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Genetic maps of diploid orchardgrass (*Dactylis glomerata* L.)

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Introduction

Orchardgrass (*Dactylis glomerata* L.) is indigenous to Eurasia and northern Africa. It has been naturalized on nearly every continent and is one of the top four economically important perennial forage grasses grown worldwide (Stewart and Ellison 2010). It has been used widely as forage due to its quality, biomass production and good shade tolerance. Despite its various agricultural uses, little information is available for functional and comparative genetic analysis and concomitant genetic improvement of this species. To date, there have been no reports of genetic linkage studies in orchardgrass.

In the present study, a genetic linkage map of diploid orchardgrass based on two-way pseudo-testcross mapping strategy was constructed using SRAP and SSR markers. This is the first step towards genomic mapping for this species.

Methods

A total of 111 individuals of an F\textsubscript{1} population were derived from a pair cross between two diploid outbred parents: 01996 (very-early flowering, broad-leaved and tall) and YA02-103 (later-flowering, narrow-leaved and short) (Xie et al. 2010). A total of 275 SSR primer pairs and 192 pairs of SRAP primers were used. Markers segregating in a 1:1 and 3:1 ratio were used. The parameters of LOD=3.0 were used to group linked markers, and the map distance was calculated using the Kosambi mapping function (Kosambi 1944). Finally, the linkage map was drawn using MAPCHART 2.1 (Voorrips 2002).

Results

The SRAP and SSR markers were used to construct the genetic linkage maps on the basis of segregation data obtained from 111 F\textsubscript{1} progeny. Two parental maps were constructed first with markers segregating in a 1:1 ratio. Those markers present in both parents that segregated in a 3:1 ratio were included later and used to find the homologous groups in the two parental maps. The paternal map was constructed with 33 SRAP and 57 SSR loci, leaving 8 SRAP and 6 SSR loci unlinked. A total of 90 marker loci were distributed in 9 LGs, with the SRAP loci distributing all the LGs except LGs 4 (Fig. 1). The average marker density in this parental map was 9.6 cM per marker. In contrast, for the maternal genetic linkage map, 87 markers (33 SRAP and 54 SSR loci) were assignable to 10 LGs at a LOD score of 3.0 and covered 772.0 cM, leaving 6 SRAP and 8 SSR loci unlinked. The length of individual LGs varied from 21.1 to 133.9 cM (mean 87 cM), comprising 2-15 loci per LG. SSR loci constituted the major part of all LGs except for LGs 4 and 5. SRAP markers were missing in LG 9. Homology between the two maps was established between 5 LGs of the male map and 5 of the female map using 10 bridging markers (Table 1).

Using method No. 4 of Chakravarti et al. (1991), we estimated a total genome size of 1070.06 cM for the male parent and 1030.87 cM for the female parent. Therefore, the coverage of male and female maps, based on these estimates for genome length, was 81% and 75%, respectively.

Conclusion

The present orchardgrass genetic maps are the first ones reported for this species. Although these genetic maps were not saturated and the male and female maps were not integrated, the 01996/YA02-103 population used for the

<table>
<thead>
<tr>
<th>Male map (01996)</th>
<th>Female map (YA02-103)</th>
<th>Number of Bridging common markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>LG1</td>
<td>LG1</td>
<td>3</td>
</tr>
<tr>
<td>LG2</td>
<td>LG2</td>
<td>2</td>
</tr>
<tr>
<td>LG3</td>
<td>LG3</td>
<td>2</td>
</tr>
<tr>
<td>LG5</td>
<td>LG5</td>
<td>2</td>
</tr>
<tr>
<td>LG6</td>
<td>LG6</td>
<td>1</td>
</tr>
</tbody>
</table>
amplify polymorphic loci. With further development on closely related species where the primer sequences also codominant markers, they should be transportable to orchardgrass-specific SSRs and other markers in the future, traits, and lay a solid foundation for orchardgrass molecular maps.


References


Figure 1. Theoretical and Applied Genetics 111 (1), 135-106.

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