Durable Resistance against *Meloidogyne chitwoodi* and *M. fallax*

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Abstract

The EU-funded Project QLRT-1999-1462 DREAM (Durable Resistance Against *Meloidogyne*) aims to contribute to sustainable production systems by developing a strategy for durable resistance management for two polyphagous quarantine root-knot nematodes *Meloidogyne chitwoodi* and *M. fallax*. The objective will be achieved by integrating expertise in breeding, nematology, botany and molecular biology. The project combines three areas of research: 1. Identification and incorporation of resistance in important arable crops: potato, pepper, ryegrass and fodder radish, 2. Study of variation in nematode virulence and of durability of the resistance, and 3. Optimising of production systems by rotation schemes. The main results expected are: resistant germplasm, characterised pathogen collections, breeding methods, knowledge of the stability of resistance, molecular markers linked to resistance and (a)virulence, resistance mechanisms and genes, genetic maps, and improved rotation schemes. The strategy and some first results will be discussed.

Keywords: *Meloidogyne chitwoodi*; root-knot nematodes; virulence; *Solanum*; *Capsicum*; *Raphanus*; *Lolium*; resistance breeding

INTRODUCTION

Nematodes cause an estimated average of 4–20% yield loss per crop world-wide. Control is preventive, mainly by nematicides and resistant crops. Banning and reduction of pesticides and the lack of sufficient resistance in major crops demands efforts in resistance breeding, especially against some polyphagous species. *Meloidogyne chitwoodi* and *M. fallax* are quarantine pests within the EU and represent a serious threat to European agriculture. *M. chitwoodi* was first described in 1980 and has been reported from 6 European countries so far. *M. fallax* was found more recently. These sedentary endoparasitic nematodes are difficult to manage because they multiply on many crops and show intraspecific differentiation, which results in different pathotypes. Damage can occur either early in the season or later on and may have either a quantitative or qualitative character, depending on the crop and on pre-planting nematode density.

Durable resistance

Nematodes have a limited spatial dispersion, few generations per year and countable units. Therefore resistance in nematology is generally defined as reduced multiplication over one or a few generations. Durable resistance encompasses both resistance that cannot be 'overcome' by a pathogen as well as a more general concept embracing sustainability of resist-

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This work is supported by EU-QLRT-1999-1462.

ance in time and across crops. Durable resistance in the practical context of a cropping system may be obtained when little or no selection for virulence occurs in a wide representation of nematode populations against a single dominant resistance gene, but equally, deployment of different resistance genes in the same or subsequent crops, even when only partially resistant, may be sufficient. The applicability of resistant crops in fields with high nematode densities requires combination of resistance with tolerance, at least when the crop yield is important. Main crops that suffer from damage due to reproduction during the season need resistance themselves, whilst other crops may profit from resistance in any preceeding resistant crop. Green manure crops are interesting targets for nematode resistance breeding as generally their characteristics requirements are less than that of main crops and because they can be deployed in rotations more flexibly.

Approach and expected achievements

The host and pathogen and their complex interaction are examined in different complementary ways. Expertise in nematology, breeding, developmental botany, agronomy, (cyto-)genetics and molecular biology are integrated. Techniques and strategies involve the detection, mapping and isolation of resistance-related genes and the testing of the durability of the resistance. Sustainable production systems will be optimised by investigating rotations of potato with resistant genotypes of the green manure crops Italian rye grass and fodder radish. New tools for durable resistance management will be generated by developing and implementing techniques and strategies for the identification of pathotypes, (a)virulence mechanisms and -genes in *M. chitwoodi* and *M. fallax*. Histological features of plant interactions with pathotypes will be linked to genomic characteristics. Markers will be developed to characterise *M. chitwoodi* and *M. fallax* with regard to their (a)virulence genes. These virulence markers will be used to develop well-characterised sets of root-knot nematode isolates and to assess the genetic variability in field populations. Based on this knowledge, predictions will be made for the durability of plant resistance, which eventually will allow an effective management of resistant varieties. Furthermore, breeding strategies will profit from this knowledge, facilitating effective combinations of *R*-genes to be incorporated into new varieties.

A unique European collection of *M. chitwoodi* and *M. fallax* is used to establish the range of genetic variation in the pathogen. Molecular characterisation is combined with cytological studies to identify key representative populations. Plant accessions identified as resistant will be used for detailed studies of interaction and inheritance and will be tested in field situations. Mapping populations will be produced and molecular marker techniques applied to obtain markers linked to resistance. This will enhance the efficiency of breeding strategies and potentially lead to the isolation of resistance genes. Resistance/virulence interactions are analysed to establish the occurrence of resistance genes and complementary virulent and avirulent pathotypes. Rates of selection for virulence will be established. The results of these experiments will identify existing pathotypes and the likely emergence of others. Histological characterisation of incompatibility will help to provide and understand temporal patterns of expression of resistance or (a)virulence. This will facilitate targeting of the studies at a molecular level, which are described in a parallel paper (BLOK *et al.* 2002).

SELECTED RESULTS

Virulent and avirulent selections of two *M. chitwoodi* isolates (discriminating on *S. bulbocastanum* genotypes) were developed. Screening methods were developed for fodder radish and Italian rye grass. For both crops gradual differences in resistance have been found. A screening of 15 *Solanum* spp. revealed resistance in 12 of them to *M. chitwoodi* and in 8 to *M. fallax* (other 7 not yet tested to *M. fallax*). A new source of resistance in pepper to *M. chitwoodi* was selected and further used for marker-assisted breeding. Results of resistant (R) X susceptible (S) cross in pepper suggest dominant monogenic inheritance of two sources of resistance. In potato, tests on a BC_1 RXS with *Solanum fendleri*, confirmed monogenic inheritance of resistance RMc2 to *M. chitwoodi* and *M. fallax* and linkage to a molecular marker. *S. schenkii* and *S. sparsipilum* were used in introgression programmes for resistance to *M. chitwoodi* and *M. fallax*, respectively. In pepper, variety X *M. chitwoodi*-isolate interaction was found, indicating the presence of pathotypes. Double haploid lines differentiated on two discriminating *M. chitwoodi* isolates and *M. incognita* and *M. hispanica* isolates. One *M. chitwoodi* isolate was virulent to all genotypes tested so far. In potato, a virulent selection on several *Solanum* spp., originating from an avirulent *M. chitwoodi* isolate, appeared to be the first found isolate belonging to host race type 1 and to the most aggressive pathotype on *S. bulbocastanum*. Histological studies of highly incompatible, moderately incompatible and compatible interactions of *M. chitwoodi* and *S. bulbocastanum* showed changes in differentiation in xylem, phloem, pericycle, and in penetration pattern in the root.

References

Blok V.C., Wishart J., Mugniery D., Bossis M., Castagnone-sereno P., Neveu C., Smant G., Zijlstra C., Zoon F.C., Phillips M.S. (2002): Molecular and genetic studies of the basis of virulence/avirulence in *Meloidogyne chitwoodi*. Proc. 6th Conf. EFPP 2002, Prague. Plant Protect. Sci., **38** (Special Issue 2), 2002: 714–716.