



Comparative Chloroplast Genome Analysis, Codon Usage Patterns and Phylogenetic Position of *Euonymus alatus*

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DESCRIPTION

Euonymus alatus, commonly known as burning bush or winged spindle tree, is a deciduous woody plant belonging to the family Celastraceae. It is recognized for its distinctive wing-like corky structures on young branches and its conspicuous autumn coloration. Beyond its horticultural importance, the species provides useful material for understanding chloroplast genome organization, molecular evolution and relationships within Celastraceae. Comparative chloroplast genomics, together with codon usage analysis and phylogenetic reconstruction, can reveal patterns of genome conservation and divergence while providing molecular information for species identification and evolutionary interpretation. The chloroplast genome is generally a compact circular Deoxyribonucleic Acid (DNA) molecule organized into a large single-copy region, a small single-copy region and two inverted repeat regions. These structural components contain genes associated with photosynthesis, transcription, translation and chloroplast maintenance.

Although chloroplast genomes are relatively conserved compared with nuclear genomes, differences in sequence composition, gene arrangement, repeat boundaries and intergenic regions can provide valuable evolutionary signals. Examining these characteristics in *Euonymus alatus* allows its chloroplast architecture to be considered in relation to closely related members of Celastraceae. Comparative analysis commonly focuses on genome length, nucleotide composition, coding sequences, ribosomal Ribonucleic Acid (RNA) genes, transfer RNA genes and the positions of major structural boundaries. The inverted repeat regions are particularly informative because expansions or contractions at their junctions can contribute to differences in total chloroplast genome size. Most essential chloroplast genes remain highly conserved, whereas non-coding regions may accumulate substitutions and insertions or deletions at comparatively greater rates. These variable regions can therefore provide useful molecular markers for distinguishing closely related taxa.

Codon usage represents another important feature of chloroplast genome evolution. Protein-coding genes are composed of codons that specify amino acids, but synonymous codons are not always used equally. This unequal preference, known as codon usage bias, can be influenced by nucleotide composition, translational selection, gene expression, mutation patterns and evolutionary history. In plant chloroplast genomes, a preference for codons ending in particular nucleotides is frequently associated with the overall base composition of the genome. Assessing codon preferences in *E. alatus* can therefore provide information about the molecular characteristics shaping its chloroplast genes. Measures such as relative synonymous codon usage and effective number of codons can help describe the strength and direction of codon bias. Highly preferred codons may occur more frequently than expected under equal synonymous usage, while other codons may be comparatively underrepresented. When these patterns are examined across multiple chloroplast genomes, similarities may reflect shared evolutionary constraints or comparable genomic composition. Differences can also highlight lineage-specific changes that accumulated during diversification.

Phylogenetic placement provides a broader evolutionary context for the chloroplast genome of *E. alatus*. Chloroplast protein-coding genes and conserved genomic regions can be aligned with homologous sequences from related species, allowing evolutionary relationships to be inferred from shared sequence characteristics. The resulting phylogenetic framework can help clarify the position of *E. alatus* within Celastraceae and indicate relationships among closely related genera. Because chloroplast genomes are generally inherited as linked units, their phylogenetic signal can be particularly useful for resolving certain taxonomic relationships. Comparing complete chloroplast genomes may provide stronger resolution than relying on a small number of individual genes. Conserved coding regions contribute stable phylogenetic information, while variable intergenic sequences may improve discrimination

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among closely related lineages. However, chloroplast-based relationships represent the evolutionary history of the chloroplast genome and may not always correspond exactly to relationships inferred from nuclear DNA because of hybridization, incomplete lineage sorting or differences in inheritance patterns.

The integration of genome structure, codon usage and phylogenetic information creates a multidimensional view of *E. alatus*. Genome comparisons can identify conserved and

variable regions, codon analysis can characterize patterns of molecular selection and nucleotide preference and phylogenetic reconstruction can place the species within a broader evolutionary framework. Together, these approaches can support accurate species identification and provide molecular resources for comparative studies of Celastraceae. Such genomic information may also have practical value. Reliable chloroplast markers can assist in distinguishing morphologically similar species, verifying plant material and supporting conservation assessments.