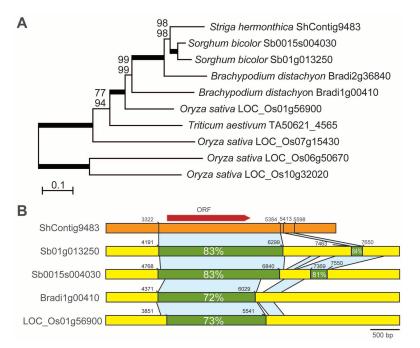
## Horizontal Gene Transfer by the Parasitic Plant *Striga hermonthica*

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**H** orizontal gene transfer (HGT) plays an important role in genome evolution (1). In plants, the majority of reported cases of HGT have been limited to exchanges between plants and microbes, mitochondrial transfer, or the translocation of mobile elements among related species (1). Parasitic plants are known to be vectors of mitochondrial HGT, but it has been unclear whether they also mediate nuclear HGT (1, 2).

Striga hermonthica (Del.) Benth. is a devastating parasitic plant that infests members of the grass family (Poaceae), including major crops such as sorghum (Sorghum bicolor) and rice (Oryza sativa). S. hermonthica belongs to the eudicot Orobanchaceae family of the order Lamiales (fig. S1) (3) and only infects monocot plants. Thus, we reasoned that we may be able to detect nuclear HGT, if it occurs, by identifying monocot-specific genes in the S. hermonthica genome. From a large-scale expressed sequence tag analysis of S. hermonthica (4), we found one gene, designated ShContig9483, which shows high similarity to genes in sorghum and rice but has no homologs in eudicots (fig. S2A and table S1) (5). Southern blot analysis revealed *ShContig9483* cross-hybridization signals from sorghum, and rice to a lesser extent, reflecting its lower similarity, whereas no signals were detected from other closely related plants in Orobanchaceae nor from any nonparasitic eudicots (fig. S2B). This indicates that *ShContig9483* most likely originated in the monocots before its transfer to *S. hermonthica*.

ShContig9483 encodes a 448–amino acid protein with unknown function. Phylogenetic analysis of ShContig9483 and related protein-coding sequences clusters S. hermonthica with sorghum (Fig. 1A). This tree conflicts with the phylogenetic position of Striga (3), suggesting that S. hermonthica acquired ShContig9483 from sorghum or a related grass species. The S. hermonthica genomic region containing ShContig9483 resides near a nuclear gene encoding a putative cis-prenyltransferase (fig. S3A). In contrast to ShContig9483, this putative cis-prenyltransferase gene from S. hermonthica clusters with genes from other eudicot species (fig. S3B).



**Fig. 1.** *ShContig9483* represents nuclear HGT in *S. hermonthica*. (**A**) Phylogenetic tree of *ShContig9483* homologs. Maximum likelihood bootstrap values (ML, top) and Bayesian inference posterior probability values (BI, bottom) are indicated at the nodes of a maximum likelihood tree. Bold lines indicate BI = 100 and ML > 95. (**B**) Comparison of genomic sequences of *ShContig9483* and its homologs from *S. bicolor* (Sb01 g013250 and Sb0015s004030), *Brachypodium distacyon* (Bradi1g00410), and *O. sativa* (LOC\_0s01 g56900). Sequences with and without similarity to *ShContig9483* are indicated in green (with identities) and yellow, respectively, and similar regions between adjacent homologs are indicated by light blue.

The genomic sequences of the sorghum homologs show similarities to the ShContig9483 locus from about 150 base pairs (bp) up- and 800 bp downstream of the putative open reading frame (ORF), except for several insertions and deletions (Fig. 1B and fig. S4). The similarity to homologs from Brachypodium and rice covers a shorter region with lower identities (Fig. 1B). The high conservation of sequence between S. hermonthica and sorghum outside the ORF suggest that transfer was a relatively recent event. Indeed, a sequence highly similar to ShContig9483 was found in S. gesnerioides but not in Orobanche minor, which is from a closely related genus (figs. S2B and S5). These data suggest that incorporation of the ShContig9483 fragment occurred before speciation of S. hermonthica and S. gesnerioides but after differentiation of the genera Striga and Orobanche. Parasitic plants form an invasive organ called a haustorium, which interconnects their vasculature with that of their hosts to allow transfer of nutrients, water, and even mRNAs (2). Thus, one possibility is that ShContig9483 was originally captured by S. hermonthica as mRNA or cDNA. Interestingly, we found 13 consecutive adenine (A) nucleotides at the 3' end of the ShContig9483 genomic region (fig. S4). This sequence may be indicative of a poly-A tail added to a transcriptional unit of the originally transferred gene. In any case, our comparative genomics analysis of a eudicot parasite and its monocot hosts presents a clear case for nuclear HGT. Because the method used in this study is limited to the detection of nuclear HGT of genes that are unusual among eudicots, we suspect that more nuclear HGT will be found if other genes are investigated in detail.

## **References and Notes**

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- 5. Information on materials and methods is available on *Science* Online.
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## Supporting Online Material

www.sciencemag.org/cgi/content/full/328/5982/1128/DC1 Materials and Methods Figs. S1 to S5

Table S1 References

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