Identification of a genetic factor determining the durability of a plant major resistance gene and quantitative resistance to virus accumulation

Julie Quenouille-Lederer, Estelle Paulhiac, Pascale Mistral, Ghislaine Nemouchi, Anne-Marie Sage-Palloix, Bruno Savio, Vincent Simon, Benoît Moury, Alain Palloix

To cite this version:

HAL Id: hal-02745421
https://hal.inrae.fr/hal-02745421
Submitted on 3 Jun 2020

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.
Identification of genetic factors determining the durability of a major resistance gene and quantitative resistance to virus.


Introduction

Genetic resistance provides efficient control of crop diseases but is limited by pathogen evolution capacities which often result in resistance breakdown.

The pepper resistance gene pvr2 coding for a eIF4E (eukaryotic initiation factor 4E), confers a recessive resistance to Potato virus Y (PVY). This resistance is broken down by single amino acid substitutions in the Vpg of PVY.

The breakdown frequency of pvr2 is highly dependent on the genetic background indicating that plant genetic factors directly affect the durability of the resistance.

Research question: Are the plant genetic factors involved in the durability of a major resistance gene and those controlling the quantitative resistance the same?

Phenotyping durability of pvr2 resistance gene and level of quantitative resistance.

Yolo Wonder pvr2 - partial resistance factor
Parental pvr2 - partial resistance factor

Population of 30 DH lines
Segregating for pvr2 and genetic background

pvr2 resistant sub-population
156 DH carrying the resistant allele pvr2

pvr2 susceptible sub-population
154 DH carrying the allele of susceptibility pvr2

Manual inoculation Wild type PVY clone

This virus is not able to infect pvr2 plants and need to evolve during the test.

Measure of resistance durability components:

- Number of DH lines
- Breakdown frequency

Each case of infection resulting of virus evolution (the pvr2 resistance is broken down)

Measure of quantitative resistance components:

- AUDPC
- Symptom assessment

Wild type PVY clone differs from the mutant PVY clone which is the breakdown of resistance gene durability and quantitative resistance

Genetic factors control pvr2 resistance gene durability and quantitative resistance

Detection of two “QTLs for durability” : QTLs affecting the breakdown frequency of the major gene pvr2 were successfully detected.

Comparative mapping: the two significant QTLs for Breakdown frequency of pvr2 allele are also involved in quantitative resistance.

Descriptive table of QTL results

<table>
<thead>
<tr>
<th>Trait</th>
<th>Additive QTLs</th>
<th>Epistatic QTLs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Resistance breakdown (%)</td>
<td>Resistance breakdown (%)</td>
<td></td>
</tr>
<tr>
<td>Number of DH lines</td>
<td>Number of DH lines</td>
<td></td>
</tr>
<tr>
<td>h² = 0.50</td>
<td>h² = 0.52</td>
<td></td>
</tr>
<tr>
<td>Breakdown frequency for pvr2 sub-population</td>
<td>AUDPC for pvr2 sub-population</td>
<td></td>
</tr>
<tr>
<td>Viral accumulation for pvr2 sub-population</td>
<td>AUDPC for pvr2 sub-population</td>
<td></td>
</tr>
<tr>
<td>Viral accumulation for pvr2 sub-population</td>
<td>Breakdown frequency for pvr2 sub-population</td>
<td></td>
</tr>
<tr>
<td>Viral accumulation for pvr2 sub-population</td>
<td>Breakdown frequency for pvr2 sub-population</td>
<td></td>
</tr>
</tbody>
</table>

Conclusion

QTLs conditioning pvr2 resistance gene durability were successfully detected. Direct selection for alleles increasing the durability of virus resistance is consequently possible and opens new ways for durable resistance breeding.

Genetic factors affecting quantitative resistance and breakdown frequency colocalize in the genome suggesting pleiotropy for the two traits.

When direct selection for resistance durability is not possible (phenotyping test not available), indirect selection for quantitative resistance traits can be expected to improve the durability of a major resistance gene.

Strategic

Construction of a doubled haploid (DH) progeny segregating for the pvr2 gene (pvr2 - susceptibility allele or pvr2 resistance allele) and the genetic background.

Phenotyping the DH progeny for:

- Breakdown frequency of pvr2 component of resistance durability.
- Virus accumulation and symptom intensity (area under the disease progress curve (AUDPC)) component of quantitative resistance.

Genetic mapping of the quantitative trait locus (QTLs) controlling each phenotyped trait.

XV International Congress of Molecular Plant-Microbe Interactions – July 29–August 2 – 2012 Kyoto – Japan