solQTL: A Tool for QTL Analysis and Linking QTLs to Annotated Genomes

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Tecle et al. BMC Bioinformatics 2010, 11:525

Overview

SGN (http://solgenomics.net)

Preconditions...

- Population types: F2, BC, RIL
- Diploid
- Phenotype data: normal dist.
- Marker sequences need to be on SGN
  - For comparative analyses

Preconditions...

Statistics...

- R/QTL
  - Single-QTL Scan
    - Interval Mapping and Single Marker Analysis
    - LOD threshold
    - 95% confidence interval
    - Explained variation
    - QTL effects

Preconditions...

QTL search results

<table>
<thead>
<tr>
<th>Trait name</th>
<th>Definition</th>
<th>QTL</th>
</tr>
</thead>
<tbody>
<tr>
<td>flesh color</td>
<td>The area of the fruit.</td>
<td>✓</td>
</tr>
</tbody>
</table>

Browse QTL populations:
- T. morrisii x T. sect. 'Florida' x L-1499 F2
- T. morrisii 'Flottat' x L-1499 F2
- T. morrisii 'Purple' x L-1499 F2

something wrong? Report a problem

SGN is supported by the NSF MCB-0722252, USDA CRIS and the USDA National Institute for Food and Agriculture. SGN is a product of the Joint Genome Institute (JGI). Visit http://www.jgi.doe.gov for links to software, web services and tools. For comments or feedback, send email to sgn-helpdesk@genome.org.

The SGN team, from top to bottom: S. Widom, P. Cogoni, P. Kim, D. Parrett, G. Skagen, A. Allard.
**Qtl populations for fruit area**

**Qtl analysis**

<table>
<thead>
<tr>
<th>Analyze Qtl in population</th>
<th>Population description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Qtl Tomato x Howard German x LA399 F2</td>
<td>Qtl Tomato Howard German</td>
</tr>
<tr>
<td>Qtl Tomato x Howard German x LA399 F2</td>
<td>Qtl Tomato Howard</td>
</tr>
</tbody>
</table>

**Qtl effects and more**

Variation explained by QTLs (interesting QTL mode)

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>LOD</th>
<th>Pedest(%)</th>
<th>Pedest()</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>2</td>
<td>207906.78</td>
<td>105936.39</td>
<td>4.18</td>
<td>55.67</td>
</tr>
<tr>
<td>Error</td>
<td>110</td>
<td>1470909.37</td>
<td>105285.26</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>Total</td>
<td>112</td>
<td>2098906.15</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

The ANOVA model is based on a single QTL: significant source of variation.

**Qtl details**

- **Qtl effects**
  - LOD 435.81
  - P-value: 0.82
  - P-value: 44.85

**Corresponding genome positions**
Website: http://solgenomics.net/qtl

Further reading: Tecle et al. BMC Bioinformatics 2010, 11:525