Common bean, root-knot nematodes, *Meloidogyne* spp., resistance genes, breeding

Common bean (*Phaseolus vulgaris* L.) is a highly susceptible host of root-knot nematodes (*Meloidogyne* spp.). Symptoms of nematode damage include yellow stunted plants, early defoliation, secondary root and stem rots, root galls, and reduced yields: up to 60% of losses or more can occur when beans are grown on heavily infected soils with *Meloidogyne* spp.. Use of resistant cultivars, in combination with crop rotation, is the least expensive and most environmentally safe way to manage root-knot nematodes problems in common bean and other crops.

A breeding program, with the aim to introduce the nematode resistance into Italian cultivated germplasm of common bean, was started 2 years ago. Different and contrasting resistant sources were evaluated with different Italian races of root-knot nematodes (*Meloidogyne* spp.), then 3 of them were used as resistance donors in a complex scheme of crosses. Several types of climbing and determinate Cannellino and Borlotta (for freezing and fresh market) as well as climbing filet or stringless types were the susceptible parents to be improved (among the 14 cvs, 5 were ISCI Kaimano, Kondor, Talento, King and Luxor). More than 2500 (2782) crosses were completed and 661 F1s were subsequently grown. In the following season more than 15% of the 28176 F2 obtained were inoculated in field and evaluated for resistance and main agronomical and morphological characters. A group of 51 different breeding resistant lines were firstly selected and then re-evaluated in glasses houses to confirm the previous results of nematodes inoculation.

Preliminary data deriving from the segregations of different F2, in field and in glasses house, are introducing the hypothesis of a qualitative inheritance of these resistance genes. A molecular analysis with RAPD and microsatellites is in progress to associate markers to these genes in order to speed up the breeding programme and consequently to identify the genes involved.

Interestingly an outbreeding depression was observed in some of progenies derived from wide crosses, *i.e.* form the crosses derived from Mesoamerican x Andean genotypes.