

QTL MAPPING FOR GRAIN AND YIELD RELATED TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT:

An F₂ mapping population derived from two contrasting bread wheat parents, PHS 1107 (low tillering) and Lok 1 (high tillering) was evaluated to identify genomic regions controlling tiller number and yield related traits using SSR markers. Among 133 SSK markers screened, 29 markers showed polymorphism and were used for genotyping 70 F₂ plants. All markers segregated according to the expected Mendelian ratio (1:2:1) indicating suitability for linkage analysis. A genetic linkage map comprising seven linkage groups was constructed using covering a total map length of 394.04 cM, with linkage groups ranging from 36.83 cM (LG7) to 80.86 cM (LG6). QTL analysis based on phenotypic data of F₂ lines identified six QTLs associated with important agronomic traits. A major QTL for tiller number per plant, qNTPP 4-1 was detected on linkage group 4 between markers Xgwm194 and Xcfd71 with a LOD score of 15.87 explaining 68.26% phenotypic variation. Two QTLs for plant height qPH-4-1 and qPH-6-1 explained 17.70% and 27.09% variation, respectively. A major QTL for 1000 grain weight, qTGW-5-1 was identified on linkage group 5 with 42.20% phenotypic variation. One QTL for grain yield per plant, qGYPP-1-1 was mapped on linkage group 1 explaining 32.64% variation. Another major QTL, QNGPS-4-1, controlling grains per spike, was located on linkage group 4 with 66.66% variation. Linkage group 4 emerged as an important genomic region harboring multiple yield related QTLs. The Identified marker-trait associations provide useful tools for marker-assisted selection and pyramiding of favorable alleles to develop high-yielding, well-adapted wheat cultivars with improved tillering ability, grain weight, plant architecture, and yield stability.

KEYWORDS: Bread wheat, Linkage and QTL mapping

INTRODUCTION:

Wheat (*Triticum* spp.) is one of the most important cereal crops in the world and serves as a staple food for a large proportion of the global population. Among cereals, wheat is an important cereal crop because of its wide adaptability, high yield potential, nutritional importance, and prominent role in international grain trade. It is cultivated across diverse agro-climatic regions ranging from temperate to subtropical environments under both irrigated and rainfed conditions. Wheat contributes nearly 20 per cent of the total dietary calories and protein consumed worldwide, making it indispensable for global food and nutritional security. According to the Food and Agriculture Organization, global wheat production in recent years has exceeded 780 million tonnes from about 220 million hectares, highlighting its strategic importance in world agriculture (FAOSTAT, 2024). Among the cultivated wheat species, bread wheat (*Triticum aestivum* (L.) em, Thell.) is the most dominant and economically important species, occupying nearly 90-95 per cent of the total wheat-growing area. Its hexaploidy nature and broad genetic adaptability have enabled its successful cultivation under a wide range of environmental conditions. India is the second largest producer of wheat in the world after China. During 2024-25, wheat was cultivated on approximately 32 million hectares with production exceeding 112 million tonnes and an average productivity of around 3.5 t ha (Ministry of Agriculture & Farmers Welfare, Government of India, 2025). Major wheat producing states include Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, and Rajasthan. Despite remarkable progress in wheat improvement, productivity is frequently constrained by abiotic stresses (Kumar et al., 2023) particularly terminal heat stress in South Asian environments. Delayed sowing due to the late harvesting of preceding rice crops often exposes wheat plants to high temperatures during anthesis and grain tilling stages, resulting in forced maturity, reduced grain weight, poor grain quality and substantial yield losses. Therefore, the development of high-yielding and heat-tolerant wheat genotypes has become a major breeding priority.

Grain yield in wheat is a complex quantitative trait governed by several component characters such as days to heading, plant height, tiller number, spike length, grains per spike, thousand-grain weight, and biomass. These traits are controlled by multiple genes and are strongly influenced by environmental factors (Kumar et al., 2020), making direct phenotypic selection less efficient. The advent of molecular marker technologies has greatly improved the precision of wheat breeding by enabling the identification of genomic regions associated

with important agronomic traits (Choudhary et al., 2022). Among different marker systems, simple sequence repeat (SSR) markers have been widely used in wheat because they are co-dominant, highly polymorphic, reproducible, chromosome-specific, and evenly distributed throughout the genome. Several studies have reported linkage maps and quantitative trait loci (QTLs) associated with grain yield, earliness, plant height, and stress tolerance in bread wheat (Manjunatha et al., 2020, Choudhary et al., 2024). QTL mapping provides valuable information on the number, position, and effects of loci controlling quantitative traits, thereby facilitating marker-assisted selection. However, many previously identified QTLs were population-specific or environment dependent, and limited information is available on the genetic architecture of yield-related traits under late-sown and heat-stressed Indian conditions using adapted parental material. Further validation of SSR markers linked with stable QTLs is essential before their effective deployment in breeding programmes. In view of the above facts, the present investigation was undertaken to dissect the genetic basis of grain yield and its component traits in bread wheat using molecular markers and segregating populations. The objectives of the study were to identify polymorphic SSR markers between the parental lines and their segregating population, to construct a genetic linkage map in bread wheat using molecular markers, to estimate the extent of genetic variation for grain yield and its component traits in F₂ lines, to identify and map quantitative trait loci (QTLs) associated with bio fortification (Sharma et al., 2024) and important agronomic characters, and to determine the contribution of individual QTLs for their utilization in marker-assisted breeding programmes.

MATERIALS AND METHODS

Experimental site and material

The present investigation entitled "QTL mapping for grain and yield related traits in bread wheat (*Triticum aestivum* L.)" was conducted at Junagadh Agricultural University. Field experiments were carried out at the Wheat Research Station, while molecular studies were undertaken in the Biotechnology Laboratory, Department of Genetics and Plant Breeding, College of Agriculture, JAU, Junagadh. Geographically, Junagadh is located at 21.5° N latitude and 70.5° E longitude with an altitude of about 60 m above mean sea level. The soil of the experimental site was medium black, alluvial in origin, and medium in organic matter content. The experimental material consisted of two diverse bread wheat genotypes, namely Lok 1 and PHS 1107, obtained from the Wheat Research Station, JAU, Junagadh. Lok 1 is a widely adapted variety suitable for timely and late-sown irrigated conditions, whereas PHS 1107 is an early-sown irrigated genotype.

The cross PHS 1107 × Lok 1 was made during Rabi 2013-14. The F_i seeds were grown during Rabi 2014-15, and seeds harvested in bulk were advanced to the F₂ generation during Rabi 2015-16. Subsequently, F₂s families were raised during Rabi 2016-17 for phenotypic evaluation and molecular analysis.

Phenotypic Evaluation

The F₂s families were evaluated at the Wheat Research Station, J.A.U., Junagadh in three replications following a Randomized Block Design (RBD). Each experimental unit consisted of a single row of 3.0 m length, with a spacing of 22.5 cm between rows and 5.0 cm between plants. Recommended agronomic practices and crop management measures were followed throughout the crop season.

Observations were recorded on important agronomic and yield-contributing traits including throughout the crop season. Observations were recorded on important agronomic and yield-contributing traits including days to first heading, plant height, tiller number per plant, spike length, grains per spike, thousand-grain weight, grain yield per plant, and other related characters. In the F₂s population, days to first heading were recorded on an individual plant basis.

Genotyping

Genotyping was carried out in the Biotechnology Laboratory, Department of Genetics and Plant Breeding, College of Agriculture, J.A.U., Junagadh using Simple Sequence Repeat (SSR) markers. Standard laboratory glassware and plasticware of reputed make were used after proper cleaning and sterilization. Analytical and molecular grade chemicals were used throughout the study. Genomic DNA was extracted from fresh young leaf samples of the parents and segregating individuals by the CTAB method as described by Doyle and Doyle (1987) with minor modifications. A pre-warmed 2x CTAB extraction buffer containing CTAB, Tris-HCL, EDTA, NaCL, PVP, and B-mercaptoethanol was used for DNA isolation. DNA was purified using chloroform: isoamyl alcohol extraction followed by precipitation with isopropanol and ethanol washing. The purified DNA was dissolved in TE buffer and treated with RNase to remove RNA contamination. The quality and quantity of extracted DNA were determined using a NanoDrop Spectrophotometer. DNA purity was assessed through the A₂₆₀/A₂₈₀ ratio, and concentration was measured in ng µl. The DNA samples were diluted and standardized to 50 ng µl for PCR amplification.

SSR Marker Analysis

A total of 133 SSR primers, procured from Integrated DNA Technologies, were screened for parental polymorphism between Lok 1 and PHS 1107. Out of these, 29 SSR markers (21.80%) showed clear polymorphism between the two parents and were used for further genotyping of the mapping population. PCR amplification was carried out in a thermal cycler using standard reaction conditions. Amplified products were separated through agarose gel electrophoresis in TBE buffer, stained with ethidium bromide, and visualized under a gel documentation system. Marker data were scored based on the presence or absence of bands.

Linkage Map Construction and QTL Analysis

The polymorphic SSR marker data generated from the segregating population were used for construction of a genetic linkage map and QTL analysis using QTL IciMapping version 4.0 (Meng et al., 2015). Linkage group construction involved three major steps, namely grouping, ordering, and rippling. Markers were grouped at a minimum LOD score of 3.0, recombination frequency of 0.30, and window size of 5 cM. Additional markers were incorporated using the "try" and "move to" functions, and the final linkage map was generated based on SSR markers. For QTL mapping, phenotypic data of the F_s population along with marker genotypic data were analyzed using the Inclusive Composite Interval Mapping (ICIM) approach available in IciMapping. The F_s and Fig genetic models were used to estimate additive and dominance effects of putative QTLs. QTL positions, logarithm of odds (LOD) values, additive effects, dominance effects, and percentage phenotypic variance explained were determined. Parameter estimation was performed using the Expectation Maximization (EM) algorithm (Dempster et al., 1977). Only QTLs exceeding the threshold LOD value were considered significant. Simple Sequence Repeat (SSR) primers obtained from Integrated DNA Technologies (IDT) Inc, USA were used in the study (Table S1).

RESULTS AND DISCUSSION

Parental polymorphism and construction of the linkage map: The parental genotypes PHS 1107, characterized by low tillering, and Lok 1, characterized by high tillering, were screened using 133 SSR markers to identify informative polymorphic loci. Of these, 29 markers showed clear polymorphism between the parents, corresponding to a polymorphism rate of 21.80%. The relatively moderate level of polymorphism is consistent with the narrow genetic diversity often observed among elite bread wheat genotypes. All 29 SSR loci exhibited the expected 1:2:1 Mendelian segregation ratio in the F₂ population, with no significant segregation distortion (Table 1). This indicated normal chromosomal segregation and provided a reliable marker dataset for linkage analysis. The absence of substantial segregation distortion is particularly important because distorted loci can affect estimates of recombination and consequently influence QTL localization. A linkage map comprising 29 SSR markers was constructed using the 70 F₂ individuals. The markers were grouped into seven linkage groups covering a total map distance of 394.04 cM, with individual linkage groups ranging from 36.83 cM to 80.86 cM. Linkage group 6 was the longest (80.86 cM), whereas linkage group 7 was the shortest (Table 2). Although the map had relatively low marker density, it was sufficient to identify major genomic regions associated with important agronomic traits. The relatively short map length can primarily be attributed to the limited number of polymorphic SSR markers and the relatively small mapping population. Larger populations and high-density SNP platforms would be expected to provide greater genome coverage and more precise QTL intervals.

The detection of agronomically important QTLs using a moderate-density SSR map is consistent with previous wheat mapping studies. Borner et al. (2002) identified QTLs for several morphological and yield-related traits in hexaploid wheat, demonstrating the usefulness of linkage analysis for dissecting complex agronomic characters. Similarly, Huang et al. (2006) identified numerous QTLs for yield-related and quality traits in wheat and reported clustering of QTLs for correlated traits in several genomic regions.

QTL for tiller number per plant

A major QTL, designated qNTTP-4-1, was detected for number of tillers per plant on linkage group 4 at 14.0 cM between Xgwm194 and Xcfd71. The QTL showed a very high LOD value of 15.87 and explained 68.26% of the phenotypic variation, indicating a major contribution of this genomic region to tillering in the PHS 1107 × Lok 1 population. The large phenotypic effect of qNTTP-4-1 suggests that this locus may be particularly useful for marker-assisted selection (Fig1). Tillering directly influences the number of productive spikes per unit area and consequently contributes to grain yield. However, selection solely for increased tiller number may not always improve yield because excessive or late-emerging tillers may compete for assimilates and fail to produce productive spikes. Therefore, the identification of a major QTL that can be evaluated together with grain number and grain weight provides a more useful breeding strategy than phenotypic selection for tillering alone. Previous studies have identified tillering-related QTLs on several wheat chromosomes, supporting the quantitative genetic basis of this trait. The present qNTTP-4-1 locus on linkage group 4 therefore represents an important genomic region for further validation. The high LOD value and large phenotypic effect observed in the present population make this region particularly attractive for validation in independent populations and environments (fig 2).

QTLs for plant height: Two QTLs were identified for plant height: qPH-4-1 on linkage group 4 and qPH-6-1 on linkage group 6 (Fig 3 a & b). These loci explained 17.70% and 27.09% of the phenotypic variation, respectively. Both QTLs showed negative additive effects, indicating that alleles contributed by one of the parents reduced plant height. Plant height is an important component of wheat plant architecture because reduced and appropriately proportioned plant stature can improve lodging resistance and enhance assimilate partitioning towards grain production. The importance of dwarfing genes such as *Rht-B1* and *Rht-D1* in modern wheat improvement is well established. The present QTLs may provide additional loci for fine-tuning plant height beyond the major dwarfing genes already deployed in breeding programmes.

The detection of qPH-4-1 in the same linkage group as qNTTP-4-1 and qNGPS-4-1 is particularly noteworthy. Such co-localization may indicate either linkage or pleiotropic effects and warrants further investigation through fine mapping and validation. The use of additional markers around this region could help determine whether the

observed associations represent closely linked loci or a common genomic factor affecting several components of plant architecture and yield.

QTL for thousand-grain weight: A major QTL, qTGW-5-1, was detected for thousand-grain weight on linkage group 5 at 4.0 cM, flanked by Wmc413 and Xgwm126 (Fig 4). The QTL recorded a LOD score of 7.77 and explained 42.20% of the phenotypic variation. The relatively large effect of qTGW-5-1 indicates that this genomic region has a substantial contribution to grain weight in the studied population. Thousand-grain weight is an important yield component and is generally considered more amenable to direct phenotypic selection than grain yield itself because of its comparatively higher heritability and more direct measurement. Nevertheless, grain weight is influenced by both genetic and environmental factors, and therefore the stability of qTGW-5-1 should be tested across environments before routine deployment.

The presence of a TGW-associated region on chromosome group 5 is consistent with previous QTL studies reporting genomic regions controlling grain size and weight in wheat. Börner et al. (2002) detected QTLs for thousand-grain weight and other yield-related characters, while subsequent studies have repeatedly identified genomic regions affecting grain weight across the wheat genome. More recent high-density mapping has also demonstrated stable QTLs for thousand-grain weight across multiple environments, emphasizing the importance of validating QTL effects before their incorporation into breeding programmes.

QTL for grain yield per plant: One QTL, qGYPP-1-1, was detected for grain yield per plant on linkage group 1 at 2.0 cM between Xgwm264 and Xcfd19 (Fig 5). It showed a LOD score of 5.01 and explained 32.64% of the phenotypic variation. Grain yield is a highly complex quantitative trait influenced by numerous genes and strong genotype × environment interactions (Kumar et al., 2022). Therefore, identification of a QTL explaining approximately one-third of the phenotypic variation is of considerable breeding interest. The qGYPP-1-1 region may affect yield directly or indirectly through its effects on component traits such as tiller number, grain number and grain size.

The present observation agrees with earlier reports showing that yield-associated QTLs can be detected on chromosome 1 in wheat. Kuchel et al. (2007), for example, identified a grain-yield QTL on chromosome 1B and demonstrated that yield QTLs may be expressed across multiple environments. However, because grain yield is strongly environment-dependent, qGYPP-1-1 should be validated across contrasting environments before being considered a robust marker for marker-assisted selection.

QTL for number of grains per spike: A major QTL, qNGPS-4-1, was identified for number of grains per spike on linkage group 4 at 26.0 cM between Xcfd71 and Xwmc48 (Fig 6). The QTL had a very high LOD score of 15.33 and explained 66.66% of the phenotypic variation. Number of grains per spike is an important determinant of wheat yield because it defines the sink capacity of the spike. Improvement in grain number can contribute substantially to yield provided that grain filling and grain weight are not adversely affected. The high phenotypic variation explained by qNGPS-4-1 indicates that this genomic region may have considerable potential for increasing grain number. The close physical/genetic proximity of qNGPS-4-1 and qNTPP-4-1 on linkage group 4 is particularly important. Both loci have large effects on yield-related traits, suggesting that this region may represent a genomic hotspot controlling several components of yield. However, the present data alone cannot distinguish between tight linkage and pleiotropy. Fine mapping, larger populations and marker-trait validation will therefore be required to establish the genetic relationship among these loci.

Previous studies have also demonstrated that grain number per spike is genetically complex and controlled by loci distributed across several wheat chromosomes. Zhang et al. (2012), using a Chinese wheat mini-core collection and SSR-based association analysis, identified grain-number-associated loci across multiple chromosomes, emphasizing the polygenic nature of this trait. More recent GWAS studies have further identified stable loci and haplotypes associated with kernel number and spike traits and have demonstrated the potential of diagnostic markers for marker-assisted selection.

Co-localization of QTLs and genetic architecture of yield: An important outcome of the present study was the identification of a cluster of QTLs on linkage group 4. The region contains qNTPP-4-1 for tiller number, qPH-4-1 for plant height, and qNGPS-4-1 for number of grains per spike. The simultaneous occurrence of QTLs for these traits suggests that linkage group 4 represents an important genomic region for wheat yield and plant architecture. The qNTPP-4-1 locus explained 68.26% of the phenotypic variation, while qNGPS-4-1 explained 66.66%. The co-localization of these major QTLs is particularly valuable because productive tiller number and grains per spike jointly determine the potential number of grains produced per plant. At the same time, the presence of a plant-height QTL in the same region provides an opportunity to manipulate plant architecture while improving yield components. However, the possibility of unfavorable linkage must be carefully examined before pyramiding these loci.

QTL clustering has been reported in earlier wheat studies. Huang et al. (2006) observed genomic regions containing QTLs for multiple correlated agronomic and quality traits, demonstrating that QTL clusters can be useful targets for breeding but may also complicate selection because of linkage or pleiotropic effects.

Implications in wheat breeding: Implications for wheat breeding the six QTLs identified in the present investigation provide useful genomic resources for improving yield and associated traits in bread wheat. In particular, qNTPP-4-1, qNGPS-4-1 and qTGW-5-1 showed relatively large phenotypic effects and therefore represent promising targets for marker-assisted selection. The markers flanking these QTLs can be used for preliminary selection of favorable alleles, followed by phenotypic evaluation in advanced generations.

The results also support a marker-assisted QTL pyramiding strategy. Favorable alleles at qNTPP-4-1, qNGPS-4-1, qTGW-5-1 and qGYPP-1-1 could potentially be combined through successive crossing and marker-assisted selection. Such pyramiding could enable simultaneous improvement of productive tillering, grain number, grain weight and grain yield. The concept is consistent with previous wheat studies demonstrating the usefulness of molecular markers for combining favorable alleles controlling yield and its components. However, the present QTLs should not be regarded as immediately deployable markers. Validation across independent genetic backgrounds, environments and seasons is essential, particularly for qGYPP-1-1 because grain yield is strongly affected by genotype $\times$ environment interaction. Kuchel et al. (2007) demonstrated that yield QTL expression can vary with environmental conditions, reinforcing the importance of multi-environment validation. The use of SSR markers is advantageous for initial validation because they are co-dominant, reproducible and locus-specific. Nevertheless, for routine breeding applications, the flanking SSR markers could be converted into high-throughput SNP or KASP assays after validation, thereby facilitating rapid screening of large breeding populations. Modern wheat genomic studies demonstrate the value of diagnostic SNP/KASP markers for translating QTL discoveries into practical marker-assisted selection. Importantly, wheat is an allohexaploid crop with a large and repetitive genome, which makes precise marker development and QTL resolution challenging. Therefore, the current SSR-based findings should be considered an important preliminary genomic resource that can be strengthened through high-density genotyping, fine mapping, haplotype analysis and validation using near-isogenic or advanced backcross populations.

CONCLUSION:

The present study successfully identified six QTLs associated with important yield and yield-related traits in bread wheat using an F₂ population derived from the contrasting parents PHS 1107 and Lok 1. The QTLs included qNTPP-4-1 for tiller number, qPH-4-1 and qPH-6-1 for plant height, qTGW-5-1 for thousand-grain weight, qGYPP-1-1 for grain yield per plant, and qNGPS-4-1 for number of grains per spike. Among these, qNTPP-4-1 and qNGPS-4-1 were major-effect QTLs explaining 68.26% and 66.66% of the phenotypic variation, respectively, while qTGW-5-1 explained 42.20% and qGYPP-1-1 explained 32.64%. The co-localization of QTLs for tiller number, plant height and grains per spike on linkage group 4 highlights this region as a potentially important genomic hotspot for wheat yield improvement. The flanking markers, particularly Xgwm194, Xcfd71 and Xwmc48, may provide useful tools for marker-assisted selection after independent validation. Therefore, the study demonstrates the potential of molecular mapping to dissect the genetic basis of yield and its components in wheat. The identified QTLs provide a foundation for marker-assisted selection and QTL pyramiding aimed at developing high-yielding, lodging-resistant and agronomically superior wheat cultivars. Nevertheless, validation across diverse genetic backgrounds and environments should precede their routine use in breeding programmes.

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Data Availability: The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

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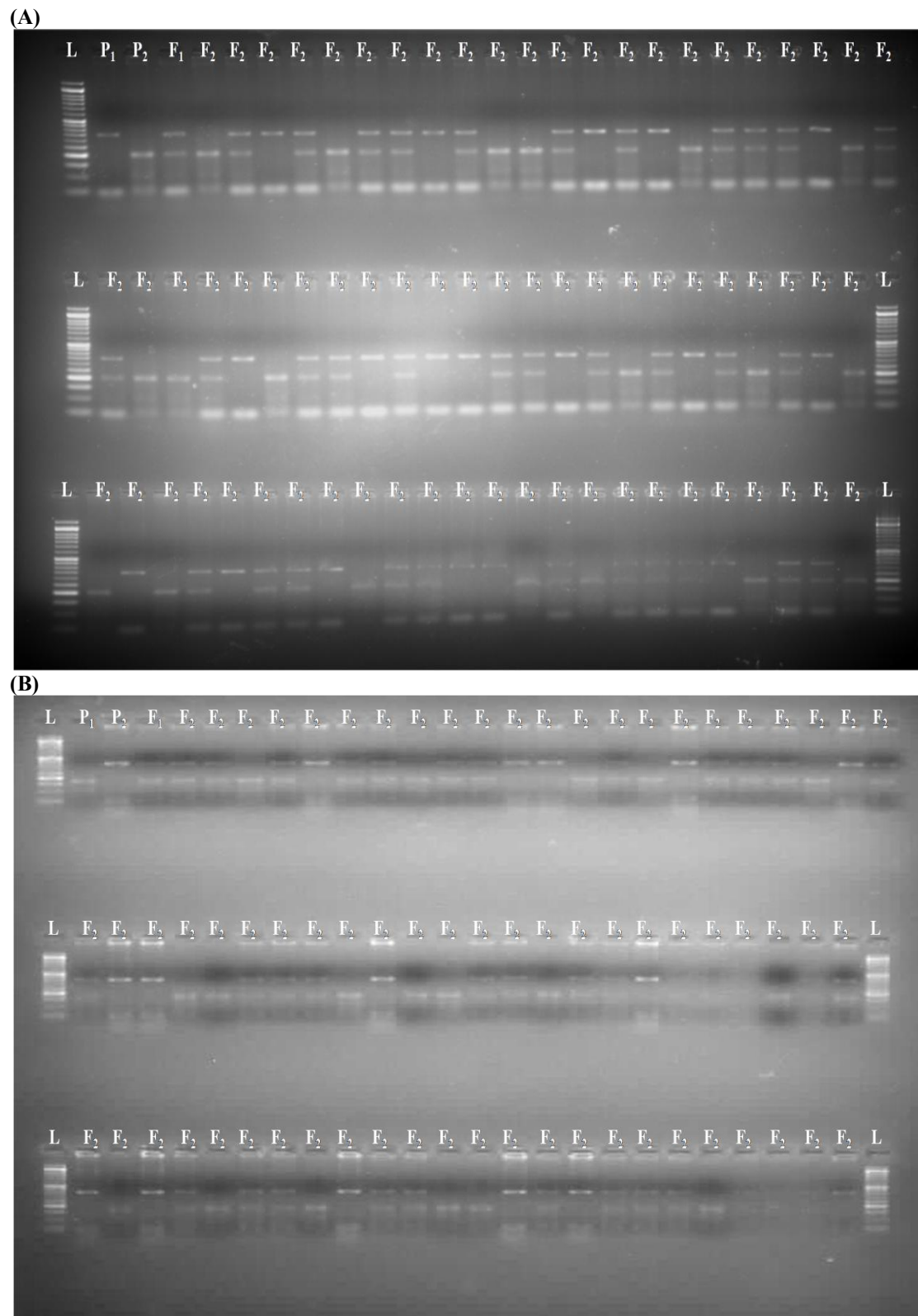


Fig. 1 Agarose gel from genotyping of SSR loci (A) Xgwm210 and (B) Xswes861.1 markers differing in size of PCR amplified in individual F_2 plants

Table 1: Chi-square tests for 29 SSR markers used to discriminate 70 individual F₂ plants equivalents to P₁, P₂ and F₁

Sr. No.	Marker Name	Chromosome	Position	Hm z A	Ht z	Hm z B	Missing marker	Chi-Square	Pr>ChiSq	Degree of Dominance
1.	Xgwm264	1	00.00	15	40	15	0	1.43	0.49	Codominant
2.	Xcfd19	1	18.96	15	38	16	1	0.74	0.69	Codominant
3.	Xgwm18	1	45.79	11	40	18	1	3.17	0.20	Codominant
4.	Xwmc344	1	50.33	15	37	17	1	0.48	0.79	Codominant
5.	Xgwm371	2	00.00	15	39	16	0	0.94	0.62	Codominant
6.	Xwmc445.2	2	29.32	17	40	13	0	1.88	0.39	Codominant
7.	Xcfa2134	2	47.87	14	40	16	0	1.54	0.46	Codominant
8.	Xbarc288	3	00.00	14	40	14	2	2.11	0.35	Codominant
9.	Xwmc262	3	22.23	20	35	15	0	0.71	0.69	Codominant
10.	Xgwm391	3	52.33	15	34	21	0	1.08	0.58	Codominant
11.	Xwms382	3	78.64	18	35	17	0	0.03	0.98	Codominant
12.	Xwmc527	4	00.00	18	30	21	1	1.43	0.49	Codominant
13.	Xgwm194	4	9.15	18	28	24	0	3.83	0.15	Codominant
14.	Xcfd71	4	17.48	15	31	23	1	2.56	0.28	Codominant
15.	Xwmc48	4	27.48	16	34	19	1	0.27	0.87	Codominant
16.	Xgwm210	4	56.23	18	33	19	0	0.26	0.88	Codominant
17.	wmc413	5	00.00	21	34	15	0	1.08	0.58	Codominant
18.	Xgwm126	5	6.68	21	31	18	0	1.17	0.56	Codominant
19.	Xgwm193	5	28.94	15	37	18	0	0.48	0.78	Codominant
20.	Xbarc334	5	43.28	16	37	17	0	0.26	0.88	Codominant
21.	gpw3087	6	00.00	21	36	12	1	2.48	0.29	Codominant
22.	wmc273	6	10.12	18	39	13	0	1.63	0.44	Codominant
23.	Xgwm111	6	31.80	13	40	17	0	1.88	0.39	Codominant
24.	Xgwm169	6	54.91	10	40	20	0	4.28	0.12	Codominant
25.	Xwmc553	6	61.63	12	39	19	0	2.31	0.31	Codominant
26.	Xswes861.1	6	80.86	18	31	20	1	0.83	0.66	Codominant
27.	Xbarc168	7	00.00	14	39	17	0	1.17	0.56	Codominant

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28	Xgwm190	7	13.53	12	40	18	0	2.45	0.29	Codominant
29.	Xgwm493	7	36.83	15	38	17	0	0.63	0.73	Codominant

hmzA = Homozygous for P₁, **hmzB** = Homozygous for P₂, **htz** = Heterozygous F₁

Table 2 QTL identification for tiller number per plant and grain yield related traits with LOD score, PVE (%), additive and dominance effects

Sr. No.	Name of trait	Name of QTL	Chromosome	Position	Left marker	Right marker	LOD score	PVE (%)	Additive effect	Dominance effect
1.	Number of tiller per plant	qNTPP-4-1	4	14.00	Xgwm194	Xcfd71	15.86	68.26	1.47	3.42
2.	Plant height	qPH-4-1	4	17.00	Xgwm194	Xcfd71	3.69	17.70	-6.58	3.30
3.	Plant height	qPH-6-1	6	40.00	Xgwm111	Xgwm169	4.49	27.09	-9.00	-2.24
4.	1000-grain weight	qTGW-5-1	5	4.00	wmc413	Xgwm126	7.77	42.20	-3.78	-0.03
5.	Grain yield per plant	qGYPP-1-1	1	2.00	Xgwm264	Xcfd19	5.01	32.64	-1.19	2.44
6.	Number of grain per spike	qNGPS-4-1	4	26.00	Xcfd71	Xwmc48	15.33	66.66	-5.35	4.89

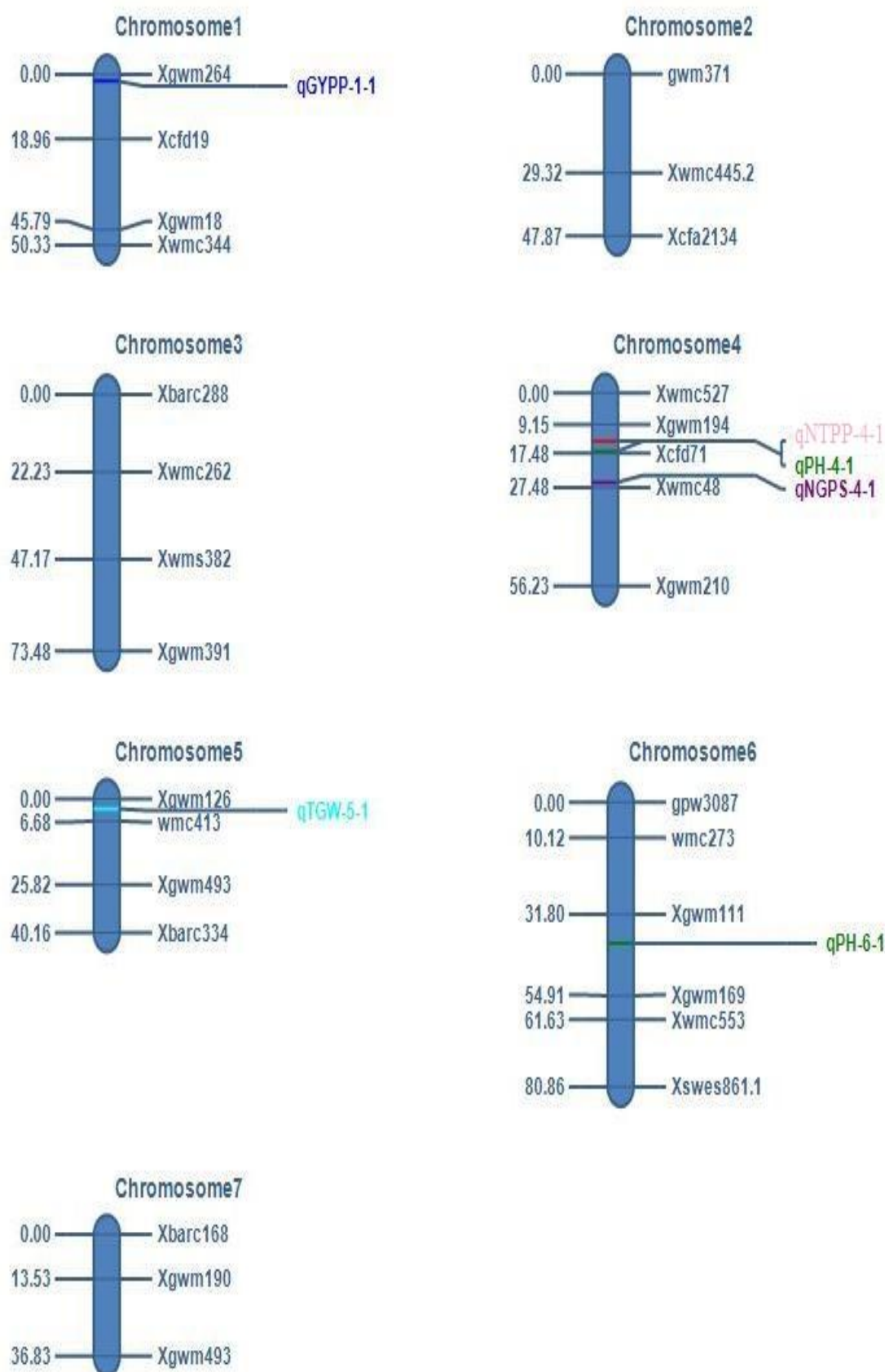


Fig 1 Position of number of tillers per plant and grain yield related QTL in whole genome

● NTPP

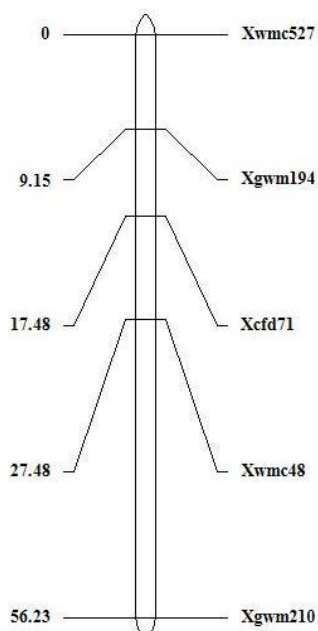


Fig 2 Position of QTL qNTPP-4-1 on chromosome 4 with LOD score

▲ PH

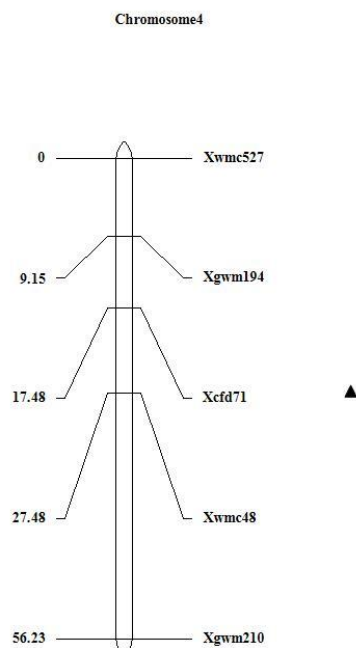


Fig 3a Position of QTL qPH-4-1 on chromosome 4 with LOD score

◆ TGW

▲ PH

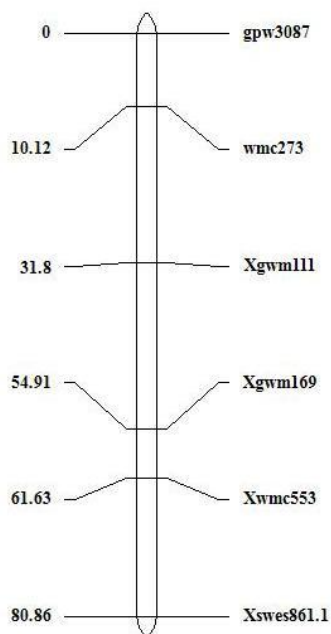


Fig 3b Position of QTL qPH-6-1 on chromosome 6 with LOD score

▲

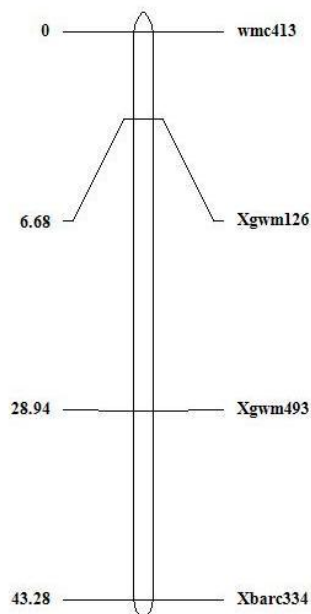


Fig 4 Position of QTL qTGW-5-1 on chromosome 5 with LOD score

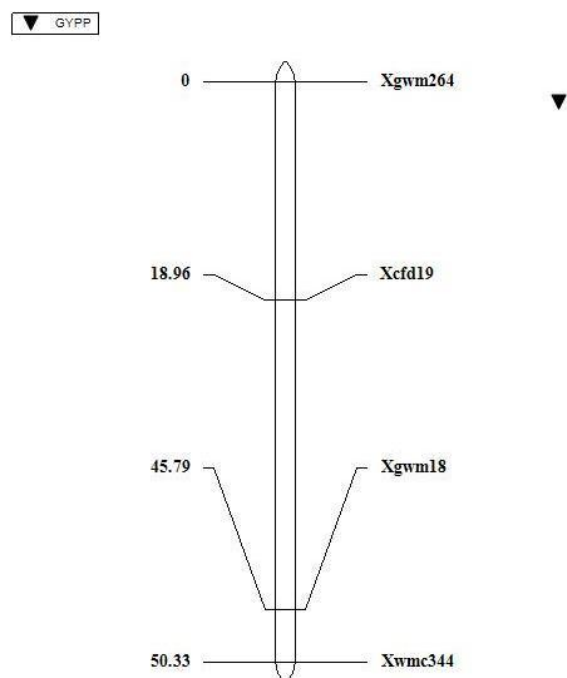


Fig 5 Position of QTL qGYPP-1-1 on chromosome 1 with LOD score

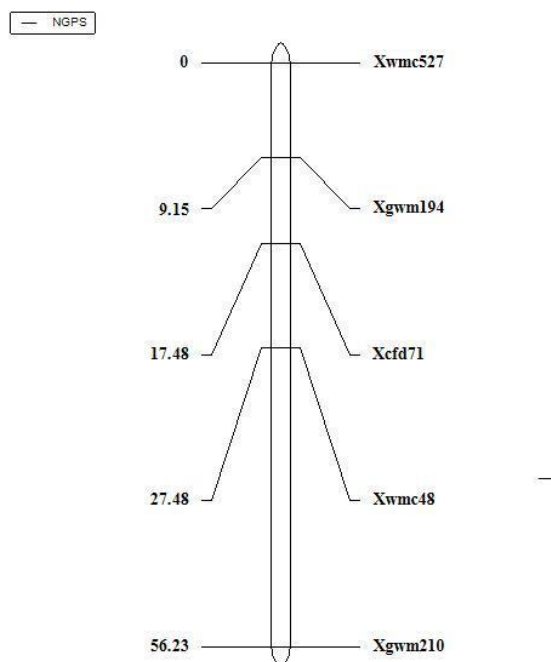


Fig 6 Position of QTL qNGPS-4-1 on chromosome 4 with LOD score