

MAIZE GENETIC REGULATION OF CUTICLE DEPOSITION AND ITS ROLE IN THE ENVIRONMENTAL ADAPTATION RESPONSE

CASTORINA G.* , DOMERGUE F.***, HORNER D.** , CHIARA M.** , CONSONNI G.*

*) Dipartimento di Scienze Agrarie e Ambientali, Università degli Studi di Milano (Italy)

**) Dipartimento di Bioscienze, Università degli Studi di Milano (Italy)

***) Université de Bordeaux Bâtiment - INRA Bordeaux Aquitaine, Villenave d'Ornon (France)

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The cuticle, the outer surface of epidermal cells, provides a primary barrier to protect from environmental stresses and has important functions in plant development. However, genetic and hormone regulation of cuticle pathways in maize are still poorly understood.

In this work we propose that functional characterization of the *ZmMYB94/Fused leaves1 (Fdl1)* transcription factor, a key regulator of cuticle deposition, which is required to establish a precise boundary between seedling organs, thus preventing organ fusion.

Biochemical analyses performed to determine the lipid profiles in *fdl1-1* mutant and wild type plants showed that *fdl1* gene is involved in the deposition of both wax and cutin components during the early phases of seedling development.

We have investigated the FDL1-dependent genetic regulation of cuticle biosynthesis during juvenile vegetative phase with an Illumina based RNA-sequencing experiment performed on *fdl1-1* mutant and wild type plants. About 1600 differentially expressed genes have been detected and, through the Gene Ontology analysis, we obtained a general overview of the metabolic pathways and cellular processes involved.

Variation in gene expression nicely correlated with cuticular differences observed at the biochemical level.

Genetic and physiological approaches have been adopted to explore the interaction between the regulatory protein FDL1 and the putative *fdl1*-target genes. In particular, physiological analysis included a chlorophyll leaching assay, as a tool to analyse leaf permeability.

Plants evolved different strategies to cope with stresses and different plant species are able to modify the cuticle to increase adaptability in response to external cues. Since *Fdl1* regulates cuticle biosynthesis, we performed some analysis to evaluate the role of FDL1 in integrating environmental signals, for example water scarcity, and promoting cutin and wax biosynthesis.