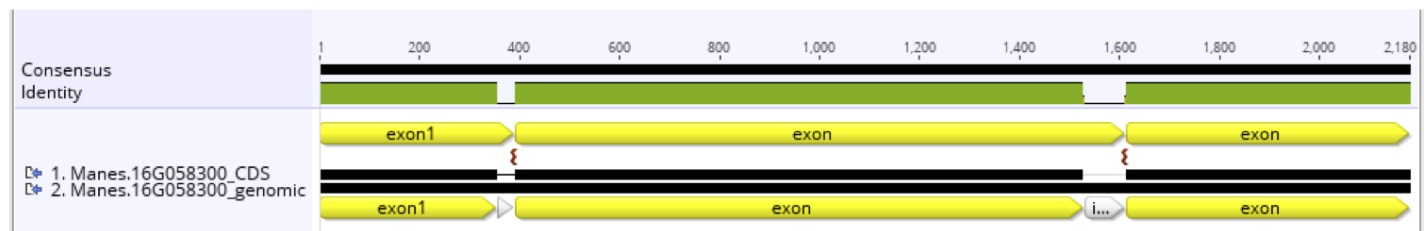


a

Presence of introns indicates a genomic transfer

Donor gene has 2 introns Alignment of the donor gene CDS and donor genomic sequence reveals two introns



Alignment of *Cuscuta* genomic against the donor genomic reveals genomic transfer containing introns (72% nucleotide identity) and the two exon-intron boundaries retain



b

The *Cuscuta* sequence becomes a pseudogene

removes introns in *Cuscuta* genomic sequence, translates, then aligns with peptide sequences of the donor (54.5% PEP identity, or 64% PEP identity in exon2-3)



However, stop codons in the coding sequence of *Cuscuta* suggests it is a pseudogene

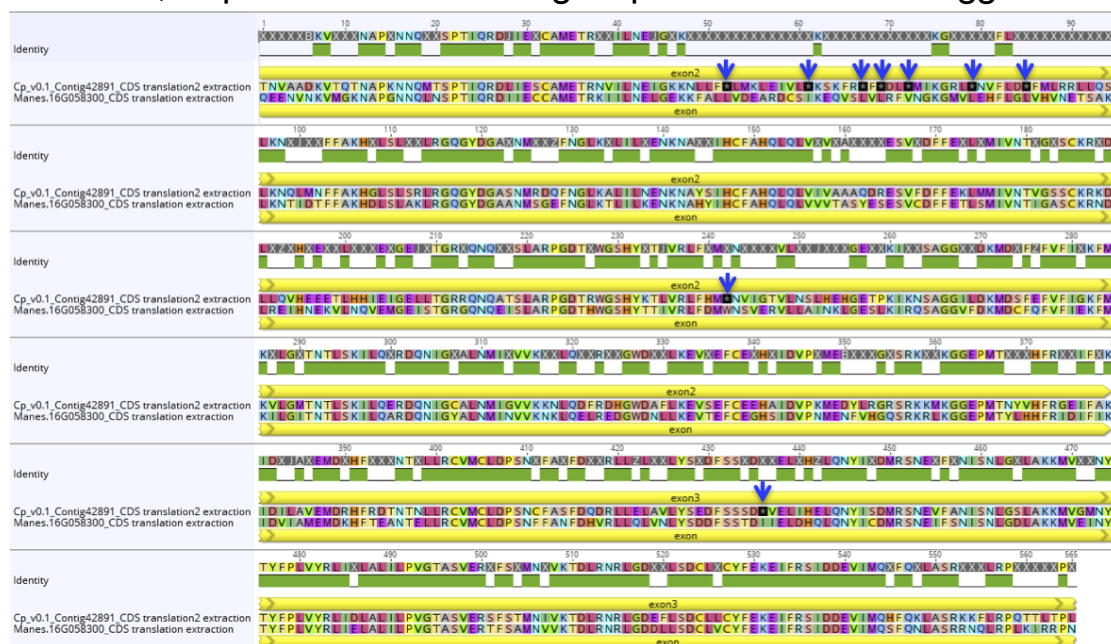


Fig. S10. Analysis workflow illustrating HGT of a *Cuscuta* gene via genomic transfer from a *Manihot* ancestor followed by pseudogenization. The presence of conserved introns between the donor and the HGT gene indicate the HGT gene was via genomic transfer (Yang et al., 2016) (a). However, the presence of multiple premature stop codons (b) indicates that the *Cuscuta* gene has become pseudogenized.

References

Yang, Z. et al. Horizontal gene transfer is more frequent with increased heterotrophy and contributes to parasite adaptation. Proc Natl Acad Sci U S A, doi:10.1073/pnas.1608765113 (2016).