Proceedings of the Joint Congress SIBV-SIGA
Milano, Italy – 8/11 September, 2015
ISBN **978-88-904570-5-0**

Poster Communication Abstract – A.21

CONTROL OF LATERAL MERISTEM FORMATION IN *ANTIRRHINUM MAJUS*: THE ROLE OF *ERAMOSA*

MIZZOTTI C.*, GALLIANI B.M.*, DRENI L.**, SOMMER H.***, MASIERO S.*

*) Department of Biosciences, Università degli Studi di Milano, Via Celoria 26, 20133 Milan (Italy)
**) School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai 200240 (China)
***) Max Planck Institut für Züchtungsforschung, Carl-von-Linné Weg 10, 50829 Köln (Germany)

Axillary meristem, branching, Antirrhinum majus, transcription factor, plant yield

Plant architecture is designed by shoot growth and branching developing from axillary meristems (AMs). The molecular and genetic networks controlling AMs formation have been studied in few species, e.g. Arabidopsis thaliana, tomato, rice and maize. These works have identified few transcription factors controlling AM.

Our effort are finalised to explore the genetic network controlling AM determination in *Antirrhinum majus*. During the vegetative phase, the snapdragon mutant *eramosa* (*era*) does not develop AMs and *era* plant develops a main stem with no lateral branches. Differently from its orthologous in Arabidopsis and tomato, *era* mutation causes severe effect also during the reproductive phase, indeed *era* plant develops very few flowers which are completely disorganized. Furthermore the analysis of *AmSTM* expression in *era* mutant background indicates that the meristematic tissue is completely absent at the axil of the bracts of this mutant.

The phylogenetic reconstruction of the ERA subfamily revealed the absence of ERAMOSA orthologues in *Medicago truncatula*, *Phaseolus vulgaris* and *Glycine max* suggesting that the molecular mechanism regulating branching is somehow modified in legumes.

Overexpression of *ERA* in *Arabidopsis thaliana* causes an increase in lateral branching formation resulting in an increased number of flower and seeds. These data paved the way to increase plant yield through the genetic control this gene.