Supercharged Plants to Fight Global Warming: Data Mining for Key Genes of Photosynthetic Acclimation to Climate Change

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The objective of this study was to investigate, at the molecular level, what makes a plant robust in photosynthesis and CO2 assimilation under heat stress. The significance of it is that efficient CO2 uptake at high temperatures is an ideal characteristic of plants in need for mitigating global warming. In nature, there are plants that perform well in warm weather whereas others are apt to grow in cooler climates. Quailbush is a notable exception: it thrives in the mild weather of 23°C as well as in hot desert temperature of 43°C. This unique feature makes Quailbush an ideal system to study photosynthetic acclimation to climate change. In this study, I conducted bioinformatics analysis on publicly available Quailbush RNAseq datasets. Results of my data mining showed that RNA transcripts encoding key enzymes of photosynthesis such as RuBisCO, were surprisingly not increased at 43°C. Instead, the CPN60 gene encoding chaperonin essential for the proper protein folding of the RuBisCO large subunit emerged as one of the most significantly increased gene transcripts at 43°C. The RNA editing apparatus was also drastically elevated. It has been reported that heat stress results in incomplete C-to-U editing of chloroplast mRNAs. My study showed, for the first time, that to compensate for that inefficiency, plants respond by increasing the expression of certain proteins participating in RNA editing. These results revealed an elaborated post-transcriptional regulation, both at the level of RNA editing and protein folding, in heat acclimation. The genes identified in this study can be used as molecular markers to screen for natural plant variations with a high capacity to perform CO2 assimilation. Plants with such traits will be indispensable in our battle against global warming.

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