# STRATEGIES FOR CONSTRUCTION OF NEMATODE RESISTANT PLANTS


## Summary

Plant-parasitic nematodes are very important pests of many crops causing up to 20-30% losses of agricultural yield. Their traditional control relies on extremely toxic nematicides and breeding resistant cultivars. As both methods have major disadvantages (environmental pollution, long time-course of breeding a new cultivar with resistance which is often broken by the pathogen after several years), an approach based on genetic engineering seems to be a promising alternative. Reproductory success of the nematodes depends on induction and development of a feeding site composed of modified plant cells. In a compatible plant/pathogen interaction, nematode secretions (pathogenicity factors) released consecutively into the root change the morphogenetic programme of plant cells via modification of expression of selected plant genes which enables nematode's migration, induction of the feeding site and its proper development into an effective feeding structure. Different strategies to stop or to impair pathogen development may be applied which interfere with nematode's development at different points of its life cycle. This approach has been adopted by an international research project „NONEMA" carried out within 5th Framework Programme of the European Community for Research, Technological Development and Demonstration. First, pathogenicity factors are sought, recognised and evaluated employing such methods as subtractive hybridisation using cDNA libraries, comparative cDNA-AFLP, microsequencing of nematode secretions, dsRNA-mediated mRNA inactivation of candidate genes in nematodes. The factors thought to be involved in: modification/dissolving of plant cell walls during migration, protection against active oxygen species produced upon infection by the host and induction of feeding cells are search for. The selected proteins – pathogenicity factors will be afterwards inactivated by „plantibodies" – specific immunoglobulins synthesised in transgenic plants. This should minimise pathogen's success during early stages of infection. Second, plant proteins up-regulated upon infection are being identified using RT-PCR, *in situ* hybridisation and immunolocalisation. These genes/proteins involved in reactivation of cell cycle (necessary for induction of feeding site development) or in modification of plant cell walls (including local dissolutions of the walls) in developing feeding sites of cyst nematodes will be inactivated using „plantibodies" or inhibited at mRNA level using antisense constructs in transgenic plants. To maximise the chances of public acceptance for genetically engineered plants special attention is paid to use promoters with minimised expression outside the area (plant tissues) of their action. Some feeding site-specific promoters are already available but they are being improved by employing promoter deletion techniques and also new ones are sought.