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MYB31 TRIGGERS WATER STRESS MEMORY RESPONSES IN MAIZE

Laetitia Virloquet¹, Sandrine Chaignon¹, Valérie Méchin¹, Marie-Pierre Jacquemot¹, Llorenç Cabrera-Bosquet², Thierry Balliau³, Charlotte Henriot¹, Sandrine Balzergue^{4,5}, Etienne Delannoy^{4,5}, Johann Joets³, Marie-Laure Martin-Magniette^{4,5,6}, Claude Welcker², Michel Zivy³, Christophe Sallaud⁷, François Tardieu², Marie Javelle⁷, Sylvie Coursol¹

¹Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, Université Paris-Saclay, RD10, 78026 Versailles Cedex, France; ²LEPSE, INRA, Université Montpellier, 34060 Montpellier Cedex 1, France; ³GQE-Le Moulon, INRA, Université Paris-Sud, CNRS, AgroParisTech, Université Paris-Saclay, 91190 Gif-Sur-Yvette, France; ⁴Institute of Plant Sciences Paris-Saclay IPS2, CNRS, INRA, Université Paris-Sud, Université Evry, Université Paris-Saclay, Bâtiment 630, 91405 Orsay, France; ⁵Institute of Plant Sciences Paris-Saclay IPS2, Paris-Diderot, Sorbonne Paris-Cité, Bâtiment 630, 91405 Orsay, France; ⁶UMR MIA-Paris, AgroParisTech, INRA, Université Paris-Saclay, 75005 Paris, France; ⁷Biogemma, Centre de Recherche, 63720 Chappes, France

sylvie.coursol@inra.fr

Water deficit directly impacts the ability of plants to intercept and convert light into biomass. Because leaf growth is one of the first processes affected by water deficit, many physiological studies concentrated in short-term responses and associated mechanisms. They demonstrated the roles of cellular and metabolic processes such as changes in cell turgor, hydraulic conductance and cell wall plasticity. However, our understanding of how water deficit impacts cell wall biosynthesis is still fragmentary. Here, we report that *ZmMYB31*, a R2R3-MYB transcription factor implicated in the regulation of lignin biosynthesis, is induced by water deficit in the growing zone of maize leaves. Consistently, we showed that *ZmMYB31* colocalizes with quantitative trait loci for growth responses to water deficit and anthesis-silking interval (ASI) under water deficit conditions. Furthermore, we showed that increasing *ZmMYB31* expression in maize had an impact on ASI that was maintained under water deficit conditions. On the basis of these data, we generated transcriptomic and proteomic data to detect transcripts and proteins that show substantial changes in abundance in the leaf growing zone of three representative independent transgene-positive homozygous maize lines compared with that of transgene-negative sibling plants grown in the PhenoArch platform under well-watered and water deficit conditions. We identified 352 genes that were transcriptionally regulated by *ZmMYB31* under well-watered conditions and displayed opposite transcription levels under water deficit conditions, suggesting that *ZmMYB31* may function in a water stress memory response pathway, which likely helps the transgenic maize enduring the water deficit stress. Our studies further revealed co-expression relationships between these genes and others from the proteome and a cell wall data sets, suggesting potential regulatory influence.

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