MAPPING AND SEGREGATION DISTORTION ANALYSIS IN THE G2333 X G19839 RECOMBINANT INBRED LINE POPULATION OF COMMON BEAN

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Introduction

Mapping populations are a critical genetic tool for gene tagging and quantitative trait loci studies but also serve to analyze the frequency of segregation distortion, where this genetic phenomenon is the deviation from expected values of observed allelic frequencies. Segregation distortion is a common aspect of mapping population analysis, especially for recombinant inbred line or double haploid populations and has important implications for linkage mapping: namely, in map regions suffering from segregation distortion, the estimate of recombination fraction might be biased leading to the inaccurate calculation of marker linkage and map distances in some map segments with a high proportion of distorted markers; however, the order of the markers seems not to be particularly affected by the inaccuracy in map distance introduced by segregation distortion when these are corrected for by two-point analysis (Lashermes et al., 2001). The number of genetic factors causing segregation distortion in a given distorted region might also affect the estimate of map distance; nevertheless, Lu et al. (2002) speculated that as a general rule only one gametophytic or sporophytic incompatibility factor is present per region of segregation distortion. The objective of this study was to develop a new linkage map of Phaseolus vulgaris L. with PCR-based markers, and to identify sets of markers showing segregation distortion.

Materials and Methods

A F₅:₈ recombinant inbred line (RIL) population of 84 genotypes was derived from the cross between G2333 and G19839 (from Mesoamerica and Andean gene pool respectively) and used for this study. Four different types of DNA based markers were analyzed: (1) 106 genomic and gene-coding microsatellites (Blair et al., 2003); (2) 34 RAPD fingerprints (primers) that had been previously tested in CIAT mapping populations (M. W. Blair, unpublished data); (3) 15 SCAR markers (http://www.ars.usda.gov/SP2UserFiles/person/3848/pdf/Scartable3.pdf); and (4) 3 STS markers linked to seed coat color. In addition the biochemical marker phaseolin (Phs) and the morphological marker flower color (V) were scored. The PCR amplifications of microsatellites markers were performed as described by Blair et al. (2003). Linkage analysis was conducted using the software MAPMAKER/EXP 3.0 (Lander et al., 1987) with the Kosambi mapping function. Groups of markers were assigned to particular linkage groups if at least two microsatellites were reported previously from that linkage group (Blair et al., 2003). These were then used for the placement of additional markers based on the most-likely interval at a minimum LOD of 2.0. The best marker order of the linkage groups was determined using a minimum LOD of 4.0. For each of the 160 polymorphic markers evaluated in the RIL population, a chi-square goodness-of-fit test against an expected 1:1 (A:B) ratio of parental alleles was carried out in order to identify markers showing segregation distortion. Heterozygous individuals were not considered in the analysis.
Results and Discussion

One hundred forty nine out of 160 polymorphic markers evaluated were assigned into 11 linkage groups for the G2333 x G19839 RIL population. The total cumulative map length was 1175 cM (Figure 1). We found 46.3% (69) of the total markers being mapped showing segregation distortion. Considering all loci together, there was preferential transmission of maternal alleles from G2333 (53.5% vs. 46.5) over paternal alleles from G19839 ($\chi^2 = 473.7$; Table 1). This significant preferential transmission of maternal alleles occurred on every linkage group (Table 1) except for linkage groups B4 and B11 where the expected 1:1 ratio was observed. Linkage group B9 showed the highest proportion of maternal alleles (67.6%). In our map, distorted markers were unevenly distributed among the 11 bean linkage groups (Figure 1). The highest proportion of skewed markers occurred on linkage groups B2 with 12 out of 16 markers distorted and B5 with 10 out of 11 markers distorted, while the fewest distorted markers were found on linkage groups B1, B4, and B11 with 1 or 2 loci each (Figure 1). Following the criteria proposed by Xu et al. (1997), we identified four well defined segregation distortion regions (SDRs) located in the bottom half of linkage group B2, the entire middle section of linkage group B5, the top half of linkage group B9, and the bottom half of linkage group B10 (Figure 1). We speculate that the high proportion of distorted markers and the preferential transmission of maternal alleles from G2333 would have been due to selection against G19839 gametes and alleles in the environmental conditions (average temperature and altitude) in which the RIL population was developed at CIAT where conditions might have been more favorable to the Mesoamerican alleles. This might be particularly true because the parents represented different gene pools, and adaptation to different agroecologies.

Table 1. Transmission of alleles in recombinant inbred population of G2333 x G19839.

<table>
<thead>
<tr>
<th>Linkage group</th>
<th>B1</th>
<th>B2</th>
<th>B3</th>
<th>B4</th>
<th>B5</th>
<th>B6</th>
<th>B7</th>
<th>B8</th>
<th>B9</th>
<th>B10</th>
<th>B11</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>G2333 allele (A)</td>
<td>332</td>
<td>753</td>
<td>645</td>
<td>677</td>
<td>552</td>
<td>551</td>
<td>563</td>
<td>780</td>
<td>580</td>
<td>603</td>
<td>401</td>
<td>6437</td>
</tr>
<tr>
<td>G19839 allele (B)</td>
<td>238</td>
<td>373</td>
<td>472</td>
<td>741</td>
<td>253</td>
<td>466</td>
<td>367</td>
<td>453</td>
<td>188</td>
<td>269</td>
<td>373</td>
<td>4193</td>
</tr>
<tr>
<td>$\chi^2$ (1:1)</td>
<td>15.5</td>
<td>128.2</td>
<td>26.8</td>
<td>2.9</td>
<td>111.1</td>
<td>7.1</td>
<td>41.3</td>
<td>86.7</td>
<td>200.1</td>
<td>127.9</td>
<td>1.0</td>
<td>473.7</td>
</tr>
<tr>
<td>$P_{0.05}$; 1df</td>
<td>***</td>
<td>***</td>
<td>***</td>
<td>ns</td>
<td>***</td>
<td>**</td>
<td>***</td>
<td>***</td>
<td>***</td>
<td>***</td>
<td>ns</td>
<td>***</td>
</tr>
<tr>
<td>Allele in excess</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>-</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
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<td>A</td>
<td>A</td>
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</tr>
</tbody>
</table>

References

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Figure 1: Genetic map of the G2333 x G19839 RIL population showing distribution of molecular markers displaying segregation distortion. Markers displaying significant distortion at 5%, 1%, 0.1%, 0.01%, and 0.001% are represented by *, **, ***, ****, and ***** respectively.