**Original article**

**Inferring Hypothesis-based Transitions in Clade-specific Models of Chromosome Number Evolution along Phylogenies**

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**Summary**

Chromosomal rearrangements have been shown to trigger diversification. For instance, several ancient rounds of polyploidization events have been inferred to promote angiosperm diversification. Dysploidy, although less studied, has been suggested to play also an important role in angiosperm diversification. In this article, we aim to elucidate the role of chromosomal rearrangements on lineage diversification by analyzing a new comprehensive sedge (Cyperaceae) phylogenetic tree.

Mode and tempo of chromosome evolution were inferred for the complete phylogeny as null hypothesis. In order to discern patterns of diversification shifts and chromosome number changes within the family tree, we tested clade-specific chromosome evolution models for several subtrees according to previously reported increments of diversification rates.

Results show that alternative hypotheses of clade-specific models of chromosome evolution are significantly supported against the null hypothesis of a single model.

This could suggest a link between diversification and changes in chromosome number evolution. Our methodological approach may allow identifying different patterns of chromosome evolution, as found for Cyperaceae, for other lineages at different evolutionary levels.

**Key words**

ChromEvol, chromosome evolution, Cyperaceae, dysploidy, diversification rates, holocentric chromosomes, phylogeny, polyploidy