

Comparative genomic analysis of Clubroot resistance in the Brassicaceae family

Aurélie Evrard, Charles Bettembourg, Olivier Dameron, Olivier Filangi, Anthony Bretaudeau, Fabrice Legeai, Regine Delourme, Maria Manzanares-Dauleux, Mélanie Jubault

► **To cite this version:**

Aurélie Evrard, Charles Bettembourg, Olivier Dameron, Olivier Filangi, Anthony Bretaudeau, et al.. Comparative genomic analysis of Clubroot resistance in the Brassicaceae family. Brassica2016, Oct 2016, Melbourne, Australia. <<http://brassica2016.com/>>. <hal-01391707>

HAL Id: hal-01391707

<https://hal.inria.fr/hal-01391707>

Submitted on 3 Nov 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Comparative genomic analysis of Clubroot resistance in the *Brassicaceae* family

A. Evrard¹, C. Bettembourg², O. Dameron², O. Filangi¹, A. Bretaudeau¹, F. Legeai¹, R. Delourme¹, M. J. Manzanares-Dauleux¹, M. Jubault¹

Introduction

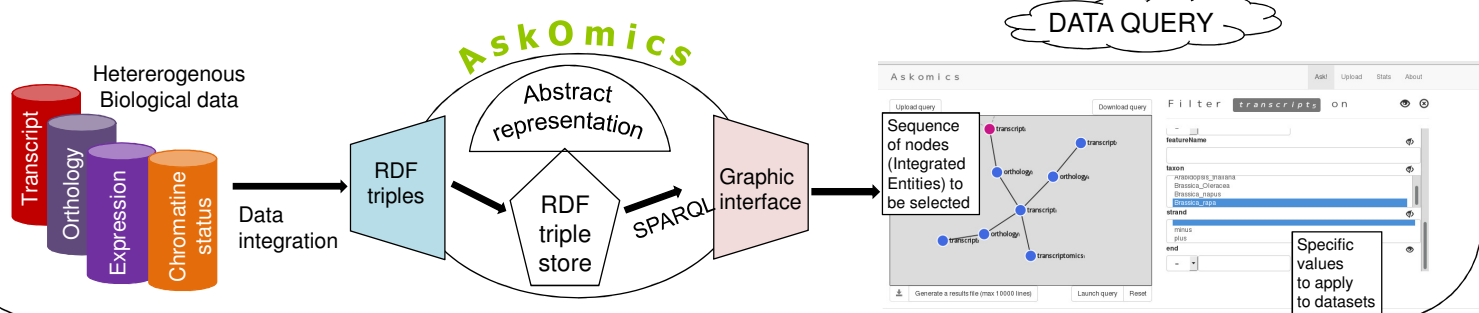
Clubroot, caused by the obligate biotroph *Plasmodiophora brassicae*, is one of the economically most important diseases of Brassica crops in the world including *B. oleracea* (coles), *B. napus* (oilseed rape) and *B. rapa* (turnip). The breeding of resistant cultivars is currently a main goal to control this disease in all Brassica crops. Very few resistant varieties are currently available especially for coles and oilseed rape. The model plant *Arabidopsis thaliana* is also a host for clubroot and shows natural variation in the responses to clubroot infection. Genetical genomics analyses of the plant response to clubroot infection are in progress in our team in order to determine which structural and functional characteristics of the resistance factors have to be taken into account to build resistant varieties in a complex environment. The aim of the present work was to investigate synteny of the regions carrying resistance factors to clubroot through a comparative structural study in the three Brassica crops (*B. napus*, *B. oleracea* and *B. rapa*) and in the model species *A. thaliana* and to identify underlying candidate genes.

Integration and query of Clubroot datasets with Semantic Web technologies : AskOmicS

AskOmicS is a tool supporting both intuitive data integration and querying while shielding the user from most of the technical difficulties underlying RDF and SPARQL
Still under development @<https://github.com/askomics/askomics>

AskOmicS advantages:

- Simple and automatic translation of biological data in RDF format and visual interface for biological query
- Interoperability for integrating multiple data sources
- Adaptability: RDF can be incremented, evolved, extended



Clubroot comparative genomics

- Major genes and quantitative trait loci (QTL) with high or moderate effect for resistance to various *P. brassicae* isolates identified in the four species were recorded.
- "Quartet" gene sets (*B. rapa*, *B. oleracea*, *B. napus* subgenomes A and C) and their *Arabidopsis* ortholog were retrieved from Chalhouh et al (2014) and were completed through BlastP analysis between *B. rapa*, *B. oleracea* and *Arabidopsis* protein databases.
- Gene sets underlying each QTL in each species were identified and compared, which allowed the identification of common and 'missing' genes between species (Fig.1).
- The comparison of the physical location of these common genes showed the synteny relationships between *Arabidopsis* and *Brassica* QTLs (Fig.2).

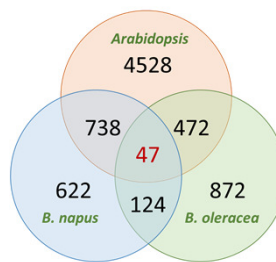


Figure1: Number of common orthologous genes underlying the QTLs of resistance to eH isolate in three Brassicaceae species. The number of genes indicated for *B. napus* and *B. oleracea* correspond to the genes that have orthologs in *Arabidopsis*. A total of 47 *Arabidopsis* genes were identified as common to the three studied species.

Prospects

Integration of structural and functional data is going on and results will be examined to infer evolutionary patterns and consequences for the construction of durable resistant varieties.

REFERENCES

- Chalhouh et al (2014) *Science*, 345: 950-953
Cheng et al (2013) *The Plant Cell*, 25: 1541-1554
Lysak et al (2016) *Current Opinion in Plant Biology*, 30:108-115
Mason et al (2016) *Genetics*, 202: 513-523

This work was supported by the French 'Institut National de la Recherche Agronomique' (INRA) and Brittany region.

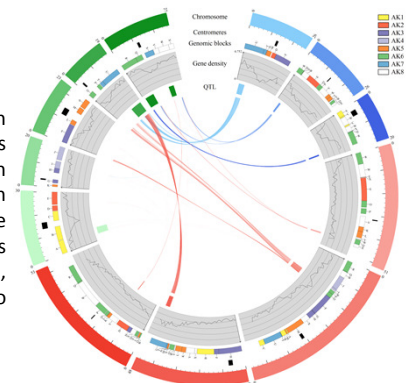


Figure2: Structural genomic position of *Arabidopsis* and *B. napus* QTL. Lines show the *B. napus* genes underneath the QTLs that have an ortholog in *Arabidopsis*. Centromeres, gene density and ancestral genomic blocks (Mason et al., 2016; Cheng et al., 2013; Lysak et al, 2016) were added to the circos plot.