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ENVIRONMENTAL EPIGENETICS IN MAIZE: ADVANCES FROM A EUROPEAN INITIATIVE

ROSSI V.*, MAINIERI D.*, FORESTAN C.**, MASCHERETTI I.*, FARINATI S.**, LAURIA M.***, VAROTTO S.**

*) Maize Research Unit, Agricultural Research Council (CRA), Via Stezzano 24, 24126 Bergamo (Italy)
**) Department of Environmental Agronomy and Crop Production, University of Padova, Viale dell'Università 16, 35020 Agripolis Legnaro (Italy)
***) Institute of Agricultural Biology and Biotechnology, National Research Council (CNR), Via Bassini 15, 20133 Milano (Italy)

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AENEAS (Acquired Environmental Epigenetics Advances: from Arabidopsis to maize) is a research collaborative project recently funded by the European Commission. The AENEAS initiative aims to assess the impact of environmental conditions on epigenetic states in the model plant *Arabidopsis thaliana* and then transfer knowledge to maize, one of the most important crops of the world. Here, we illustrate some of the recent advances obtained by studying maize epigenetics within AENEAS project.

A first objective of AENEAS is to characterize three epi-regulatory pathways in maize. These pathways are: the autonomous flowering (AF), the CpG methylation (mCG), and the small RNA (sRNA) pathway. These pathways are well characterized in Arabidopsis, particularly for their interaction with environmental signals in mediating changes into the epigenome. The expected outcome of our study is the production of maize tools (e.g. mutants and epi-targets) for analyzing epigenetic-mediated response to environmental cues. In this context, we have focused our study on the maize homolog of the Arabidopsis *FVE* gene, named *nfc102*, which encodes a MSI-like WD-repeat protein belonging to AF pathway. The *nfc102* gene is ubiquitously expressed, but its RNA accumulates in actively dividing tissues and *nfc102* antisense transcripts were detected in specific tissues. Phenotypic analysis of *nfc102* RNAi mutants reveals that plants exhibit several developmental defects, suggesting a pleiotropic *nfc102* function. Among sequences showing differences in RNA accumulation in *nfc102* mutant compared to wild-type plants is enclosed the maize homolog of the Arabidopsis florigen *FT* gene (*ZCN8*). Our results suggest that *nfc102* is involved in the regulation of *ZCN8* sense and antisense RNA processing. Additional targets of *nfc102* are different types of transposons and retrotransposons (TEs), which show an increase of their RNA level in *nfc102* mutants. The *nfc102* down-regulation also provokes in the targeted TEs a decrease of histone marks associated with transcription activation and an increase of histone modifications related to silencing, thus corroborating the *nfc102* role in epigenetic-mediated silencing.

Since *nfc102* regulates the RNA level of various TEs and because it is well known that TEs are sensitive to different environmental cues, we have performed experiments to analyze TEs response in *nfc102* mutants concomitantly with application of temperature stresses. In these experiments we have enclosed the *rmr6* mutant, affecting the function of the maize homolog of the

Arabidopsis *NRPD1* gene, which encodes the largest subunit of RNA polymerase IV. Since retrotransposition occurs through retrotranscription of TE-derived RNAs, the level of both transcripts and extrachromosomal DNA copies for the TEs was detected. The analysis was performed immediately after stress removal and after some days of recovery to assess maintenance of changes through mitotic division. Preliminary results from these experiments will be illustrated and discussed.