

RESEARCH

Thirteen genomes

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Abstract

Background: Text for this section.

Results: Text for this section.

Conclusions: Text for this section.

Keywords: genome sequence; cotton; *Gossypium*; molecular evolution

Background

The American diploid “D-genome” cottons (subgenus *Houzingenia*) comprise a monophyletic clade of cytogenetically and morphologically distinct species largely distributed from Southwest Mexico to Arizona, with additional disjunct species distributions in Peru and the Galapagos Islands [Corrinne](#). Among the 13 species currently included in the D-genome /note[Corrinne]although see Ulloa 2013 are *G. raimondii* (D5), the model diploid progenitor to wild and domesticated allopolyploid cotton, and *G. harknessii* (D2-2), an important species for cytoplasmic male sterility in cotton. Classic cytogenetic research regarding interspecific meiotic pairing patterns revealed that the origin of one allopolyploid progenitor was derived from subgenus *Houzingenia* [Corrinne](#). The close relationship of *Houzingenia* to the agronomically important polyploid species, along with the relative ease of sampling this subgenus for early cotton taxonomists, led to the much of the current understanding of the relationships among D-genome species.

These early taxonomists divided subgenus *Houzingenia* into two sections and six subsections, whose species alliances have largely been retained by subsequent phylogenetic studies [Corrinne](#). Several molecular datasets have been used to evaluate these relationships, including chloroplast restriction sites [Corrinne](#); simple sequence repeat (SSR) and expressed sequence tag (EST)-SSR markers [Corrinne](#); random amplified polymorphic DNA (RAPD) markers [Corrinne](#); internal transcribed sequences (ITS) [Corrinne](#); and few single-copy nuclear genes [Corrinne](#). Relationships among the six subsections, however, remain unclear despite numerous, and often conflicting, studies [Corrinne](#). Determining the closest living relative of the D-genome ancestor to the polyploid, however, has been met with greater success. Early morphological and cytogenetic comparisons using intergenomic hybrids quickly identified *G. raimondii* as the closest living relative to the D-genome ancestor of polyploid cotton species (Stephens, 1944b Hutchinson et al., 1945, 1947; Gerstel and Phillips, 1958; Phillips, 1964; reviewed in Wendel and Cronn 2003). Subsequent analyses have largely supported this observation (Abdalla et al., 2001; cronn 1999, liu 2001, Cronn et al., 1996 Seelanan et al., 1997 Small et al., 1998; Small and Wendel, 2000a,b), with few

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conflicts (see, however Wendel et al., 1995b; I know there are others. . . . What are they?).

Results

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Results subsection

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Discussion
Conclusions
Methods

Competing interests
The authors declare that they have no competing interests.

Author’s contributions
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Figures

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Figure 2 Sample figure title. Figure legend text.

Tables

Table 1 Sample table title. This is where the description of the table should go.

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