

ABSTRACT

Alternative oxidase (Aox) has been proposed as a functional marker for breeding stress tolerant plant varieties. This requires presence of polymorphic Aox allele sequences in plants that affect plant phenotype in a recognizable way. In this review, we examine the hypothesis that organization of genomic Aox sequences and gene expression patterns are highly variable in relation to the possibility that such a variation may allow development of Aox functional markers in plants. Aox is encoded by a small multigene family, typically with four to five members in higher plants. The predominant structure of genomic Aox sequences is that of four exons interrupted by three introns at well conserved positions. Evolutionary intron loss and gain has resulted in the variation of intron numbers in some Aox members that may harbor two to four introns and three to five exons in their sequence. Accumulating evidence suggests that Aox gene structure is polymorphic enough to allow development of Aox markers in many plant species. However, the functional significance of Aox structural variation has not been examined exhaustively. Aox expression patterns display variability and typically Aox genes fall into two discrete subfamilies, Aox1 and Aox2, the former being present in all plants and the latter restricted in eudicot species. Typically, although not exclusively, the Aox1-type genes are induced by many different kinds of stress, whereas Aox2-type genes are expressed in a constitutive or developmentally regulated way. Specific Aox alleles are among the first and most intensively stress-induced genes in several experimental systems involving oxidative stress. Differential response of Aox genes to stress may provide a flexible plan of plant defense where an energy-dissipating system in mitochondria is involved. Evidence to link structural variation and differential allele expression patterns is scarce. Much research is still required to understand the significance of polymorphisms within AOX gene sequences for gene regulation and its potential for breeding on important agronomic traits. Association studies and mapping approaches will be helpful to advance future perspectives for application more efficiently.

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