

COMPARISON OF CUTICULAR WAX METABOLISM IN MAIZE AND ARABIDOPSIS

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Arabidopsis is widely used as a model plant for molecular biology research although it displays substantial developmental and metabolic diversity compared to several economically important species such as maize.

Cuticular waxes cover the aerial surfaces of all terrestrial plants as an indispensable lipid protection against several biotic and abiotic stresses. Many wax mutants of maize (*glossy, gl*) and Arabidopsis (*eceriferum, cer*) have been isolated. Through the characterization of most *cer* genes, the wax biosynthetic pathway of Arabidopsis was defined while corresponding studies in maize have lagged behind. Of the three *Glossy* genes cloned so far, only *Gl8* has been characterized as to its metabolic function whereas *Gll* and *Gl2* have a still undefined role in wax biosynthesis.

Biochemical analysis of wax composition in *gll* mutants supports two alternative conclusions:

either the maize wax biosynthetic pathway differs from the analogous pathway in Arabidopsis or the wax phenotype of *gll* mutants is misleading in defining the function of the gene product.

To discriminate between these hypothesis, a physiological approach to *Gll* gene silencing was employed. It turned out that under different environmental stress (drought, osmotic stress, high salinity, cold) *Gll* expression is repressed. Analysis of parallel changes in wax composition disclosed a different wax profile compared to what is observed in *gll* mutants and supported the idea that wax biosynthesis in maize and Arabidopsis is achieved through overlapping metabolic steps. However, when the modulation of this pathway under stress was analyzed, important differences were disclosed, pointing to the existence of specific regulatory mechanisms in each species and highlighting the little utility of Arabidopsis in deciphering stress induced regulation of wax metabolism in maize.