

Table S1: Mean squares of F_{2:3} mapping population evaluated under artificial *Striga* infestation at both Abuja and Mokwa in 2018 growing season.

Source of variation	Df	Grain yield, kg/ha	Ears per plant	Emerged <i>Striga</i> count	<i>Striga</i> damage
Env	1	1524536672**	0.34**	106.05**	14.59**
Block (Rep*Env)	52	831223**	0.06**	0.86**	0.86**
Rep (Env)	2	115992597**	0.25**	18.14**	18.91**
Genotype	195	1228060**	0.12**	0.80**	0.86**
Genotype x Env	195	649661**	0.04	0.45	0.46*
Error		376449	0.04	0.39	0.41

Table S2: Shapiro-Wilk's normality tests for *Striga* resistance/tolerance indicator traits for F_{2:3} population derived from the cross between TZEEI 79 and TZdEEI 11.

Trait	Skewness	Kurtosis	Shapiro-Wilk's test	
			Statistic	P value
Grain yield	0.24	-0.04	0.991	0.296
Ears per plant	0.23	0.89	0.970	0.000
<i>Striga</i> damage	-0.15	-0.13	0.986	0.053
<i>Striga</i> count	-0.52	0.29	0.977	0.003

Table S3: Candidate genes associated with the identified QTL for key *Striga* resistance/tolerance indicator traits under artificial *Striga* infestation.

Trait	QTL	LG:start-end position*	Gene ID and sequence description
Grain yield	<i>qgy-1.1</i>	1:35591728-39591728	GRMZM2G408305 - ARM repeat superfamily protein
			GRMZM2G703555 - cl35724_1 - Chaperone DnaJ-domain superfamily protein
			GRMZM2G105362 - TIDP3455 - Phospholipase A2-alpha
			GRMZM2G072376 - bhlh56 - bHLH-transcription factor 56
			GRMZM2G372398 - pza03344
			GRMZM2G174236 - pco141386
			GRMZM2G062210 - fus6 - fusca homolog
			GRMZM2G001696 - phosphoenolpyruvate carboxykinase
			GRMZM2G030422 -tpl2 - topless-related2
			GRMZM2G066120 - mkkk11 - MAP kinase kinase kinase11
			GRMZM2G161337 - pco121713
			GRMZM2G093217 - si486090a03
			GRMZM2G049041 - IDP92
			GRMZM2G079112 -coi4 - coronatine insensitive4
			GRMZM2G128206 - limtf1 - LIM-transcription factor 1
			GRMZM5G886952 - pco106297a
			GRMZM2G007055 - umc2185
			GRMZM2G160198 - limtf2 - LIM-transcription factor 2
GRMZM2G141799 - AY110052			
<i>qgy-2.1, qsd-2</i>	<i>qsd-2</i>	2:138980014-142980014	GRMZM2G053466 (cl61_3) - uncharacterized protein
			GRMZM2G162286 -AW681281
			GRMZM2G115451 - invan5 - invertase alkaline neutral5
			GRMZM2G133716 - fha6 - FHA-transcription factor 6
<i>qgy-7, qepp-7, qsd-7</i>	<i>qsd-7</i>	7:840233-4840233	GRMZM2G047486 (cdpk11 - calcium dependent protein kinase11)
			GRMZM2G302778 (hagtf32 - GNAT-transcription factor 32)
			GRMZM5G872216 -senescence-associated-like protein
			GRMZM2G090824 -umc1788a
			GRMZM2G179429 - pco096998
			GRMZM2G436981 - krp11 - kinesin-related protein11
			GRMZM2G135739 - mstr1 - monosaccharide transporter1
			GRMZM2G420733 - dir11 - dirigent protein 11
			GRMZM2G120563 - alt7 - alanine aminotransferase7
			GRMZM6G199466 - hsp3 - heat shock protein3
			GRMZM2G022120 - cl24641_1
			GRMZM2G019200 - IDP1417
			GRMZM2G072582 - mads3 - MADS3
			GRMZM5G845755 - cka4 - CK2 protein kinase alpha 4
			GRMZM2G100176 - glk28 - G2-like-transcription factor 28
GRMZM2G033014 (nactf28 - NAC-transcription factor 28)			
GRMZM2G044060 - umc1672			

			GRMZM2G044194 (psk1 - phytosulfokine peptide precursor1)
			GRMZM2G008234 - ereb114 - AP2-EREBP-transcription factor 114
			GRMZM2G465226 - prp4 - pathogenesis related protein4
			GRMZM2G028041 - rs1 - rough sheath1
			GRMZM5G831780 - rpl5 - mitochondrial ribosomal protein
			GRMZM2G426154 -EMB2219 -putative mitochondrial transcription termination factor family protein
			GRMZM2G064799 - TIDP3457 - succinate dehydrogenase1
EPP	<i>qepp-1</i>	1:217230073 - 221230073	AMADH1b, GRMZM2G016189 (aldh9 - aldehyde dehydrogenase9) Description=betaine aldehyde dehydrogenase
			GRMZM2G015642 - signal recognition particle binding
			GRMZM2G160560 - Zm00001d032212
			GRMZM2G166687 - tcptf11 - TCP-transcription factor 11
			GRMZM2G124203 - pco070813(750) - Threonine endopeptidase
			GRMZM2G106133 - hmga102 - high mobility group family A 102
			GRMZM2G056400 - kan1 - KANADI1
			GRMZM2G135949 - cl5297_1(517) - hypothetical protein
			GRMZM2G101000 - putative inositol polyphosphate phosphatase (synaptogenin-like) family protein
			GRMZM2G016189 - AMADH1b- betaine aldehyde dehydrogenase
			GRMZM2G324999 - wrky25 - WRKY-transcription factor 25
	<i>qepp-2.1</i>	2:4272353 - 8272353	GRMZM2G422938, gpm120 - putative alpha amylase
			GRMZM2G026223 - zag6 - agamous-like6
			GRMZM2G054225 - nrpd2/e2 - nuclear RNA polymerase D2/E2
			GRMZM2G174917 - ereb47 - AP2-EREBP-transcription factor 47, dehydration responsive element binding protein
			GRMZM2G023163 - pco095943 - Glycerol kinase
			GRMZM2G019404 - mha2 - plasma-membrane H ⁺ ATPase2
			GRMZM2G086801 - COP9 signalosome complex subunit
			GRMZM2G086920 - zim32 - ZIM-transcription factor 32
			GRMZM2G032977 - pco102923 -Endonuclease 202
			GRMZM2G166281 -mir3 - maize insect resistance3
			GRMZM2G174784 - EREB197 - putative AP2- EREBP transcription factor superfamily protein
			GRMZM5G882708 - cl34132_1b
			GRMZM2G022192 - ami4 - amidase4
			GRMZM2G131961 -bzip27 - bZIP-transcription factor 27
			GRMZM2G106056 - mre11a - meiotic recombination protein 11 homolog A
			GRMZM2G106245 - sgb101 - silencing gene B101
			GRMZM2G106393 - umc1497a - wound-responsive family protein
			GRMZM2G106578 - dgk3 - diacylglycerol kinase3
			GRMZM2G164400 - pza03747 - peroxisome biogenesis protein
			GRMZM2G164277 - MYND finger family protein
			GRMZM2G114861 - KIN6 -kinesin related protein
			GRMZM2G155217 - umc1961 - putative HLH DNA-binding domain superfamily protein

	<i>qepp-3</i>	3:119393084-123393084	GRMZM2G114613, cl889 GRMZM2G114924, GRMZM2G114930 - S-adenosyl-L-methionine-dependent methyltransferase superfamily protein GRMZM2G162988 - Pentatricopeptide repeat-containing protein mitochondrial GRMZM2G701689 - cpp10 - CPP-transcription factor 10 GRMZM2G066321, gpm829 - Methylsterol monooxygenase MIR167g - In Arabidopsis, soybean and maize, miR167 was reported to play critical roles in lateral root development and architecture GRMZM2G152470 - hmt3 - homocysteine S-methyltransferase 3 GRMZM2G178102 - hb25 - Homeobox-transcription factor 25 GRMZM2G104396 - ca2p12 - CCAAT-HAP2-transcription factor 212
	<i>qepp-8.1</i>	8:35493871-39493871	GRMZM2G009719 - universal stress protein GRMZM5G842965 - negatively light-regulated protein GRMZM2G001024 - putative RING2FU-box superfamily protein GRMZM2G053503 - ERF1, ethylene-responsive factor-like protein; ereb148 - AP2-EREBP-transcription factor 148 GRMZM2G051528 - myb95 - myb transcription factor95
RAT2	<i>qsd-5.1</i>	5:170001287-174001287	GRMZM2G172158 - Ubiquitin carboxyl-terminal hydrolase family protein GRMZM2G108267 - hypothetical protein GRMZM2G059851 - HSF-6, heat shock factor protein GRMZM2G059671, gpm318 - Serine threonine-protein kinase CTR1 GRMZM2G139300 - incw1 - cell wall invertase1 GRMZM2G099334 - myb3 - WD40 repeat protein GRMZM2G162663 - pco084078 - Acetyl-coenzyme A synthetase chloroplastic/glyoxysomal protein GRMZM2G172230 - chaperone protein ClpD chloroplastic GRMZM2G032628 - ae1 - amylose extender1 GRMZM2G113332 - csu308 - Copper transport protein CCH GRMZM2G074017 - umc1966 - ATPase inhibitor GRMZM2G039089 - cl31997_1 - chaperone protein dnaJ-related
ESP2	<i>qsc-3.1</i>	3:21951408-25951408	GRMZM2G054050 - Multicopper oxidase GRMZM2G114552; umc1742 - Bowman-Birk type trypsin inhibitor GRMZM2G121066 - gpm141 -Mannose-6-phosphate isomerase GRMZM5G853361 - Actin-interacting protein GRMZM2G340342; ARM repeat superfamily protein GRMZM2G130800 - pco131712 - Glycosyltransferase family protein GRMZM2G059358 - GRMZM2G152689; ZCN10 GRMZM2G345840 - pco087404 - C2 domain-containing protein GRMZM2G162709 - myb137 - MYB-transcription factor 137 GRMZM2G130800 - pco131712 - Glycosyltransferase family 61 protein

*Linkage group start and end positions within 2.0Mb interval downstream and upstream of the significant associated SNPs

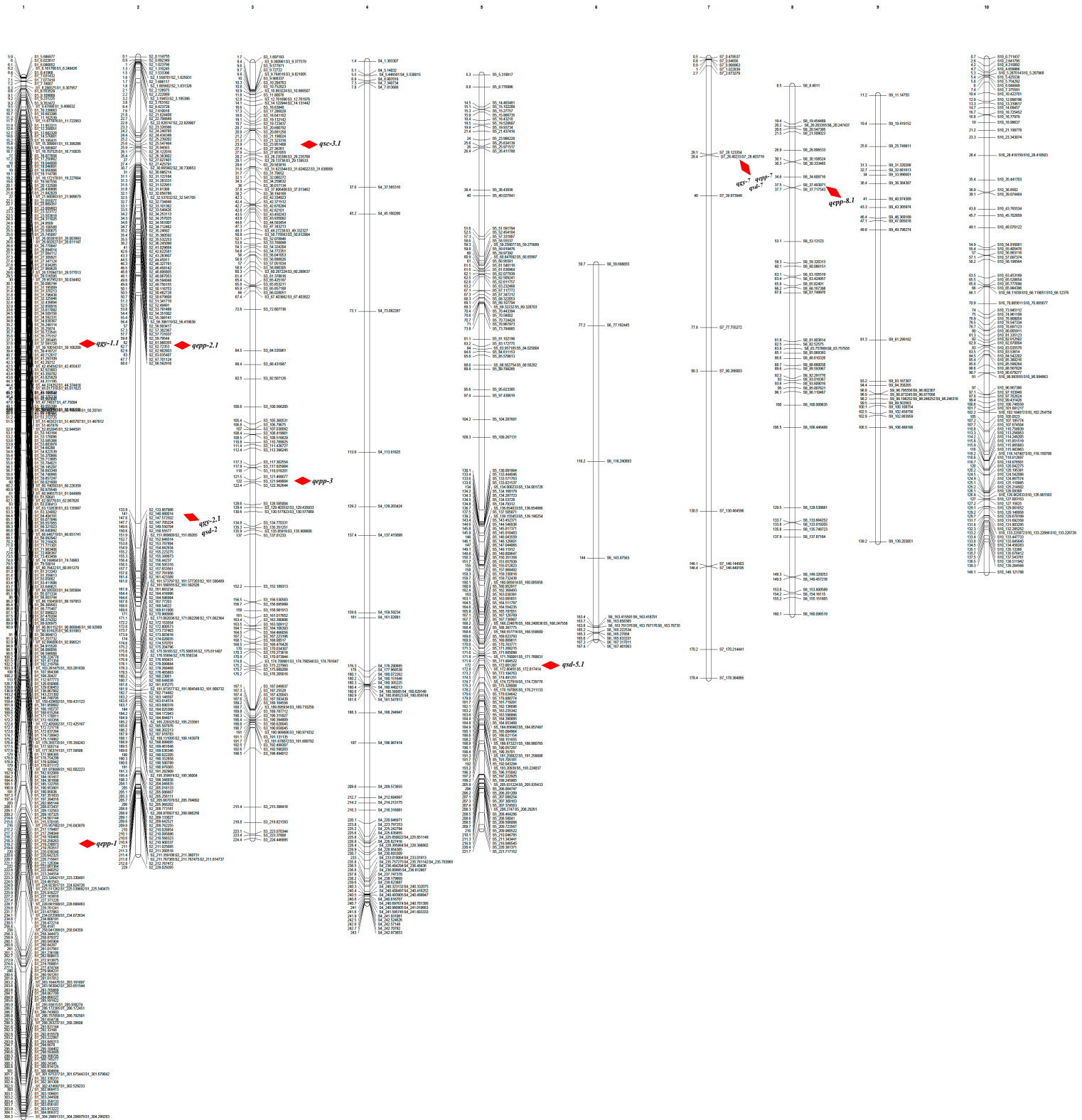


Figure S1: Linkage map of F2:3 mapping population based on 1,139 DARTseq markers. Left bar of the linkage map indicates cM distance while right bar of linkage map displayed the marker names. Red bars and letters indicate QTL identified across *Striga* infested environments.

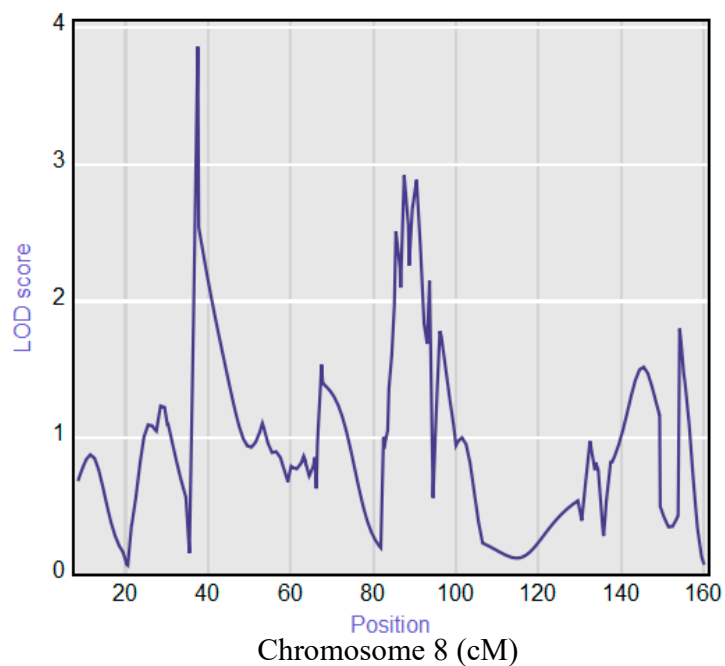
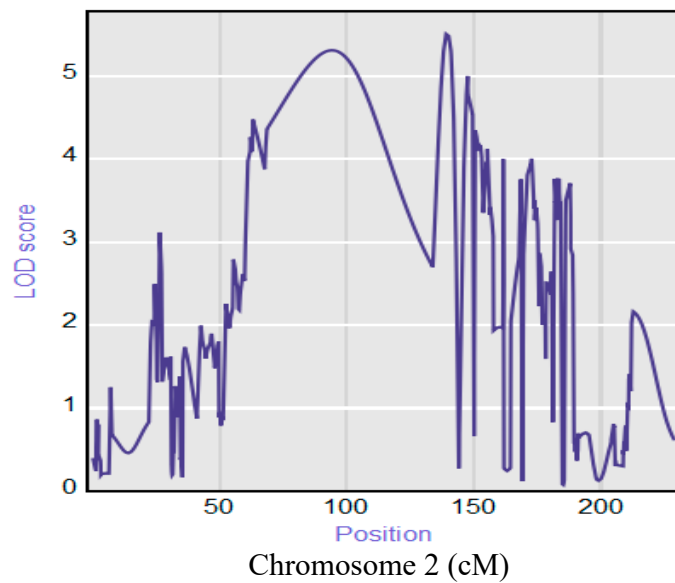
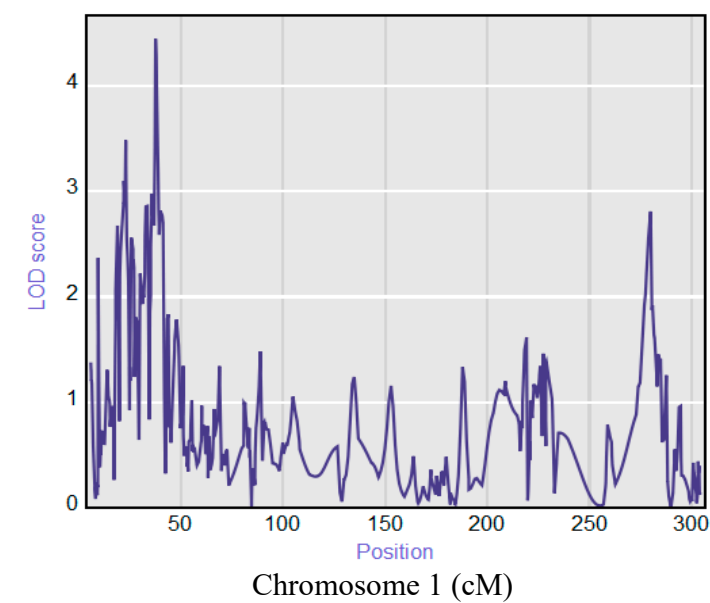


Figure S2. Major QTL identified for *Striga* resistance in extra-early yellow mapping population. A likelihood of odds (LOD) scan showing the QTL identified on chromosomes 1, 2, and 8 explaining $\geq 10\%$ phenotypic variation.