Identification of *Meloidogyne* and *Heterodera* species by molecular methods and using MAS for the resistance of wheat varieties.

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Identification of plant-parasitic nematodes has traditionally been based on comparative morphology and there are several diagnostic keys. The use of morphometric characteristics to differentiate species is very time consuming and can be unreliable and difficult to use and, more recently, techniques based on protein or DNA differences have been implemented.

Root-knot nematodes cause a great deal of economic losses on many cultivated fruits and vegetables in Turkey. Population of root-knot nematodes were collected from different geographical regions of Turkey. Samples of root-knot nematodes were first homogenized. Then, DNA extraction from egg masses was carried out. rDNA-RFLP and species-specific primers were used to diagnose the important root-knot nematode species. *M. arenaria, M. javanica* and *M. incognit* were determined. At the end of this study, root-knot nematode map of Turkey will be established.

Cereal cyst nematodes are also very important pests in central Anatolia wheat production areas. Protein electrophoresis has successfully been used to distinguish *Heterodera* species, however requires a large number of nematodes and is therefore useful only where pure populations can be obtained. The use of PCR-RFLP overcomes this problem as DNA can be amplified from only one nematode if required, and discrimination of both cyst nematode species has been achieved from 1-10 nematodes. This technique has been successfully implemented in Turkey. These molecular techniques are useful, however given we are still improving our understanding of the complexity of CCN with respect to both the number of species and pathotypes which are representative, further characterization of a greater number of isolates from global collections are needed and PCR probes are needed. It would also be of tremendous value to use to relate this genetic diversity of the pathogen to the source (evolution) of the host genetic resistance which has been found, as most of the identified sources of resistance to *H. avenae* have been found predominantly in wild relatives of wheat in the *Aegilops* genus. Six out of the seven named *Cre* genes for *H. avenae* resistance in wheat as well as *Rkn2* for resistance to both *M. naasi* and *H. avenae* came from four *Aegilops* species and have already been introgressed into hexaploid wheat backgrounds for breeding purposes.

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Another important aspect of research is the both the idenfication of gene(s) of resistance against the CCN complex, followed by and understanding of the both the number of genes, location and the identification of a diagnostic maker to the gene of interest. We know to date all genetic resistance identified for CCN in cereals is controlled by a single dominant gene. Molecular technologies have been applied to identify markers for various CCN plant resistance genes using techniques such as RAPD and RFLP, in both barley McIntosh *et al.* (2001) presented information about introgression, substitution and molecular characterization of these resistance sources in cereals. In several Australian cereal breeding programmes, and in CIMMYT International markers for both wheat and barley are being implemented using marker assisted selection (MAS) to pyramid resistance genes against *H. avenae*, pathotype Ha13. However we must not forget the identification and implementation of markers in this way requires sufficient understanding of the biology of the pathogen and genetic control of the resistance.