

Phylogeny, character evolution, and biogeography of *Cuscuta* (dodders; Convolvulaceae)

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The parasitic genus *Cuscuta*, containing some 200 species circumscribed traditionally in three subgenera, is nearly cosmopolitan, occurring in a wide range of habitats and hosts. Previous molecular studies, on subgenera *Grammica* and *Cuscuta*, delimited major clades within these groups. However, the sequences used were unalignable among subgenera, preventing the phylogenetic comparison across the genus. We conducted a broad phylogenetic study using *rbcL* and nrLSU sequences covering the morphological, physiological, and geographical diversity of *Cuscuta*. We used a variety of methods to reconstruct phylogeny, ancestral states for taxonomically important characters, and historical biogeography. Four well-supported major clades are resolved. Two of them correspond to subgenera *Monogynella* and *Grammica*. Subgenus *Cuscuta* is paraphyletic, with section *Pachystigma* sister to subgenus *Grammica*. Dehiscent fruits and globose stigmas are inferred as ancestral character states, whereas the ancestral style number is ambiguous. These results disagree with scenarios of evolution (polarity) previously proposed for several taxonomically important morphological characters, and with their usage and significance. Biogeographical reconstructions suggest an Old World origin for the genus and subsequent spread to the Americas as a consequence of one long-distance dispersal. While several cases of long-distance dispersal are inferred, vicariance or dispersal to adjacent areas emerges as the dominant biogeographical pattern.

The vast majority of relationships within this subgenus are congruent between plastid- and nuclear-derived phylogenies. However, we also discovered a number of cases of strongly supported discordance between them. We interpreted them as results of 9-10 independent hybridization events. Some cases involve species whose progenitors are derived from different major groups of subgenus *Grammica*, and which are clearly allopatric in their present distribution. This is consistent with more ancient hybridization events. However, most of these cases likely represent relatively recent reticulations because each of them involves more closely related species, always confined within the same section as their putative parental species, and are currently sympatric or parapatric with them. One such small group of species that contains recent and repeated hybridization, resulting in multiple polyploid hybrid species, *Cuscuta* section *Denticulatae*, will be discussed in detail. We are currently developing this tractable natural system to address questions about the pace of genetic, epigenetic, and evolutionary change, and to study broader implications of repeated polyploidy (i.e., does genomic/genetic evolution repeat itself in polyploids of multiple origin, does parental genotype matter in polyploidization, to what extent, etc.).