB database version (RefGen\_v4).

Table 1: Phenotyping and genotyping of the four mapping populations.

Maturity group	Extra-early White	Extra-early Yellow	Early white	Early white
Resistant parent	TZEEI 29	TZEEI 79	TZdEI 352	TZdEI 352
Susceptible parent	TZEEI 23	TZdEEI 11	TZEI 811	TZEI 916
Generations	BC1S1	F2:3	BC1S1	F2:3
No of progenies	198	194	232	223
Phenotyping locations	Abuja, Mokwa	Abuja, Mokwa	Abuja, Mokwa	Abuja, Mokwa
Years	2018	2017	2019	2020
No of SNPs used	2516	1139	1,983	1,918

## Results and Discussion

Significant mean squares for genotypes under each and across environments revealed the existence of genetic variability for resistance to *Striga* among the genotypes (Table not shown). Moderate heritability estimates were observed for most traits under each and across environments, implying the increased influence of single nucleotide polymorphism (SNP) detection in the mapping population. Twelve *Striga* resistance QTLs were identified from the extra-early yellow F<sub>2:3</sub> mapping population, 14 QTLs from the extra-early backcross mapping population, 19 QTLs from the early white backcross population, 23 QTLs from the early white F<sub>2:3</sub> population (Table 2), and 24 significant SNPs from the association mapping panel study. The phenotypic variation explained by QTLs across the four mapping populations ranged from 1.5 to 34 %, indicating the complex nature of the *Striga* resistance traits. However, the QTLs contributed significantly to observed variation in the four mapping populations. Kompetitive Allele-Specific Polymerase Chain Reaction (KASP) assays were designed from selected 11 SNP markers linked to key candidate genes associated with plant defense mechanisms under *Striga* infestation (Table 3). Genotype × environment interaction QTLs are important as they significantly influence the total phenotypic variance and additive effect of the main effect QTL located inside or close to them. In our studies, we detected significant G × E interaction QTLs for *Striga* resistance indicator traits. Similar signs of additive effects observed for some of the MET-QTLs and main effect QTLs revealed that these MET-QTLs had positive effects on the total additive value of the traits. The implication is that these MET-QTLs had a positive effect on the *Striga* resistance alleles which improved the phenotypic expression resulting in increased grain yield and reduced *Striga* damage under *Striga* infestation. Three of the SNP markers snpZM00246, snpZM00253, and snpZM00259 were identified to possess the highest prediction accuracy in the validation populations (Figures 1 and 2).

Table 2. The 23 QTLs mapped in the F2:3 population derived from TZdEI 352 × TZEI 916 under *Striga* infestation at Abuja and Mokwa, 2019 – 2020.

Trait	QTL	Chr	Position	LOD	PVE(%)	Add	LeftCI	RightCI
Grain yield	qgy2	2	23.8	4.03	8.2	-159.29	22.3	25.3
	qgy4	4	230.8	5.45	10.8	219.62	228.3	232.3
	qgy5	5	76.8	6.15	11.6	235.60	72.3	80.3
	qgy8	8	168.1	4.48	8.7	-125.21	167.6	168.6
Striga damage	qsd2	2	172.8	3.35	7.4	0.13	171.3	173.3
	qsd2	2	181.8	3.83	8.9	-0.17	178.3	186.3
	qsd2	2	201.8	2.80	4.1	0.11	199.3	202.3
	qsd3	3	13.9	2.89	5.3	-0.09	10.4	15.4
	qsd3	3	168.9	3.79	6.8	-0.17	168.4	169.4
	qsd5	5	76.8	3.86	10.2	-0.18	70.3	80.3
	qsd8	8	164.1	3.49	8.6	0.07	161.6	164.6
	qsd10	10	110.7	2.55	5.9	0.17	109.2	112.2
	qsc2	2	12.8	4.84	8.0	2.89	12.3	13.3
	qsc2	2	215.8	5.40	12.6	-0.14	215.3	216.3
Striga count	qsc3	3	11.9	3.36	4.6	-0.01	11.4	13.4
	qsc5	5	212.8	2.96	6.1	-0.10	211.3	214.3
	qsc6	6	110.0	3.26	7.0	2.81	107.5	110.5
	qsc7	7	41.8	3.17	14.4	4.73	40.3	42.3
	qsc7	7	109.8	3.70	7.1	-0.14	101.3	111.3
	qsc8	8	166.1	3.65	7.3	0.13	165.6	166.6
	qsc9	9	14.2	5.13	11.3	0.17	13.7	16.7
	qsc9	9	14.2	5.13	11.3	0.17	13.7	16.7
Ears per plant	qepp1	1	46.8	2.72	6.0	-0.03	43.3	52.3
	qepp6	6	0.96	3.87	8.3	-0.04	0.96	1.46

Table 3. KASP markers validated for *Striga* resistance traits in the early and extra-early maize.

S/N	Intertek	SNP ID	SNP ID	Trait	Gene	Reference Allele	Alternative Allele
1	snpZM00241	S5_215584707	S5_215584707	Ears per plant	GRMZM2G083138	G	A
2	snpZM00242	S5_203246961	S5_203246961	Grain yield	GRMZM5G891295	T	C
3	snpZM00245	S10_133224801	S10_133224801	Grain yield	GRMZM2G164743	G	T
4	snpZM00246	S3_135810411	S3_135810411	Striga count	-	C	G
5	snpZM00248	S3_23951418	S3_23951418	Striga count	GRMZM2G086583, GRMZM2G317835	T	C
6	snpZM00250	S1_102219805	S1_102219805	Striga count	GRMZM2G033876	A	G
7	snpZM00252	S2_140980050	S2_140980050	Striga damage	GRMZM2G053466	A	G
8	snpZM00253	S2_181171702	S2_181171702	Striga damage	GRMZM2G347743	G	A
9	snpZM00254	S3_144672580	S3_144672580	Striga damage	GRMZM2G164502	T	C
10	snpZM00256	S8_167850221	S8_167850221	Striga damage	GRMZM2G166873	A	C
11	snpZM00259	S9_154978435	S9_154978435	Striga damage	GRMZM2G010017	G	A

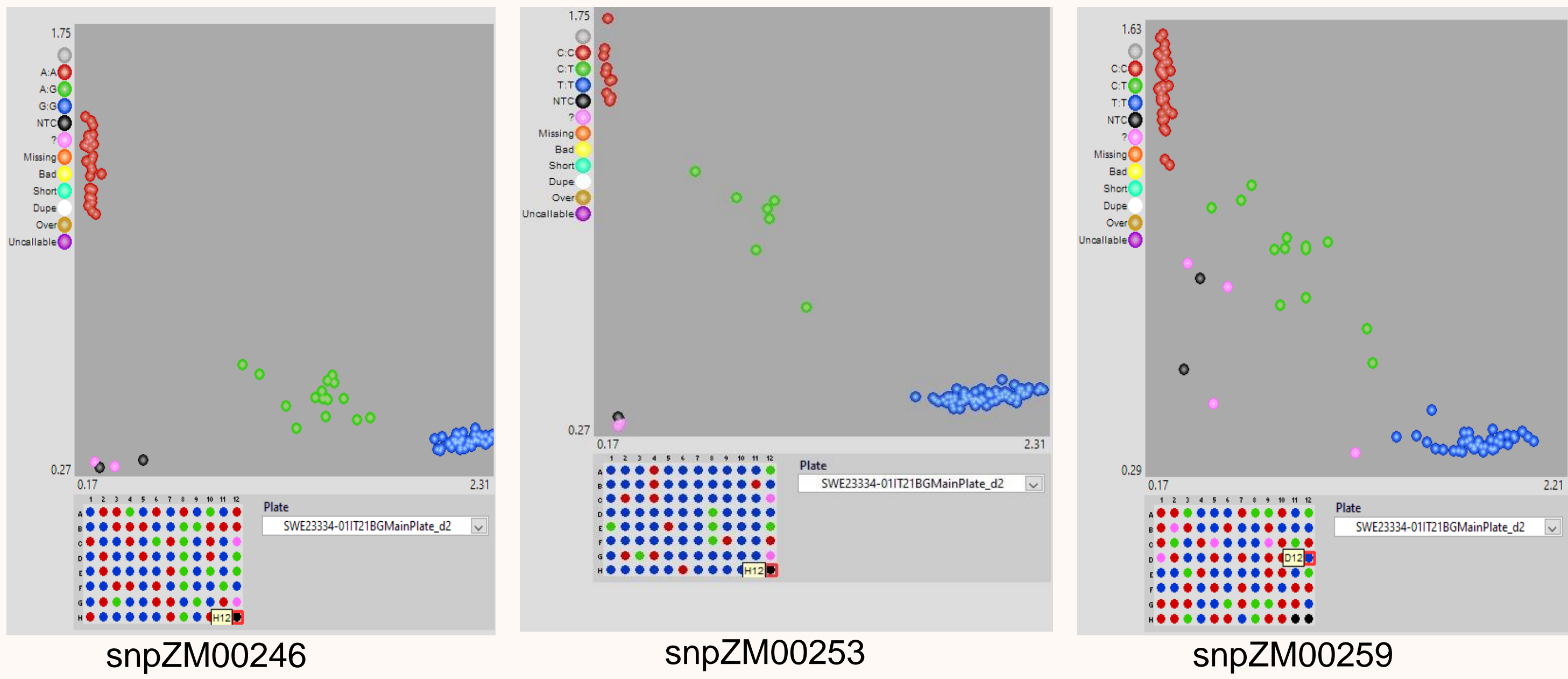


Fig. 1. KASP assay profile of snpZM00246, snpZM00253, and snpZM00259 showing SNPs genotyping in *Striga* resistant and susceptible inbred lines and F1 progenies.

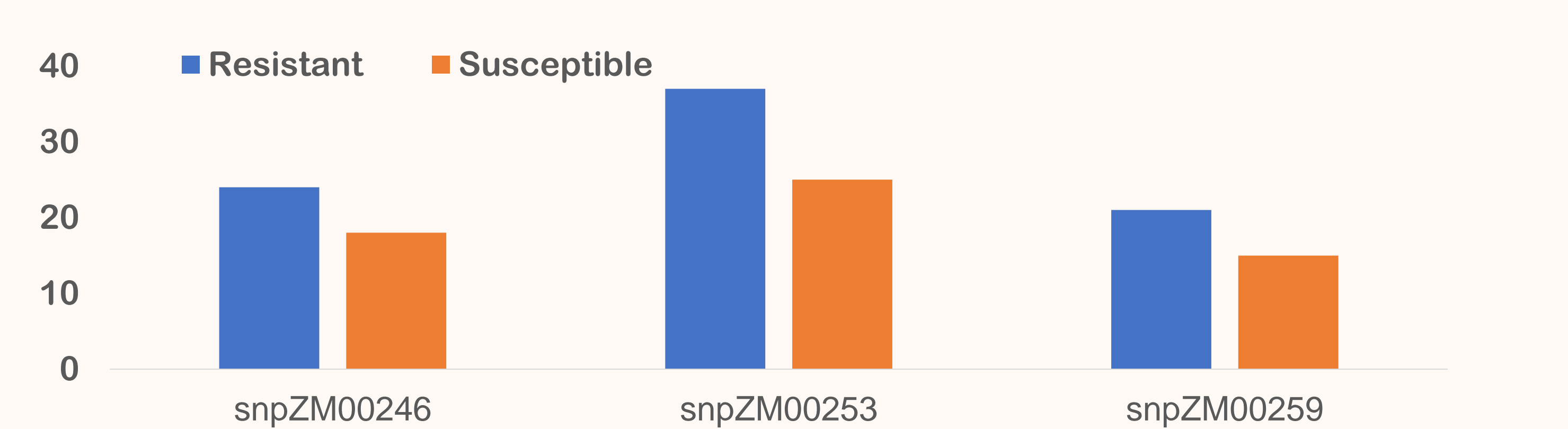


Fig. 2. Count of resistant and susceptible haplotypes in the validation population for KASP markers snpZM00246, snpZM00253 and snpZM00259.

## Conclusion

This study provides further insights into the genetic mechanisms of resistance to *Striga* parasitism in maize. The validated markers snpZM00246, snpZM00253, and snpZM00259 are presently being used in MAS for screening new breeding lines for *Striga* resistance to accelerate the introgression of resistance genes into susceptible maize genotypes.

## Reference

Badu-Apraku B. and Fakorede M. A. B. 2017. Advances in genetic enhancement of early and extra-early maize for sub-Saharan Africa. Springer.

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