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Thirteen genome sequences representing the entire subgenus *Houzingenia* (*Gossypium*): insights into evolution of the New World diploid cottons

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Abstract

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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 Corrinne are*G. harknessii* (D2-2), an important species for cytoplasmic male sterility in cotton, and *G. raimondii* (D5), the model diploid progenitor to wild and domesticated allopolyploid cotton Corrinne. The close relationship of *Houzingenia* species to the agronomically important polyploids, combined with the relative ease of sampling this subgenus for early cotton taxonomists, facilitated 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 Corrinne. 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 conflicts Corrinne.

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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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References
Figures

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Figure 2 Sample figure title. Figure legend text.

Tables

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