An intervarietal genetic linkage map of Indian bread wheat (Triticum aestivum L.) and QTL maps for some metric traits

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Summary

Bread wheat (Triticum aestivum L.) exhibits very narrow genetic diversity and hence there is high relatedness among cultivated varieties. However, a population generated from an intervarietal cross, with the parents differing in a large number of traits, could lead to the generation of QTL maps which will be useful in practice. In this report a genetic linkage map of wheat is constructed using a cross between two Indian bread wheat varieties: Sonalika and Kalyansona. The linkage map consisted of 236 markers and spanned a distance of 3639 cM, with 1211.2 cM for the A genome, 1669.2 cM for the B genome, 192.4 cM for the D genome and 566.2 cM for unassigned groups. Linkage analysis defined 37 linkage groups of which 24 were assigned to 17 chromosomes. The genetic map was used to identify QTLs by composite internal mapping (CIM) for three metric traits, viz. culm length (CL), flag leaf length (FLL) and flag leaf breadth (FLB). Of 25 QTLs identified in this study, 15 have not been reported previously. Multitrait CIM (MCIM) analysis was carried out for traits that were significantly correlated such as FLB–FLL and CL–FLB–FLL. Detection of a large number of QTLs for the three traits analysed suggests that in parent cultivars that are not too diverse, the differences at genetic level detected as polymorphisms may be mostly associated with QTLs for the observed differences.

1. Introduction

Wheat (Triticum aestivum L.) is a major food crop of the world and the second most important crop in India. It is a segmental allopolyploid containing three distinct but genetically related (homoeologous) genomes: A, B and D. It is a hexaploid containing 42 chromosomes. The haploid DNA content of bread wheat genome is approximately 1.7 × 10^9 bp.

In bread wheat several genetic linkage maps have been published either in the form of separate homoeologous groups, such as groups 1 to 7 (Phillips & Vasil, 2001), or as complete maps (Liu & Tsunewaki, 1991; Gale et al., 1995; Messmer et al., 1999). Owing to the poor levels of polymorphism often encountered in wheat, mapping strategies most often used wide crosses involving either a synthetic wheat and a variety such as Chinese Spring (Gale et al., 1995) or Opata (Nelson et al., 1995a–c) as parents, or crosses between Chinese Spring and Triticum spelta (Liu & Tsunewaki, 1991; Messmer et al., 1999).

The development of genetic maps is a prerequisite for the understanding of QTLs governing complex agronomic traits and their use in plant breeding via marker-assisted selection. The first intervarietal map of bread wheat, based on restriction fragment length polymorphism (RFLP) markers, was published by Cadalen et al. (1997). An updated version of this Chinese Spring–Courtot genetic map was published by Sourdille et al. (2003). More recently three intervarietal maps based on Australian bread wheat varieties were reported by Chalmers et al. (2001) and other intervarietal maps by Paillard et al. (2003), Liu et al. (2005), Quarrie et al. (2005), Suenaga et al. (2005) and Torada et al. (2006). Some of these maps have also been used for QTL analysis (Sourdille et al., 2003; Liu et al., 2005; Quarrie et al., 2005; Suenaga et al., 2005; Semagn et al., 2006).

The major trait governing plant stature is plant height (culm length). Several major genes reducing
plant stature have been identified in wheat. Introduction of genes Rht-B1b (Rht1) and Rht-D1b (Rht2) for reduced height (Peng et al., 1999) into commercial wheat cultivars resulted in the Green Revolution. The other Rht genes in hexaploid wheat include Rht4, Rht5, Rht7 and Rht12.

Leaf size has a positive effect on biomass and yield of plants. In wheat, the flag leaf makes important contribution of photosynthates, particularly during grain filling. Several flag leaf morphogenetic parameters have been identified which contribute to the moisture stress tolerance of wheat. Flag leaf length and flag leaf breadth are components which contribute to photosynthesis. Searching for loci controlling these quantitative traits will be useful as they are of agronomic importance (Lupton, 1987).

The aim of this study was to obtain a genetic linkage map of wheat (Triticum aestivum L.) using a cross between the Indian bread wheat varieties Kalyansona and Sonalika and to obtain a QTL map for three different stages of growth. For this purpose an F2 population derived from Chinese Spring was used. All plants were grown at Trombay under field conditions.

2. Materials and methods

The mapping population consisting of 150 F2 plants was derived from a cross between the varieties Sonalika and Kalyansona (bread wheat: Triticum aestivum L.). A set of nullitetrasomic lines derived from Chinese Spring were used. All plants were grown at Trombay under field conditions.

(i) DNA extraction and estimation

DNA was isolated and quantitated from leaf tissue by a new method of DNA isolation suitable for long-term storage (Nalini et al., 2004).

(ii) Phenotypic data collection

The data on three agronomic traits, viz. culm length (CL), flag leaf length (FLL) and flag leaf breadth (FLB), among 150 F2 individuals were recorded at different stages of growth.

(iii) PCR analysis

All PCR amplifications were carried out on an Eppendorf Mastercycler-Gradient Thermal Cycler.

(a) AP-PCR analysis

PCR amplification was carried out in a volume of 25 µl containing 100 ng of template DNA, 2 mM MgCl2, 25 pmol of primers, 200 µM each of dNTPs and 1 unit of Taq DNA polymerase. The cycling condition was as follows: 1 cycle of 5 min at 94 °C, 5 min at 45 °C and 5 min at 72 °C, and 35 cycles of 1 min at 94 °C, 1 min at 45 °C and 1 min at 72 °C, followed by a final 10 min extension at 72 °C.

(b) RAPD analysis

PCR amplification was carried out in a volume of 25 µl containing 100 ng of template DNA, 2 mM MgCl2, 10 pmol of 10mer primers, 200 µM each of dNTPs and 1 unit of Taq DNA polymerase. The cycling condition was as follows: 1 cycle of 5 min at 94 °C, 5 min at 42 °C and 5 min at 72 °C, and 45 cycles of 1 min at 94 °C, 1 min at 42 °C and 1 min at 72 °C, followed by a final 10 min extension at 72 °C.

(c) ISSR analysis

PCR amplification using a 3’ anchored I SSR primer was carried out in a volume of 25 µl. The reaction mixture contained 100 ng of template DNA, 2 mM MgCl2, 25 pmol of ISSR primer, 200 µM each of dNTPs and 1 unit of Taq DNA polymerase. The cycling condition was as follows: 1 cycle of 5 min at 94 °C, 5 min at 50 °C and 5 min at 72 °C, 45 cycles of 1 min at 94 °C, 1 min at 50 °C and 1 min at 72 °C, followed by a final 10 min incubation at 72 °C.

The PCR products of AP-PCR, RAPD and ISSR were separated by electrophoresis using 1x TBE buffer on a 2% agarose gel. The DNA fragments were stained with ethidium bromide and viewed under ultraviolet light and photographed.

(d) AFLP analysis

The AFLP analysis was carried out essentially by the method described by Vos et al. (1995). Genomic DNA (100 ng) was digested with EcoRI and MseI. Ligations of the EcoRI and MseI adapter sequences, the pre-selective amplifications and the selective amplifications were carried out using the primer pairs E+3′/ M+2 as described previously. Equal amounts of the selective amplification products and formamide loading dye were mixed. The samples were denatured for 3 min at 90 °C, chilled on ice and fragments were separated by electrophoresis on a denaturing 5%
polyacrylamide gel in a vertical cassette. The DNA fragments were stained by the silver staining method.

(e) STMS analysis

PCR amplifications were carried out using 84 STMS primers for the A, B and D genomes of bread wheat, viz. two each on either arm of the seven A, B, D chromosomes (Roder et al., 1998). The PCR reaction mixture (25 μl) contained 10 mM Tris-HCl pH 9.0, 2 mM MgCl₂, 10 pmol of each left and right primer, 200 μM of each dNTP, 1.0 unit of Taq DNA polymerase (Bangalore Genei, India) and 100 ng of template genomic DNA. The cycling condition was as follows: 1 cycle of 3 min at 94 °C and 45 cycles of 1 min at 94 °C, 1 min at 62 °C and 20 s at 72 °C followed by a final 10 min incubation at 72 °C. The PCR products were separated on 2.5% agarose gel and some STMS were analysed on denaturing 5% polyacrylamide gels.

(iv) Extraction and analysis of seed proteins

Total protein was extracted from five seeds each of Sonalika, Kalyansona and F₂ seeds from F₂ plants. High molecular weight (HMW) glutenin subunit and other seed proteins were analysed by SDS-PAGE (Payne & Lawrence, 1983).

(v) Analysis of gene-specific loci

(a) PCR-RFLP of the ITS region

ITS region from 18S-5.8S-26S rRNA was amplified using the primers G₁: 5'-TCCGTAGGTACGCTACTG-3' and C₂: 5'-TCCTCCGCTTTATTGATGTTG-3' as detailed by Saini et al. (2000). An aliquot of the PCR product was digested with a restriction endonuclease (4 units) in a 10 μl reaction mixture according to the manufacturer’s instructions. Digested fragments were separated on a 3% high-resolution agarose gel and then stained with ethidium bromide.

(b) PCR of puroindoline genes

The wild-type allele of pinA (Pina-D1a) was PCR-amplified using the allele-specific primers PinA-D1F-5'-CCCTGTAGAGACAAGCTAA-3' and PinA-D1R-5'-CACCAGTAATAGCCAAATAGTG-3' as described by Gautier et al. (1994).

(c) Rht-B1 and Rht-D1 amplification

The wild-type and mutant alleles of Rht-B1 and Rht-D1 were PCR-amplified using allele-specific primers according to Ellis et al. (2002).

(vi) Nullisomic-tetrasomic analysis

A series of nullisomic-tetrasomic lines of Chinese Spring (CS) (Sears, 1966) was used to physically map 22 AFLP primer combinations.

(vii) Data analysis and linkage mapping

In the case of a dominant marker the polymorphic band positions were scored as ‘0’ or ‘1’ for absence or presence of band, respectively. In the case of a co-dominant marker, the allele from the female parent was scored as ‘1’, the allele from the male parent was scored as ‘2’ and presence of the two alleles together (heterozygotes) was scored as ‘3’. The observed segregation ratios were tested by chi-square analyses (3:1). The linkage analysis was performed using MapMaker v.3.0b (Lander et al., 1987) for the F₂ population. Recombination frequencies were converted to centimorgans (cM) using Kosambi's mapping function (Kosambi, 1944). The linkage groups were constructed using the ‘two-point/group’ command with a LOD threshold of 3.0 and a maximum distance of 50 cM.

(viii) QTL mapping

QTL Cartographer v.2.5 (Wang et al., 2005) was used for QTL analysis. Zmap QTL, Model 6 with a window size of 10 cM, was used for composite internal mapping (CIM) analyses. The number of markers for the background control was set to five. For each trait, a minimum LOD value of 2.5 was used for the identification of putative QTLs. Association of a marker with a QTL was analysed by a two-population t-test. The F₂ population was divided into two groups based on the alleles of a marker closest to a QTL. The trait means of the two groups were subjected to a t-test for significance. QTL effects (R² values), also referred to as phenotypic variation, were obtained from the output file of CIM. Two combinations of the quantitative traits, viz. (1) FLB–FLL, (2) CL–FLB–FLL, were used for joint multitrait CIM (MCIM) using the module JZmapqtl available in QTL Cartographer.

3. Results

(i) Genetic linkage map

A genetic linkage map referred to as an ‘SK’ map consisting of 236 loci with a marker density of 15.4 cM was obtained. The map consisted of 37 linkage groups and spanned 3639 cM, with 1211.2 cM for the A genome, 1669.2 cM for the B genome, 192.4 cM for the D genome and 566.2 cM for unassigned groups. Twenty-four linkage groups were assigned to
Table 1. Number of markers and length of each linkage group

<table>
<thead>
<tr>
<th>Linkage group</th>
<th>Chromosome</th>
<th>No. of markers</th>
<th>Length in cM (Kosambi)</th>
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<tr>
<td>1</td>
<td>1A</td>
<td>04</td>
<td>57.9</td>
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<td>2</td>
<td>1A</td>
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</tr>
<tr>
<td>35</td>
<td>–</td>
<td>12</td>
<td>206.0</td>
</tr>
<tr>
<td>36</td>
<td>–</td>
<td>07</td>
<td>112.2</td>
</tr>
<tr>
<td>37</td>
<td>–</td>
<td>04</td>
<td>31.6</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>–</td>
<td><strong>236</strong></td>
<td><strong>3639</strong></td>
</tr>
</tbody>
</table>

17 chromosomes; however, none were assigned to chromosomes 1D, 2D, 4D and 7D (Table 1). The number of markers mapped was highest in the B genome (97) followed by the A genome (72) and D genome (17) (Fig. 1).

(ii) Segregation distortion

Of the 280 markers analysed, 89 (31%) deviated significantly (\(P<0.05\)) from a 3:1 ratio and this was not specific to any marker type. Of the 89 distorted markers, 74 were mapped and 15 remained unlinked. Thirty-nine mapped markers (53%) showed a segregation distortion in favour of Kalyansona and 35 (47%) in favour of Sonalika, indicating no bias towards a particular parent.

(iii) Frequency distribution, ANOVA and correlation among the traits

The frequency distribution of each of the three traits in the segregating population was found to be different. While FLB showed a normal distribution, FLL showed a distribution skewed towards shorter leaf length. A skewed distribution indicates higher frequency of a phenotype. The skewed distribution could arise due to (a) dominance of the alleles responsible for shorter leaf length, (b) epistatic action of leaf length inhibitor as well as (c) genotype \(\times\) environment interactions. CL showed a double bell-shaped curve distribution. This is due to segregation for the two major semi-dwarfing genes present in the parents, viz. Kalyansona harbours \(Rht-B1b\) while Sonalika harbours the \(Rht-D1b\) gene. In the absence of major dwarfing genes the population would have shown a normal distribution. Further analysis showed that three combinations, viz. CL–FLL, CL–FLB and FLL–FLB, among the three quantitative traits were positively correlated.

(iv) Composite interval mapping (CIM) of QTLs

Twenty-five QTLs with LOD scores above 2.5 spread over seven chromosomes were detected for the three traits (Table 2). Eight QTLs for CL with LOD scores ranging from 2.5 to 4.3 and phenotypic variation (QTL effect, \(R^2\)) ranging from 21.6% to 66.5% were found on chromosomes 2B, 3A, 5A, 6A, 6B, 7B and linkage group 12. Twelve QTLs for FLL with LOD scores ranging from 2.5 to 7.2 and phenotypic variation ranging from 8.2% to 39.0% were found on chromosomes 1B, 2B, 5A, 6A, 6B and 7B. Five QTLs for FLB with LOD scores ranging from 2.5 to 3.3 and phenotypic variation ranging from 10.9% to 34.9% were found on chromosomes 2B, 5A, 6A, and linkage groups 1 and 11.

(v) Multitrait composite interval mapping (MCIM)

Of the various combinations of the quantitative traits that were used for correlation analysis, two combinations, viz. FLB–FLL, CL–FLB–FLL, which showed positive correlation, were chosen for MCIM analysis. The results are described below.

(a) Flag leaf breadth and flag leaf length

The results of MCIM are given in Table 3. Twenty-two QTLs were detected in joint MCIM, of which nine were also detected by CIM.

(b) Culm length, flag leaf breadth and flag leaf length

The results of MCIM are given in Table 4. Forty-three QTLs were detected in joint MCIM, of which
Mapping and QTL identification in bread wheat

Fig. 1.
Fig. 1. Genetic linkage map of bread wheat using an F₂ population derived from a cross between Sonalika and Kalyansona. The name of the chromosome or group is given on the top of individual linkage group. The names of markers are given on the right-hand side and the distance (in centimorgans) between markers on the left-hand side of the linkage groups. The arrows on chromosomes 3A1, 5A4 and 6A indicate the markers E16_M5D, E3_M5B and Xgwm1696A, respectively, which are lying closest to the QTLs for the trait culm length (CL). The arrows on chromosome 5A2 indicate the markers E1_M7G and OPAA07C, which are lying closest to the QTLs for the trait flag leaf length (FLL). The black coloration within the linkage group indicates the QTL at these locations. The STMS markers indicated as ‘MS’ are the ‘Xgwm’ series of STMS described by Roder et al. (1998). The arrows on chromosomes 2B1 and 6B indicate the markers E7_M4H, SS13RA and E2_M7C, respectively, closest to the QTLs for CL. The arrows on chromosomes 1B, 2B1 and 7B indicate the markers E14_M5J, Proi, OPAB18A, VM13RA, and SS26LB, respectively, closest to the QTLs for FLL. The arrow on linkage group 1 indicates the marker E17_M7M closest to the QTL for trait flag leaf breadth (FLB). The arrows on linkage groups 11 and 12 indicate the markers OPAB08A, and E19_M7A closest to the QTLs for traits FLB and CL, respectively.
were also detected by CIM. As an example a representa-
tive QTL Cartographer plot involving chro-
mosome 6B obtained using MCIM involving three
correlated metric traits – trait 1, culm length; trait 2,
leaf breadth; trait 3, leaf length – is shown in Fig. 2.

(vi) Association of molecular markers with
quantitative traits by t-test

Thirty markers that were closest to the QTLs were
analysed further. The means for the trait concerned
were estimated for each of the two-allele classes and
subjected to a t-test. Among five of the markers, the
differences between the allele classes were found to be
significant, indicating that these markers show as-
sociation with the respective traits (Table 2), viz. one
marker associated with CL, two for FLB and two for
FLL.

4. Discussion

The aim of the study was to develop a linkage map
based on varieties which were extensively used in
cultivation and in wheat breeding, with the purpose
of identifying associations between markers and
QTLs. In this study an intervarietal map has been
constructed based on the Indian bread wheat cultivars
Kalyansona and Sonalika. In general, cultivated wheat
varieties exhibit narrow genetic diversity. However,
the two varieties used in this study showed differences
in 10 agronomically important traits and also ex-
hibited considerable DNA polymorphisms. The dif-
ferences at DNA level detected as polymorphisms
were observed to be mostly associated with QTLs for
the observed differences. An F₂ population was used
as it is available earlier and expected to be unbiased.

(i) Genetic linkage map

The length of the SK map (3639 cM) is comparable
with reported wheat maps lengths such as the
Courtot × Chinese Spring intervarietal map (3685 cM;
Sourdille et al., 2003) and the Cranbrook × Halberd
intervarietal map (4110 cM; Chalmers et al., 2001),
and is less than the Synthetic W7984 × Opata 85
(ITMI) map (> 5000 cM; for review see Langridge

Table 2. Composite interval mapping (CIM) for three quantitative traits

| Sr. no. | Trait and 
| linkage group | LOD score | QTL position 
| and interval (cM) | Closest marker | QTL effect 
| | | | (R²%) |
|---|---|---|---|---|---|
| Culm length (CL) | | | | |
| 1 | 2B1 | 3.3 | 76.7 (18) | E7_M4H (18) | 40.5 |
| 2 | 3A1 | 4.3 | 205.7 (24) | E16_M5D (20) | 65.3 |
| 3 | 5A4 | 3.1 | 120.0 (24) | E3_M5B (5-6) | 46.8 |
| 4 | 6A | 3.7 | 40.0 (30) | Xgwm1696A (40) | 66.5 |
| 5 | 6B | 4.3 | 30.0 (56) | SS13RA (30) | 21.6 |
| 6 | 6B | 3.2 | 156.2 (40) | E2_M7C (8) | 30.2 |
| 7 | 7B | 2.5 | 22.4 (36) | E17_M7A* (4) | 21.6 |
| 8 | Linkg12 | 3.3 | 99.6 (28) | E19_M7A (26) | 59.2 |
| Flag leaf breadth (FLB) | | | | |
| 1 | 2B1 | 2.7 | 56.3 (14) | SSR112B (12) | 11.7 |
| 2 | 5A3 | 2.6 | 24.4 (28) | Xgwm3045A* (6) | 10.9 |
| 3 | 6A | 2.5 | 77.1 (8) | E18_M7G* (0-1) | 20.9 |
| 4 | Linkg1 | 3.1 | 19.6 (6) | E17_M7M (6) | 34.9 |
| 5 | Linkg11 | 3.3 | 8.0 (24) | OPAB08A (8) | 14.4 |
| Flag leaf length (FLL) | | | | |
| 1 | 1B | 3.9 | 372.7 (12) | E14_M5F** (4) | 20.7 |
| 2 | 1B | 3.9 | 90.1 (40) | Prot (30) | 32.9 |
| 3 | 1B | 3.3 | 181.5 (19) | OPAB18A (0) | 8.2 |
| 4 | 2B1 | 7.2 | 104.0 (17) | VM13RA (8) | 26.5 |
| 5 | 5A1 | 2.9 | 12.3 (6) | CT2D* (0) | 8.5 |
| 6 | 5A2 | 5.1 | 16.0 (16) | E1_M7G (16) | 34.8 |
| 7 | 5A2 | 5.5 | 178.3 (19) | OPAA07C (12) | 29.4 |
| 8 | 5A3 | 2.5 | 6.0 (18) | E17_M7J (6) | 11.3 |
| 9 | 6A | 2.7 | 59.5 (16) | E18_M7F (0) | 39.0 |
| 10 | 6B | 2.6 | 81.3 (37) | Xgwm6446B (18) | 22.6 |
| 11 | 6B | 2.9 | 427.8 (41) | E7_M4G (30) | 8.9 |
| 12 | 7B | 3.4 | 45.6 (13) | SS26LB (0) | 11.6 |

*, ** Means for marker allele classes, which differed significantly at \( P<0.05 \) and \( 0.01 \) respectively. The markers associated
with the traits are shown in bold.

a Intervals in cM were obtained by marking positions \( \pm 1 \) LOD from the peak.

b Values in parentheses are the distances (cM) of the marker from the peak.

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et al., 2001). The number of markers in the ITMI map is 1065, while it is 659 in the Courtotr Chinese Spring map and 902 in the Cranbrookr Halberd map. The mean interval between two markers on the ITMI map is 5.8 cM, while on the Courtotr Chinese Spring intervarietal map it is 5.6 cM and on the Cranbrookr Halberd map it is 4.5 cM and on the SK map it is 15.4 cM. The large difference in the marker frequency could be attributed to the number of markers on the map.

In the SK map, maximum number and proportion of markers were mapped onto the B genome (97, 41%), followed by the A genome (72, 31%) and then the D genome (17, 7%). Chromosomes 1D, 2D, 4D and 7D were not represented at all. A low level of polymorphism in the D genome observed is in agreement with the reports available in the literature and with the hypothesis suggesting a recent and monophyletic introduction of the D genome in bread wheat (Lagudah et al., 1991). The higher proportions of markers placed on the chromosomes 1B, 6B and 5A indicated that the two parents could be carrying more variations in these chromosomes than the rest.

The lengths of chromosomes 3A, 2B, 5B, 6B, 7B and 3D in the SK map are comparable to the sizes reported by others. The lengths of chromosomes 1A, 2A, 4A, 6A, 7A, 5D, 6D, 3B and 4B in the SK map are shorter than the lengths reported in the ITMI genetic linkage map. This could be due to the lower number of markers in the map. In contrast, the lengths of chromosomes 5A and 1B in the SK map are longer than the lengths reported in previous maps. Apparently addition of more markers was not the only
reason for the increase in the length of chromosomes 5A and 1B, because for chromosome 6B, which had a similar number of markers to 5A and 1B, the chromosome length was comparable to that reported in the literature. The majority of the markers on chromosomes 5A and 1B were AFLP markers, and this may have led to map stretching. To test the effect of the type of marker on chromosome length, the lengths of chromosomes 1B and 5A were estimated using two modifications: (1) selectively withdrawing AFLP markers located on these chromosomes and (2) withdrawing non-AFLP markers. The results showed that withdrawal of AFLP markers resulted in a larger change in chromosome length (Table 5, chromosome 1B, rows 2–6) while withdrawal of non-AFLP markers resulted in a smaller change in length (Table 5, chromosome 1B, rows 7–9). It was also observed that withdrawal of AFLP markers resulted not only in compression at the interval per se but also all over the chromosome (Table 5). For example, when AFLP marker E6_M4A from chromosome 1B was removed the compression at the interval per se was only 7 cM but the overall length of the chromosome reduced by 20 cM. Similar results were found for other chromosomes including chromosome 6B. Stretching of linkage maps with the incorporation of AFLP markers in the map along with other markers such as RAPD, ISSR and SSR has been shown previously in several studies on cereals (Becker et al., 1995; Maheswaran et al., 1997; Castiglioni et al., 1999; Lotti et al., 2000; Saal & Wricke, 2002). The stretching of the map in the case of durum wheat (Lotti et al., 2000), barley (Becker et al., 1995) and rice (Maheswaran et al., 1997) was 52.5%, 70.9% and 68.9%, respectively. Map stretching could occur due to the addition of map distances as new markers are discovered and also due to differences in methods used in the construction of an existing map and the new data being superimposed. In the present case the methods used for the earlier mapping and the superimposed markers were same; therefore the increase in map distances could be due to addition. Genetic distances are subject to modification as new loci are discovered between the existing ones.

The distortion in segregation ratios for the markers observed (31%) in the SK map is comparable to the segregation distortion reported by others in wheat (27%, Cadalen et al., 1997; 35%, Messmer et al., 1999). Segregation distortion is reported among F$_2$ progenies of wheat (Liu & Tsunewaki, 1991). The segregation distortion in the SK map was not biased towards a particular marker type; also, when all markers were considered together, the segregation distortion was not found to be biased towards any parental allele. The segregation distortion observed could be (a) due to the polymorphic band being amplified from more than one loci or (b) the phenotypes associated with the marker may influence selection towards a particular allele. Segregation distortion is also reported among F$_2$ progenies in other plants such as rice (McCouch et al., 1988), lettuce (Landry et al., 1987) and tomato (Helentjaris et al., 1986).
Marker order and distances of some regions on the SK map and the reported maps were found to be comparable. Specific gene/loci markers such as Rht-B1b, Glu-B1 loci and the Nor-B1 locus along with the STMS loci allowed the comparison of two different intervals on the SK map with microsatellite (Roder et al., 1998) and consensus genetic (Somers et al., 2004) maps. The distance between Rht-B1 and the microsatellite marker Xgwm368-4B on chromosome 4B in the SK map was 9.2 cM, which is similar to the reported distance of 9.0 cM (Roder et al., 1998).

The reported distance between Glu-B1 and the Nor-B1 loci on chromosome 1B (22 cM) (Payne et al., 1984; Ellis et al., 2002; Ram et al., 2002) is shorter than the distance estimated in this study (29 cM). This could be due to addition of a marker between the two loci and/or the computational method used.

(ii) QTL mapping

In recent years the availability of DNA markers and powerful biometric analytical tools has led to considerable progress in QTL mapping in plants. There are several types of experimental designs for QTL analysis and the choice of method depends on the mating system of the crop species. Most QTL analyses in plants involve populations derived from pure lines and use several approaches to associate QTLs with molecular markers. In this study an F_2 population was used to detect the loci significantly contributing to the traits of interest.

The SK map was used for QTL analysis of three metric traits that differed between the parents. We used CIM and MCIM, which are often recommended for power and precision of QTL analysis. CIM and MCIM have been used recently in bread wheat (Kulwal et al., 2003; Campbell et al., 2003; Marza et al., 2006). CIM is an extension of simple interval mapping (SIM) that considers both the markers flanking the QTL and background markers, which could be or need not be linked to the QTL. CIM is said to give more power and precision in the detection of QTLs than SIM. CIM has been used in QTL mapping in wheat (Shah et al., 1999; Campbell et al., 2003; Kulwal et al., 2003). One of the most important advantages of CIM is that the markers can be used as boundary conditions to narrow down the most likely QTL position. The resolution of QTL locations can be greatly increased.

(a) Culm length (CL)

Culm length (or plant height) is an important trait that contributes to the plant’s stature. Classical genetic studies have shown that genetic control of CL in bread wheat is complex, and most chromosomes harbour factors (loci) that can affect it (Law et al., 1973). To date 21 loci with major effect on plant height have been identified (Worland et al., 1998). The two most common semi-dwarfing genes, Rht-B1b and Rht-D1b, are present on the short arms of chromosomes 4B and 4D (Ellis et al., 2002), respectively, and are gibberellic acid (GA)-insensitive. Both Sonalika and Kalyansona are semi-dwarf genotypes, and harbour Rht-D1b and Rht-B1b, respectively. Of the eight QTLs that were detected for CL in this study, the QTL on chromosome 6A showed the highest phenotypic variation (66.5%). The QTL with the highest LOD score of 4.3 and a phenotypic variation of 65.3% was on chromosome 3A1 with E16_M5D as the closest marker. The STMS marker Xgwm169-6A is closest to the QTL for plant height on chromosome 6A. Since genes for plant height are known to be present on chromosome 6A, this STMS marker could be linked to one of these genes.

In addition to Rht-B1b and Rht-D1b, a large number of QTLs for CL have been reported by many workers (Table 6). Two major QTLs on chromosome 6B, with LOD scores of 3.2 and 4.3, have been observed in this study. A QTL for CL on chromosome 6B has not
been reported, although previous cytogenetic studies have indicated that a gene for plant height is also present on chromosome 6B (Goud & Sridevi, 1988). The two parents Sonalika (average CL = 57.75 ± 1.6 cm) and Kalyansona (average CL = 49.3 ± 2.34 cm) are semi-dwarf genotypes. The phenotype exhibited is contributed to by the eight QTLs in addition to the two dwarfing genes.

(b) Flag leaf length (FLL) and flag leaf breadth (FLB)

FLL and FLB determine area, which is an important trait. QTLs for leaf breadth reported in the literature are listed in Table 6. Monosomic analysis has shown that chromosomes 1A, 2A, 3A, 3B, 4B, 6D and 7D affect FLB (Iqbal & Vahidy, 1992). Among the five QTLs identified for FLB in this study, the QTL with the highest phenotypic variation (34.9%) is present on unassigned linkage group 1. STMS marker Xgwm3045A was lying closest to the QTL on 5A showing a phenotypic variation of 10.9%. A QTL on chromosome 5A with a phenotypic variation of 14.9% has been reported by Keller et al. (1999). QTLs for FLB on chromosome 2B have not been reported previously.

Monosomic analysis of FLL in bread wheat had indicated that chromosomes 1A, 2A, 5A, 6A, 2B, 3B, 4B, 5B and 6D affected FLL (Iqbal & Vahidy, 1992). Of the 12 QTLs for FLL identified in this study, those on chromosomes 5A, 6A and 2B were also identified by monosomic analysis and the one exhibiting maximum phenotypic variation (39%) was on chromosome 6A.

(c) General observation

For CL and FLL, often, more than one QTL for the same trait was identified on a chromosome. However, more than one QTL within the same interval, if present, cannot be identified since CIM does not have the power to resolve such linked QTLs. Among QTLs for a trait located on the same chromosome, two QTLs for CL were located on 6B and three QTLs for FLL were located on 1B, two on chromosome 5A2 and two on chromosome 6B. Such QTLs on the same chromosome were not linked. In all cases QTLs on the same chromosome were separated by long genetic distances ranging from 13 to 280 cM, thus suggesting absence of close linkage or no linkage between the QTLs.

(iii) Multitrait composite interval mapping (MCIM)

MCIM has been used recently as a means of improving the power and precision of QTL detection for correlated traits, as information on the traits acts like repeated measurements. Using MCIM, loci showing pleiotropy on the traits CL, FLB and FLL were analysed.

(a) Flag leaf breadth – flag leaf length

The traits FLB and FLL showed significant positive correlation ($r = 0.53; P < 0.01$), indicating that there could be some loci affecting both the traits. Of the 22 QTLs detected by joint MCIM, the nine QTLs which were also detected by CIM in addition to joint MCIM are the QTLs which influences both the traits in the combination. Of these nine, the QTL on chromosome 7B was also detected for CL. Two of these nine QTLs located on chromosomes 1B and 5A1 were the same as those for which the corresponding molecular markers showed significant association with the traits in question (see later).

(b) Culm length – flag leaf breadth – flag leaf length

Positive correlation was observed between CL and FLL ($r = 0.22; P < 0.05$) and between CL and FLL

<table>
<thead>
<tr>
<th>Name of trait</th>
<th>QTLs detected in the present study</th>
<th>QTLs reported in literature</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Culm length (CL)</td>
<td>2B1, 3A1, 5A4, 6A, 6B, 7B, Linkg12</td>
<td>4BS, 4DS, 6A 7AL, 7BL</td>
<td>Cadalen et al. (1998)</td>
</tr>
<tr>
<td>Flag leaf breadth (FLB)</td>
<td>2B1, 5A3, 6A, Linkg1, Linkg11</td>
<td>1A, 1B, 2A, 3B, 5A, 5B, 6A</td>
<td>Borner et al. (2002)</td>
</tr>
<tr>
<td>Flag leaf length (FLL)</td>
<td>1B, 2B1, 5A1, 5A2, 5A3, 6A, 6B, 7B</td>
<td>1A, 2A, 3A, 3B, 4B, 6D, 7D</td>
<td>Keller et al. (1999)</td>
</tr>
</tbody>
</table>

QTLs in bold are detected in this study.
(r = 0.22; P < 0.05), indicating that there could be some loci influencing all three traits. MCIM analysis on FLB, FLL and CL detected a few more QTLs in addition to the ones detected by MCIM analysis on FLB and FLL. In addition to MCIM analysis on FLB and FLL, additional QTLs were detected when all three traits were analysed together for multitrait analyses. Seven QTLs located on chromosomes 3A1, 3B, 5A4, 6B, 7B and linkage group 12 were detected exclusively for CL by CIM but were also detected by joint MCIM for all three traits. Joint MCIM detected more QTLs jointly affecting CL, FLL and FLB than the QTLs jointly affecting only FLL and FLB. Of the 43 QTLs detected by joint MCIM, 17 which were also detected by CIM in addition to joint MCIM were the QTLs which influence both the traits in the combination. Three of the 17 QTLs located on chromosomes 1B, 3A2 and 7B are the same as those for which the corresponding molecular markers showed significant association with the traits in question (see later).

In both the above MCIM analyses the LOD scores for the common QTLs were higher in MCIM than in CIM. This shows that the level of confidence in MCIM for QTL detection is higher even than for CIM. The repeated finding of a QTL by two methods such as CIM and MCIM confirms the QTL only in the available data. However, a separate set of data would be needed to confirm the presence of a QTL. A similar finding has been reported by Kulwal et al. (2003), although with a different combination of traits. The QTLs detected by joint MCIM could suggest pleiotropy as the possible cause of correlation among the correlated traits. This inference may be taken into account while designing experiments involving molecular MAS aimed at improving more than one trait simultaneously.

(iv) Markers associated with quantitative traits

The significance of marker–trait association was analysed by t-test to check their usefulness in MAS and in detecting probable false QTLs. For instance OPAB18A (FLL) and SS26LB (FLL) were coincident with the QTL positions but did not show a significant association with the trait. It was noticed (Table 2) that the marker–trait association was not always correlated either with the distance of the marker from the QTL position or with the size of confidence interval. Also, no significant correlation between marker–trait associations and the magnitude of the LOD score was detected, in contrast to that reported by Kulwal et al. (2003). Markers having lower LOD values but showing association could be due to a lower confidence interval and the marker being very close to the QTL position. A few markers with LOD values higher than 3.9 did not show association with the trait in question. This could be due to the lower contribution to phenotypic variation or the larger distance between the marker and the QTL position or larger confidence interval. Of the five marker–trait associations found, four were also detected by MCIM for the trait(s) in question and these markers could prove to be useful in MAS.

5. Conclusions

An intervarietal genetic linkage map based on a cross between the two wheat Indian varieties Sonalika and Kalyansona was developed. These two varieties have served as the starting material for many of the later-developed cultivars and hence the markers thus obtained would be useful for future breeding programmes involving parents related to the two varieties. Several QTLs were detected for three quantitative traits, of which 15 have not been reported previously. Cultivated Indian bread wheat varieties have narrow diversity; however, we found many agronomically important traits which differed among Kalyansona and Sonalika and also sufficient polymorphisms at the DNA level. The four markers that showed association with quantitative traits could be useful in MAS.

Although genetic maps of wheat have been developed previously, many of which using the ITI populations, there is a need to develop maps for specific populations for actual use. The Indian cultivars, for example, are spring wheats many of which carry cytogenetic variations. Also varieties adapted to certain agroclimatic conditions could carry variations. Hence an independent map based on Indian wheat varieties will thus be more useful.

References


