

Year of CfP: 2010

Project N° 1002-003

Project title: Identification of nematode (<i>Meloidogyne</i> spp.) effectors of pathogenicity in rice (<i>Oryza sativa</i>)
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Units managing the project: UMR RPB "Plant resistance to pests and diseases" (CIRAD, IRD, UMII)

Project leader: Fernandez, Diana (diana.fernandez(a)ird.fr)

Countries involved in the project: Brazil and Benin

Sub-thematic axes: IPB-1 (Integrative Plant Biology 1: Genetics and genomics, plant breeding, ecophysiology)

Objectives:

The diseases caused by parasitic nematodes in plants are major factors that decrease production and quality of the agricultural products. Root-knot nematodes (*Meloidogyne* spp.) are one of the three most economically damaging genera of plant-parasitic nematodes on horticultural and field crops in all temperate and tropical areas (Trudgill and Block, 2001).

The main hypothesis of this project is that *Meloidogyne* nematodes secrete a rich assortment of effectors that interact with or manipulate host plants during infection. An exhaustive mass spectrometry analysis of *M. incognita* secretions allowed the direct identification of proteins that could play a role in the interactions between *M. incognita* and its host plants. We propose in this project to search for essential *M. incognita* proteins among a set of candidate secreted proteins and to assess their possible role as effectors involved in interactions with the host plant. This objective can be achieved by a multi-disciplinary project combining functional genomics (transcriptomics, reverse/forward genetics, biological assays), basic plant pathology (nematode sampling in fields and identification) and genetic variability analysis of candidate genes in nematode populations.

The proposed program will associate the functional analysis of *Meloidogyne* candidate genes with field surveys for the sampling of nematode populations and assessment of candidate gene variability at a regional scale in Brazil and Africa. A set of *M. incognita* secreted proteins has been selected in IRD and Embrapa-Cenargen as putative virulence effector candidates. Once these proteins are confirmed to be secreted during parasitism, functional analysis of candidate genes will be assessed through combined forward and reverse genetic approaches using genetic transformation of rice.

The study of proteins secreted during interactions with host plants should significantly widen our knowledge of molecular players contributing to nematode pathogenicity, opening new avenues for *Meloidogyne* spp. control strategies in rice and other crops of interest for Brazil and Africa which are highly susceptible to *M. incognita*. The major goals of this project will be (i) to identify and functionally characterize *M. incognita* effector proteins involved in virulence against the host plant, (ii) to assess *M. incognita* gene polymorphism among natural populations in rice fields from Brazil and Benin and (iii) to generate rice plants with potential anti-nematode activity against *Meloidogyne* spp.

Total Agropolis Fondation funding: €19,999

Funding category: Work mission of professors, faculty members, scientists and/or researchers

Project duration: 01 March 2011 – 28 february 2013

Keywords: *Meloidogyne* nematode, disease, virulence, effector proteins, reverse genetic approach.