Proceedings of the 56th Italian Society of Agricultural Genetics Annual Congress
Perugia, Italy – 17/20 September, 2012
ISBN **978-88-904570-1-2**

Poster Communication Abstract – 3.53

FUNCTIONS OF MICRO AND SMALL INTERFERING RNAS IN MAIZE STRESS RESPONSE

FORESTAN C.*, DE PAOLI E.**, LUNARDON A.*, FARINATI S.*, VAROTTO S.*

*) Department of Agronomy Food Natural resources Animals Environment - DAFNAE, University of Padova, Viale dell'Università 16, 35020 Legnaro (Italy)
**) Department of Agricultural and Environmental Sciences - DISA, University of Udine, Via delle Scienze 206, 33100 Udine (Italy)

epigenetics, siRNA, microRNA, environmental stress, Zea mays

In both animals and plants it is well documented that specific regulatory small RNAs act in post-transcriptional and transcriptional gene expression regulation, mainly directing epigenetic modifications on DNA and chromatin condensation of target regions. At present, different types of RNA silencing pathways have been described in plants involving different types of small RNAs referred to as microRNA (miRNA) and small interfering RNA (siRNA), which can be further subdivided in heterochromatin-associated siRNA (hc-siRNA) and trans-acting siRNA (ta-siRNA).

In particular, the hc-siRNA pathway generates 24 nt siRNAs associated with transposable elements and highly repetitive sequences. Their biogenesis involves the production of transcripts by a plant-specific RNA polymerase (POL IV). which are then made double-stranded by RDR2, an RNA-dependent RNA polymerase, and diced by DCL3. Resulting hc-siRNAs, after incorporation into AGO4, AGO6 and/or AGO9 silencing complexes, recruit chromatin modifiers and target transcripts generated by the plant-specific POL V to direct DNA methylation at cytosine residues and deposition of epigenetic marks typical of heterochromatin. Since many sRNAs derive from repeats and transposons situated in heterochromatic regions, their main role seems to be the silencing of these elements to maintain a stable 'architecture' of plant genomes. Both miRNAs and siRNAs are involved in plant stress response, as it has been shown in many plants species from model to crops.

Focusing on the maize system, we are using Illumina deep sequencing technology (sRNA-seq) to analyze the dynamics of different populations of both miRNAs and siRNAs that are produced in B73 inbred line following drought, salt and drought plus salt stress treatment. Stresses were applied in greenhouse conditions for ten days and small RNA population abundances have been analyzed at the end of stress application and after a recovery stage of seven days. The same stress protocols were applied to *rmr6* mutant (a mutant of POL IV involved in hc-siRNAs biogenesis) and preliminary data show significant differences in small RNA accumulation after stress application in wt and mutant plants. Results of siRNA target analysis and the most evident changes observed during stress treatment will be presented and examined.