Mapping of botrytis resistance in gerbera & validation of Candidate genes

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Introduction

Gerbera hybrida

• G. jamesonii & G. viridifolia

• abundance of colours, sizes and shapes
• outbreeding crop
• highly heterozygous diploid (2n=50)

Gerbera grey mould

• Caused by Botrytis cinerea
• The symptom of Botrytis infection on Gerbera
• High humidity situation

Phenotyping

• inoculated Botrytis spore
  ✓ Visual (whole flower)
  ✓ Bottom
  ✓ Petal
• 48hpi, RT, 100%rh
• Scored 0~5

QTL mapping for Botrytis resistance

Selected two populations from 20 cross populations

• S_pop: SP1:PS × SP2:CK
  276 offspring

• F_pop: FP1:KK × FP2:LL
  276 offspring

Disease scores
Marker development: EST-SNPs

Marker selection from RNA-seq data

- Selection over both populations
  - Specific SNPs - polymorphic between parents
  - Common SNPs - polymorphic in two populations

- Genotyping
  - 677 SNP markers for S-pop
  - 675 SNP markers for F-pop
  - 477 common markers
  - Genotyping success 70%, diploid segr.

Overview of all linkage groups:

\[ S1=30 \] S_1G=23 \[ S2=29 \] F1=27 \[ F_1G=20 \] F2=28

QTL found for visual, bottom and petal in two populations

<table>
<thead>
<tr>
<th>QTL</th>
<th>Parents</th>
<th>Flanking Markers</th>
<th>LG</th>
<th>MQM</th>
<th>LOD % expl (GW)</th>
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<tr>
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<tr>
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<tr>
<td>SBP6</td>
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Candidate gene approach

- Many CG described (~60 currently)
  1. Find the homologous gene in gerbera

CGs approach

Many CG described (~60 currently)
1. Find the homologous gene in gerbera
2. Look for SNP in gerbera homolog CG
• develop SNP marker

3. Mapping CGs in gerbera populations
29 mapped

14 CGs show statistically significant difference.

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Hit</th>
<th>F1/F2</th>
<th>CM</th>
<th>P-value</th>
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<td>WGC8244_216_S2F2</td>
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<td>PG1_15001_1052</td>
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PETAL
0
5
F2_21

SCAR from agro-
infiltration by scratching

VIGS experiment

Silencing

29 candidate genes were mapped.

4. Look for co-localisation
• Mapping of CG improved QTL mapping
  ● Shift of QTL peak e.g. for PG1
  ● Addition of other QTL

Co-localization with QTLs

WAGENINGEN
groent & natuurwetenschappen

PG21

candidate gene from test of

SS SS_5198_1668 SP1 bottom
AO AO_19807_6510 FP1
PG2 PER62 PER62_31923_540 FP2
PG1 PG1_15001_1052 FP2
CH1 CH1_22447_285 FP1
Silencing

- Differences between parents in PDS silencing response both in bleaching as in silencing transcription
- SP1 and SP2 show bleaching, FP1 seems unresponsive

Lesion size

- Lesion sizes smaller in SP1, SP2

Summary

- Detected several QTL for Botrytis resistance from visual, bottom and petal.
- Mapped CGs related to Botrytis resistance
- Co-localised CG are upregulated upon infection
- VIGS indicate possible functional role in resistance
- Allelic variation being assessed on F2 plants

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- Schreurs Holland BV
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- Wen Fang
- Jan van Kan
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QUESTIONS?