

***r1* GENE IS TIGHTLY ASSOCIATED TO A QTL INVOLVED IN MAIZE YIELD**

PILU R.*, BUCCI A.*, CASELLA L.*, LAGO C.*, CERINO BADONE F.*, CASSANI E.*, LANDONI M.**, REGINELLI D.***

*) Dipartimento di Produzione Vegetale, Università degli Studi di Milano, Via Celoria 2, 20133 Milano (Italy)

**) Dipartimento di Scienze Biomolecolari e Biotecnologie, Università degli Studi di Milano, Via Celoria 26, 20133 Milano (Italy)

***) Azienda Agraria “Angelo Menozzi”, Università degli Studi di Milano, Landriano (Italy)

Zea mays, *r1* gene, anthocyanins, QTL analysis

Anthocyanins are a class of water-soluble molecules produced only in plants and conferring a red-blue colour depending by the vacuole pH where they are stored in glycosylated form. These substances play important roles in several physiological processes such as UV protection, male fertility, antimicrobial activity and in general they are involved in protection against oxidative damage. In maize, anthocyanins are synthesized by a pathway made up by about 20 genes activated by transcription factors belonging to two gene families: *c1/pl1/pl* (MYB genes) and *r1/b1* (bHLH genes). Anthocyanin accumulation in a specific tissue requires the presence of a member of both families: from the MYB family, *Pl* is required for pigment accumulation in the plant and *CI* acts in the aleurone while *r1/b1* acts in the seed and plant tissues depending on the nature of the alleles present.

In this work we produced and studied for three years two synthetic populations of maize differing in their constitution only for the selected alleles present at the *red color 1* (*r1*) locus (*R-sc* vs *r-r*). The *R-sc* allele confers pigmentation only in the aleurone seed layer, while the *r-r* allele confers pigmentation in several tissues such as root, silk and anther but the seed is colourless. The colourless population (*r-r/r-r*) was characterized by improved agronomic features such as ear weight and plant height compared with the *R-sc/R-sc* coloured population. This finding was confirmed studying single F₄ *R/r* families where the presence of the *r-r* allele conferred positive features, acting as a dominant trait.

Quantitative trait locus (QTLs) analysis performed using molecular markers on the long arm of chromosome 10 (bin 10.06) where the *r1* gene maps, identified a QTL map position for plant height tightly associated to the *r1* gene. Thus the *r1* gene may represent a major QTL or it could be closely linked to another gene involved in the agronomic performance of the two populations studied.