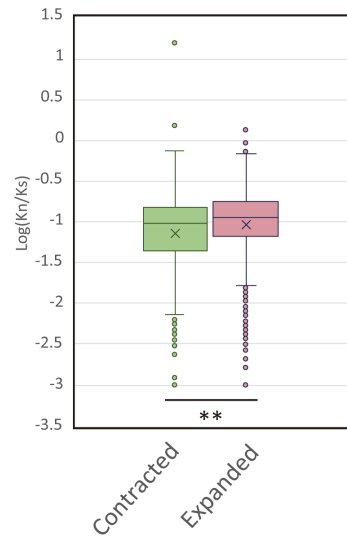


## Supplemental Information

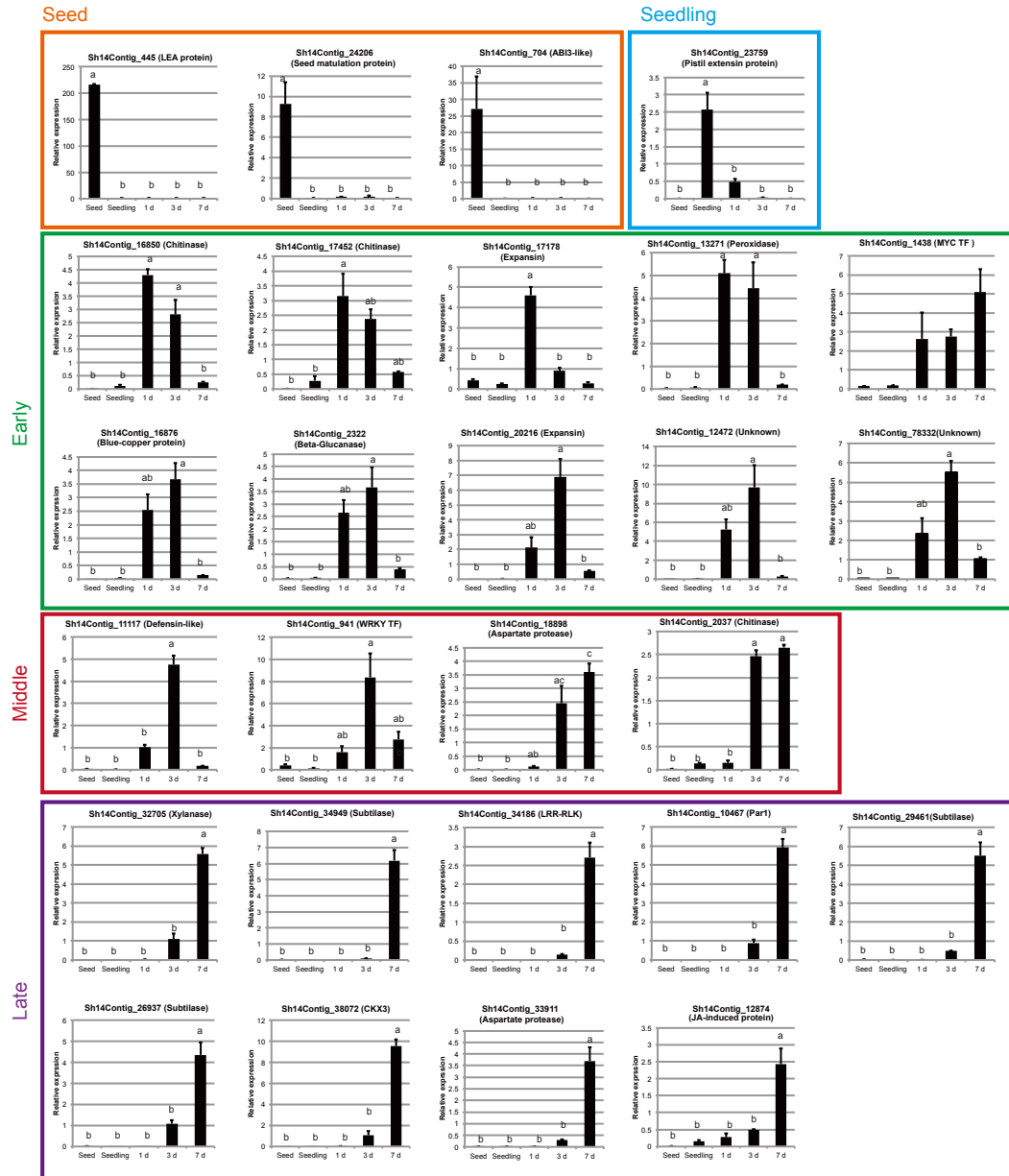
### Genome Sequence of *Striga asiatica* Provides Insight into the Evolution of Plant Parasitism

Satoko Yoshida, Seungill Kim, Eric K. Wafula, Jaakko Tanskanen, Yong-Min Kim, Loren Honaas, Zhenzhen Yang, Thomas Spallek, Caitlin E. Conn, Yasunori Ichihashi, Kyeongchae Cheong, Songkui Cui, Joshua P. Der, Heidrun Gundlach, Yuannian Jiao, Chiaki Hori, Juliane K. Ishida, Hiroyuki Kasahara, Takatoshi Kiba, Myung-Shin Kim, Namjin Koo, Anuphon Laohavisit, Yong-Hwan Lee, Shelley Lumba, Peter McCourt, Jenny C. Mortimer, J. Musembi Mutuku, Takahito Nomura, Yuko Sasaki-Sekimoto, Yoshiya Seto, Yu Wang, Takanori Wakatake, Hitoshi Sakakibara, Taku Demura, Shinjiro Yamaguchi, Koichi Yoneyama, Ri-ichiroh Manabe, David C. Nelson, Alan H. Schulman, Michael P. Timko, Claude W. dePamphilis, Doil Choi, and Ken Shirasu



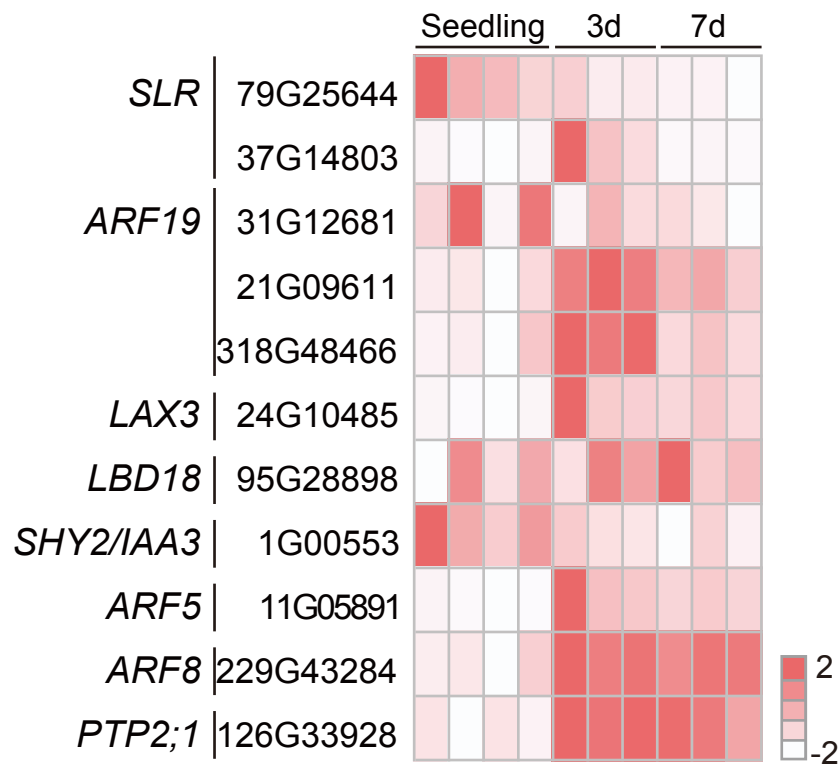
**Figure S1. Kn/Ks ratios between *Striga* and *Mimulus* orthologues in expanded and contracted gene families. Related to Figure 2.**

Ratios of non-synonymous and synonymous substitutions between *S. asiatica* and *M. guttatus* orthologous genes present in syntenic regions were calculated and plotted depending on their evolutionary categories in *S. asiatica* genome. Expanded gene families show significantly higher Kn/Ks ratio compared to contracted gene families (Student's t-test,  $p < 0.00001$ ).



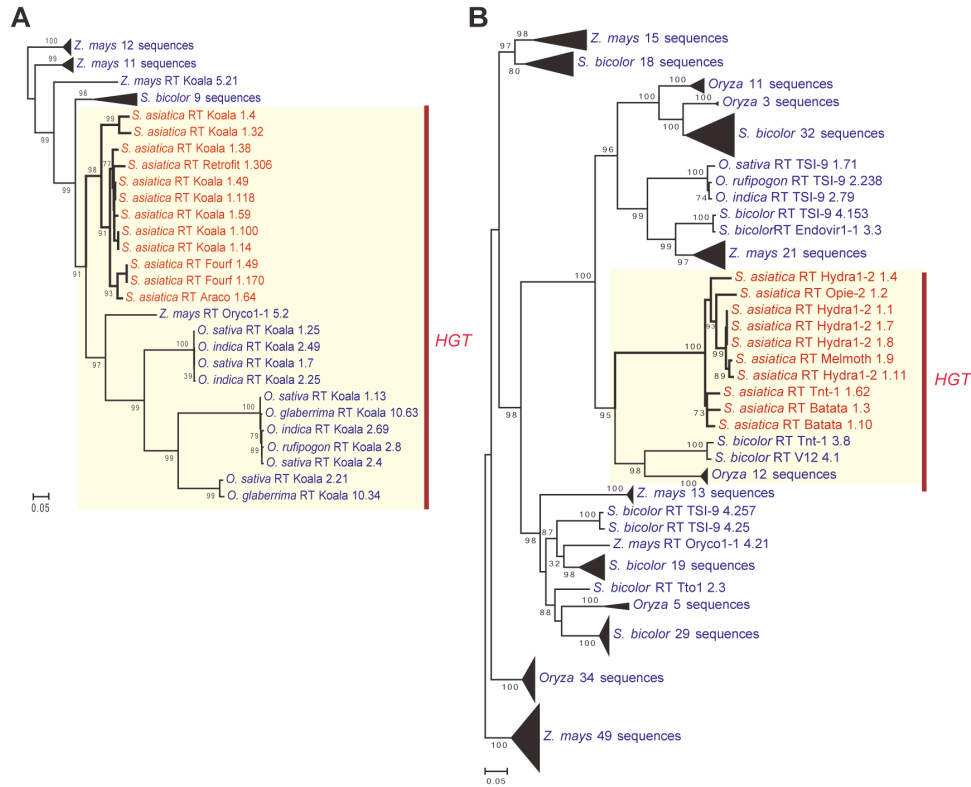
**Figure S2. Stage-specific gene expression in *S. hermonthica*. Related to Figure 4.**

RT-qPCR confirmation of stage-specific expression of selected genes. Relative expression values were normalised by expression of an internal control gene (CHYLOPHILIN). Each value was obtained as the mean of three biological replicates with SE. Statistically significant differences were tested by Tukey's test and shown in different alphabetic characters ( $P < 0.05$ ).



**Figure S3. Expression patterns of lateral root development gene orthologues in *S. asiatica* during host infection. Related to Figure 6.**

The relative expression levels of the LRD genes in *S. asiatica* were measured by RT-qPCR. Seedlings were sampled at 2 d after strigol treatment, and for 3 d and 7 d samples, the *S. asiatica* plants were harvested at 3 d and 7 d post infection of rice roots (cv. Koshihikari).



**Figure S4. Phylogenetic tree of RT domains of HGT candidate retrotransposons. Related to Figure 7.**

**A, B.** Unrooted phylogenetic trees for two RT sequences from *S. asiatica* *Copia* nested to Poaceae sequences drawn by FastTree (v.2.1.10). Local support values are shown at each node, and were calculated by the Shimodaira-Hasegawa test on the three alternate topologies (NNIs). Clades involving the horizontal transfer events are highlighted with pink background.

Annotation/Contig ID	Forward primer sequence	Reverse primer sequence	Gene annotation
<b>Primers used for RT-qPCR in <i>S. asiatica</i></b>			
SGA2.0.scaffold15G07404	TCAATTTGGCCGTGCAATG	CATGGAACTGAGGGTCATCT	SaKAI2c1
SGA2.0.scaffold62G21329_1	GAGGTCATCAACACCGAAGG	CCGGCCACCCCAAGAAT	SaKAI2i1
SGA2.0.scaffold1G00812	CCTCACTCACTTGCTGCAAT	AATACCTCCGTCGGAACCT	SaKAI2d1
SGA2.0.scaffold1G00810	AGTCACTCGTCTGCAATGTC	GTGGGAAGTCCGTCGTG	SaKAI2d2
SGA2.0.scaffold21G09436	GGTCACGATTCTGTGATTCT	AAAGGAGAATGGGCACCTAAA	SaKAI2d3
SGA2.0.scaffold21G09439_1	GAGGTCACGGTTCCAATCAT	CGAAGACTTGTCAAATCCTAATGG	SaKAI2d4
SGA2.0.scaffold21G09439_2	CCCCGTGATTCTCCGTCATATAAA	AAGGAGAATGCGCACCTAAA	SaKAI2d5
SGA2.0.scaffold69G23336	ATACATATCGGACCGACACCGGA	TAGACGGTGCTAATTACTTTAGC	SaKAI2d6
SGA2.0.scaffold62G21329_3	GTCTGTATGATATCGGGCCTTGAC	CACCTCCACCACAGACTTAC	SaKAI2d7
SGA2.0.scaffold62G21329_4	CACCTCTCCGCCACATAAAAT	AGCGTTACCAAAACAGCTCTA	SaKAI2d8
SGA2.0.scaffold12G06040	GTCAAGTCCTAATGGTGGGT	TCCGATCATTCTTCGCCATATAA	SaKAI2d9
SGA2.0.scaffold29G12288	ACGTGACAAGTTATGCTTTAGGA	GTTATTGGCCGGTGCTAGTTA	SaKAI2d10
SGA2.0.scaffold29G12289	AGCACCTCTTACTGTTACTCTTG	GGGCTTGGTTTGATGTCATTAG	SaKAI2d11
SGA2.0.scaffold166G38380	CTGCTTCCACACCGACTG	GTGGATCGGTTTCATCGTCATA	SaKAI2d12
SGA2.0.scaffold8G04626_1	CATCGCGGATCAGTGAAGAT	TAACATCCACACACACACACTC	SaKAI2d13
SGA2.0.scaffold8G04626_2	AAGACAGGACATCGAGGTTTAG	CACACACATACACTCACACTTTC	SaKAI2d14
SGA2.0.scaffold8G04621	GCCACATCAGACAAGACATCA	CACACACACACACTCTCTC	SaKAI2d15
SGA2.0.scaffold29G12335	TCATAAACCCGGTGTGCTC	CTACAAGATGCTCGGCGTATAG	SaKAI2d16
SGA2.0.scaffold11G05891	TTGGAGGCCTTGTGTACTATT	GGGAGAGATTCGGATAGTTTGG	ARF5
SGA2.0.scaffold229G43284	GGCTATCAGAACCCCTCTGTATG	CCAATGTCCAATGACCTACCA	ARF8
SGA2.0.scaffold79G25644	CTGCTGATTCCGACCCAAA	TTGGCAGGTGGTTTCATAACC	SLR/IAA14
SGA2.0.scaffold37G14803	AGGCGATGTAATGAACGAGAA	TCTCCAATAACATCCAATCCC	SLR/IAA14
SGA2.0.scaffold1G00553	CGGAACGCGAAGGCTATAAA	CGAGCCTCTCATGATCCTTAATC	SHY2/IAA3
SGA2.0.scaffold24G10485	AGGTTGCCAGTGGTTATTCC	GTGATCCAACGGTCGAGTTTAT	LAX3
SGA2.0.scaffold126G33928	CATTGGGTTTGGCCTGTTTC	GCCTTGTCTTCCGTAAT	PIP2;1
SGA2.0.scaffold95G28898	ATGCGGTGGTCACGATATG	TGCTGGAGGGCAAGATG	LBD18
SGA2.0.scaffold92G28259	CCATCGGAAGTTCAGCAGAT	ACTTCCGAGATTAGCCGTTATTA	ARF5
SGA2.0.scaffold162G37941	GGAAGAGGGAATGCAGCTT	AGTACATAGGTTAAGACCCATCTT	ARF5
SGA2.0.scaffold31G12681	AGTGAAGGCACCTGCATAAA	ATGCTTGGAAGTCCACATGA	ARF19
SGA2.0.scaffold21G09611	ACTCCGCTCGTTAATATTCATG	GGTTTGGGTAGTTCGGGATT	ARF19
SGA2.0.scaffold318G48466	TGAGCTTGGATGGCGATT	GGAAGAAGAATAAGTTGGCATTGT	ARF19
SGA1.0.scaffold382G00010	GTAATGGGACTGGTGGAGAATC	CCCTGCATTTGCCATTGATAATA	SaCyclophilin (for <i>S. asiatica</i> internal control)
SGA2.0.scaffold119G32689	GTGGGAAGACTAAACCGCCT	GATACACTCTCGCAGAGCCG	SaRPS2(for <i>S. asiatica</i> internal control)
<b>Primers used for in situ hybridisation in <i>S. hermonthica</i></b>			
Sh14Contig_26937	TACAGGGACCTCCTCCTCCT	TTTATGAGGGGCAACAATGC	Subtilase1
Sh14Contig_34949	AAGCACGATCGACAGGAGGT	ACCAGTCGGGATGTGCATT	Subtilase2
Sh14Contig_33911	AATCCG GCTGTACCTTTCTCT	CTGGTCCGTTGGAAGTCTGAT	Aspartate protease
Sh14Contig_34186	TGTGCATACCTGCCATGTCTG	TGGTGTGGCTTATGTCCAGA	LRR kinase
Sh14Contig_38072	ATTCCACGTGGGGACAATCC	TTGACGGTGTGGACAGTCTG	Cytokinin dehydrogenase
Sh14Contig_13271	AGACGGCTATCCCAAACCAA	GCCGAAGAATTTCACGCGA	Peroxidase
<b>Primers used for qRT-PCR in <i>S. hermonthica</i></b>			
Sh14Contig_11117	CCCATCACCAAATCATTACTGC	CGTATGCATGGCTTCTCAAAAT	defensin-like protein
Sh14Contig_20216	TCCAGAGCTTGAATCTGGTGAA	TCGGCAAACTGAAGAAATTACG	LRR kinase
Sh14Contig_38072	ATGGCGAAGGCTTGTGTTGTT	AATCCGTTTGTGGCCCTAAGT	cytokinin dehydrogenase
Sh14Contig_10467	TTGAGATGGCTAGGGAAGGAC	TCCCCTAATAGCAAAGCAAAGC	photoassimilate responsive protein Par1
Sh14Contig_18898	CAGTACGGAGCCTCCAAGTTCT	CACCCCACATCATGACATCTTT	aspartate protease
Sh14Contig_2037	ACTGGATTGGATCGGGTATGAC	CATTGACAGCCCAAGAAGATG	mammalian chitinase
Sh14Contig_12874	CCCCTTACCCTCATGTTATCCA	TGTAGACGATTGCCTCCTTTGA	Jasmonate-induced protein
Sh14Contig_32705	ACGGCCAGCTATATTTTGAGA	CTTGGTGGGATTTCCAATCTTC	endo-beta xylanase c
Sh14Contig_13817	CATTGTGCTCTCGTCATTGAT	AGGTGGACAAGACGAAGAAAGG	polyphenol oxidase
Sh14Contig_445	GGAAACTAGATCCGACCCGTTA	CATAAACCCCAACAACAGAACGA	LEA protein
Sh14Contig_24206	GGATTACAGTCGACAAGATCCA	GCCTAGATCGTCTTGTCTCG	seed maturation protein
Sh14Contig_704	TGCACCTCTCAAGCTAGCCATA	GAAAAACGAGCAAAAGCCACTT	abi3-like
Sh14Contig_23759	GCTGGAGAGGAAAACCAAGAAA	ATCAAGAACACCCGGCAATATC	120 kda pistil extensin-like protein
Sh14Contig_941	ATTTCGTGGCTCGTGCACTGTGA	TCGACAATCTTGAGGACGGATA	WRKY transcription factor
Sh14Contig_1438	GAAATTTGCGACGAATTCCTA	GTTTTTCATGCTGCTACGGTTG	MYC transcription factor
Sh14Contig_16850	CCTGCCCTCGATTACTCACTG	GCCACAGTAGTCATCGGTTGTG	class iv chitinase
Sh14Contig_2322	GAAGTGGCCTCGTACATCAACC	GTGAAGAGCGCGTAGTCCAAGT	beta-glucanase
Sh14Contig_33911	ATTATTGTTGTGGCTGGCTGCT	ATTCCACTCTCGGCAATTTTCA	aspartate protease
Sh14Contig_13271	ATGGGTGCCGGGATTGTCTC	CCGTGGGCGAGTTGAAGGTGCG	proxidase precursor
Sh14Contig_17452	ACCGCGCGGACATTATCGTA	GACGTACGGCCAGATCGTGA	chitinase
Sh14Contig_78332	GGCCCTCTCGGCTTCATAGC	CGAGAATAACGTTGGGGTGCTC	no hit
Sh14Contig_17178	TGCGGTGGCCATAGAGTACG	CCACTTTCCAACCGAAACCCC	beta-expansin
Sh14Contig_16876	GCGCGACACAATTTGTACCTGTT	ATGTCCCGGCTTATTTAGCGTCA	blue copper protein
Sh14Contig_12472	TTACCATAACCGTCAAGCGCAAGC	ACTCCGTCAGCTCCATACAAACCA	unknown protein
Sh14Contig_20216	GAAACGATGTTAACGCGTGCGGAA	TGGCCCGAGCATATATCCAACGAA	expansin b1
Sh14Contig_26937	GTGTCGATAAGCCCAACGAT	CACCACAAGAAGCTGGGATT	Subtilase1
Sh14Contig_29461	ACCAGGTTCCCTTTCTCCTG	CATGCTTTTGGGATTTCTAT	Subtilase3
Sh14Contig_34949	AGGAGACCAAGCTGGCTATGA	GCCGCTCTGATTTTCTCGTC	Subtilase2
Sh_Cyclophilin_1	TCGCCGACGAGAATTTGTGAAGA	TCTTCGCGGTGCAGATGAAGAACT	cyclophilin (for rice interaction internal control)
Sh_Cyclophilin_2	GTCGTGATGGAGCTTTTCGC	CCTTGTAGTGGAGGGGCTTG	cyclophilin (for nonhost interaction internal control)

**Table S1. Primers used in this paper. Related to STAR Methods.**