

SESSION III: BREEDING AND UTILIZATION OF GENETIC RESOURCES

POSTER PRESENTATION

QTL Analyses for Three Grain Quality Traits in Bread Wheat Using Intervarietal Mapping Populations

H. S. BALYAN, P. K. GUPTA, P. L. KULWAL and N. KUMAR

*Molecular Biology Laboratory, Department of Genetics & Plant Breeding, Ch. Charan Singh
University, Meerut-250 004 (UP), India, e-mail: hsbalyan@rediffmail.com*

Abstract: QTL analysis in bread wheat for three grain quality traits, namely grain protein content (GPC), pre-harvest sprouting tolerance (PHST) and grain weight (GW) has been conducted by us utilizing four intervarietal mapping populations, two each for GPC and PHST and one for GW. The approaches used included simple regression analysis (SMA), simple interval mapping (SIM), composite interval mapping (CIM), and an analysis involving detection of epistatic QTLs (E-QTLs) using QTLMapper. A large number of QTLs were detected in each case, and markers were developed which may prove useful in marker-assisted selection (MAS). An important result of this investigation is that for some quantitative traits like GPC, the major part of the genetic variation is due to E-QTLs and the $Q \times E$ interactions, and that the main effects contributed very little to the genetic variation. In contrast to GPC, PHST was controlled mainly by main effect QTLs and E-QTLs. For more detailed studies, one chromosome (3A) carrying a major QTL was selected for PHST and three chromosomes (1A, 2B, 7A) were selected for GW. A major, new, definitive and stable QTL (*QPhs.ccsu-3A.1*) for PHST that is independent of red-grain colour was detected on 3AL at a distance of ~183 cM from centromere. This QTL explained 24.68% to 35.21% variation in individual environments and 78.03% variation in pooled environment. For GW, one QTL each was identified on 1AS (*QGw.ccsu-1A.1*), 2BS (*QGw.ccsu-2B.1*) and 7AS (*QGw.ccsu-7A.1*). The variation explained by these individual QTLs in GW in different environments ranged from 9.0% to 19.85%. These studies should prove useful in QTL cloning and wheat improvement through marker aided selection (MAS).

Keywords: QTL analysis; grain quality traits; grain protein content; pre-harvest sprouting tolerance; grain weight; mapping populations; bread wheat

In the majority of QTL studies on bread wheat involving different traits, QTLs only having main effects were detected leaving out many QTLs, which do not have any main effect but are involved in interaction among themselves (QQ epistasis) or with the

environment (QE/QQE). In the present study, QTL analyses for grain protein content (GPC), pre-harvest sprouting tolerance (PHST) and grain weight (GW) were conducted following single-locus (including SMA, SIM and CIM) and two-locus analyses.

MATERIALS AND METHODS

Mapping populations and their evaluation. Among the four mapping populations (PI to PIV), PI was evaluated in five environments, PII was evaluated in four environments and PIII and IV were each evaluated in six environments. The environments were created using years and locations and the data were recorded on the respective traits (Table 1).

Molecular maps. For QTL analyses, whole genome maps were used for PI and PII (PRASAD *et al.* 2003; KULWAL *et al.* 2004, 2005) and partial maps were used for PIII (chromosome 3A) and PIV (chromosomes 1A, 2B, and 7A).

QTL analyses. Single-locus QTL analyses: Single-locus QTL analysis for main-effect QTLs (M-QTLs) was performed using QTL Cartographer (BASTEN *et al.* 2002). In PI, M-QTLs for GPC were detected following SMA, SIM and CIM. In the remaining three populations, M-QTLs for different traits were detected following only CIM. QTLs detected at LOD scores 2.5 were considered as suggestive while QTLs detected above threshold LOD scores were considered as definitive QTLs (DOERGE & CHURCHILL 1996).

Two-locus QTL analysis: Two-locus analysis was conducted for GPC (PI & II) and PHST (PII) using QTLMapper Version 2.0 (WANG *et al.* 1999). This led to detection of main effect QTL (M-QTLs), epistatic QTLs (QQ/E-QTLs) and QTLs interacting with environments (QE/QQE).

RESULTS AND DISCUSSION

QTL analyses for GPC

Single-locus QTL analysis. For GPC, a total of 13 M-QTLs (following SMA, SIM and CIM) in PI and seven M-QTLs (following CIM) in PII were detected (PRASAD *et al.* 2003; KULWAL *et al.* 2005). Out of these M-QTLs, seven QTLs in PI and three QTLs in PII were definitive and the remaining QTLs were only suggestive.

Two-locus QTL analysis. A total of 26 QTLs for GPC were detected in the two populations

(14 in PI and 12 in PII) using two-locus analysis. These QTLs included M-QTLs, E-QTLs, and QTLs involved in QE and QQE interactions. However, none of the individual QTL was detected in both the populations. Further, five M-QTLs each in PI and PII accounted for a mere 7.24% and 7.22% of the phenotypic variation (PV), respectively.

In PI, two digenic QQ epistatic interactions (involving four E-QTLs), and in PII, three digenic QQ epistatic interactions (involving six E-QTLs) accounted for 2.68% (PI) and 6.04% (PII) PV. In PI, each of the two epistatic combinations and in PII only one epistatic combination exhibited QQE interactions. However, none of the E-QTLs involved in digenic epistatic interactions were individually involved in significant QE interaction. In PI, out of eight QTLs, which were involved in significant QE, three QTLs each had neither any main effect nor any epistatic effect. The remaining five QTLs exhibiting QE interactions were M-QTLs. In PII, only one QTL was involved in QE interaction and this was an M-QTL. All QE interactions together accounted for 24.24% (PI) to 21.19% (PII) PV.

Substantial QQE interactions (26.80% PV) were also noticed in PII, although in PI these interactions were rather minimal (1.67% PV). Three QQEs involving six QTLs (including two M-QTLs) were identified in PII, but only one of these interactions had significant additive (QQ) epistatic effect. In PI, although the four QQE interactions accounted for a mere 1.67% PV, two of them had significant QQ epistatic interactions. Taken together, the results indicated that a substantial proportion (25.91% in PI and 47.99% in PII) of PV is contributed by QE and QQE interactions.

QTL analyses for PHST

Single-locus QTL analysis: Following CIM, five M-QTLs for PHST were identified in PII (KULWAL *et al.* 2004). Three of these QTLs were identified each in more than one environment, but none of them could be detected in all the four environments. Two of the above five QTLs were definitive.

Table 1. Details of mapping populations and the traits studied

RIL mapping population	Trait studied	Reference
GPC population (Population I = PI)	GPC	PRASAD <i>et al.</i> (2003)
ITM _I pop (Population II = PII)	GPC & PHST	KULWAL <i>et al.</i> (2004, 2005)
PHST population (Population III = PIII)	PHST	KULWAL <i>et al.</i> (2005b)
GW Population (Population IV = PIV)	GW	Unpublished

A similar analysis in PIII detected a major QTL (*QPhs.ccsu-3A.1*) on 3AL (~183 cM from centromere) explaining 24.68% to 35.21% variation in individual environments and 78.03% variation in pooled environment (KULWAL *et al.* 2005a).

Two-locus QTL analysis: Following two-locus analysis, 14 PHST QTLs including M-QTLs, E-QTLs and QTLs involved in QE and QQE interactions were resolved. Eight M-QTLs together accounted for 47.95% PV. Five of these eight QTLs were also involved in QQ interactions, and two QTLs were involved in QQE interactions; none of the eight M-QTLs showed significant QE interaction with any of the environments. In contrast, one QTL (*QPhs.ccsu-5D.1*) had neither any main effect nor any epistatic effect, but was involved in QE interaction. Eight E-QTLs (including five of the above M-QTLs) were involved in four QQ interactions and accounted for 28.73% of PV. None of these four epistatic combinations exhibited QQE interaction. Four QTLs were involved in two interactions and accounted for 3.24% of PV. Two QTLs that were detected in more than one environment at LOD scores above the threshold values were located on 3BL and 3DL presumably in the vicinity of the dormancy gene *TaVp1*. Another QTL on 3B was perhaps located in close proximity of *R* gene for red grain colour.

QTL analysis for GW

Single-locus QTL analysis following CIM in PIV identified three QTLs for GW. Two of the three QTLs (*QGw.ccsu-2B.1* and the *QGw.ccsu-7A.1*) were definitive and were detected in at least four different environments and also in the pooled environment. The individual QTLs explained 9.06% to 19.85% PV.

CONCLUSIONS

(i) Besides M-QTLs, QTLs having no main effects but involved in QQ and QQE interactions also contribute to the total variation of a trait. Hence, ignoring these QTLs will cause bias in the QTL analysis. (ii) Nature of QTLs differs from trait to trait. (iii) Results for GPC suggest that often more than one mapping population should be used for QTL analysis in order to detect as many QTLs as possible. (iv) QTLs with major effect such as that for PHST on 3AL (*QPhs.ccsu-3A.1*) are candidates for QTL cloning.

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