Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – A.13

A NEW MUTATION OF DWARF8 MAIZE GENE

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maize, dwarf mutants, gibberellins, DELLA domain

The large increase in rice and wheat yields during the years of the so-called ''Green revolution'' largely resulted from the introduction of monogenic dwarfing traits into plants in combination with the application of large amounts of pesticides and fertilizer. Height reduction has been associated with increases in yield in several different crop species. The new varieties used today are shorter, more resistant to storm damage and have an increased grain yield in comparison with the older ones. The reduction in size of these varieties is caused by the abnormal response to the gibberellins (GAs), which are essential endogenous regulators of plant growth, suggesting that this hormone is central to the control of plant stature. Much of the current progress with regard to GA metabolism comes from the isolation and characterization of single-gene mutants.

However, the elongation of plant organs is a complex phenomenon mediated by many plant hormones, including auxins and brassinosteroids as well as the gibberellins. More than 20 independent dwarf mutants have been mapped in maize altogether representing a very heterogeneous category of dwarfing mutations.

In this work we have isolated a new dwarf mutant that arose in a F1 maize population. It is characterized by reduced stature, due to shortening of internodes rather than reduction of internodes number, and dark green, crinkly leaves. Mutant plants exhibit ectopic anthers in the ear and show variation in the flowering time. Based on morphology and on response to treatments with GA3 the mutant was classified as dwarf with little response to gibberellic acid.

The genetic analysis performed to understand the inheritance of this mutation, named *D*1023*, demonstrated a monogenic dominant inheritance of this trait.

Furthermore, using SSRs (Simple Sequence Repeats) molecular markers on a segregating F_2 population it has been established the mapping position of *D*1023*.

The results obtained from this analysis showed that *D*1023* maps on chromosome 1 (bin 1.09), where *D8-ref*. was localized. Expression analysis carried out using RT-PCR did not show any significant difference between the level of expression of *D8* gene in mutant and wild type.

The novel mutant allele was cloned and the alignment with *d8*(+) wild type alleles present in the database has shown the molecular lesion: an insertion of 3bp within VHYNP domain, localized in the 5' of the gene, near the DELLA domain, responsible for the GA response.

Further data will be presented to better characterize this new mutation.