

## Aox gene structure, transcript variation and expression in plants

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### 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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Received 28 April 2009; revised 20 July 2009

DOI:10.1111/j.1399-3054.2009.01284.x

Full article available: <http://www3.interscience.wiley.com/journal/122578542/abstract>