

DEEP SEQUENCING-BASED CHARACTERIZATION OF BARLEY miRNome IN PLANT EXPOSED TO LOW TEMPERATURES

GIUSTI L.* , FACCIOLI P.* , COLAIACOVO M.* , ORRÙ L.* , CATTIVELLI L.* ,
CROSATTI C.*

*) CRA- Genomics Research Centre, Via S Protaso 302, 29017 Fiorenzuola d'Arda (Italy)

***) CRA-Cereal Research Centre, S.S. 16 Km 675, 71122 Foggia (Italy)

microRNA, drought, cold, stem-loop qRT-PCR

Plant miRNAs are 19-24 nt-long endogenous gene regulators that act at the post-transcriptional level through sequence-based interaction with target mRNAs. Transcription factor families comprise most of the highly conserved miRNA targets. MiRNA are known to play key regulatory roles in plant response to stress, besides being involved in development and morphogenesis.

To verify experimentally the barley miRNAs and their involvement in stress response the barley miRNome of plants exposed to low temperatures has been characterized by a deep sequencing approach on Illumina GAIIX. In details, 18 libraries have been obtained from the 2 cultivars, 2 stress levels and 3 replicates and yielded approximately, on average, 6 million unfiltered sequence reads. Many of the known miRNAs have been found as different isomeric variants, so-called isomiRs, which might increase the target repertoire of the miRNA gene they derive from. Candidate stress-regulated microRNAs were identified and their expression patterns were validated by a qRT-PCR approach. Interestingly, differential expression of miRNA genes between cvs. under control and stress conditions was also found.