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**Post-transcriptional regulation of the oxidative stress response in plants**

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**ABSTRACT**

Due to their sessile lifestyle, plants can be exposed to several kinds of stresses that will increase the production of reactive oxygen species (ROS) such as hydrogen peroxide, singlet oxygen and hydroxyl radicals in the plant cells and activate several signaling pathways that cause alterations in the cellular metabolism. Nevertheless, when ROS production outreaches a certain level, oxidative damage to nucleic acids, lipids, metabolites, and proteins will occur, finally leading to cell death. Until now, the most comprehensive and detailed readout of oxidative stress responses is undoubtedly obtained at the transcriptome level. However, transcript levels often do not correlate with the corresponding protein levels. Indeed, together with transcriptional regulations, post-transcriptional, translational, and/or post-translational regulations will shape the active proteome. Here, we review the current knowledge on the post-transcriptional gene regulation during the oxidative stress response *in planta*.

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