

Intron polymorphism pattern in *AOX1b* of wild St John's wort (*Hypericum perforatum*) allows discrimination between individual plants

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ABSTRACT

The present paper deals with the analysis of natural polymorphism in a selected alternative oxidase (AOX) gene of the medicinal plant, St John's wort. Four partial AOX gene sequences were isolated from the genomic DNA of a wild plant of *Hypericum perforatum* L. Three genes belong to the subfamily AOX1 (*HpAOX1a*, *b* and *c*) and one to the subfamily AOX2 (*HpAOX2*). The partial sequence of *HpAOX1b* showed polymerase chain reaction (PCR) fragment size variation as a result of variable lengths in two introns. PCR performed by Exon Primed Intron Crossing (EPIC)-PCR displayed the same two-band pattern in six plants from a collection. Both fragments showed identical sequences for all exons. However, each of the two introns showed an insertion/deletion (InDel) in identical positions for all plants that counted for the difference in the two fragment sizes. The InDel in intron 1 influenced the predictability of a pre-microRNA site. The almost identical PCR fragment pattern was characterized by a high variability in the sequences. The InDels in both introns were linked to repetitive intron single nucleotide polymorphisms (ISNP)s. The polymorphic pattern obtained by InDels and ISNPs from both fragments together was appropriate to discriminate between all individual plants. We suggest that AOX sequence polymorphism in *H. perforatum* can be used for studies on gene diversity and biodiversity. Further, we conclude that AOX sequence polymorphism of individual plants should be considered in biological studies on AOX activity to exclude the influence of genetic diversity. The identified polymorphic fragments are available to be explored in future experiments as a potential source for functional marker development related to the characterization of origins/accessions and agronomic traits such as plant growth, development and yield stability.

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