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Research article

Deciphering the genetic architecture of β-glucan content in oats (*Avena sativa* L.) through QTL mapping

Gagandeep Kaur*, Rahul Kapoor, Lalit Pal, Puja Srivastava and Priti Sharma

Punjab Agricultural University, Ludhiana-141004, India
*Corresponding author e-mail: gagansekhon2021@gmail.com

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Abstract

Oat is a cereal grain grown for human and animal nutrition. It is known for its high dietary fibre content, phytochemicals, and nutritional value. The primary component of oat fibre is β-glucan, a group of polysaccharides comprising mixed-linkage (1,3) (1,4)-D-glucose units. The β-glucan concentrations of oat cultivars usually range from 3 to 6% and are considered a polygenic trait controlled by multiple genes with additive effects. The primary goal of this study was to identify quantitative trait loci (QTLs) for β-glucan content. Two contrasting parents for β-glucan content, OL10 (5.8%) and OL11 (0.8%), were selected from 91 germplasm lines, and an $F_{2:4}$ mapping population was generated for QTL mapping. Five genotypes with the highest levels of β-glucan content were observed. The QTLs affecting β-glucan content were identified using QTL cartographer, employing single marker analysis (SMA) and composite interval mapping (CIM). Two putative QTL regions were identified, one on linkage group (LG) 1 and the other on LG 4, with LOD (logarithm of the odds) scores of 3.7 and 4.3, respectively, explaining 31 and 33% of the phenotypic variation. The information generated is important in identifying the genomic regions responsible for β-glucan content in oats.

Keywords: Composite interval mapping, Oats, QTL mapping, Single marker analysis, β –glucan

Introduction

Oat is one of the important cereal grains belonging to the family Poaceae. The centre of origin of oats is unknown but is thought to be in the Middle East or Mediterranean basin (https://cropforlife.com/). Wheat and barley were domesticated far earlier than oats, and the domestication of oats took place beyond the range of genetic variation for the crop. Oats have a polyploid number of taxonomic patterns, including diploid, tetraploid, and hexaploid, with a fundamental chromosomal number of seven (x = 7). The genetic makeup of the cultivated oat is AACCDD, where 2n = 6x = 42. The genus *Avena* has over 70 species, and the three most widely cultivated species of oats are *A. sativa*, *A. nuda* and *A. byzantina*. The *Avena* genus has significant diversity, as seen by its genome size, mainly determined by its ploidy levels (Yan *et al*., 2016). Oat is a multipurpose crop used for staple food directly for human consumption and indirectly for livestock feed (Varma *et al*., 2016; Hilli *et al*., 2021).

Oats are primarily grown in central and northwestern parts of India during the *rabi* season as a fodder crop. Nowadays, it is also grown in the eastern regions of the nation. About 1.04 million hectares of the country are under cultivation of oats (Anonymous, 2019). Uttar Pradesh has the largest area, followed by Punjab, Bihar, and Haryana. The remaining region is shared by Gujarat, Maharashtra, Orissa and Uttaranchal. In Punjab, oats are mostly grown for fodder. The oat crop can grow on a variety of soils. The crop requires healthy, well-drained soil with the proper moisture and temperature. Oats thrive on soils with an approximate pH of 4.5. After being cut, oats display excellent growth with a good forage quality due to their good regeneration ability.

The common oat (*A. sativa*) is a cereal grain primarily farmed for animal feed and used as oatmeal for humans. The richness of oats in antioxidants such as α-tocotrienol, α-tocopherol and avenanthramides as well as total dietary fibre, including the soluble fibre β-glucan makes it valuable for consumption (Arora *et al*., 2020). The soluble fibre content is the primary factor determining the crop's benefit for consumption. It is regarded as the most affordable and abundant source of soluble dietary fibre. The primary element of soluble fibre in oats is β-glucan, a group of polysaccharides (Miller *et al*., 1995).

In barley and oats, β-glucan consists of mixed-linkage (1, 3) (1, 4) - *β*- D- glucose units (Tohamy *et al.*, 2003). Oat is also called 'supergrain' because of its positive health benefits (Smulders *et al.*, 2016). Oat β-glucan is directly related to health benefits like reducing both systolic and diastolic blood pressure, lowering bad cholesterol, and improving diabetes and immune response (Keenan *et al.*, 2002; Braaten *et al.*, 1994; Jenkins *et al.*, 2002; Estrada *et al.*, 1997; Kaur *et al.*, 2019).

Genetic diversity is a prerequisite for any crop improvement programme (Poonia *et al.*, 2020). The primary step in any breeding programme is to assess the variation in the characters within a large germplasm collection to define the valuable genotypes/lines to be considered further (Kumar *et al.*, 2023). To develop new oat cultivars, germplasm selected from various eco-geographic regions is regarded as the finest natural resource in providing the required variation in traits. The more diverse the individuals, the more heterotic effects and desirable segregants are observed in the crossing programme. Better characterization of the exotic germplasm is needed to facilitate its use in research and plant breeding. Owing to the significant health and nutritional benefits of oats, there was an urgent need to screen a large number of oat germplasm for high dietary quality, *i.e.*, β-glucan content (Priyanka *et al.*, 2022). Genotypes with high β-glucan content can help to enhance the β-glucan content of local germplasm lines through different breeding strategies (Ahmad *et al.*, 2014).

Materials and Methods

Plant materials and methods: A total of 96 genotypes belonging to the diverse regions of the world collected from NBPGR, New Delhi, were evaluated morphologically for β-glucan character (Table 1). The entries were planted in the field in two rows, each of 2 m in length, in augmented design during the *rabi* season 2016-17 at the Forage Section of Punjab Agricultural University, Ludhiana (India). The control varieties (OL 9, OL 10 and Kent) were repeated randomly in every block to obtain an error estimate. The recommended package of practices was followed strictly to raise the healthy crop.

In order to make crosses and generate a mapping population, the collected germplasm lines was used to select the contrasting parents for the β-glucan. The genotypes were subjected to biochemical examination to determine the amount of β–glucan. OL10 and OL11 were selected as the contrasting parents for β-glucan because they had the highest 5.8 and the lowest 1.8 per cent of β-glucan content, respectively.

The F_1 hybrids were generated by crossing parents OL10 and OL11 (*rabi* 2016-17). The hybrids were further raised in rabi 2017–18 to generate F_2 seeds. Then, in offseason 2018, F_2 seeds were planted in Keylong and F_3 seeds were harvested. About 91 F_2-derived F_3 progenies were grown in forage fields in 2018-19, and $F_{2:4}$ seeds were harvested and used as the mapping population. Half of the $F_{2:4}$ seeds were kept for sowing, and the rest was used for phenotyping. Seeds of each of the 91 individuals were used to estimate the amount of β-glucan by alkaline method as outlined by Wood *et al.* (1977).

Genomic DNA of 91 $F_{2:4}$ individuals and parents (OL10 and OL11) was isolated using the CTAB (cetyl trimethyl ammonium bromide) method as given by Murray and Thomson (1980). Young leaves were freshly harvested from each of the 91 $F_{2:4}$ individuals grown in the trays kept in cold chambers and DNA isolation process was carried out.

Parental polymorphism survey: The parental polymorphism was performed using 213 SSR markers (Table 2). The polymorphic markers were then analyzed on the genomic DNA of 91 lines of $F_{2:4}$ population as per Li *et al.* (2000) and Dumlupinar *et al.* (2016). In-vitro, amplification of the DNA was performed in an Eppendorf master cycler employing SSR primers using the protocol given by Oliver *et al.* (2011). PCR was performed using the reaction volume of 20 µL containing the template DNA, forward and reverse primers, $MgCl_2$, dNTPs, Taq polymerase and PCR buffer. After the amplification of the PCR product, 6% polyacrylamide gel electrophoresis (PAGE) was used to resolve the products. About 10 µL of each sample was loaded in the gel, and bands were resolved at 300 volts. The bands were seen under UV light and were photographed by Alpha imagerHP, AlphaInnotech.

The banding pattern generated by the SSR markers was then scored in a co-dominant way. 'A' was scored for the parent with a higher β-glucan value, 'B' for the band similar to the parent with lower β-glucan and 'M' was scored as missing data.

Construction of linkage map: 'MAPDISTO' program version 1.7.7 was used for the construction of linkage map (Lorieux, 2007). All markers were assigned to a linkage group using pair-wise analysis, with a minimum LOD score of 3.0 and a maximum recombination frequency of 0.3. Kosambi mapping function was used to calculate the map distances from recombination frequency. The command 'Auto Order' was used to order the markers on the linkage group using multipoint analysis. Reconfirmation of the final and last order of the markers on the linkage groups was done using the command ripple. Composite interval mapping (CIM) was used to identify the QTLs. The combinatorial approach of interval mapping and regression analysis was used. For greater accuracy, the regression method, which was selected as the parameter for performing the analysis, was the forward and backward method. One thousand

Table 1. List of germplasm lines acquired from NBPGR, New Delhi

Genotype	Origin	Genotype	Origin	Genotype	Origin
IC 372496	Indigenous	EC 605835	Exotic	EC 246158	Exotic
IC 372457	Indigenous	EC 18850	Exotic	EC 528925	Exotic
IC 372452	Indigenous	EC 537878	Exotic	EC 209576	Exotic
IC 372467	Indigenous	EC 528896	Exotic	EC 246178	Exotic
IC 372563	Indigenous	EC 537869	Exotic	EC 246112	Exotic
IC 372503	Indigenous	EC 537811	Exotic	EC 528874	Exotic
EC 605839	Exotic	IC 372478	Indigenous	EC 528902	Exotic
EC 209589	Exotic	IC 372474	Indigenous	EC 246132	Exotic
IC 372523	Indigenous	IC 372493	Indigenous	IC 372529	Indigenous
IC 372527	Indigenous	IC 372441	Indigenous	EC 528899	Exotic
IC 372437	Indigenous	EC 209570	Exotic	EC 528923	Exotic
EC 209272	Exotic	EC 528871	Exotic	EC 246166	Exotic
EC 605833	Exotic	EC 209402	Exotic	IC 372462	Indigenous
P 7 292561	Exotic	IC 372424	Indigenous	EC 209452	Exotic
IC 108477	Indigenous	EC 528906	Exotic	EC 246176	Exotic
IC 372510	Indigenous	EC 209307	Exotic	EC 537850	Exotic
IC 372530	Indigenous	EC 537834	Exotic	EC 246181	Exotic
IC 372531	Indigenous	EC 537825	Exotic	EC 537853	Exotic
IC 372481	Indigenous	EC 209346	Exotic	EC 246131	Exotic
EC 605829	Exotic	EC 528919	Exotic	EC 528908	Exotic
EC 537851	Exotic	IC 372415	Indigenous	EC 537885	Exotic
EC 537849	Exotic	EC 537819	Exotic	EC 528905	Exotic
EC 537856	Exotic	EC 537924	Exotic	EC 372463	Exotic
EC 528864	Exotic	EC 528907	Exotic	EC 537867	Exotic
IC 372489	Indigenous	EC 528916	Exotic	IC 372482	Indigenous
EC 537808	Exotic	EC 537836	Exotic	EC 537875	Exotic
IC 372497	Indigenous	IC 372502	Indigenous	EC 537855	Exotic
IC 372442	Indigenous	IC 372466	Indigenous	EC 246120	Exotic
EC 533788	Exotic	EC 209524	Exotic	EC 246147	Exotic
P 7 295932	Exotic	EC 528888	Exotic	OL 11	Ludhiana
EC 246179	Exotic	EC 246200	Exotic	IC 372477	Indigenous
IC 372458	Indigenous	EC 537815	Exotic	EC 131639	Exotic

permutations at a 5% level of significance were used to calculate the threshold LOD score.

Results and Discussion

Variability and distribution of beta-glucan content in germplasm: The biochemical analysis led to the estimation of β-glucan percentages varied from 0.43 to 6.90% (Table 3). Only four genetic lines considerably outperformed standard control OL 10 (5.79%), while 27 lines outperformed standard control OL 9 (4.03%) and Kent in terms of β-glucan (3.79%). It was observed that 65 genotypes had lower β-glucan percentages than the controls. Also on $F_{2:4}$ seed, the estimated content of β-glucan showed continuous distribution. Among the parents, OL10 had the highest concentration of β-glucans (5.8%), while OL11 had the lowest content (0.8%). Only a small number of individuals were found

Table 2. SSR markers used for parental polymorphism survey

S. No.	Marker name	S. No.	Marker name	S. No.	Marker name
1	AM1	46	AM46	91	AB_AM_124
2	AM 2	47	AM47	92	AB_AM_130
3	AM3	48	AM48	93	AB_AM_155
4	AM4	49	AM49	94	AB_AM_183
5	AM5	50	AM50	95	AB_AM_185
6	AM6	51	AM51	96	AB_AM_202
7	AM7	52	AM52	97	AB_AM_219
8	AM8	53	AM53	98	AB_AM_223
9	AM9	54	AM54	99	AB_AM_226
10	AM10	55	AM55	100	AB_AM_227
11	AM11	56	AM56	101	AB_AM_232
12	AM12	57	AM57	102	AB_AM_238
13	AM13	58	AM58	103	AB_AM_242
14	AM14	59	AM59	104	AB_AM_258
15	AM15	60	AM60	105	AB_AM_259
16	AM16	61	AFO33096	106	AB_AM_260
17	AM17	62	AM87	107	AB_AM_269
18	AM18	63	AM102	108	AB_AM_275
19	AM19	64	AM112	109	AB_AM_283
20	AM20	65	HVM4	110	AB_AM_285
21	AM21	66	HVM20	111	AB_AM_290
22	AM22	67	HVM62	112	AB_AM_299
23	AM23	68	L39777	113	AB_AM_303
24	AM24	69	M83381	114	AB_AM_322
25	AM25	70	Xgwm88	115	AB_AM_323
26	AM26	71	Xgwm471	116	AB_AM_324
27	AM27	72	Z48431	117	AB_AM_327
28	AM28	73	AB_AM_059	118	AB_AM_329
29	AM29	74	AB_AM_065	119	AB_AM_340
30	AM30	75	AB_AM_066	120	AB_AM_342
31	AM31	76	AB_AM_068	121	AB_AM_349
32	AM32	77	AB_AM_070	122	AB_AM_354
33	AM33	78	AB_AM_073	123	AB_AM_361
34	AM34	79	AB_AM_074	124	AB_AM_397
35	AM35	80	AB_AM_076	125	AB_AM_399
36	AM36	81	AB_AM_077	126	AB_AM_400
37	AM37	82	AB_AM_079	127	AB_AM_425
38	AM38	83	AB_AM_081	128	AB_AM_431
39	AM39	84	AB_AM_083	129	AB_AM_439
40	AM40	85	AB_AM_087	130	AB_AM_451
41	AM41	86	AB_AM_093	131	AB_AM_453
42	AM42	87	AB_AM_095	132	AB_AM_457
43	AM43	88	AB_AM_108	133	AB_AM_467
44	AM44	89	AB_AM_111	134	AB_AM_469
45	AM45	90	AB_AM_123	135	AB_AM_483

S. No.	Marker name	S. No.	Marker name
136	AB_AM_485	175	AB_AM_888
137	AB_AM_488	176	AB_AM_897
138	AB_AM_491	177	AB_AM_905
139	AB_AM_493	178	AB_AM_906
140	AB_AM_494	179	AB_AM_907
141	AB_AM_512	180	AB_AM_908
142	AB_AM_541	181	AB_AM_911
143	AB_AM_550	182	AB_AM_912
144	AB_AM_553	183	AB_AM_913
145	AB_AM_554	184	AB_AM_914
146	AB_AM_576	185	AB_AM_915
147	AB_AM_577	186	AB_AM_916
148	AB_AM_603	187	AB_AM_956
149	AB_AM_680	188	AB_AM_993
150	AB_AM_688	189	AB_AM_994
151	AB_AM_689	190	AB_AM_1003
152	AB_AM_692	191	AB_AM_1013
153	AB_AM_709	192	AB_AM_1015
154	AB_AM_805	193	AB_AM_1024
155	AB_AM_814	194	AB_AM_1025
156	AB_AM_824	195	AB_AM_1045
157	AB_AM_825	196	AB_AM_1052
158	AB_AM_829	197	AB_AM_1055
159	AB_AM_831	198	CWM 26
160	AB_AM_833	199	CWM 48
161	AB_AM_839	200	CWM 65
162	AB_AM_842	201	CWM 90
163	AB_AM_844	202	CWM 162
164	AB_AM_845	203	CWM 163
165	AB_AM_846	204	CWM 340
166	AB_AM_847	205	KSUM 37
167	AB_AM_851	206	KSUM 69
168	AB_AM_853	207	GWM 3
169	AB_AM_854	208	GWM 6
170	AB_AM_858	209	GWM 247
171	AB_AM_863	210	GWM 577
172	AB_AM_873	211	HVM 3
173	AB_AM_874	212	Wisc 48
174	AB_AM_878	213	Wisc 115

to have β-glucan levels beyond the parental range, demonstrating transgressive segregation. The population levels of β-glucan content ranged from 1.05 to 6.08%. The frequency distribution of the individuals of the $F_{2:4}$ population was also recorded (Fig 1).

***Parental polymorphism analysis and linkage mapping*:** A total of 213 SSR markers were employed for parental polymorphism (Table 2). The parental polymorphism survey of SSR markers was recorded (Fig 2). The first band in each pair indicated the first parent, OL10, and

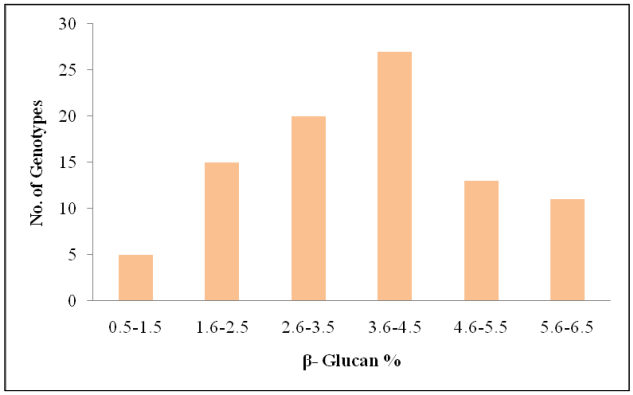

Fig 1. Frequency distribution of the segregating individuals for β-glucan

the second band represented OL11, the second parent. Out of 213 SSR markers, 52 were found to be polymorphic between the parents. The genotypic data from these 52 markers were analyzed for segregation ratios in F2:F4 generation, ensuring adherence to Mendelian principles. Out of these, 25 markers exhibited no significant distortion in segregation and were consequently employed in constructing the linkage map. The results of the population survey carried out with the polymorphic marker AB_AM_87 was also recorded (Fig 3). Besides, the polymorphic SSR markers between parents and their linkage map position on the OT linkage map was recorded (Oliver *et al.*, 2010; Table 4).

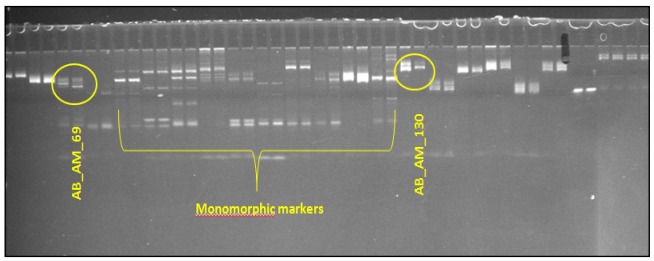

Fig 2. PAGE gel showing parental polymorphism survey

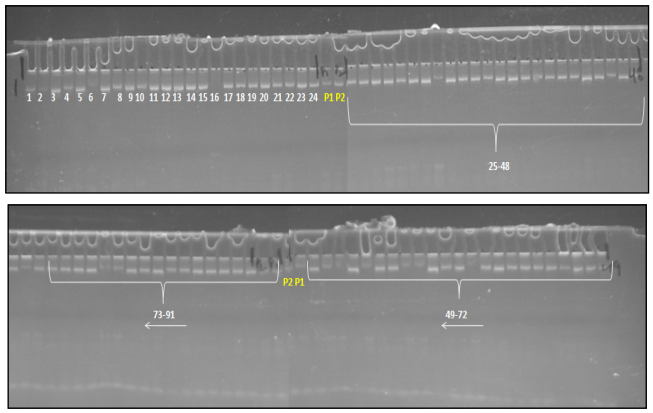

Fig 3. PAGE plates showing the population survey with the polymorphic marker AB_AM_ 87

A linkage map was constructed using MAPDISTO with an LOD score of 3.0 and a recombination percentage of 0.3 for genotypic data of 91 lines of $F_{2:4}$ population using 25 SSR markers. From this data, four linkage groups were produced (Fig 4). The markers of one OT linkage group were found to be linked together (Oliver *et al.*, 2010). The marker interval between AB_AM_183 and AB_AM_847 on linkage group (LG) 1 was discovered to have a maximum distance of 97.7 cM. On LG 3, the marker interval between AB_AM_823 and AB_AM_913 was found to have a minimum distance of 8.2 cM. On LG 1, the maximum number of markers (10) and on LG2 the minimum number of markers (4) were discovered. The smallest map length of 41.2 cM was found on LG 3, and the map length (97.7 cM) of LG 1 was found to be the longest.

QTL analysis for β-glucan content: The integration of genotypic and phenotypic data from $F_{2:4}$ populations for β-glucan involved employing a QTL Cartographer with both single marker analysis (SMA) and CIM techniques to identify the QTLs associated with β-glucan content (Fig 5). In Simple interval mapping (SIM), three markers from LG 1 marker AB_AM_915, AB_AM_69 and AB_AM_123 showed the probability of linkage with 0.1, 0.1 and 5% levels of significance, respectively.

SIM and CIM were also employed by Kianian *et al.* (2000) to locate the QTLs for β -glucan. They found that regions on the linkage groups 11 and 14 of the hexaploid oat

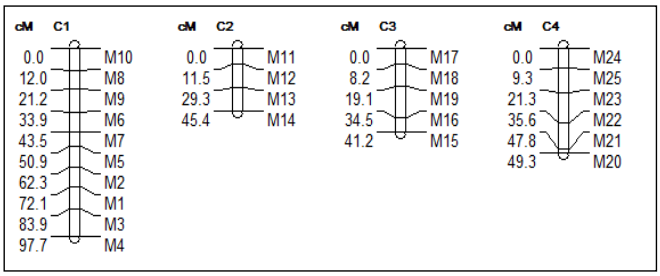

Fig 4. Linkage groups generated by MAPDISTO

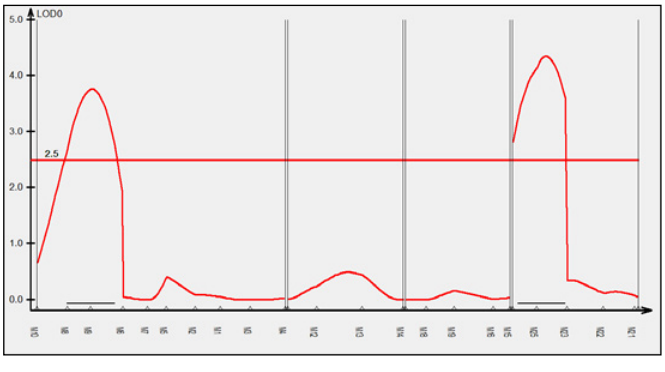

Fig 5. QTL map for β-glucan content in oat (*A. sativa* L.) using composite interval mapping

Table 3. Mean beta glucan content in germplasm and control

Germplasm	β-glucan (%)	Germplasm	β-glucan (%)	Germplasm	β-glucan (%)
Kent	3.79	EC 246179	1.43	EC 246200	0.50
OL 9	4.03	IC 372458	4.43	EC 537815	1.00
OL 10	5.79	IC 372477	3.43	EC 131639	3.50
IC 372496	1.50	EC 605835	2.43	EC 246158	6.50
IC 372457	1.50	EC 18850	2.93	EC 528925	3.00
IC 372452	4.00	EC 537878	3.43	EC 209576	4.00
IC 372467	2.50	EC 528896	5.00	EC 246178	3.50
IC 372563	2.00	EC 537869	3.50	EC 246112	4.50
IC 372503	4.00	EC 537811	1.50	EC 528874	6.50
EC 605839	5.00	IC 372478	3.00	EC 528902	3.80
EC 209589	3.50	IC 372474	3.50	EC 246132	4.80
IC 372523	5.50	IC 372493	4.50	IC 372529	3.80
IC 372527	2.00	IC 372441	1.50	EC 528899	2.30
IC 372437	1.00	EC 209570	2.50	EC 528923	3.30
EC 209272	4.00	EC 528871	1.50	EC 246166	3.30
EC 605833	0.77	EC 209402	5.00	IC 372462	3.80
P 7 292561	3.77	IC 372424	1.50	EC 209452	1.30
IC 108477	2.77	EC 528906	2.50	EC 246176	3.30
IC 372510	2.77	EC 209307	3.60	EC 537850	4.30
IC 372530	5.27	EC 537834	2.10	EC 246181	2.80
IC 372531	5.27	EC 537825	2.60	EC 537853	1.30
IC 372481	4.27	EC 209346	2.60	EC 246131	0.90
EC 605829	1.27	EC 528919	3.10	EC 528908	1.40
EC 537851	6.27	IC 372415	4.10	EC 537885	2.90
EC 537849	3.77	EC 537819	3.10	EC 528905	4.90
EC 537856	5.27	EC 537924	0.60	EC 372463	6.90
EC 528864	1.27	EC 528907	3.10	EC 537867	2.40
IC 372489	0.43	EC 528916	4.60	IC 372482	1.40
EC 537808	5.43	EC 537836	3.10	EC 537875	0.90
IC 372497	4.93	IC 372502	4.60	EC 537855	2.90
IC 372442	1.93	IC 372466	1.00	EC 246120	2.90
EC 533788	2.93	EC 209524	1.50	EC 246147	2.40
P 7 295932	1.93	EC 528888	5.50	OL 11	1.70

RFLP map influenced the β-glucan levels in populations Kanota x Ogle and Kanota x Marion. In barley, three QTLs for malt β-glucan were identified by interval mapping. The QTL on chromosome 2 H had the largest effect on β-glucan (Han *et al*., 1995). In wheat, by using GWAS, seven QTLs for β-glucan were identified on 1A, 2A (2), 2B, 5B, 7A (2) (Marcotuli *et al*., 2016). The research presented here represents a significant advancement in identifying the genomic loci controlling β-glucan content. Also, the markers AB_AM_453, AB_AM_915453, AB_AM_878, AB_AM_219, and AB_AM_692 on LG 4 showed the probability of linkage with 0.1, 0.01, 0.1, 5, 5% levels of significance respectively. Similarly. CIM was also done with Windows QTL Cartographer version 2.5_011 to recognize the chromosomal regions spanning β-glucan QTLs. However, the utilisation for marker-assisted selection (MAS), QTLs must be concentrated in a small area that has a close association with the associated

Table 4. List of polymorphic markers along with the linkage map positions

Marker	Marker name	Position on OT linkage map (Oliver *et al.*, 2010)	Marker	Marker name	Position on OT linkage map (Oliver *et al.*, 2010)
M1	AB_AM_183	34	M14	AB_AM_833	6
M2	AM 22	32-33	M15	AB_AM_709	13
M3	AB_AM_847	34	M16	AB_AM_907	19-26
M4	AB_AM_912	34	M17	AB_AM_829	12
M5	AB_AM_512	32-33	M18	AB_AM_913	12
M6	AB_AM_123	32-33	M19	AB_AM_1055	12
M7	AB_AM_488	32-33	M20	AB_AM_1003	16
M8	AB_AM_915	31	M21	AB_AM_692	16
M9	AB_AM_69	32-33	M22	AB_AM_219	16
M10	AB_AM_905	31	M23	AB_AM_878	4
M11	AB_AM_894	1	M24	AB_AM_453	20-29
M12	AB_AM_87	1	M25	AB_AM_130	5
M 13	AB_AM_897	10			

markers. Thus, precise mapping of potential QTL will aid in discovering genes influencing β-glucan content. These findings might thus be helpful for genetic and breeding research on β-glucan content and the development of markers for MAS.

Conclusion

Based on the comprehensive QTL mapping study conducted to elucidate the genetic basis of β-glucan content in our selected germplasm lines, several significant findings were emerged. Utilizing advanced QTL mapping methodologies including single marker analysis (SIM) and CIM, the key QTLs associated with β-glucan content were identified. Whereas fine mapping of potential QTLs facilitated the eventual identification of genes that influenced β-glucan content. Importantly, our study identified promising germplasm lines (OL10, EC 237851, EC 246158, EC 528874 and EC 372463) exhibiting high β-glucan content, which could serve as valuable donors in future breeding programs aimed at enhancing β-glucan levels in crop varieties. In conclusion, the successful integration of biochemical analysis, genotyping with SSR markers and sophisticated QTL mapping techniques has advanced our understanding of β-glucan regulation at the genetic level. The identified QTLs and potential donor germplasm lines represent valuable resources for the development of β-glucan enriched crops with enhanced nutritional and industrial value.

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