Cross-species primer design with primers4clades: probing chloroplast genes as phylogenetic markers

http://floresta.eead.csic.es/primers4clades

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Chloroplast genomes are the main source of molecular data for phylogenetic analyses among plants. Here we take the set of chloroplast gene families annotated in CholoroplastDB[1] and analyze them with primers4clades[2], an easy-to-use web server that implements a fully automatic PCR primer design pipeline for cross-species amplification of novel sequences belonging to user-specified clades or taxa. Results: 1) Assessment of the phylogenetic value of chloroplast genes present in 10+ genomes finds that matK and rbcL, broadly accepted as universal barcoding candidates for land plants[3], are among the most informative genes. In addition several other loci are found with similar phylogenetic information content.

2) Analysis of 32 matK gene sequences illustrates how the server can help targeting primer design to selected clades of interest, and how the number and quality of obtained pairs of primers depends on the variability of the input nucleotide sequences.