QTL Mapping of Five Agronomic Traits in Maize

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Abstract: Agronomic traits have significant influence on stability and adaptability in maize production. In this investigation, using a population with 266 F₂:₃ families from Yuyu22×Zong3×87-1two-location field tests were conducted in Wuhan and Xiangfan in 2001 with a randomized complete block design to characterize five agronomic traits: ear height, tassel branch number, stalk diameter, days to pollen, and days to silk. Correlation analysis of field performance indicated that ear height, tassel branch number, and stalk diameter were significantly positive correlated with single-plant yield, days to pollen, and days to silk were highly positive correlated with each other, and tassel branch number was significantly positive correlated with stalk diameter too. Utilizing data of field tests and molecular markers, the Composite Interval Mapping (CIM) method was used to localize the quantitative trait loci of these traits and 500 times permutation test was conducted to have proper LOD threshold value. As the results, total seven QTL of ear height, nine QTL of tassel branch number, eight QTL of stalk diameter, nine QTL of days to pollen, and seven QTL of days to silk were mapped on 10 chromosomes of maize, all of these QTL distributed unevenly on chromosomes and tended to cluster together. According to analysis of this investigation, the phenotype correlations of quantitative traits may result from the correlations of QTL controlling those traits. Those will be helpful to further understand genetic basis of agronomic traits in maize.

Key words: maize, agronomic traits, quantitative trait loci, QTL
玉米是重要的粮食和饲料作物,经济地位十分重要。在玉米育种过程中,除了对玉米产量性状的选择外,对农艺性状的选择也十分重要,因为农艺性状的优劣对玉米的稳产性和适应性有重要影响。例如:穗位高与玉米的抗倒伏性密切相关;茎粗是玉米营养生长健壮程度的重要指标,且与玉米的抗倒伏性高度相关;雄穗分支数与玉米的种子繁殖能力有关,抽雄期和吐丝期与玉米的熟期早晚及花期协调性有关。这些因素的存在,都会影响到玉米的最终产量。研究这些性状的遗传规律,对于提高玉米的稳产性和适应性具有重要的意义。

对于玉米的许多产量相关性状,如穗长、穗粗、行数、行粒数等,国内外都进行了较为深入的研究,定位了大量的QTL位点,并分析了它们的遗传规律[8-10],为玉米育种提供了很好的指导意义。对于农艺性状,只有株高的研究十分深入[11],而穗位高、茎粗、雄穗分支数、抽雄期、吐丝期这几个重要的农艺性状,总体上的研究都不够深入,国外有少量的报道[12-13],国内相关研究的报道较少。本研究以玉米强优势杂交种“豫玉”构建的34个家系为材料,构建分子标记遗传连锁图,通过一年两点的田间试验,定位穗位高、茎粗、雄穗分支数、抽雄期、吐丝期5个性状的QTL位点,并剖析它们的遗传特性。
母本综的特点是穗位较低，抽雄期和吐丝期略晚；父本综的特点是穗位较高，抽雄期和吐丝期略早；F_{1}代的穗位高、茎粗和雄穗分支数都高于双亲，抽雄期和吐丝期提前，表现了不同程度的杂种优势；家系的平均表现只有穗位高高于双亲，其他性状的都介于双亲之间。对武汉和襄樊两点的比较发现，两点的性状存在一定的差异，特别是抽雄期和吐丝期。正态分布检验表明，在武汉、襄樊两点，所有个性状的表型值均符合正态分布，并达到极显著水平。

### 表 1 田间表现

<table>
<thead>
<tr>
<th>Location</th>
<th>Material</th>
<th>EH [cm]</th>
<th>TBN</th>
<th>SD [cm]</th>
<th>DTP [d]</th>
<th>DTS [d]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wuhan</td>
<td>3</td>
<td>40.51</td>
<td>8.87</td>
<td>1.62</td>
<td>76.33</td>
<td>83</td>
</tr>
<tr>
<td></td>
<td>87-1</td>
<td>53.3</td>
<td>13.17</td>
<td>1.61</td>
<td>79</td>
<td>85</td>
</tr>
<tr>
<td></td>
<td>F_{1}</td>
<td>89.17</td>
<td>19.17</td>
<td>2.16</td>
<td>74.67</td>
<td>78.67</td>
</tr>
<tr>
<td></td>
<td>F_{2:3}</td>
<td>61.98 ± 11.15</td>
<td>13.04 ± 3.56</td>
<td>1.75 ± 0.17</td>
<td>77.86 ± 1.94</td>
<td>83.15 ± 1.97</td>
</tr>
<tr>
<td>Xiangfan</td>
<td>3</td>
<td>46.83</td>
<td>13.27</td>
<td>2</td>
<td>73</td>
<td>78</td>
</tr>
<tr>
<td></td>
<td>87-1</td>
<td>58.55</td>
<td>11.47</td>
<td>2.16</td>
<td>75</td>
<td>80</td>
</tr>
<tr>
<td></td>
<td>F_{1}</td>
<td>78.23</td>
<td>18.33</td>
<td>2.43</td>
<td>72.33</td>
<td>75</td>
</tr>
<tr>
<td></td>
<td>F_{2:3}</td>
<td>62.07 ± 10.13</td>
<td>13.92 ± 3.09</td>
<td>2.24 ± 0.17</td>
<td>74.51 ± 1.84</td>
<td>79.02 ± 1.86</td>
</tr>
</tbody>
</table>

### 表 2 单株产量与五个农艺性状的相关分析

<table>
<thead>
<tr>
<th>Location</th>
<th>Trait</th>
<th>Yield per plant</th>
<th>EH</th>
<th>TBN</th>
<th>SD</th>
<th>DTP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wuhan</td>
<td>EH</td>
<td>0.3298 *</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>TBN</td>
<td>0.2659 *</td>
<td>0.3556 *</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>SD</td>
<td>0.4467 *</td>
<td>0.3506 *</td>
<td>0.5707 *</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DTP</td>
<td>−0.0855</td>
<td>0.3703 *</td>
<td>0.1635</td>
<td>0.0759</td>
<td></td>
</tr>
<tr>
<td></td>
<td>DTS</td>
<td>−0.3129 *</td>
<td>0.1028</td>
<td>0.1016</td>
<td>−0.0368</td>
<td>0.6987 *</td>
</tr>
<tr>
<td>Xiangfan</td>
<td>EH</td>
<td>0.3076 *</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>TBN</td>
<td>0.1862 *</td>
<td>0.1231</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>SD</td>
<td>0.1987 *</td>
<td>0.0016</td>
<td>0.3154 *</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DTP</td>
<td>−0.1238</td>
<td>0.3761 *</td>
<td>−0.1506</td>
<td>0.1882</td>
<td></td>
</tr>
<tr>
<td></td>
<td>DTS</td>
<td>−0.3079 *</td>
<td>0.1796</td>
<td>−0.1263</td>
<td>0.1091</td>
<td>0.7526 *</td>
</tr>
</tbody>
</table>

* 显著水平为 0.01 0.01 0.01 0.01 0.01
* *显著性水平为 0.01 0.01 0.01 0.01 0.01

### 2.2 QTL

通过排列测验，武汉和襄樊两点穗位高定位的阈值分别为 98.1% 和 99.2%。以此为标准，在武汉点检测到 98.1% 个 Q8*，在襄樊点检测到 99.2% 个 Q8*，其中 98.1% 个 Q8* 在两点同时被检测到，因此共定位了 98.1% 个穗位高 Q8*（表 1），这些 Q8* 解释的表型变异方差介于 98.1% 之间。两地共有的 98.1% 个 Q8* 分布在 98.1% 号、99.2% 号和 98.1% 号染色体，全部由来自父本综的等位基因起增效作用。
定位了

测到

因此共定位了

予以降低,

点检测到

茎粗的表型变异方差介于

染色体上的

体的数量及提高遗传图谱的标记密度予以降低;对

数量性状的基本方法。在检测主效

第二类的错误是真实存在的

对于雄穗分支数

自

年

个

在两地同时被检测到,因此共定位了

- 个共同的

由来自母本综

在武汉点检测

襄樊点为

襄樊点为

个

号染色体上。

在武汉点检测

襄樊点检测

的几率就越

阈值来

减少发生两种错误的几率。本文采用复合区间作图

的方法,用以确定

个

号染色体的

号和

号染色体上定位了

段,

和襄樊两地,

和

相同区域。因此在

本文与前人研究结果有较高的一致性。例如

本文与前人研究结果有较高的一致性。例如

http://www.maizegdb.org/cgi-bin/QTl_loci_summary_table.cgi

3.2 QTL 研究

3.1 QTL 研究

1986 Weller

http://www.maizegdb.org/cgi-bin/QTl_loci_summary_table.cgi

Beavis 17 Berke 18 Veldboom 19 20

26 QTL qEH3 qEH5-2 Beavis 17 qearht7 qearht8

Veldboom 19 qearht13 bin5.05

Berk 21 1999 20

Mickelson

2002 QTL qTNB3-3 qTNB4-1 qTNB4-2

Koester 22 23 Bohn
3.3 Tuberosa

The study of Tuberosa revealed that

3.4 QTL

The results showed that

References


