

## A NEW MUTANT ALLELE OF BRACHYTIC 2 MAIZE GENE

E. CASSANI\*, D. VILLA\*, S. CURIALE\*, M. LANDONI\*\*, F. CERINO BADONE\*,  
D. PANZERI\*, D. REGINELLI\*\*\*, R. PILU\*

\*) Dipartimento di Produzione Vegetale - University of Milan, Via Celoria 2, 20133 Milano, Italy

\*\*) Dipartimento di Scienze Biomolecolari e Biotecnologie - University of Milan, Via Celoria 26, 20133 Milano, Italy

\*\*\*) Azienda Agraria “Angelo Menozzi” - University of Milan, Landriano (PV), Italy

*maize, mutant, green revolution, brachytic, P-glycoprotein*

Plants with short stature have had a big impact on agriculture. World rice and wheat grain yields increased dramatically in the 1960s and 1970s (green revolution) because farmers adopted new varieties that were shorter and more resistant to storm damage.

Brachytic/dwarf varieties have not been exploited commercially in maize, partly because of the excessively severe nature of the original mutant alleles. However similar mutations have been used extensively in sorghum production since the 1950s.

To our knowledge, there are three brachytic mutants isolated so far in maize: *brachytic1 (br1)*, *brachytic2 (br2)* and *brachytic3 (br3)* that show a short stature and gibberellin insensitive phenotype

A maize brachytic mutant of agronomic potential is the recessive *br2* mutation, which results in the shortening of lower stalk internodes. *br2* was cloned by transposon tagging with *Mu* element by Multani et al., in 2003 and it encodes a putative protein similar to adenosine triphosphate (ATP)-binding cassette transporters of the multidrug resistant (MDR) class of P-glycoproteins (PGPs) involved in polar movement of auxins.

The spontaneous maize mutant, named *brachytic-23\* (br\*-23)*, described in this work has a short stature and compact lower stalk internodes compared to wild type control. The genetic analysis indicated that *br\*-23* was inherited as a monogenic recessive trait.

In allelism tests our mutant failed to complement the *br2* mutant, thus it became obvious that *br\*-23* represents a mutation in the *br2* gene. Following the guidelines provided by the Maize-GDB, we renamed the new mutation *br2-23*.

In order to investigate the molecular lesion in the *br2-23* allele, we designed specific primers on the basis of the sequence of the *br2* gene cloned by transposon tagging by Multani et. al., in 2003. The genomic PCR fragments obtained from a homozygous mutant and a wild type plant (B73 inbred line) were subcloned and sequence analyses were performed. Preliminary alignment of *Br2* (B73 Allele) and *br2-23* sequences, performed using the CLUSTALW program, revealed that the mutant carries a eight nucleotide deletion in the coding region. The presence of this deletion in the coding region was also confirmed by using allele-specific primers.

Details of further genetic, molecular, and histological characterization of this mutant will be presented.