

Analysis of the CAD2 gene polymorphism in *Eucalyptus urophylla* population along altitudinal gradient in Timor Island

Favreau B., Bouvet J-M

Forest Genetics Unit (UPR 39), Biological System Department, TA A-39/C, 34398 Montpellier Cedex 5, FRANCE

E-mail: benedicte.favreau@cirad.fr

We study the nucleotidic variability within the Cinnamyl Alcohol Dehydrogenase (CAD2) gene, a structural gene of the lignin biosynthesis pathway, within a representative sample of *E. urophylla* distributed at various altitudes in the Timor Island. We sequenced 100% of the CAD2 gene from 10 individuals by direct sequencing of the PCR product.

The gene has a total length of 5395 bp, 5 exons and 4 introns, and shows a 93% similarity with the *E.gunnii* CAD2 gene. We identified 160 SNPs and 16 INDELS with a heterogeneous polymorphism distribution in the exonic regions (1 SNP/74 bp) and the intronic regions (1 SNP /21 bp). Four SNPs are non synonymous and 1 SNP is translated in polar/non polar aminoacids.

The diversity in the silent regions is higher ($\pi=10.8 \times 10^{-3}$) than in the non synonymous sites ($\pi=0.74 \times 10^{-3}$). The sliding window analysis detects polymorphism variation along the gene with 5 peaks showing high π values in the silent region.

The D Tajima test is negative but not significant for the whole gene, showing no impact of the natural selection. However, the sliding window approach detects 2 regions, exon 3 and exon 5, with a negative significant Tajima and Fu and Li's D and F tests.

Divergence between 2 populations (superior to 1000 m and inferior to 1000 m) vary also along the gene and 1 peak corresponds to a positive Tajima D values and high polymorphism.

A detail analysis of variation in exons 3 and 5 is undertaken with 85 individuals distributed along the altitudinal gradient.



