

Differential expression and co-regulation of carrot AOX genes (*Daucus carota*)

Maria Doroteia Campos ^a, Hélia Guerra Cardoso ^a, Bettina Linke ^b, José Hélio Costa ^c, Dirce Fernandes de Melo ^c, Lígia Justo ^a, António Miguel Frederico ^a and Birgit Arnholdt-Schmitt ^{a,*}

^a EU Marie Curie Chair, ICAAM, University of Évora, Apartado 94, 7002-554 Évora, Portugal

^b Department of Biology, Humboldt University, Invalidenstr. 42, D-10115 Berlin, Germany

^c Department of Biochemistry and Molecular Biology, Federal University of Ceará, PO Box 6029, 60455-900, Fortaleza, Ceará, Brazil

Correspondence to * e-mail: eu_chair@uevora.pt

ABSTRACT

Alternative oxidase (AOX) is a mitochondrial protein encoded by the nuclear genome. In higher plants AOX genes form a small multigene family mostly consisting of the two subfamilies AOX1 and AOX2. *Daucus carota* L. is characterized by a unique extension pattern of AOX genes. Different from other plant species studied so far it contains two genes in both subfamilies. Therefore, carrot was recently highlighted as an important model in AOX stress research to understand the evolutionary importance of both AOX subfamilies. Here we report on the expression patterns of *DcAOX1a*, *DcAOX1b* and *DcAOX2a* and *DcAOX2b*. Our results demonstrate that all of the four carrot AOX genes are expressed. Differential expression was observed in organs, tissues and during de novo induction of secondary root phloem explants to growth and development. *DcAOX1a* and *DcAOX2a* indicated a differential transcript accumulation but a similar co-expression pattern. The genes of each carrot AOX sub-family revealed a differential regulation and responsiveness. *DcAOX2a* indicated high inducibility in contrast to *DcAOX2b*, which generally revealed low transcript abundance and rather weak responses. In search for within-gene sequence differences between both genes as a potential reason for the differential expression patterns, the structural organization of the two genes was compared. *DcAOX2a* and *DcAOX2b* showed high sequence similarity in their open reading frames (ORFs). However, length variability was observed in the N-terminal exon1 region. The predicted cleavage site of the mitochondrial targeting sequence in this locus is untypical small for both genes and consists of 35 amino acids for *DcAOX2a* and of 21 amino acids for *DcAOX2b*. The importance of structural gene organization and the relevancy of within-gene sequence variations are discussed. Our results strengthen the value of carrot as a model plant for future studies on the importance of AOX sub family evolution.

Received 19 May 2009; revised 5 August 2009

DOI: 10.1111/j.1399-3054.2009.01282.x

Full article available: <http://www3.interscience.wiley.com/journal/122574752/abstract>