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Original article

Mapping of genes controlling secondry metabolits in barley (*Hordeum volgare* L.) under salinity stress

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Extended abstract

Introduction

Barley (*Hordeum vulgare* L.) is one of the four important cereals in the world. Soil salinity is one of the major barriers to the production of important agricultural products. Crops are one of the most important factors affecting the level of secondary metabolites present in plants under protective conditions. Secondary metabolites help plants to survive and survive external disturbances (such as pests and pathogens) and stress environmental conditions (such as drought or unfavorable soil conditions). Many agriculturally important traits are controlled by many genes and are known as quantitative. The regions within genomes that related to genes associated with a particular quantitative trait are known as quantitative trait loci (QTLs). The identification of QTLs based only on classic phenotypic evaluation is not possible. A major breakthrough in the characterization of quantitative traits that created opportunities to select for QTLs was initiated by the development of DNA markers. One of the main uses of DNA markers in research has been in the providing of linkage maps. Linkage maps have been used for identifying chromosomal regions that contain genes controlling simple traits and quantitative traits using QTL analysis.

Materials and methods

In order to locate secondrey metabolits of salinity tolerant genes in barley in vegetative and reproductive stages, 106 F8 lines caused Badia and Kavir crosses was used and cultivated as augumented design.This research was conducted in the research greenhouse of Gonbad Kavous University in 2019 and 2020. The seeds of 106 lines as well as were parents planted in the pot. For salinity stress, the lines were kept normal until the end of the vegetative phase and then irrigated with 16 $dS.m^{-1}$ in the reproductive stage. At the end of grain filling period, leaf samples were taken from flag leaf and secondary metabolites of sugar, phenol, catalase and peroxidase were measured. The linkage map was provided with markers with clear and consistent Mendelian segregation markers (152 SSR markers, 72 ISSR alleles, 7 IRAP alleles, 29 CAAT alleles, 27 Scot alleles and 15 iPBS alleles). Four methods of mapping CIM, ICIM, STMIM and STPLM were used to identify the control QTLs and estimate the effect genetic of one of them.

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Results

Gene loci were detected for the sugar content using CIM, ICIM and STPLME in the region of chromosome 1 at 26 cM and near the Bmaq0211. Also, for the peroxidase effective loci on chromosome 3 were identified in 44 cM flanked Bmac0067 and HVM33. The SMIM method was identified at position 118 cM between ISSR13-1 and ISSR16-4 for the sugar content, phenol, peroxidase of a gene locus on chromosome 4.

Conclusions

qSUG-4 QTLs (sugar content on chromosome 4) with a coefficient of 20.2 as well as qPHE-1 and qPHE-2 QTLs (phenol content on chromosomes 1 and 2) with coefficients of determination of 21.3, 29.21 and qPER-1, qPER-4b, qPER-5, qPER-7 (peroxidase on chromosomes 1, 4, 5 and 7) are a siutable candidate for marker-assisted selection programs in the barley recombinant line population

***Keywords*:** Barley, QTL, Salinity stress, Secondary metabolites

Table 1. Soil properties of the experiment site (0-30 cm depth)

Sand	Silt	Clay	K	P	N	Organic carbon	Neutral substances	pH	EC
----------%----------			---------ppm---------		----------%----------				ds/m
13	58	29	316	11.4	0.09	0.9	9.5	7.6	1.19

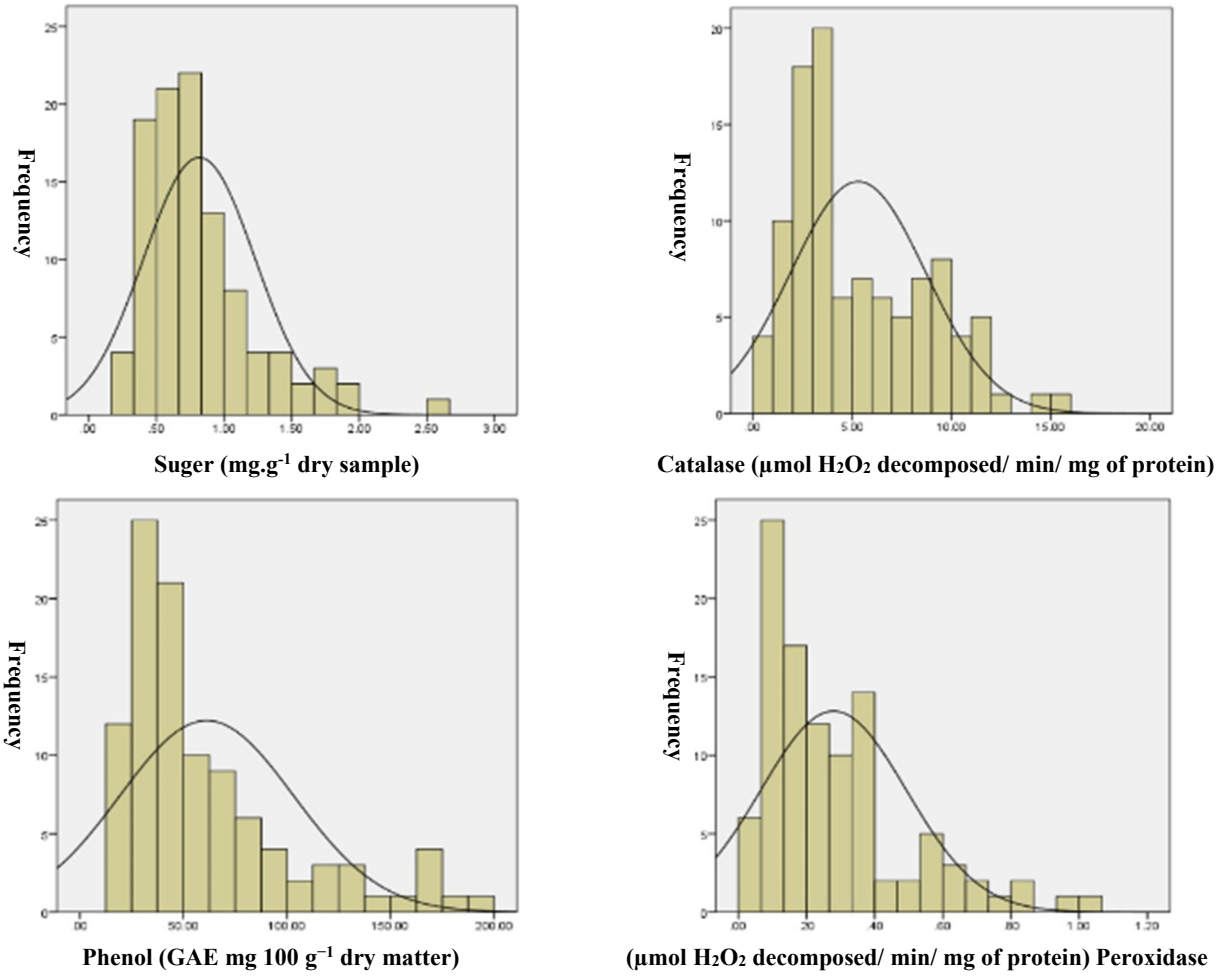

Fig. 1. Histogram for traits studied in 106 lines derived from cross between Badia and Kavir under salinity stress

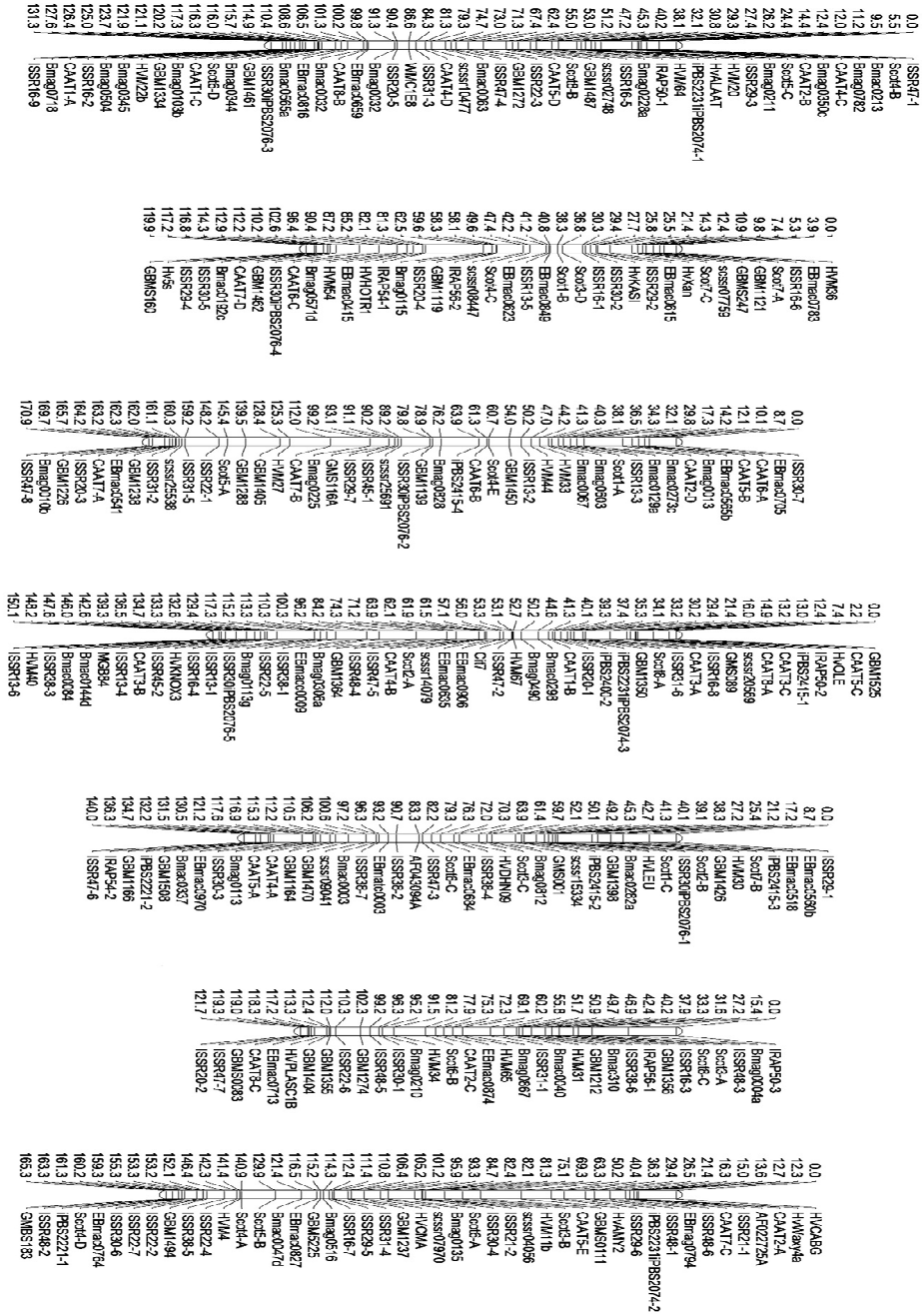

Fig. 2. Linkage map in barley RIL population caused Badia × Kavir crosses using 152 SSR, 72 ISSR, 7 IRAP, 29 CAAT, 27 Scot and 15 iPBS alleles

Table 2. QTLs Detected for Traits Containing Sugar, Phenol, Catalase and Peroxidase in a Population of Recombinant Lines from Kavir and Badia Cross

Traits	QTL	Chr	Position	Flanking markers	LOD	Add effect	R^2	Allele direction
Composite Interval Mapping								
Suger	qSUG-1	1	26	Scot5-Bmaq0211	2.808	0.161	11.80	Kavir
Phenol	qPHE-1	1	126	ISSR16-2-CAAT1-A	2.792	-52.738	11.7	Badia
Peroxidas	qPER-3	3	44	Bmac0067-HVM33	3.35	-0.85	13.9	Kavir
	qPER-4	4	60	Ebmac0635-Scssr14079	3.333	-0.96	13.8	Kavir
Inclusive Composite Interval Mapping								
Suger	qSUG-1	1	26	Scot5-Bmaq0211	2.808	0.161	11.80	Kavir
Phenol	qPHE-1	1	126	ISSR16-2-CAAT1-A	2.792	-52.738	11.7	Badia
Peroxidas	qPER-3	3	44	Bmac0067-HVM33	3.35	-0.85	13.9	Kavir
	qPER-4	4	60	Ebmac0635-Scssr14079	3.333	-0.96	13.8	Kavir
Single Trait Multiple Interval Mapping								
Suger	qSUG-1	1	14	Bmag0350c-CAATc	2.682	0.48	11.3	Kavir
	qSUG2-a	2	6	ISSR16-6-Scot7-A	3.323	0.451	13.8	Kavir
	qSUG2-b	2	32	ISSR16-1- Scot3-D	4.622	-0.456	18.7	Badia
	qSUG-4	4	118	ISSR13-1- ISSR16-4	5.045	.489	20.2	Kavir
	qSUG-5	5	132	GBM1508- iPBS2221-2	2.526	0.465	10.7	Kavir
	qSUG-7	7	76	Scot3-B- HVM11b	4.259	0.491	17.3	Kavir
Phenol	qPHE-1	1	34	iPBS2231iPBS2074-1-HVM64	5.369	44.752	21.3	Kavir
	qPHE-2	2	102	CAAT6-C-ISSR30iPBS2076-4	7.704	-45.978	29.1	Badia
	qPHE-4a	4	42	CAAT1-B- Bmac0298	2.544	44.811	10.8	Kavir
	qPHE-4b	4	118	ISSR13-1- ISSR16-4	4.631	47.347	18.7	Kavir
	qPHE-7	7	144	ISSR22-4- ISSR38-5	7.454	44.289	28.3	Kavir
Peroxidas	qPER-1	1	82	CAAT4-D- ISSR31-3	5.037	0.24	20.2	Kavir
	qPER-3a	3	44	Bmac0067- HVM33	3.57	-0.84	14.8	Badia
	qPER-3b	3	66	iPBS2415-4-Bmag0828	4.902	0.243	19.7	Kavir
	qPER-3c	3	150	ISSR22-1-ISSR31-5	3.565	0.239	14.7	Kavir
	qPER-4a	4	60	EBmac0635-scssr14079	2.718	-0.082	11.4	Badia
	qPER-4b	4	118	ISSR13-1-ISSR16-4	6.399	0.236	24.9	Kavir
	qPER-5	5	26	Scot7-B-HVM30	6.443	0.244	25	Kavir
	qPER-7	7	76	Scot3-B-HVM11b	5.183	0.238	20.7	Kavir
ST- penalized likelihood method								
Suger	qSUG-1	1	26.2	Bmag0211	2.868	0.117	12	Kavir
Catala	qCAT-2	2	58.1	IRAP56-2	3.608	1.144	14.9	Kavir
Proxidaz	qPER-3	3	44.2	HVM33	3.468	0.071	14.4	Kavir
phenol	qPEO-2	2	102.5	ISSR30iPBS2076-4	3.05	-18.519	12.7	Badia