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RESEARCH ARTICLE

QTL analysis of yield and yield related traits in bread wheat under salt-stress conditions

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ABSTRACT: In order to identify yield and yield component QTLs under control and salt-stress conditions, a population of 254 recombinant inbred lines (RILs), derived from a cross between two bread wheat cultivars, (Roshan / Sabalan), was assessed. Parents and their 254 recombinant inbred lines (RILs) were evaluated in an alpha-lattice design with two replications in two control and saline environments of Yazd in 2011-2012 cropping season. Yield and yield-related traits were evaluated at harvest time. The genotyping was carried out using SSR and DArT markers. A, B and D genomes were covered by 411.8, 620.4 and 67.5 cM, respectively. Also, a total of 48 QTLs were detected on 11 chromosomes for grain yield, biological yield, harvest index, thousand-kernel weight, grain number per spike, spike weight and spikelet number per spike. Roshan (salt tolerance) alleles were associated with an increase yield under saline conditions. SSR markers including *gwm146, gwm577, gwm249* (on chromosomes 2A and 7B) were tightly associated with different QTLs. The major effect QTLs were located on chromosomes 1A and 7B for grain yield, harvest index and spike weight, which were explained 10.2%, 12.98% and 29 % of the total phenotypic variance, respectively. These QTLs and markers could be suitable for marker-assisted selection and gene stacking techniques. Moreover, co-located QTLs were detected on chromosome 2B for evaluated traits.

KEYWORDS: Bread wheat, QTL, Salt- stress, Grain yield

INTRODUCTION

Wheat has allocated the most area under cultivation and production around the world. Soil salt-stress is one of the most important unfavorable factors and abiotic stress that have undesirable effect on crops qualitative and production [5]. Salt-tolerant was defined as genotype capacity for growth and well yield in an environment that was assessed as more biomass production or yield under saline and non-saline conditions [30]. Overall, if

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salt-stress occurs previous or during plant transmission from vegetative to generative stage, it will have significant effect on vegetative and generative growth. In this case, salt-stress was caused generative growth acceleration and influence spike growth. Finally, salt stress decrease wheat yield potential by reducing the number of fertile tillage and grains [12, 26]. In majority of cases, genotypes that showed resistance under control conditions, didn't showed resistance under field salt-stress soil because of horizontal and vertical non-monotonous of soil physical and chemical characteristics, high temperate and low humidity. Therefore, it is necessary to assessed plant under actual and variable field conditions [31]. Spike weight, grain number per spike, the number of fertile spike, sodium and potassium value on two upper leaves, leaf surface and the number of sterile spikelets are convenient criteria for screening of salt-tolerant wheat genotypes in both field and greenhouse conditions [13]. Grain yield of wheat is one of the most important targets of its breeding programs and salt-tolerant criterion [23]. The major components of grain yield, including spikelet number per spike, spike number per plant, grain number per spike, thousand-kernel weight are quantitative traits controlled by several genes. Some yield components have less sensitive to the environment and have inheritance higher than grain yield. Therefore, it is useful to evaluate yield components when assessments of grain yield to provide specific information about the genetic control and relationship between yield and its components [8]. Genetic mapping of yield and yield components have been conducted under control conditions by many researchers [1, 4, 7, 8, 18, 20, 24, 25, 27, 29]. Cuthbert and et al. [8] detected 53 QTLs on 12 chromosomes using a population of 186 double haploid on six sites and were located 5 QTLs for seed yield on chromosomes 5A, 3B, 2D and 1A. They found 34 QTLs for six agronomical traits. Börner and et al. [4] identified 17 QTLs for yield components on 5A, 4A, 3A and 2D chromosomes, using 114 recombinant inbred lines in both field and greenhouse conditions. Of these, co-located QTLs were detected for heading time, spike seed number, thousand-kernel weight and seed weight per spike. Quarrie et al. [36] reported two QTLs for yield on chromosomes 5B and 5D under saline conditions. A population of 127 recombinant inbred lines derived from across Chuanmai 42 variety and a wheat variety of china spring, namely, Chuannong 16 was assessed on six sites. A total of 76 QTLs were identified for these traits. One QTL were detected for grain yield on chromosome 4D on 4 out of 6 environments. Seven clusters of co-located QTL were identified for yield on chromosomes 7D, 4D, 5B, 3B, 4A, 1A [38]. Marza et al. [28] were detected 206 QTLs for yield, yield components, agronomical traits, using a population of 214 recombinant inbred lines. Thirty-five QTLs were identified for yield, yield components on chromosomes 1A, 1B, 2A, 2D, 3B, 4D, 5A, 5B, 5D, 6A, 7A, 7B and 7D, using a population of back cross [19]. QTLs were located for grain yield, thousand-kernel weight, spikelet number per spike, grain number per spike, the number of fertile spikelet per spike and spike number per plant on 21 chromosomes and four co-located QTLs clusters on chromosomes 7D, 6B, 2A and 1D [22]. Kumar et al. [25] reported six pleiotropic QTLs for yield-related traits. Furthermore, one QTL was detected for spikelet number per spike on chromosome 4AL. Several pleiotropic QTLs were mapped for thousand-grain weight and grain filling rate on chromosomes 1B, 2A, 7D, 3B, 4D, 6D and 1A [40]. Salt- tolerant cultivars production, genetic diversity identification and mechanisms knowledge of genetic control of salt-tolerant are essential. It would be done using molecular marker technologists and effective QTLs mapping of salt tolerant. For this purpose, a trial was conducted to identify loci controlling salt-tolerant traits, using 254 recombinant inbred lines derived from a cross between two cultivars, namely, Roshan and Sabalan.

MATERIALS AND METHODS

Plant material

In the current study, a population consisting of 254 F8 recombinant inbred lines (RILs) derived from a cross between two parents, namely, Roshan and Sabalan through single seed descent method were used. Roshan is considered as relatively tolerant variety to salt-stress stress. Sabalan is relatively susceptible to salt-stress.

Genotyping

Two hundred and fifty-four RILs and their parents were assessed for genotyping. DNA was extracted from leaves of 254 RILs and their parents using the Triticale plant DNA extraction protocol (triticarte.com.au/content/DNA-preparation.html).

Quality and quantity of DNA samples were determined

using 1% agarose gel electrophoresis and Nano Drop (ND1000) instrument, respectively. Genotyping was carried with 2112 Diversity Arrays technology (DArTs) markers (Australia; http://www.triticarte.com.au). Also, a total of 232 simple sequence repeat (SSR) markers were tested according to Röder et al. [37]. At first, polymorphic SSR markers were determined. The PCR program for SSR primers was an initial denaturation at 95^{o}C for 5 min, followed by 30 cycles of 94^{o}C for 1 min, 50-65^{0}C (depending on the primer annealing) for 30 s, 72^{0}C for 1 min, and a final extension of 5 min at 72^{0}C before cooling to 4^{0}C. The PCR products were separated on 6% denatured polyacrylamide gel and visualized by silver staining. Out of 232 SSR and 2112 DArTs evaluated markers, 47 SSR markers and 463 DArTs markers were showed polymorphism, respectively.

Field trial

Two hundred and fifty-four RILs and their parents were studied using an alpha-lattice design under control and salt-stress conditions (The electrical conductivity level of soil and the irrigation water were 12 and 10 ds m^{-1}, respectively). Each plot consisted of two 2 m-long rows, each spaced 40 cm apart. All agricultural practices were done as recommended. Grain yield, thousand-kernel weight, grain number per spike, spikelet number per spike, spike length, plant height, biological yield, and harvest index were recorded on harvest time.

Data analysis

Map-Maker/EXP ver.3 [21] was used to construct the linkage map using Kosambi mapping function and the Logarithm of odds (LOD) threshold of higher than 3. Deviation from a Mendelian ratio at each locus was tested using chi-square test (P< 0.01). Overall, markers that indicated distorted segregation were excluded from the map. Normality distribution of traits was tested using SPSS 19. Trait mean was calculated in both control and salt-stress sites separately using SAS v.9.1. The QTL analysis for each trait was performed with the means of two control and salt-stress sites separately. At first, to identify markers significantly associated with each trait, single marker analysis using the linear regression method option of QTL Cartographer v.2.5 was performed. Therefore, QTL analysis was performed by the composite interval mapping (CIM) method using QTL Cartographer v.2.5. The LOD threshold were calculated by thousand permutation and P=0.05. The percentage of explained phenotypic variance was estimated for each QTL (R^2). Epistatic effects were estimated using QTL Network v.2.1 and P=0.05 was used as the threshold for detecting epistatic QTLs.

RESULTS

Analysis of variance showed significant difference for all traits except spikelet number per spike (Table 1). These results indicated that genetic variation exists among genotypes. Data normalization is one of the requirement principles for QTL analysis. Frequently distribution of population displayed approximately normal distribution for all traits under salt-stress conditions. Values of evaluated traits for some RILs were out of parents range and established in each two ends of frequently distribution diagram (Figure 1).

This issue shows transgressive segregation. The salt-tolerant parent, Roshan, had a higher value than susceptible parent, Sabalan, for grain yield under salt-stress conditions (Table 2). This issue presumably caused to higher salt-tolerant of Roshan variety. This result is in agreement with the result of Poustini and Siosemardeh [35]. Yld mean of 254 RILs was reduced under salt-stress conditions in compared to control conditions. To identify markers that significantly associated with each trait, single marker analysis was performed, using linear regression method. *Gwm146* and *gwm577* on chromosome 7B were tightly linked to Blyd and Yld, respectively under stress site (P<0.001and P<0.0001, respectively) (Table 3). *Gwm249* marker on chromosome 2A was significantly associated with QTLs of Gns (P<0.001) under control conditions.

Table 1. Combined analysis of variance for yield and yield components

S. O. V	df	Ms						
		Yld (g/plot)	Blyd (g/plot)	Tkw (g)	Sl (cm)	Sw (g)	Sns	Gns
Location	1	23438390.8**	393438985.5**	2090.7	55118.5**	64.9**	2770**	3812**
Error (a)	2	16460.1	2146588.1	348.6	766.3	0.45	102.6	113.4
Treatment	255	15203.8**	80661.3**	44.6**	113.6**	0.4**	3.89	68.69**
Treatment× Location	255	13714.3**	56339.4	18.1**	56.3	0.25**	1.95	37.14**
Error (b)	510	6624.6	54569.9	14.7	77.4	0.11	4.47	24.4
CV (%)		19	17.5	10.6	9.96	15.2	13.7	15.1

Table 2. Means of relevant traits in two parents and RILs population under control (C) and salinity (S) conditions.

Genotype	Environment	Yld (g/plot)	Blyd (g/plot)	Tkw (g)	Sl (cm)	Sw (g)	Sns	Gns	Hi
Sabalan	C	749.35	2010	34.5	100.58	1.98	15.75	38	37.01
	S	305.45	809.26	33.7	85.96	1.55	12.16	27.93	37.58
Roshan	C	500.1	1850	36.7	91.29	2.16	17.22	37.25	26.81
	S	407.57	1004.49	35.1	89.7	2.03	15.83	35.07	40.93
RILs	C	56v7.71	1974.48	39.9	95.06	2.36	17.03	34.18	29.72
	S	282.53	755.25	37.6	81.25	1.89	13.94	30.82	37.57

Linkage mapping of evaluated population in this study has been provided by Ghaedrahmati et al. [16].

QTL analysis

Biological yield

A total of seven QTLs were distributed on 6chromosomes, including 1A, 6A, 1B, 2B, 3B and 7B on both sites (Table 3). These QTLs were explained between 3.2-7% of phenotypic variation. Only QTL effects on chromosomes 6A and 1B was negative under salt-stress conditions. Of these QTLs, positive alleles for four QTLs on chromosomes 2B, 3B and 7B were derived from Roshan, and the other positive alleles that contributed positively to Blyd were from Sabalan. The strongest QTL for Blyd was located in the marker interval between *gwm146-wPt9515* on chromosome 7B, with a LOD=5.4 and R^2=7%. *Gwm146* and *wPt9515* markers were tightly linked with this QTL (P<0.001 and P<0.0001, respectively).

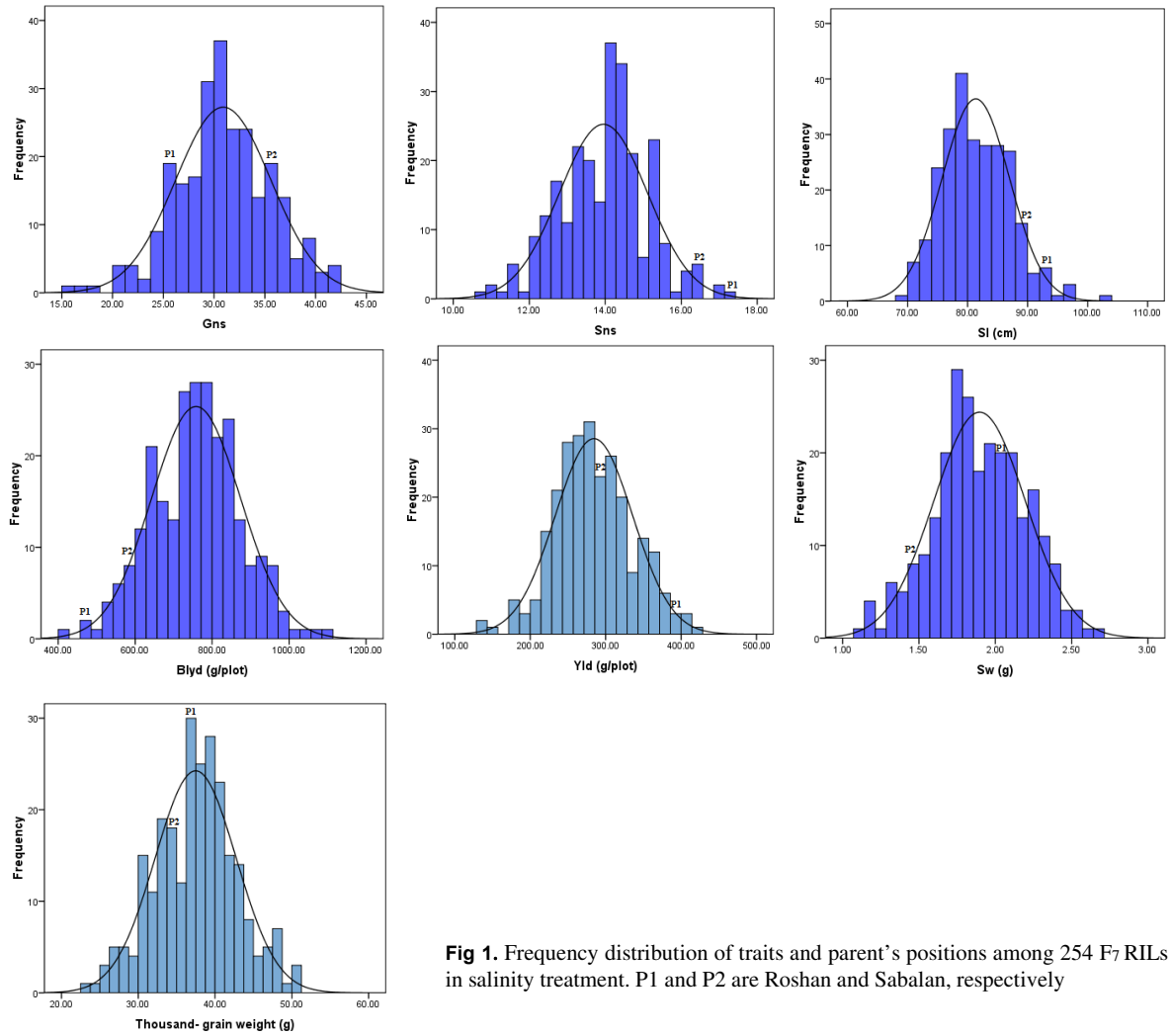

Fig 1. Frequency distribution of traits and parent's positions among 254 F_7 RILs in salinity treatment. P1 and P2 are Roshan and Sabalan, respectively

Table 3. Location, additive effects and contribution rate of QTL for yield and yield-related traits under control (C) and salinity (S) conditions

Trait	Environment	QTL	Position (CM)	Marker interval	LOD	Additive effect [a]	Allele	R^2% [b]
Blyd	C	*QBlyd.abrii-2B*	128	*gwm257-wPt7883***	3.6	73.85 g/plot	R	6
	C	*QBlyd.abrii-1A*	86.4	*wPt743317-wPt7030*	2.8	51.05 g/plot	S	3.6
	C	*QBlyd.abrii-3B*	12.4	*wPt4569**-wPt0302*	4.2	68.84 g/plot	R	4.7
	S	*QBlyd.abrii-7B*	10.5	*gwm146****-wPt9515****	4.5	31.51g/plot	R	7
	S	*QBlyd.abrii-6A*	27.4	*wPt3091-wPt730711*	3	-23.54 g/plot	S	3.8
	S	*QBlyd.abrii-1B*	2.2	*wPt0983**-wPt4343*	2.9	-22.15 g/plot	R	3.2
	S	*QBlyd.abrii-2B*	84.6	*gwm55-wPt0408*	2.8	23.28 g/plot	R	3.4
Tkw	C	*QTkw.abrii-1A*	112.2	*wPt664972-wPt5316*	2.7	-25.56 g	R	2.8
	C	*QTkw.abrii-3A*	0	*wPt733571-wPt2698*	2.5	-25.69 g	S	2.5
	C	*QTkw.abrii-3A*	13.2	*wPt9049-wPt8699*	3.2	29.67 g	R	3.8
	C	*QTkw-abrii.6B*	26.7	*wPt1048-gwm219**	3	26.33 g	R	3.7
	S	*QTkw.abrii-.2B*	105.5	*wPt0408-wPt3561**	3	1.3 g	R	5.7
	S	*QTkw.abrii-2B*	108.4	*wPt3561**-wPt4301**	3.6	1.26 g	R	5.3
Yld	C	*QYld.abrii-1B*	16.9	*wPt5899-wPt8682*	3.2	24.59 g/plot	S	4
	C	*QYld.abrii-6A2*	0	*wPt733035**-wPt3091*	5	-29.75 g/plot	S	6
	C	*QYld.abrii-7B*	12.8	*wPt9813**-wPt0494**	4.3	28.72 g/plot	R	5
	S	*QYld.abrii-7B*	31.7	*wPt0465-gwm577****	3.3	15.43 g/plot	R	8
	S	*QYld.abrii-2B*	82.6	*gwm55-wPt0408*	3	11.32 g/plot	R	4.5
	S	*QYld.abrii-1B*	6.1	*wPt2762**-wPt743523*	3.1	-10.7 g/plot	S	3.7
	S	*QYld.abrii-2B*	95.4	*wPt0408-wPt3561*	3.6	19.26 g/plot	R	10.2
Gns	C	*QGns.abrii-1B*	72.7	*wPt664250-wPt3202*	2.8	-0.926	S	3.1
	C	*QGns.abrii-7A*	1.9	*wPt6768-wPt5524*	2.9	0.916	R	3.2
	C	*QGns.abrii-2A*	17.3	*gwm249***-wPt8596****	5.7	-1.437	S	8
	S	*QGns.abrii-6B*	52.6	*gwm88**-wPt667798*	3.1	-1.487	S	6.4
SL	C	*QSl.abrii-1B*	3.4	*wPt4343-wPt1560*	3	1.98 cm	S	3.8
	C	*QSl.abrii-1B*	0	*wPt7422-wPt0983*	3.1	2.06 cm	S	3.8
	C	*QSl.abrii-1D*	2.56	*wPt4196-wPt3790*	2.7	-2.09 cm	S	7.4
	C	*QSl.abrii-3B*	0	*wPt1336-wPt4569*	2.9	-1.45cm	S	3.3
	C	*QSl.abrii-6A*	40.2	*wPt732741-wPt733051*	3.2	-1.52 cm	S	3.6
	S	*QSl.abrii-3B*	47.2	*tPt8621-wPt0439*	2.9	-1.06 cm	S	3.5
	S	*QSl.abrii-3B*	37.3	*gwm533-wPt8781*	2.7	-1.34 cm	S	5.7
	S	*QSl.abrii-3B*	54.8	*wPt7677-wPt11218*	2.7	-1.14 cm	S	4
	S	*QSl.abrii-3B*	47.7	*wPt0439-wPt9579*	3.5	-1.18 cm	S	4.2
	S	*QSl.abrii-1A*	99.4	*wPt7030-wPt8347*	2.8	1.21cm	S	2.9
SW	C	*QSw.abrii-1A*	173.9	*wPt9752-wPt731807*	18	-1.65 g	S	29
	C	*QSw.abrii-6B*	30.4	*gwm219**-wPt740675*	3	0.12 g	R	5.7
	C	*QSw.abrii-6B*	36.3	*wPt740675-gwm626*	3.2	0.124 g	R	6
	S	*QSw.abrii-5B*	42.2	*wPt3289-wPt2810*	3.2	0.093 g	R	5.7
	S	*QSw.abrii-5B*	92.9	*wPt7240-wPt1505*	3.3	-0.085 g	S	6.8
	S	*QSw.abrii-7B*	69	*wPt7925-wPt665112*	3.1	-0.084 g	S	5.6

[a] Positive and negative value indicate the Roshan and Sabalan alleles increased phenotypic

[b] Phenotypic variation explained by each QTL

, *, **** Present significant levels at P<0.01, P<0.001, P<0.0001

Grain yield

Seven QTLs were located on chromosomes 1B, 2B, 7B and $6A_2$ under both conditions (Table 3). LOD values were varied among 3-5 for Yld QTLs that each QTL was explained 3.7- 10.2% of phenotypic variation. The most significant QTL was in the marker interval between *wPt040-wPt3561* on chromosome 2B, explaining 10.2% of yield variation. It seems that the alleles increasing grain yield at the 1B, 2B and 7B loci came from Roshan *Gwm577* marker on chromosome 7B was tightly

Table 4. AA additive effect; AAE1 and AAE2 epistasis associated with environments of control and stress, respectively

Trait	QTL	Marker interval	Position (CM)	QTL	Marker interval	Position (CM)	AA	AAE_1	AAE_2
Blyd	*QBlyd.abrii-2B*	*wPt7883-wPt0880*	138.8	*QBlyd.abrii-2A*	*Gwm249-wPt8596*	8	67.03	46.21	-48.62

Table 5. Correlation coefficients between different traits under salinity conditions

Traits	Yld	Blyd	Tkw	Sl	Sw	Sns	Gns	Hi
Yld		0.71^{**}	0.23^{**}	0.08	0.31^{**}	0.14^{*}	0.15^{**}	0.55^{**}
Blyd			-0.22^{**}	0.22^{**}	0.001	0.29^{**}	0.08	-0.17^{**}
Tkw				-0.33^{**}	0.38^{**}	-0.32^{**}	-0.23^{**}	0.56^{**}
Sl					0.02	0.24^{**}	0.23^{**}	-0.09
Sw						0.42^{**}	0.57^{**}	0.42^{**}
Sns							0.5^{**}	-0.15^{*}
Gns								0.12^{*}
Hi								

Yld: rain yield, Blyd: Biological yield, Tkw: Thousand kernel weight, Sl: Spike length, Sw: Spike weight, Sns: Spikelet number per spike, Gns: grain number per spike, Hi: Harvest index

*, ** P<0.05, P<0.01 respectively.

associated with QTL of Yld (P<0.0001) under salt-stress conditions. Additive alleles were distributed between two parents under control conditions.

Spike weight

Six QTLs were found for Sw on chromosomes 5B, 6B, 7B and 2D (Table 3). The presence of alleles from Roshan at these QTLs resulted in an increase in spike weight. A major effect QTL was located on chromosome 1A with LOD=18 and R^2=29% (in marker interval between *wPt9752* and *wPt731807*). Additive effect of this QTL reduced Sw by 1.65 gr.

Spike length

Ten QTLs were observed for Sl on chromosomes 1A, 3B and 6B at both salt-stress and control sites (Table 3). Detected QTLs for Sl had minor effect. Chromosome 3B with five QTLs was allocated the most QTLs number that a totally explained 20.7% of phenotypic variation.

Spikelet number per spike

Two QTLs were identified on chromosomes 6B and 2D that explained 10% of trait phenotypic variation (Table 3). Alleles that increased Sns were found at loci *QSns.abrii-6B* and *QSns.abrii-2D* were contributed by Roshan.

Thousand kernel weight

Six QTLs were found for Tkw on chromosomes 1A, 3A, 6B and 2B (Table 3). Four QTLs for TKW from Roshan (*QTkw.abrii-3A, QTkw-abrii.6B, QTkw.abrii-.2B* and *QTkw.abrii-2B*) had a positive effect.

Harvest index

Six QTLs were detected for Hi under both control and salt-stress conditions (Table 3). The strongest QTL for harvest index was located chromosome 2B (in interval wPt7883-wPt0880) with LOD=4.1 and R^2=12.98%. Alleles of this QTL came from Sabalan and reduced Hi by 1.82.

Epistatic QTLs

Epistatic interactions were identified for only Blyd. Two QTLs were involved in QQ, QQE1 and QQE2 interaction (Table 4).

DISCUSSION

Different factors caused deviation from a mendelian ratio which lead to a biased estimate of marker-trait association [15, 17, 33]. As a result, markers that had deviation from a mendelian ratio were not used on QTL analysis in current study. The total length map was 1099.7 cM withan average distance of 4.7 cM between adjacent markers. Low length and low marker densities for linkage map could be due to two reasons: 1) the parental genomic structure and 2) the fact that these molecular markers are not well-distributed across all chromosomes and do not sufficiently cover the genome. In current study, there was variation in marker number, map length, marker density according to genome type. Length and marker number of D genome was lower than A and B genomes. It can be concluded that there were lower DArT markers for D genome. Of these, marker number, density and map length were the greatest in B

genome. Ayman et al. [2] reported the greatest density and marker number on genome B. In current study, the genome D had the fewest QTL among the three genomes. This was reported by some researchers [3, 7, 25, 36, 39]. There were large gaps and inadequate coverage on our map. These gaps in this map could be due to: 1- lack of available markers for some genomic regions, especially in the D genome 2- exclusion of markers exhibiting segregation distortion 3- genomic regions in which the two parents are identical by descent [29]. Thereby, more markers addition will make more complete genome coverage and eventually more important QTL will detect [7]. Forty-eight QTLs were identified for yield and yield related traits in current study. Of these QTLs, 25 and 23 QTLs were detected under control and salt-stress conditions, respectively. These QTLs explained 2.5-29 % of the phenotypic variance. QTLs had been detected for yield and yield components on 21 chromosomes in previous studies [1, 4, 7, 8, 10, 14,19, 25, 27, 28, 34, 36, 38]. The majority studies related to QTLs of yield and yield components were carried under natural growth conditions. Seldom researches were done about effective QTL under salt-stress conditions [3, 9, 32, 36]. *Gwm88* marker on chromosome 6B, was significantly associated with QTL of Gns ($P<0.01$). Huang et al. [19] were detected one QTL for grain yield linked to this marker. *Gwm219* marker on chromosome 6B was associated with three QTLs of Tkw, Sw and Sns($P<0.01$). These QTLs are potential selection targets for improving salt-stress tolerance of wheat. One QTL for Gns on chromosome 2A was linked tightly to *gwm249* in this study. This marker was linked closely to QTL-related fertile spikelet number trait that identified by Gang et al. (14). Three SSR markers, namely, *gwm577, gwm249, gwm146* were significantly linked to different QTLs and explained 7%, 8% and 8% of phenotypic variance, respectively. These markers could be increased efficiency of marker-assisted selection technique in future breeding studies. A major QTL for SL explained to 29% phenotypic variance was located on chromosome 1A under salt-stress conditions. QTLs explaining at least 15% of phenotypic variance were called major QTLs [11]. The most detected QTLs were located on chromosomes 6B, 3B and 2B. It seems, several clusters were located on different regions of these chromosomes under salt-stress conditions. Therefore, these regions could be used as important target for salt-tolerant improvement on wheat. Detected QTLs for assessed traits were explained low phenotypic variance. This may be result of complexity and polygenic nature of yield and yield components. Some QTLs were detected and concentrated in certain region on chromosome 2B (Table 2). QTLs controlling three yield-related traits, including Blyd, Yld and Tkw were identified in the interval of *gwm55-wPt0408-wPt3561* on chromosome 2B. Therefore, the selection of these traits could be concluded through these markers of *gwm55, wPt0408, wPt3561*. The positive alleles for the QTLs-related to these traits in this marker interval were contributed by the Roshan parent (salt-tolerant parent). QTLs that have favorable alleles from one of the parent across population mapping will have greater value for MAS [6]. Therefore, Roshan can be used effectively on wheat breeding program transfer pleiotropic and co-located gene using closely linked these molecular marker (*gwm55-wPt0408-wPt3561*). However, the co-localization of the QTLs controlling these traits could be suggested that 1) two closely linked genes each affecting a separate trait 2) one gene with a pleiotropic effect 3) one gene with a single function that initiates a sequence of causally related events (1). Also, co-located QTLs have been reported for Yld and Yld components [3, 36]. Moreover, significant and positive correlation among these three traits observed in current study (Table 5), confirms association among these traits. The positive and strong correlation among these traits suggests the presence of common genes controlling these traits. Positive and significant correlation was found between QTL of Yld and Yld component by some researchers [4, 8, 14, 25, 36]. However, in other cases, the QTLs for different traits were located at different position that suggests the absence of pleiotropic effects. Spike length is one of the most important components of spike morphology. The DArT marker *wPt7677* on chromosome 3B, was identified to be linked to a SL QTL detected in current study and by Yu et al. [41]. In current study, QTL of Yld co-located with Tkw enhancement. This suggested that selection for Tkw could be effectively increased Yld. In future, this research could be applied to develop with yield enhancement through functional (DNA sequence) marker in conventional breeding or molecular targets for genetic engineering.

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تجزیه QTL عملکرد و صفات مرتبط با عملکرد گندم نان تحت شرایط شرایط تنش شوری

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چکیده

به منظور شناسایی QTLهای عملکرد و صفات مرتبط با عملکرد تحت شرایط نرمال و تنش شوری، جمعیتی شامل ۲۵۴ لاین اینبرد نوترکیب حاصل از تلاقی روشن × سبلان مورد ارزیابی قرار گرفتند. والدین و ۲۵۴ لاین اینبرد نوترکیب در یک طرح آلفا لاتیس با دوتکرار در دو محیط نرمال و شور یزد در سال زراعی ۹۱-۱۳۹۰ ارزیابی شدند. در زمان برداشت، عملکرد و صفات مرتبط با عملکرد دانه اندازه‌گیری شدند. ارزیابی ژنوتیپی با استفاده از نشانگرهای SSR و DArT انجام شد. ژنوم‌های A، B و D به ترتیب ۴۱۱/۸، ۶۲۰/۴ و ۶۷/۵ سانتی‌مورگان از نقشه ژنتیکی را پوشش دادند. همچنین، در مجموع ۴۸ QTL بر روی ۱۱ کروموزوم برای عملکرد دانه، عملکرد بیولوژیک، شاخص برداشت، وزن هزار دانه، تعداد دانه در سنبله، وزن سنبله و تعداد سنبلچه در سنبله شناسایی شد. نشانگرهای SSR شامل *gwm146*، *gwm249* و*gwm577*(بر روی کروموزوم‌های 2A و 7B) از همبستگی بالایی با QTLهای مختلف برخوردار بودند. QTLهای بزرگ اثری بر روی کروموزوم‌های 1A و 7B مکان‌یابی شدند که به ترتیب ۱۰/۲، ۱۲/۹۸ و ۲۹ درصد از کل واریانس فنوتیپی را توجیه نمودند. QTLها و نشانگرهای مذکور می‌توانند برای تکنیک‌های ژن استکینگ و انتخاب به کمک نشانگر مفید باشند. به‌علاوه، QTLهای همپوشان برای صفات مورد بررسی بر روی کروموزوم 2B شناسایی شدند.

کلمات کلیدی: گندم نان، QTL ، تنش شوری، عملکرد