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GENETIC AND PHYSIOLOGICAL ANALYSIS OF THE *GLOSSY1* GENE OF MAIZE

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The cuticle is a lipidic water-repellent layer covering the aerial surfaces of land plants. It consists of a polyester matrix, the cutin, interspersed and overlaid by waxes, which are the main determinants of the cuticle functions. In spite of its importance as a preformed defence against several environmental stresses, genetic analysis of cuticle biosynthesis has been very limited and focussed mainly on two model species, maize and Arabidopsis.

Several wax deficient mutants (*glossy* or *gl*) have been isolated in maize but only three genes involved in cuticular wax biosynthesis have been cloned and characterized: *Glossy1* (*Gl1*), *Glossy2* (*Gl2*) and *Glossy8* (*Gl8*), all conditioning wax accumulation in the juvenile stage of maize development. Mutations in the *Gl1* gene have a pleiotropic effect affecting wax production, trichome development and cuticle membrane formation, though the GL1 protein appears to be a metabolic enzyme belonging to a class of membrane bound hydroxylases-desaturases widespread in both prokaryotes and eukaryotes.

To determine whether the different effects of the *gl1* mutations are due to the impairment of a single biosynthetic step or depend on a multifunctional nature of the enzyme, we analyzed a collection of 20 stable independent mutations of the *Gl1* locus all impairing wax biosynthesis. Sequence analysis of the transcripts, when present, gave indications of some functional domains involved in wax biosynthesis whereas analysis of trichome morphology and distribution in the same mutants did not support the hypothesis of the presence of multiple catalytic domains.

To analyze the regulation of the wax biosynthetic pathways in maize seedlings, *Gl1*, *Gl2* and *Gl8* expression was assayed in plant subjected to environmental stresses (drought and high salinity) and in response to light. All these factors are known to cause an increase of wax load on leaf surfaces. Contrary to *Gl2* and *Gl8*, *Gl1* transcription was down regulated by water stress and light indicating the presence of multiple regulatory pathways in the control to wax biosynthesis or an indirect involvement of *Gl1* in this metabolic process.