



Kinetic transcriptomic approach revealed metabolic pathways and genotoxic-related changes implied in the Arabidopsis response to ionising radiations

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Résumé en anglais	<p>Plants exposed to ionising radiation (IR) have to face direct and indirect (oxidative stress) deleterious effects whose intensity depends on the dose applied and led to differential genome regulation. Transcriptomic analyses were conducted with CATMA microarray technology on Arabidopsis thaliana plantlets, 2 and 26 h after exposure to the IR doses 10 Gy and 40 Gy. 10 Gy treatment seemed to enhance antioxidative compound biosynthetic pathways whereas the 40 Gy dose up-regulated ROS-scavenging enzyme genes. Transcriptomic data also highlighted a differential regulation of chloroplast constituent genes depending on the IR dose, 10 Gy stimulating and 40 Gy down-regulating. This probable 40 Gy decrease of photosynthesis could help for the limitation of ROS production and may be coupled with programmed cell death (PCD)/senescence phenomena. Comparisons with previous transcriptomic studies on plants exposed to a 100 Gy dose revealed 60 dose-dependent up-regulated genes, including notably cell cycle checkpoints to allow DNA repairing phenomena. Furthermore, the alteration of some cellular structure related gene expression corroborated a probable mitotic arrest after 40 Gy. Finally, numerous heat-shock protein and chaperonin genes, known to protect proteins against stress-dependent dysfunction, were up-regulated after IR exposure.</p>
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