What is the epigenetic contribution to quantitative resistance to pathogen?

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Resistance and Adaptation

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Social-economic context

As part of an environmentally friendly agriculture aiming at reducing input uses, disease genetic control is a major concern for plant breeding.

Scientific context

Continuous variation observed for complex traits, and more particularly for response to biotic stress, is traditionally attributed to the action and interaction of numerous DNA sequence polymorphisms and environmental factors. However, genome expression strongly depends on upstream mechanisms, called epigenetics, which modulate chromatin structure and regulate thus genomic region accessibility to transcriptional machinery. Genome-wide segregation of numerous epialleles could therefore constitute an unexplored variability source.

Objectives

The aim of the project is thus to study the contributions of epigenetic regulations in quantitative resistance and to make the connection between genetic and epigenetic variations, more particularly in *Brassicaceae* response to clubroot, one of the major diseases of Brassica crops.

Results

This thesis will be structured in two parts:

(i) The first one focus on the identification of epigenetic profiles associated with clubroot partial quantitative resistance and susceptibility in the model species Arabidopsis. This part will allow to determine the genomic regions whose epigenetic regulation modifications lead to variability in the plant response to clubroot. The identification is based on two approaches:

- ✓ epiQTLs detection. Pathological tests were carried out on the 123 epiRILs obtained from the cross between *ddm1* (partially resistant) and Col-0 (susceptible) (Johannes *et al.*, 2009) and enabled to identify 6 epiQTLs on chromosomes 1, 3, 4 and 5 of Arabidopsis. Some of these epiQTLs co-localized with clubroot resistance QTLs identified by Jubault *et al.* (2008) and the major gene *RPB1* (Arbeiter, 2002) and regions controlling development. These preliminary results showed that one part of the clubroot resistance is under the control of epigenetic modifications and potentially associated with development. After validation of these preliminary results, the reduction of epiQTLs confidence intervals would lead to a list of regions involved epigenetically in clubroot resistance response.
- ✓ Analysis of chromatin structure changes in two genotypes displaying contrasted responses to clubroot. The comparison of open chromatin regions, in progress, is performed using FAIRE sequencing.

Epigenetic marks will be then precisely determined by bisulfite-PCR and ChIP-PCR in the regions identified by comparison between the lists obtained in the two approaches.

(ii) In order to determine if these epigenetic regulations are maintained amongst *Brassicaceae*, genomic regions identified in Arabidopsis will be validated (or not) in *Brassica napus* genotypes showing different susceptibility levels to clubroot.

Perspectives

Integration of epigenetic data, acquired during the thesis, to genetic data already available in the lab on both species will be carried out to establish the respective contributions of genetic and epigenetic variabilities in *Brassicaceae* quantitative resistance to clubroot. These data will also bring valuable information on the impact of duplications and structural rearrangements on organisation, effect and diversity of genetic and epigenetic factors involved in quantitative resistance to clubroot. Epigenetic polymorphisms, if heritable, could be exploited in breeding, especially with biomarkers development.

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