QTL MAPPING FOR ROOT ARCHITECTURE AT THE SEEDLING STAGE IN MAIZE


*) Dept. of Agroenvironmental Science and Technology, University of Bologna, Italy
**) KWS SAAT AG, Maize Breeding, Einbeck, Germany

Zea mays, root traits, Quantitative trait loci (QTL), introgression library(IL)

The root system architecture is a complex trait involved in the plant's ability to acquire water and nutrients from the soil as well as in root-lodging resistance. In order to elucidate the genetic control of root architecture in maize, an introgression library (IL) developed from the cross between two parents contrasting for root traits (B73 and Gaspé Flint) was studied. The IL collection included 75 lines, most of which retaining one single chromosome introgression of the donor genome (Gaspé Flint) with an average length of ca. 40 cM. It has been estimated that ca. 70% of the Gaspé Flint genome is represented within the collection.

The IL lines were evaluated for root characteristics by applying two different methodologies, i.e. a paper-roll based protocol and a pot-growing system (seedlings grown until the fourth-leaf stage in sand/clay pebble pots). Root traits (e.g. length and dry weight of the primary and seminal roots, number of seminal roots) and seedling traits (dry weight, etc) at the seminal and early stages of development were recorded. Highly significant differences were observed between the two parental lines and among the IL lines for the number of seminal roots developing from the scutellar node. B73 produced an average of 2.8 seminal roots per plant while Gaspé Flint did not show any seminal root. Among the IL lines, a few showed a Gaspé-like phenotype, implying that the QTLs controlling this trait are localized on the corresponding introgressions. Five QTLs for seminal root number were identified in the paper roll experiment, three of which were also confirmed in the pot experiment.

In order to better characterize the QTL on chromosome 1 (Seminal root 1, Sr1), F2 plants from the cross between B73 and the IL line carrying the introgression on chromosome 1 have been analyzed for both phenotype, using the paper roll system, and genotype using SSRs mapped in the introgressed region. A major QTL for seminal root number has been confirmed on chromosome 1 bin 1.02; the QTL is characterized by a LOD value equal to 16, spans ca. 7 cM and is localized in the proximity of locus Rtec1 (Taramino et al., 2007. Plant J. 50: 649-659) controlling root architecture. Thus phenotypic and preliminary fine mapping data indicate that the two loci do not coincide.

Positional cloning of Sr1 is underway.