Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - C.21

CHARACTERIZATION OF THE *Ra1* MAIZE GENE INVOLVED IN INFLORESCENCE ARCHITECTURE

E. CASSANI*, M. LANDONI**, R. PILU*

*) Department of Crop Science - University of Milan, Via Celoria 2, 20133 Milano, Italy
**) Department of Biomolecular Sciences and Biotechnology University of Milan, Via Celoria 26, 20133 Milano, Italy

maize, inflorescence, ra1 mutant, zinc finger domain

Plant and floral architecture has an enormous impact on yield, either by altering the numbers of fruits and seeds produced by the inflorescence, or by making plants more compact allowing them to be grown under stringent conditions. In maize, increasing the number of branches in the tassel increases pollen yield, which influences overall yield as well as F1 production.

Several mutations have been described that affect the development of the maize inflorescence, but only *ramosa1* (*ra1*) causes a change in a specific branching pattern of the inflorescence without a concomitant loss of any tissue types.

Ra1 gene was cloned and preliminarily characterized by Martienssen et al., it encodes a small zinc finger transcription factor (patent number: WO 01/90343 A2).

In the present work, we have characterized a new mutation of *Ra1* gene, named *ramosa1-154* (*ra1-154*), isolated in the progeny of a selfed B73 inbred line plant. This spontaneously arising ramosa maize mutant shows over-branching in the male and female inflorescences. This over branching causes a net increase of the number of spikelets in the tassel of about 50% respect to wild type.

Also heterozygous *Ra1/ra1-154* plants exhibited a consistent increase in number of branches and spikelets in the tassel compared to wild type, this might indicate that one single-functional gene copy is not sufficient to warrant the wild phenotype. This data indicate that the number of tassel branches is closely linked to RA1 level just as, most probably, the different average number of tassel branches present in several inbred lines might be due to different expression level of different *Ra1* alleles.

We cloned and sequenced *Ra1* gene in *ra1-154* mutant and wild type. The comparison of the sequences showed the presence of AAG deletion (position +157) in the coding region in *ra1-154* mutant. This small deletion causes the loss of the K residue at the position 53 in the predicted putative zinc finger domain of RA1 protein.

This is the first evidence of single amino acid deletion in the zinc finger domain that knocks out the function of the RA1 protein.

This result strongly suggests that the RA1 protein functions by acting as a DNA-binding protein, likely involved in transcriptional regulation and in particular, the presence of ERF-associated amphiphilic repression (EAR) motif in RA1 protein sequence supports the hypothesis that *Ra1* gene might acts as repressor of genes involved in the inflorescence branch meristems.