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Poster Abstract – A.73

INHERITANCE OF A TASSEL SEED CHARACTERISTIC IN MAIZE RESULTING FROM *IN VITRO* CULTURE

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Regeneration from in vitro tissue culture can give rise to plants showing genetic variation, which can be of classical as well as of novel types. In a previous study in maize (*Zea mays*, L.), we conducted three cycles of recurrent selection aimed at improving plant regeneration capacity from callus cultures of immature embryos, using as source population the double cross (A188 x W64A) x (A634 x B79). The population resulting from the third selection cycle (C_3) was subjected to one selfing generation and in the subsequent S_1 population a plant showing tassel seed phenotype (*ts*) was identified. An inbred line (Bo22) was then developed from this *ts* plant. Throughout the selfing process the *ts* phenotype proved to be stable. Objectives of this study were to: (a) gain information on the inheritance of the trait, and (b) map the locus/loci responsible for such phenotype by means of molecular marker analysis.

The *ts* inbred line Bo22 was crossed to the three wild type (*wt*) inbred lines W23, B73 and Lo976; then corresponding F_2 as well as BC_1 (using Bo22 as recurrent parent) generations were produced. The three F_1's always showed the *wt* phenotype. For the cross Bo22 x W23 and Bo22 x B73, the F_2 and BC_1 generations showed phenotypic frequencies (*wt:ts*) consistent with 15:1 and 3:1, respectively, in accordance with the hypothesis of duplicate gene action. On the other hand, the generations derived from Bo22 x Lo976 showed segregating ratios not consistent with this simple inheritance hypothesis.

Bulk Segregant Analysis (BSA) using 114 publicly available SSR markers was carried out on bulked samples of *ts* and *wt* plants from the two BC_1 populations (Bo22 x Lo976) x Bo22 and (Bo22 x B73) x Bo22. Association of the *ts* phenotype with one chromosome region (chrom. bin 6.07, near umc2165) was confirmed after the analysis of both BC_1 populations. The same 6.07 markers confirmed the association of bin 6.07 with the *ts* phenotype in two other small F_2 populations. No *ts* mutations have been previously mapped in this chromosome region.

In conclusion, two genes with duplicate action seem to be responsible of the *ts* phenotype shown by the inbred line Bo22 at least in two of the three analysed crosses, and one of these two genes appears to map in bin 6.07. Further analyses are now in progress to identify and map the other gene involved.