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## GENOME-WIDE CLASSIFICATION OF MYB-REGULATORY GENES IN THE PERENNIAL GRASS *ERAGROSTIS CURVULA* AND IDENTIFICATION OF THE *ZMFDL1* ORTHOLOGUE

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*Eragrostis curvula* is a perennial grass native to Southern Africa that was introduced into semiarid regions of Australia, USA, and Argentina as forage grass. In the recent years, *E. curvula* has been considered one of the model organisms for the study of the molecular mechanisms underlying apomixis in plants. However, this species has also received much interest for its ability to adapt to marginal environments. Ecotypes with different drought stress response are characterized by changes in cuticle wax deposition, a trait that may influence plants capability to maintain a high-water content.

Aim of this work is to isolate key regulatory genes of wax biosynthesis and deposition in *E. curvula* and investigate their involvement in drought stress response. The recent availability of *E. curvula* genome sequence allowed us to identify the whole family of MYB transcription factors. The construction of a phylogenetic tree allowed to establish the relationships among MYB genes of *E. curvula* and closely related grasses. This analysis highlighted the presence, among different candidates, of the *Eragrostis curvula* orthologue of the *ZmMYB94/fused leaves1 (fdl1)* gene. This MYB factor is required in maize for a proper cuticle deposition in the juvenile phase of plant development, and its expression, which is confined to seedling tissues, is modulated by drought stress. *Ecdfll* is also expressed in the aerial parts of the plant, however, differently from what observed in maize, it is specifically expressed in adult tissues. The *Ecdfll* transcript level was measured in *Eragrostis* ecotypes characterized by different drought stress tolerance and wax content. Variations of *Ecdfll* gene expression observed in four ecotypes nicely correlated with differences in the amount of waxes.

Our results indicate that the two MYB orthologs are characterized by distinct spatial-temporal expression patterns in the perennial *E. curvula* and the annual *Zea mays* plants. They may contribute to a general understanding of the cuticle role in stress adaptation mechanisms.