

TRANSCRIPTOME RESPONSE OF *POPULUS ALBA* TO ULTRAVIOLET-B RADIATION

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Depletion of stratospheric ozone has led to an increase of ultraviolet-B radiation (UVB) on earth surface; UVB radiation induces several physiological and morphological responses and is potentially deleterious to plant growth and development. The molecular mechanisms of UVB perception and UVB induced acclimation processes are still unclear. A microarray technology approach was used to assess UVB induced transcriptome change in poplar (*Populus alba L.*) under a realistic simulation of UVB radiation increase carried out in a controlled environment. The UVB radiation causes a dramatic change in gene expression, with more than 570 upregulated ESTs and 750 downregulated ESTs differentially expressed between irradiated and control plants after 30 hours of treatment. UVB radiation induced transcriptome change involves many pathways, with a strong down regulation of photosynthetic genes and the up regulation of the phenylpropanoid (lignin and flavonoid) and oxidative stress metabolism. Some pathways influenced by UVB radiation are shared with other biotic (Pathogenesis related proteins) and abiotic stresses (dehydration, heat shock, wounding); nevertheless UVB radiation seems to affect also specific molecular targets such as DNA repair pathways and nucleic acid and protein turnover. This first microarray transcriptome analysis of poplar under UVB radiation highlights main pathways for future research.