

Loss of matK RNA editing in seed plant chloroplasts

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Abstract: Background. RNA editing in chloroplasts of angiosperms proceeds by C-to-U conversions at specific sites. Nuclear-encoded factors are required for the recognition of cis-elements located immediately upstream of editing sites. The ensemble of editing sites in a chloroplast genome differs widely between species, and editing sites are thought to evolve rapidly. However, large-scale analyses of the evolution of individual editing sites have not yet been undertaken. **Results.** Here, we analyzed the evolution of two chloroplast editing sites, matK-2 and matK-3, for which DNA sequences from thousands of angiosperm species are available. Both sites are found in most major taxa, including deep-branching families such as the nymphaeaceae. However, 36 isolated taxa scattered across the entire tree lack a C at one of the two matK editing sites. Tests of several exemplary species from this *in silico* analysis of matK processing unexpectedly revealed that one of the two sites remain unedited in almost half of all species examined. A comparison of sequences between editors and non-editors showed that specific nucleotides co-evolve with the C at the matK editing sites, suggesting that these nucleotides are critical for editing-site recognition. **Conclusion.** (i) Both matK editing sites were present in the common ancestor of all angiosperms and have been independently lost multiple times during angiosperm evolution. (ii) The editing activities corresponding to matK-2 and matK-3 are unstable. (iii) A small number of third-codon positions in the vicinity of editing sites are selectively constrained independent of the presence of the editing site, most likely because of interacting RNA-binding proteins. © 2009 Tillich et al.

Index Keywords: nucleotide; angiosperm; article; chloroplast; chloroplast genome; DNA sequence; gene; matK 2 gene; matK 3 gene; nonhuman; plant seed; RNA editing; classification; cytology; evolution; genetics; metabolism; molecular genetics; nucleotide sequence; phylogeny; Codon (angiosperm); Magnoliophyta; Nymphaeaceae; Spermatophyta; Angiosperms; Base Sequence; Chloroplasts; Evolution; Molecular Sequence Data; Phylogeny; RNA Editing; Seeds

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