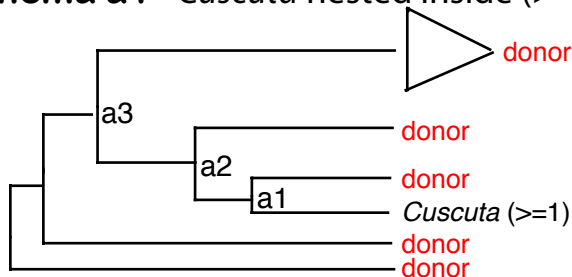
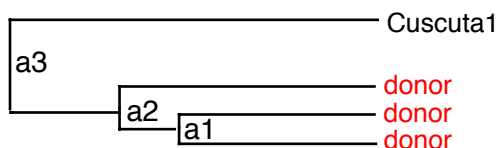


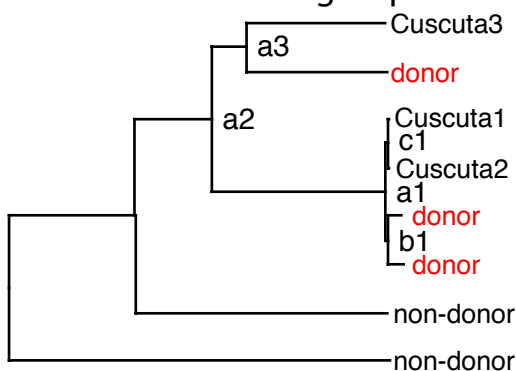
Schema a1 - *Cuscuta* nested inside (≥ 1 *Cuscuta*)



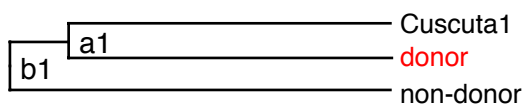
Schema b1 - *Cuscuta* grouped outside (1 *Cuscuta*)



Schema b2 - *Cuscuta* grouped outside (≥ 2 *Cuscuta*)



Schema c1 - only one supported node (1 *Cuscuta*)



Schema c2 - only one supported node (≥ 2 *Cuscuta*)

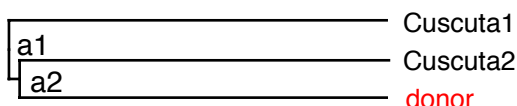


Fig. S2. Three models for phylogenetic identification of HGT.

Schema a1: 1) *Cuscuta* sequence is nested within its donor clades. *Cuscuta* drawn here can be one or more sequences; if more than one sequence, a1 is the ancestral node of the first donor sequence. 2) At least two values out of (a1, a2, a3) ≥ 50 . **Schema b1:** 1) One single *Cuscuta* sequence is outside of the donor nodes. 2) at least two values out of (a1, a2, a3) ≥ 50 .

Schema b2: 1) More than two *Cuscuta* sequences are outside of the donor nodes. 2) at least two values out of (a1, a2, a3) ≥ 50 . **Schema c1:** 1) One single *Cuscuta* sequence groups with donor with just one strong node (only a1 ≥ 50). **Schema c2:** 1) More than two *Cuscuta* sequences group with donor, (2) but only one strong node: only one value of (a1, a2) ≥ 50 .