

SUPPLEMENTARY MATERIAL

Table S1. Local names, status and collection site of sorghum landraces, improved cultivars, and exotic material used

No	local name	Status	Collection site
1	Aklamoi	Landrace	East Sudan
2	Arfa Gadamak	Improved cultivar	East Sudan
3	Baham	Landrace	Red Sea (Sudan)
4	Bari	Landrace	South Sudan
5	Botana	Improved cultivar	East Sudan
6	Dabar	Landrace	Central Sudan
7	Dari	Landrace	South Sudan
8	Debeikri	Landrace	North Sudan
9	Fakimustahi	Landrace	East Sudan
10	Feterita Geshaish	Landrace	White Nile
11	Feterita Geshiash	Landrace	White Nile (Sudan)
12	Framida	Exotic	Uganda
13	Gadam Elhamam	Improved cultivar	East Sudan
14	Hakika	Exotic	Tanzania
15	Hariri	Landrace	East Sudan
16	Hazaztokarwe	Landrace	Red sea (Sudan)
17	Hemisi	Landrace	North Sudan
18	IS 15401	ICRISAT	ICRISAT
19	IS-9830	Landrace	Central Sudan
20	Kolom	Landrace	Blue Nile (Sudan)
21	Korokollow	Landrace	East Sudan
22	Markoob	Landrace	West Sudan
23	Mogud	Landrace	North Sudan
24	N13	Landrace	Exotic India
25	Najad	Landrace	West Sudan
26	Naten	Landrace	Blue Nile (Sudan)
27	SRN39	Synthetic	ICRSAT (Sudan)
28	Tabat	Improved cultivar	Central Sudan
29	Tafsagabeid	Landrace	Blue Nile (Sudan)
30	Tetron	Landrace	West Sudan
31	Tokarawee	Landrace	Red Sea (Sudan)
32	Wad Ahmed	Improved cultivar	Central Sudan
33	Wad Baco	Landrace	East Sudan
34	Wad Elmardi	Landrace	West Sudan
35	Wad Fahel	Landrace	White Nile (Sudan)
36	Zahrat Elgadambalia	Improved cultivar	East Sudan

Source: Plant Genetic Resources Unit, Agricultural Research Corporation

Table S2. Genotypic variation in strigolactone production in sorghum. Levels of 5-deoxystrigol, sorgomol and orobanchol in root exudates of sorghum genotypes. C18 and silica purified root exudates were analysed using liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS). Peak area means of 4 replicates. Least significant differences of means at P = 0.05 were determined by ANOVA. Means within a column followed by the same letter(s) are not significantly different according to the Duncans' pairwise comparison (P < 0.05).

No	Genotype	5-deoxystrigol*	sorgomol*	orobanchol*
1	Aklamoi	114 abcdefghi	2.65 defghji	0.28 efghji
2	Arfa Gadamak	95.9 abcdefgh	0.00 m	0.08 jk
3	Baham	118 abcdef	0.02 jklm	0.02 cdef
4	Bari	92.2 fhgji	3129 a	2.57 cde
5	Botana	32.6 abcdefhgi	0.09 klm	1.92 cdef
6	Dabar	21.1 abcdefhgi	0.08 hjkl	0.11 efghji
7	Dari	125 abcdegh	1362 a	2.14 cdef
8	Debeikri	602 ab	0.18 hgjik	0.44 cdefgh
9	Fakimustahi	261 abcdef	270 ab	0.07 jk
10	Feterita	427 abcd	0.09 defgh	0.09 defghi
11	Feterita Geshaish	262 abcd	0.80 efhgjki	0.57 defghi
12	Framida	189.15 abcdefhgi	0.75 jkl	7.56 bc
13	Gadam Elhamam	172 abcdef	0.69 defhgi	0.38 cdefgh
14	Hakika	0.21 kl	1.32 cdefgh	1.36 cdef
15	Hariri	2.03 kijl	9.45 cd	0.05 cdefe
16	Hazaztokarwe	361 abcd	0.22 hgjik	0.11 efghji
17	Hemisi	2832 abcdefhg	26.6 cdefg	4.80 cdef
18	IS 15401	7.64 fhgji	2.10 cdefgh	0.26 efghji
19	IS-9830	0.12 l	0.00 m	28.7 cd
20	Kolom	579 a	0.13 hgjik	0.22 defghi
21	Korokollow	14.6 cdehfgji	0.00 m	0.23 defghi
22	Markoob	179 abcdef	0.96 fhgjik	0.18 ghijk
23	Mogud	8.49 efhigj	0.01 lm	0.14 defghi
24	N13	817 a	3.45 cdef	0.59 cdefghi
25	Najad	524 abcdef	6.58 cd	1.97 cdef
26	Naten	10.1 defhgi	19.8 bc	0.26 defghi
27	SRN39	3.05 hjki	5.71 cde	197 ab
28	Tabat	558 abc	2.93 cdefg	0.58 cdefg
29	Tafsagabeid	328 abcde	0.13 hgjikl	0.04 hjik
30	Tetron	2.62 jkl	0.00 m	183 a
31	Tokarawe	192 fhgji	4.48 defhgi	0.41 efghji
32	Wad Ahmed	244 abcdef	1.73 m	2.56 cdef
33	Wad Elmardi	187 abcdef	1335 a	2.28 cdef
34	Wad Baco	3.18 hgjik	1.68 cdefg	0.48 cdefg
35	Wad Fahel	111 abcdefg	18.6 bc	0.11 efghji
36	Zahrat Elgadambalia	86.2 abcdefgh	4.43 cde	0.35 cdefgh

\*Peak area x10<sup>5</sup>

Table S3. Principle components, Eigenvalues, loadings, and percentage of total variance explained in principal component analysis on the concentration of three strigolactones in the root exudate of 36 sorghum genotypes and their germination stimulant activity (belonging to the data shown in Fig. 7A) or the concentration of three strigolactones in the root exudate of 20 sorghum genotypes and *S. hermonthica* infection in a pot experiment (belonging to the data shown in Fig. 7B).

For data shown in Fig. 7A								
PC	E*	Total variance (%)				Eigen vector loading for		
		In	Cum	5-de	sorg	orb	Germ	
1	1.85	47.29	47.29	0.61	0.24	-0.44	0.60	
2	1.09	26.84	74.13	0.15	0.82	0.52	-0.11	
3	0.62	15.72	89.84	0.27	-0.45	0.72	0.43	
4	0.48	10.16	100.00	-0.72	0.21	0.01	0.65	
For data shown in Fig. 7B								
PC	E	Total variance (%)				Eigen vector loading for		
		In	Cum	5-de	sorg	orb	Striga	Germ
1	2.63	52.67	52.67	0.45	0.31	-0.49	0.53	0.40
2	1.02	20.49	73.16	0.25	0.79	0.18	-0.12	-0.50
3	0.74	14.86	88.03	0.59	-0.05	0.51	-0.36	0.49
4	0.35	7.08	95.11	-0.60	0.51	0.10	-0.13	0.57

\* E, Eigen value; In, Individual; Cum, Cumulative; 5-de, 5-deoxystrigol; sorg, sorgomol; orb, orobanchol; Germ, Germination %; Striga, Striga plants per pot.

Table S4. Emergence rate calculated as days to the first Striga emergence calculated as mean emergence time per 4 replicates. Least significant differences of means at  $P = 0.05$  were determined by ANOVA. Means within a column followed by the same letter(s) are not significantly different according to the Duncan's pairwise comparison ( $P < 0.05$ ).

No.	genotype	Days to first Striga emergence
1	Aklamoi	15 i
2	Arfa Gadamak	24 f
3	Botana	27 e
4	Fakimustahi	18 h
5	Feterita Geshiash	15 i
6	Framida	24 f
7	Hariri	31 d
8	Gadam Elhamam	18 h
9	IS-9830	33 c
10	Korokollow	23 g
11	Mogud	24 f
12	Najad	24 f
13	Naten	27 e
14	N13	24 f
15	SRN39	36 a
16	Tabat	15 i
17	Tetron	33 c
18	Tokarawe	24 f
19	Wad Ahmed	35 b
20	Wad Baco	27 e
21	Wad Fahel	16 i
22	Zahrat Elgadambalia	18 h

Table S5. Pearson Correlation between emerged number of Striga/pot, total Striga biomass per pot and emergence rate (days to first Striga emergence)

Striga number	Striga biomass (mg)	Days to first Striga emergence	Striga number
Striga numbers	1	0.43*	-0.53*
Striga biomass (mg)		1	-0.56*
Days to first Striga emergence			1

Table S4A. *D27* (DWARF 27) sorghum orthologous putative gene sequence identified by BLASTn using rice *D27* published sequence in the NCBI database (<http://www.ncbi.nlm.nih.gov/;cloneID-FJ641055>).

Gene symbol	<i>SbD27</i>	Gen. Bank ID
Gene description	Sb05g022855.1	8062677
Gene type	protein coding	Ref sequence: X_M002449722.1
Location:	chromosome: 5	

> SbD27: Sb05g022855.1  
ATGGAGGTGCGCCGCACTTGCATGCCCCTTGCTCACGCTCATGGCGTTGGTGTCCCTACCGGCATGGTCG  
TCACCGTCGACAGCAGCAGCAACAGCACGCTCCGTGACGAGGCAGAGCTACACCTACACGAGGAGGA  
AGCGCCTCGCCACCGCGGAGGCGTCATGGCGAGGCCGAGGAGGTGGTGGTGGCGCCGGCGCCACC  
AGCGAGGCCGACACCACCACCAACAACAACAAGGAGAGAACAGCGCTGGCGCCGCGCCACC  
ACCACCACGTACCACGACAGTTGGTTCGACAAGCTGGCCATCGGGTACCTGTCCCAGAACCTTCAAGA  
AGCTTCTGGGATGAAGAACGGAAAGGACGGCTACGAAGGCCTGATAGAGGCGGCACTGGCCATCTCC  
GCGCTGTTCAAGGTTGATCAGCAGTTGGAGACTGTGGCCAAGGCTCTCGAACAGGCCTTCCCAGCTA  
CATCCTCACAATGGCAAGAGATAAACACAAGGTATCTATTATAGACGGTTTAGAAAGTAGGTTGTTCT  
TTGAATATAAGATAAAGATAATGATGCCACCCTCGAGATTTTCTCGAGAGTACTTTGCCGCCTTACCA  
CGATATTCTTCCCTTGGCTCGTTGGACCATGTGAGGTCAGGGAATCCGAAGTTGATGGAAGGAAAGAG  
AAGAATGTGGTCTACATACCCAAATGCAGATTTCTGGAAAGCACCAACTGTGTGCGGAATGTGCACGAA  
CCTTTGCAAATCCCATGCCAGAAGTTCATCCAAGATTCACCTGGCACGGCTGTACTACATGTCTCCAA  
TTTTGAGGACATGAGCTGTGAGATGATCTTTGGACAGCAACCTCCTGAAGATGATCCAGCACTGAAGC  
AGCCCTGCTTCCGGACAAAA

Table S4B. *CCD7* (CAROTENOID CLEAVAGE DIOXYGENASE 7) orthologous putative gene sequence identified by BLASTn in Phytozome (<http://www.phytozome.org>) using published rice *CCD7* sequence in ([www.gramene.org](http://www.gramene.org)) as described by Vallabhaneni et al., 2010; Guan et al., 2012 and Priya and Siva, 2014.

Gene symbol	<i>CCD7</i>	Gen. Bank ID
Gene description	Carotenoid cleavage dioxygenase	8055963
Gene type	Sb06g024560 protein coding	Ref sequence: X_M002446857.1
Location:	chromosome: 6	
<hr/>		
>SbCCD7: Sb06g024560		
ATGCACGCCGCCGTGCACCACCACCACCCTGGCCACCGCGCACCGCCGCCTCGCCGCTGCTCTCGCGG CCACGGGCGCAGCAGCGTCCGCTCCGCGCCGCGGCCACCACCGTACCAGCACCCGGGCGCC GCGGCGACAGCGCCGACTCGCCGTCCGCGTCGTTCTGGGACTACAACCTCCTGTTCCGGTTCGAGCG CGCCGAGTGCCGCGACCCCGTCCGCGTCCGCGTACCAGAGGGCGCGATCCCGGCGGACTTCCCGTCCG GCACCTACTACCTCGCCGGTCCGGGGATGTTACCGACGACCACGGGTCCACCGTGCACCCGCTCGAC GGCCACGGCTACCTCCGCTCGTTCGGCTCCGACGGCGCGCCGGCGCGCTACTCCGCGCGGTA CGTGGAGACGGCGGCGAAGCGGGAGGAGCACGACGCGCCGCGCTCGTTCGTGGCGGTTACGCACCGG GGCCCCTTCTCGGTGCTGCAGGGCGGGACCCGGGTGGGCAACGTGAAGGTGATGAAGAACGTGGCCA ACACCAGCGTGCTGCGCTGGGGCGGCCGCGTGCTCTGCCTCTGGGAAGGCGGCGAGCCGTACGAGCTG GACCCGCGGACGCTGGAGACCATCGGCCCGTTCGACATCCTCGGCCGCCTCGCCACCGGCGGCGAAGC GGCAGGAGACGACGACAGCAGCGAGGCTGCGCGTCTCGGGCGCCGGCGGCCGTGGCTGCAGGAGGCA GGGATCGACGTGGCCGCGCGCCTGCTGCGACCGGTCTCGGTGGTGTCTTACGATGCCGGCCAAGCG GCTGCTCGCGCACTACAAGATCGACCAGGAGAGGAACCGGCTGCTCATGGTGGCCTGCAACGCCGAG GACATGCTCCTCCCGCGCTCCAATTCTACTTTCTACGAGTTCGACGCCGACTTCGCGCTGGTGCAGACG CGGGAGTTTGTCTTGCCGGACCACCTGATGATCCACGACTGGACCTTACGGACAGCCACTACGTCTCT CCTCGGCAACAGAATCAGGCTGGACATTCCAGGTTGCTGCTGGCGCTCACGGGCACTACCCAATGA TCGCGGCCCTCGCCGTGGACCCGAGCCGGCAGTCCACGCCCGTCTACCTGCTGCCGCGTCCCCGGAG GCCGAGCCCCCGGCCGACTGGAGCGTGCCCATCGAGGCGCCATCGCAGATGTGGTCCATGCACGT CGGCAACGCCTTCGAGGAGCGCAACGCCCGGGGCGGCATCAACATTAGCTCCACATGTCCGGCTGCT CTTACCAGTGGTTCAACTTCCACAGGATGTTTGGTTACAATTGGCAGAACAAGAAGCTGGACCCGTCC TTCATGAACATAGCCAAGGGCAGGGAATGGCTACCTCGTCTTGTACAGGTGTCCATCGACCTCGACAA GAGAGGAACGTGCCGAGGATGCTCCGTCCGGAGATTGTCCGACCAGTGGACCAGGCCGGCGGACTTC CCGGCGATCAACCCAGGCTTCGCCAACCGGAGGAACCGGTTTCATCTACGCCGGCGGCGCCTCCGGTTC ACGACGATTCTTGCCGTAATCCCTTCGACAGCGTCGTCGAGGTAGACGTCGCTGATGGATCAGCGC GGTCGTGGTTCAGTCCCGGGCGCAAGTTCGTTGGTGGAGCCGGTCTTTCGTCGCCGACCGGCAGTAGCGAG GATGACGGCTATGTTCTGCTTGTGAGTATGCAGTGTCTGATCACAGGTGCCATCTGGTGGTGTGGAC GCAAGGAAGATCGGGGAAAGGGACGCAGTTGTGGCAAACTTGAGGTGCCAAGCACCTCACCTTCC CAATGGGATTCATGGGTTCTGGGCAGATGAATGA		
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Table S4C. *CCD8* (CAROTENOID CLEAVAGE DIOXYGENASE 8) orthologous putative gene sequence identified by BLASTn in Phytozome (<http://www.phytozome.org>) using published rice *CCD8* sequence obtained from ([www.gramene.org](http://www.gramene.org)) as described by Vallabhaneni et al., 2010; Guan et al., 2012 and Priya and Siva, 2014.

Gene symbol	<i>CCD8</i>	Gen. Bank ID
Gene description	Carotenoid cleavage dioxygenase Sb03g034400.1	8062181
Gene type	protein coding	Ref sequence: X_M002458432
Location:	chromosome: 3	
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>SbCCD8: Sb03g034400.1		
ACCAGTACACACCACACTCTCGGCTAGCTAGCTAGCGAGCTACTACTGACCTCTCCTTTTCTTAT TAGCTCCAAATTAAGAGCCCGCCCTGGTACTACAACCCTAGCAAGAGCATTTTGCCATGTCTCCCAC TATGGCTTCGTCGCTCTGCGTGTTCAGCGATGTCTGGCGCCACCGGCAGGCCGTCGTCGACCGGTG CTCGGTGGTGCCGCCGGGCGCTGTCCAGTACTGCACAGGGGACCAAGGGAAAGAGGGGCCGTGGTG CAGCCTCTCGCGGCTAGCGTCGTGACGGACACGCCGACGCCGACGCCGGCCATAGCTCCGGCGCCCC GCCAGCTCGGCCAGTCGTCGACGCCCGCGCCCGCTGGGGGCCGCGGCACCGGCGAGCACGCGGCG TGGAAGAGCGTCCGGCAGGAGAGGTGGGAGGGGGCGCTGGAGCTGGAGGGAGAGCTGCCGCTCTGGC TGGATGGCACGTACCTGAGGAACGGCCCCGGCCTGTGGAACCTGGGCGACTACGGCTTCCGGCACCTG TTCGACGGCTACGCGACGCTGGTCCGCGTCTCGTTCCGCAACGGGCACGCGGTGGGCGCGCACCGGCA GATCGAGTCGGAGGCGTACAAGGCGGCGCGCGGAACGGCAAGGTGTGCTACCGCGAGTTCTCGGAG GTGCCAAGGCGGACAGCTTCTCTCCACGTGGGCCAGCTCGCCACCCTCTTCTCGGGCTCCTCGCTC ACCGACAACCTCAACACGGGCGTGGTCAGGCTCGGCGACGGCCGCGTGTGTGCCTGACGGAGACCA TCAAGGGCTCCATCGTGGTCGACCCGGACACGCTGGACACCCTCGGCAAGTTCGAGTACACGGACAAG CTGGGCGGCCTCATCCACTCGGCGCACCCCATCGTGACGGACACCGAGTTCTGGACGCTGATCCCGGA CCTCATCCGCCCCGGGCTACTCGGTGGTGCAGATGGACGCCGGGACCAACGAGCGGCGGTTTCGTGGCA GGGTGGACTGCCGCGGCGGGCCGGCGCCCGGTGGGTGCACTCGTTCCCCATCACGGACACTACGTG GTCGTGCCGGAGATGCCGCTCCGGTACTGCGCCAGGAACCTCCTCCGCGCGGAGCCACCCCGCTGTA CAAGTTCGAGTGGCACCTCGAGTCCGGCAGCTACATGCACGTATGTGCAAGGCCAGCGGCAGGGTCG TGGCAGCGTGGAGGTGCCGCCCTTCGTACCTTCCACTTCATCAACGCGTACGAGGAGAAGGACGAG GAGGGCCGCGTCACGGCGATCGTCGCCGACTGCTGCGAGCACAACGCCAACACCACCTCCTCGACA AGCTCCGGTCCAGAACCTCCGCTCTTCCACCGGGCAGGACGTCCTCCCGGACGCCAGGGTGGGCCGG TTCAGGATCCCGCTGGACGGGAGCCCGTTTCGGCGAGCTGGAGTCGGCGCTGGACCCGGACCAGCACG GCCGCGGGATGGACATGTGCAGCATCAACCCGGCCACGTCGGCAAGAAGTACCGGTACGCCTACGC CTGCGGCGCCAGCGGCCGTGCAACTTCCCAAACACCCTACCAAGATCGACCTGGTGGAGAAGACG GCCAAGAAGTGGTACGAGGAGGGCGCCGTGCCGTCAGAGCCCTTCTTCGTGCCGCGCCGGGCGCCGT GGAGGAGGACGACGGCGTTGCGATTTTCGATGGTGAAGCGCAAGGACGGATCGGCGTACGCGCTAGTG CTGGACGCCAAGACGTTCCAGGAGATCGCGCGGGCCAAGTTCCTGACGCGATGCCCTACGGTTTGA CTGCTGCTGGGTGCCTAGGACCACCTCAGACGCGTAG		

**Table S4D.** *SbMAX*, orthologous putative gene sequence identified by BLASTn in PlantGDB (<http://www.plantgdb.org/>) using *Arabidopsis thaliana* *MAX1* (AT2G26170) published sequence obtained from ([www.arabidopsis.org](http://www.arabidopsis.org)).

Gene symbol	SbOrtholog ( <i>MAX1</i> ) Sb03g032220	Gen. Bank ID
Gene description	SbOrtholog ( <i>MAX1</i> ) cytochrome P450	8068068
Gene type	protein coding	Ref sequence: XM_002456168.1
Location:	chromosome: 3	

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>SbMAX1: Sb03g032220  
ATGGAGATGGGCACGGTTCTGGGTGCCATGGAGGAGTACACCTTCACCTTCCTGGCCATGGCCGTGGG  
GTTCCCTAGTGCTTGTGTATCTGTACGAGCCGTAAGGAGTGCAGCCACGTGCCCCGGGCCCGTGCCGCT  
GCCGCTCATCGGCCACCTCCACCTGCTGGCGAAGCACGGCCCAGACGTCTTCCCTGTGCTCGCCAAGA  
AGCACGGGCCTATCTTCAGATTTACGTGGGAAGGCAGCCATTGATCATCGTGGCCGACGCAGAGCTC  
TGCAAGGAGGTGGGCATCAAGAAGTTCAAGAGCATGCCTAACCGGAGCTTGCCTTCGCCATCGCCAA  
TTCTCCATACATCGGAAAGGCCTCTTCGCTACAAGGGATTGAGGTGGTGGCGATGCGAAACGTTA  
TCGTCTCGATCTACCAGCCGTCGCACCTCGCCGGCTGATGCCGACCATGGAGTCGTGCATCGAGCGC  
GCTGCGACGACGAACCTCGGCGATGGCGAGGAGGTCGTCTTCTCCAAGCTGGCGCTGAGCCTCGCCAC  
CGACATCATCGGGCAAGCGGCTTCGGCACAGACTTTGGCCTCTCGGGAAAGCCGGTGGTGCCTGACG  
ATGACATGAAGGGTGTGCGACGTCGTCGTGGAGATGCAGCGAAGGCGAAGGCGTCATCATCGGAATT  
CATAAACATGCACATCCACTCGACCACGTCGCTCAAGATGGACCTGTCGGGGTCGCTCTCCACCATCG  
TTGGCGCGCTCGTGCCCTTCTGCAGAATCCGCTGCGGCAGGTGCTCTTGAGGGTCCCCGGCTCCGCCG  
ACCGGGAGATCAACCGTGTGAACGGCGAGCTCCGTAGGATGGTGGACGGCATCGTCGCCGCCCGCGC  
AGCGGAGAGGGAGCGTGCGCCGGCGGCGACAGCAGCACAGCAGCACAAGGACTTCTCTCCGTGGTG  
CTGGCGGGGAGGGAGAGCGACGCTCCACGCGGGAGCTGCTCTCGCCGACTACTTGAGCGCGTTGA  
CCTACGAGCACCTCATCGCTGGGCCGCGACCGCGGGCTTACGCTGTCCTCCGTGGTCTACCTCGTCCG  
CCAAGCACCCGGAAGTGGAGGAGAAGCTGCTTAGGGAGATGGACGCGTTTCGGCCCTCGCGGCAGTGT  
GCCACGGCGGATGATCTTCAGACCAAGTTCCCTACCTCGATCAGGTGGTGAAGGAGTCGATGAGGC  
TGTTTCATGGTGTGCCATTGGTGGCGCGAGAGACCTCCGAGCGAGTGGAGATCGGTGGCTATGTGCTT  
CCAAAGGGGCGCATGGGTGTGGATGGCACCAGGGGTCCTCGCCAAGGACGCCCACTTCCCGGACC  
CGGAGCTGTTCCGACCAGAGCGGTTTCGACCCAGCCGGCGACGAGCAAAAAGAAGCGTCACCCATACGC  
GTTTCATCCCTTTTGAATCGGCCCCAGGGTTTGCATCGGCCAGAAGTTCGCCATCCAGGAGATCAAGC  
TCGCGATAATCCACCTCTATCAGCACTATGTGTTCCGGCATTCTCCAGCATGGAGTCCCCTCTAGAGT  
TTCAGTTTGGGATTGTGGTCAACTTCAAGCATGGTGTCAAGCTTCACGTATCAAGAGGCATGTGGAA  
AATAATTAA

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Table S5A. Primers used for quantitative RT-PCR

Predicted locus/ Gene symbol	Primer pair
SbD27	F_TG TTCAGGGTTGATCAGCAG
Sb05g022855.1	R_CGAGGGTGGCATCATTATCT
SbCCD8	F_GAGTACTTTGCCGCCTTCAC
Sb03g034400.1	R_ACTTCTGGCATGGGATTTTG
SbCCD7	F_ACGCAGATTCTTGCCGTACT
Sb06g024560	R_CAAGCAGAACATAGCCGTCA
SbMAX1	F_GTGGAGATCGGTGGCTATGT
Sb03g032220	R_AAAAGGGATGAACGCGTATG
SbActin1	F_ACATTGCCCTGGACTACGAC
Actin	R_TGATGACCTGTCCATCAGGA

Table S5B. Primers used for quantitative PCR for Marker analysis:

Sequence Name	Sequence
SB3344-F	GCC TCT GCC TCT TGG AAT CAG TTA
SB3344-R	AAG AAA GGG AGT AAC CGG ATG AGC

Table S6. Correlation coefficients between strigolactone peak area in the root exudates, and expression of biosynthetic genes D27 and CCD8 Striga germination and Striga emergence in a pot experiment employing 20 sorghum genotypes.

	5-deoxystrigol	sorgomol	orobanchol
<i>D27</i>	0.70**	0.73**	-0.38NS
<i>CCD8</i>	-0.80**	-0.71	0.21NS

\*\*indicates significance at P<0.05