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Published in: Frontiers in Plant Science

DOI: 10.3389/fpls.2014.00197

Publication date: 2014

Document Version
Publisher's PDF, also known as Version of record

Citation for published version (APA):
Quantification of amylose, amylopectin, and β-glucan in search for genes controlling the three major quality traits in barley by genome-wide association studies

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INTRODUCTION

Over the last 30 years, glycemic index (GI) of food has been taken as guideline for controlling diabetes, obesity and other nutritional related diseases (Kirpitch and Maryniuk, 2011) and due to its low GI, barley is being promoted for healthy food products. Barley is an excellent source of complex carbohydrates and β-glucans and ranks the fourth most widely cultivated and utilized cereal worldwide after maize, rice and wheat (Newton et al., 2011). The main carbohydrate in barley is starch ranging from 62 to 77% of the grain dry weight. Amylose and amylopectin are the two components of starch, according to amylose content, barley can be classified into normal type (25–27% amylose), waxy type (non-detectable and below 5% amylose), and high-amylose type (>35% amylose). Variations in the amylose content can affect the physicochemical and functional properties of starch which may in turn affect its utilization in various industrial applications. High-amylose barley contributes toward a low GI and also promotes bowel health (Asare et al., 2011) and hence it is an excellent source of dietary fiber. Barley waxy type starches which are almost devoid in amylose were shown to have excellent freeze/thaw stability making them suitable in frozen foods (Bahatty and Rossangel, 1997).

β-glucan is the primary component of the cell wall in the starchy endosperm of barley accounting for around 75% of endosperm cell wall mass. β-glucan consists of D-glucose monomers linked by different β-glicosidic linkages such as 1,3/1,4 bonds and ranges from 4 to 10% of the dry weight across barley varieties (Brennan and Cleary, 2005; Burton and Fincher, 2012). Although the levels of β-glucans contribute little to the total grain weight, they have great influence on the nutritional value, functionality and uses of barley. β-glucans are regarded to be the most important factor determining malting potential and brewing yield by regulating the rate of endosperm modification and the viscosity of wort during brewing (Brennan and Cleary, 2005). High β-glucan and waxy phenotypes are regarded unfavorable for brewing and feed stuff, but they are considered to be a

Genome-wide association studies (GWAS) for amylose, amylopectin and β-glucan concentration in a collection of 254 European spring barley varieties allowed to identify 20, 17, and 21 single nucleotide polymorphic (SNP) markers, respectively, associated with these important grain quality traits. Negative correlations between the content of amylose and β-glucan (R = −0.62, P < 0.01) and amylopectin and β-glucan (R = −0.487, P < 0.01) were found in this large collection of spring barley varieties. Besides HvCslF6, amo1 and AGPL2, sex6, and waxy were identified among the major genes responsible for β-glucan, amylose and amylopectin content, respectively. Several minor genes like HvGSL4, HvGSL3, and HvCesA6, PWD were also detected by GWAS for the first time. Furthermore, the gene encoding β-fructofuranosidase, located on the short arm of chromosome 7H at 1.49 cM, and SRF6, encoding “leucine-rich repeat receptor kinase protein” on chromosome 2 H, are proposed to be new candidate genes for amylopectin formation in barley endosperm. Several of the associated SNPs on chromosome 1, 5, 6, and 7H mapped to overlapping regions containing QTLs and genes controlling the three grain constituents. In particular chromosomes 5 and 7H carry many QTLs controlling barley grain quality. Amylose, amylopectin and β-glucan were interacted among each other through a metabolic network connected by UDP showing pleiotropic effects. Taken together, these results showed that cereal quality traits related each other and regulated through an interaction network, the identified major genes and genetic regions for amylose, amylopectin and β-glucan is a helpful for further research on carbohydrates and barley breeding.

Keywords: Hordeum vulgare, GWAS, β-glucan, amylose, amylopectin, co-regulation

Abbreviations: AGPase, ADP-Glc pyrophosphorylase; CESA, Cellulose synthase A; CSL, cellulose synthase-like; GBSSI, granule-binding starch synthase I; GDP, guanosine diphosphate; GSL, glucan synthase-like; GT, glycosyltransferase; GTP, guanosine triphosphate; GWAS, genome wide association scan; ID, linkage disequilibrium; QTL, quantitative trait loci; SBE, starch branching enzyme; SNP, single nucleotide polymorphism; SS, starch synthase; UDP, uridine diphosphate.
valuable source of soluble fiber in human diets showing potential functions in reducing GI and serum cholesterol levels, flattening the postprandial blood glucose levels and insulin rises (Thondre and Henry, 2009; Ahmad et al., 2012). The ability of β-glucan to lower the GI is dependent on the barley starch type (Finocchiario et al., 2012) and other grain chemicals, especially the total content of fiber (Aldughassi et al., 2012).

The amylose and β-glucan content are primarily under genetic control but environmental factors especially during grain filling has a smaller contribution to the final grain composition (Baik and Ullrich, 2008). Amylose concentrations in barley are controlled mainly by the *amo1* (amylose) and *waxy* loci mapped on chromosome 1HS (5S) and chromosome 7HS (15S), respectively; another locus *sex6* on 7H is also responsible for amylose content (Morell et al., 2003). Several quantitative trait loci (QTLs) controlling amylose accumulation had been further mapped on chromosome 1, 5, and 7H, respectively (Islamovic et al., 2012).

The amount of β-glucan was shown to be controlled by several QTLs located on chromosome 2 and 5H (Han et al., 1995), 4H (Gao et al., 2004; Wei et al., 2009), and 7H (Li et al., 2008). Cellulose synthase (*CseA*, EC2.4.1.12), cellulose synthase-like (*Gsl*) superfamily and glucan synthase-like (*Gsl*) (EC2.4.1.34) gene family are involved in the synthesis of most β-linked polysaccharides of the cell wall (Farrokhi et al., 2006). *Gsl* is believed to encode enzymes that synthesize the backbone of various non-cellulosic β-linked polysaccharides and have been classified into 8 gene families, designated *Gsla* to *GslH* (Farrokhi et al., 2006; Dhugga, 2012). A cluster of *GslF* genes has been found on chromosome 2H (Burton et al., 2006) and valuable single nucleotide polymorphism (SNP) markers of the *HvCslF6* gene on chromosome 7H have been developed (Cory et al., 2012). Several QTLs for β-glucan content overlap with QTLs for amylose accumulation (Islamovic et al., 2012) probably/likely due to co-localization or interaction between genes.

Here we use genome association studies to map loci and genetic regions responsible for amylose, amyllopectin and β-glucan content, respectively, using a large spring barley variety collection already genotyped with SNPs. To our knowledge, there are no reports on simultaneous genetic analysis of β-glucan, amylose and amyllopectin content by genome-wide association studies (GWAS). This approach can provide new insights into the regulation and interaction mechanisms among genes involved in carbohydrate metabolism in the starchy barley endosperm, and thus highlight markers for crop improvement and breeding of barley varieties with suitable amylose and β-glucan content. As rice genome sequencing has been completed and most genes have been annotated (http://rice.plantbiology.msu.edu/), by analyzing each candidate gene according to syntenous and comparative genomics with rice we were able to elucidate part of the co-regulation network among the biosynthetic pathways of amylose, amyllopectin and β-glucan at the same time.

**Materials and Methods**

**Germplasm and Genotyping**

A population of 254 spring barley varieties obtained from the *Hordeum vulgare* Core Collection of EXBARDIV (http://www.era refunded.org/publicitem?mikey=everyone&pgid=18622&trail=/everyone/9587/18624/18614/18622) (Tondelli et al., 2013) was used for amylose and β-glucan analysis. All material was grown at Scottish Crop Research Institute, now James Hutton Institute Dundee, Scotland (UK) 2010. After harvesting, grains were air-dried and ground into flour, passed through 65 mesh sieves and stored at 4°C in sealed plastic bags until use. All varieties had been genotyped by TraitGenetics, GmbH, Gatersleben (Germany) using the iSelect set of 7864 SNP markers (Comadran et al., 2012).

**Amylose, Amylopectin, and β-glucan Quantification**

Amylose and amyllopectin content was measured according to the Chinese National standard method GB7648-87 and Wang et al. (2010), respectively, with minor modifications: 10 ± 0.1 mg barley grain flour were weighed into a 14 mL tube with caps, dispensed in 0.1 mL 95% ethanol, and treated with 0.9 mL 1 M NaOH for 16 h at room temperature. The samples were mixed and 10 μL supernatant were pipetted into 96-well plates, 190 μL freshly prepared I2-KI solution (3% iodine solution diluted 100 times in 0.01 M HCl before use) were added and incubated for 10 min, potato amylose and amyllopectin (Sigma-Aldrich Co.) were treated in the same way and used to construct the standard curve. Amylose and amyllopectin content was measured according to the absorbance at 620 nm (OD620) and OD550–OD740, respectively. The results were calculated based on sample weight. β-glucan content was quantified according to the assay for barley using Megazyme mixed-linkage β-glucan kit (K-BGLU, Megazyme). All analyses were run in triplicate with independent samples.

**Association Analysis**

Association analyses were all conducted as described in a recent study of diversity and history of European barley (Tondelli et al., 2013). The genetic structure of 254 spring barley cultivars was analyzed using Structure 2.3.3 (Pritchard et al., 2000) with 6810 SNPs. Linkage disequilibrium analyses of the 6810 SNPs were conducted with TASSEL 3.0.9 (http://www.maizegenetics.net/tassel). We employed a naïve model without correction for population structure, a Q model and a Q + K model, both to correct for population structure. For the Q + K model we employed the Kinship matrix and 4 principal components. We also examined P + K models based on Bayesian information criterion (BIC) (Zhu and Yu, 2009). Markers were declared significant at the $P = 0.001 \{−\log (P) = 3\}$ threshold for amylose and amyllopectin and $P = 0.002 \{−\log (P) = 2.75\}$ for β-glucan with the selected model according to a liberal approach proposed by Chan et al. (2010).

**Synteny to Rice and Brachypodium Genomes**

The homologous gene of barley SNP(s) defining the QTL was located in the genome zipper (Mayer et al., 2011) and Strudel (Milne et al., 2010). SNPs with significant associations were used to search for genes functionally related to starch and glucan metabolism according to the annotations of barley genes (http://barleyfcl.dna.afrc.go.jp) and also by taking advantage of the synteny between barley and the annotated rice and *Brachypodium* genomes, respectively. These SNPs or genes close to the SNPs in barley were considered to be candidate genes. Probabilistic
functional gene networks of candidate genes in starch metabolism were integrated based on the data from KEGG (http://www.kegg.com) and RiceCyc (http://pathway.gramine.org).

RESULTS

TRAIT VARIATIONS

The quantification of amylose, amylopectin and β-glucan in the spring barley collection showed normal distributions (Figure 1) and varied from 16.74 to 30.92, 26.47 to 42.97, and 1.34 to 3.20%, respectively. The average amylose content in 212 2-row and 42 6-row types was 24.54 ± 2.36 and 24.35 ± 2.31%, respectively, and the average β-glucan content in 2-row and 6-row types was 2.20 ± 0.38 and 2.15 ±0.35%, respectively (Table S1). Data were consistent with the variances in the whole panel and showed no correlation with geographic origin, year of release or row-type (data not shown). The amylopectin content had the same distribution trend with average content of 33.79 ± 3.42 and 32.92 ± 2.91% in 2-row and 6-row types, respectively. The analysis of the 254 spring barley varieties showed that β-glucan content is significantly negatively correlated with both amylose content ($R = -0.62$, $P < 0.01$) and amylopectin ($R = -0.487$, $P < 0.01$) (Figures 1D,E).

MARKER-TRAIT ASSOCIATION AND MODEL COMPARISON FOR ASSOCIATION ANALYSIS

Tondelli et al. (2013) evaluated this barley collection for population structure and linkage disequilibrium, and arrived at $K = 4$ as the number of principal components in the Q+K model. In order to decrease the false negative associations and still maintain a strong prediction power, the optimization of the model used for the specific case under evaluation was necessary. Naïve, Q, PCA, Kinship (K), Q+Kinship (Q+K), and PCA+Kinship (PCA+K) were performed and interpreted based on BIC and the fitting plot (observed against expected probability, PP-plot). Among the 6 models, naïve, Q and PCA showed skewed P–P plot, the other 3 models equipped with Kinship showed better fitting plot and similar BIC value. Because K model showed the smallest BIC with better fitting plot, the association analyses were based on K model (Figure 2) for all three traits.

MAPPING RESULTS AND ALLELIC EFFECTS

Significant marker-trait associations for β-glucan content using a threshold of $-\text{Log}(P) > 2.7$ ($P < 0.002$) was found for 21 SNPs, and 20 and 17 significant SNPs were identified for amylose and amylopectin, respectively, using a threshold of $-\text{Log}(P) > 3$ ($P < 0.001$) level (Table 1). Most of the SNPs identified accounted for 5–7% of the variation, except 2 SNPs for amylopectin, SCR1_RS_6792 and SCR1_RS_208186 that accounted for 14.5 and 46.9% of the variation, respectively. Almost 40% of the SNPs were located on chromosome 7H, the remaining are distributed on 1, 4, 5, and 6H. The SNP for amylopectin accounting for 14.5% of the variation was the only located on chromosome 2H (Table 1). Using the genetic position in Table 1, all SNPs were included in the OPA 2009 consensus map (Figure 3) together with previously mapped genes relevant to this study in order to identify overlap among the three traits and known genes and QTLs.

Three significant SNP regions associated with amylopectin were detected on chromosome 7H. Five SNPs detected at the region from 12.75 to 15.37 cm on 7H are very close to the waxy locus. Besides this locus, new SNPs have been identified for candidate genes controlling amylopectin content in the present GWAS. The SNP at 1.49 cm (SCRI_RS208186) was detected for the first time and accounted for about 46.9% of the variation (Table 1), which should represent the major locus responsible for amylopectin content. The significant SNP region from 126.56 to 127.55 cm on chromosome 7H might be linked to Amy2 locus, which had been mapped at 126 cm.

Barley chromosome 7H also has 6 SNPs significant for β-glucan content located around 71 cm showing the highest genetic effect and each SNP accounted for 5–6% variations (Table 1, Figure 3). These SNPs map close to cellulose synthase like gene HvCsf6 which had been mapped around 71 cm according to the comparative barley map (http://wheat.pw.usda.gov).

Barley chromosome 1H have four possible SNPs for amylose content located close to the amo1 gene located at 56.5 cm between marker lca1 and Jso074 (Barley BinMap 2005, http://wheat.pw.usda.gov) close to 60 cm on the map of OPA2009 consensus.

CANDIDATE GENES FOR β-GLUCAN CONTENT

The significant SNPs associated with β-glucan content on chromosome 7H around 71 cm are within a 1–2 cm of the HvCsf6 gene (Figure 3). HvCsf6 was found essential for 1,3; 1,4)-β-D-glucan biosynthesis from UDP-glucose (Figure 4). Other significant SNPs for β-glucan content identified in this study are located on chromosome 4 and 6H. The gene containing SCR1_RS_156130 SNP on 4H is coding for glucan synthase-like 3 (EC 2.4.1.34, HvGSL3) which is known to be involved in the generation of β-glucan by catalyzing the transfer of sugar moieties from activated donor molecules to specific acceptor molecules to form glycosidic bonds. This gene showed 99% identity to Brachypodium GSL3 gene (Bradi2g40460), and 83% identity to rice 1,3,β-glucan synthase gene (LOC_Os03g30610). HvGSL3 belong to the callose synthase gene family of the GLS family and catalyzes the synthesis of 1,3-β-glucan (Figure 4). Another SNP (BOPA1_1565-514) at 66.08 cm on 6H shows synteny to a gene encoding 60S ribosomal protein L31 (MLOC_36568, LOC_Os06g21480 and Bradi3g53460) which catalyzes GTP to GDP hydrolysis in maize (www.gramine.org).

CANDIDATE GENES FOR AMYLOSE CONTENT

Based on this study, and considering a LD of 4–6 cm (Tondelli et al., 2013), associated SNPs for amylose located on chromosome 1H are likely to be close to the amo1 gene as they were all mapped within a 1–2 cm region (Figure 3). However, when analyzing the genes according to barley genome sequence, amo1 gene is far from these SNPs, which can be due to mistakes in assembling of the particular barley contig or amo1 is not the significant locus in this case. Within this genomic region, one (1,3,1,4)-β-glucanase gene (MLOC_61746) was found.

The SNP SCR1_RS16118 located on chromosome 5H at 71 cm close to a glycogen debranching enzyme gene (MLOC_10776) which is almost identical to HvISA3 and the other significant SNPs on chromosome 5H at the region
FIGURE 1 | Quantification of barley grain constituents. The distribution of amylose content (A), amylopectin content (B) and β-glucan content (C) and the correlation between amylose content and β-glucan content (D), amylopectin content and β-glucan content (E) in 254 barley spring cultivars.
of 152.36–155.42 cM was found syntenous with the region of rice genome containing several GT genes. In which LOC_Os03g60939, syntenous to SNP SCRI_RS_132308, codes for dolichyl-phosphate β-glycosyltransferase (EC2.4.1.117) belonging to the GT2 family which includes cellulose synthase acting on UDP-glucose and participating in n-glycan biosynthesis. Furthermore, HvAGPL2 was found only 3458 bp upstream SCRI_RS_132308.

CANDIDATE GENES FOR AMYLOPECTIN CONTENT

For amyllopectin content, the significant associated SNP SCRI_RS_98829 on chromosome 7H located at 15.37 cM is located in the starch synthase gene (MLOC_66457, GBSSI), also designated as waxy. It is essential for the synthesis of amyllose and in addition it has a role in the elongation of amyllopectin carbon chains (Denyer et al., 1996). The significant associations around 126 cM on chromosome 7 should be Amy2 which catalyzes the hydrolysis of (1→4)-α-D-glucosidic linkages in starch degradation (Figure 3). sex6 locus (SSIIa), one major gene responsible for amyllopectin synthesis, was mapped around 126 cM on 7H according to barley genetic map OPA2005 (http://wheat.pw.usda.gov), however, according to its’ physical position, sex6 should be close to SCRI_RS_158266 and SCRI_RS_17908 located on 12.75 cM (Figure 3). These two SNPs are located in the phosphoglucom water dikinase gene (PWD, MLOC_73759). PWD catalyze the transfer of the β-phosphate of ATP to a glucosyl residue of amyllopectin that has specifically been phosphorylated at the C-3 positions by α-glucan water dikinase (Kotting et al., 2009). The phosphorylation of a portion of the glucosyl residues is a prerequisite for transient starch mobilization. It still remains to show how PWD acts in cereal endosperm starch metabolism, whether the influence is directly on the amyllopectin synthesis or indirectly by regulating amyllopectin metabolism through interactions.

Another two SNPs SCRI_RS_208186 and BOPA1_7172-1536 at 1.49 cM on chromosome 7H were orthologous to rice genes encoding β-fructofuranosidase (EC 3.2.1.26) (LOC_Os02g01590) and polygalacturonase (EC3.2.1.15) (LOC_Os03g03350), respectively. Both enzymes belongs to the glycoside hydrolase family and β-fructofuranosidase catalyzes sucrose (sucrose-6P) or stachyose degradation to actuate D-glucose (glucose-6P) to recycle (Figure 4). LOC_Os07g42626 (SRF6, Leucine-rich repeat transmembrane protein kinase 1) ortholog to SNP SCRI_RS_6792 on chromosome 2H with the high P-value (Table 1) might also be very important for polysaccharide synthesis or transport. The SNP SCRI_RS_205669 on chromosome 1H was located on β-1,3-galactosyltransferase-like protein gene (MLOC_16945), orthologs to rice galactosyltransferase family.
Table 1 | Associated SNPs for β-glucan, amylose and amylopectin content with the highest possibility called by K model.

<table>
<thead>
<tr>
<th>Traits</th>
<th>SNPs</th>
<th>CH</th>
<th>Position</th>
<th>P-value</th>
<th>R²</th>
<th>Alleles</th>
<th>Annotation</th>
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<tbody>
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<td>β-glucan</td>
<td>BOPA2_12_30118</td>
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<td>67.56</td>
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<td>T/C</td>
<td>Methyladenine glycosylase domain containing protein</td>
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<td>67.56</td>
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<td>0.046</td>
<td>C/T</td>
<td>Heat shock protein DnaJ</td>
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<tr>
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<td>–</td>
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<td>2.88E-04</td>
<td>0.059</td>
<td>A/G</td>
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<td></td>
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<td>Aquaporin protein</td>
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<td>C/G</td>
<td>Glycoside hydrolase, family 28, putative, expressed</td>
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protein gene (LOC_Os07g09670), which belong to glycosyl transferase family 31 and catalyzes the transfer of galactose.

**THE INTERACTIONS OF CANDIDATE GENES ON BIOSYNTHESIS OF AMYLOSE, AMYLOPECTIN AND β-D GLUCAN**

The SNP BOP2_12_30716 located on chromosome 5H detected for amylose codes for lysosomal alpha-mannosidase, 70 kb upstream from *HvCslF7* which was confirmed to mediate the synthesis of cell wall components (Burton et al., 2006), furthermore, *CESA2* was downstream this gene (Figure 3). *HvCslF7* and *HvCESA2* were confirmed to be responsible for the synthesis of cell wall 1,3,1,4-β-glucan and primary cell wall assembly which was the predominant cell wall components in endosperm cell (Burton et al., 2006; Held et al., 2008). Other genes like MLOC_61808 (BOPA1_6781-1073) encoding 1,3-β-glucosidase (EC3.2.1.39), hydrolyze 1,3-β-glucan to D-glucose (Figure 4) which is used in metabolism of starch, sucrose and other carbohydrates. Another candidate gene MLOC_61746 locating around 55.5 cM on chromosome 1H, also detected for amylose content, encoding (1,3;1,4)-β-glucanase (EC3.2.1.73), was functionally linked to the hydrolysis of (1,4)-β-D-glucan linkages and acts on lichenin and cereal β-D-glucans containing (1,3;1,4)-bonds (Figure 4).

Furthermore, the SNP at 2.55 cM on chromosome 7H detected for amylopectin was close to glucan synthase-like 8 gene which was very similar to *HvGSL4* and was mapped close to marker ABG704 at the intervals of 0–5 cM on the short arm of chromosome 7H (Schobert et al., 2009). On its syntenous rice genome region, the ortholog was also adjacent to one of the rice cellulose synthase genes (LOC_Os06g02260). The gene containing SNP BOPA1_3345-247 on chromosome 7H containing around 55.5 cM on chromosome 1H, also detected for amylose content (Asare et al., 2011). Lines showed that in addition to waxy type also high-amylose barley lines (Hang et al., 2007) as described in another study of 5 hull-less barley lines (Lee et al., 2011), while a study of ten hull-less barley lines showed that in addition to waxy type also high-amylose barley had higher β-glucan content compared to barley with normal amylose content (Asare et al., 2011).

**SNPs ASSOCIATION WITH β-D GLUCAN, AMYLOSE AND AMYLOPECTIN**

Barley, being self-pollinator, has a relative high LD of 4–6 cM based on a threshold $r^2$ value of 0.15 making gene discovery by GWAS feasible (Comadran et al., 2012). Significant SNPs for β-glucan were distributed across chromosome 1, 4, 5, 6, and 7H. A QTL for β-glucan located on the short arm near the telomere (13.6–21.5 cM) on chromosome 4H between MWG077-Olel was mapped based on both “Morex” and “Steptoe” background (Gao et al., 2004). The major SNPs region on chromosome 7H detected by present GWAS contains *HvCslF6*, which is consistent with other studies. One QTL mapped in a recombinant inbred line mapping population was also located in the region containing *HvCslF6* (Islamovic et al., 2012). A major QTL explaining up to 39% of the β-glucan concentration was reported to be located on the centromeric region of chromosome 7H (Li et al., 2008). Three associated SNP markers on chromosome 7H around 111 cM were identified with GWAS, among which nud (naked caryopses gene) locus should be the determiner for β-glucan content (Mezaka et al., 2011). The nud gene was found to be linked with the bgl gene which has been mapped to the centromeric region of chromosome 7H and the bgl (β-glucanless) phenotypes co-segregated with *HvCslF6* and caused by the mutation of *HvCslF6* (Tonoooka et al., 2009).

**DISCUSSIONS**

**COLORIMETRIC METHOD AND CORRELATIONS BETWEEN AMYLOSE AND β-D GLUCAN**

Amylopectin was measured in parallel with amylose using a dual-wavelength colorimetric method, although the widely used method for quantifying amylopectin is by calculating the difference between total starch and amylose measured. The colorimetric method is easy to operated and economic in use and using dual wavelength has already been proven to be a valid method to measure amylopectin content (Wang et al., 2010).

Though the amylose content determined with the L_{2}/KI method showed a little higher value compared with those obtained by Megazyme Kit when analyzed several barley samples, there were positive correlations between the colorimetric method and Megazyme Kit (data not shown) and for genetic analysis was considered valid. The negative correlations between amylose and β-glucan is consistence with two previous studies based on a much small number of specialty barley lines. β-glucan was found to be negatively correlated with amylose in a study of 27 barley lines (Hlang et al., 2007) as described in another study of 5 hull-less barley (Lee et al., 2011), while a study of ten hull-less barley lines showed that in addition to waxy type also high-amylose barley had higher β-glucan content compared to barley with normal amylose content (Asare et al., 2011).

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For amylose content, a number of QTLs for starch or amylose content have also been mapped on chromosome 1, 5, and 7H in the same regions (Islamovic et al., 2012; Pasam et al., 2012) as the chromosome regions detected here.

Waxy locus associating to amylopectin in the present GWAS was earlier mapped between markers ABG320 and ABC151A located around 10.1–20.5 cM (http://wheat.pw.usda.gov) and produced a high level of amylopectin. Islamovic et al. (2012) also found one of three QTLs were mapped to chromosome 7H might be the waxy locus, using 297 markers in a population of 146 F6-derived RILs. Besides these major loci mapped before, two new SNPs located at 1.49 cM on chromosome 7H were first detected here. That indicate GWAS is effective in identifying major loci as well as detecting some new loci. Furthermore, some associated SNPs were overlapped among amylose, amylopectin and β-glucan, which indicated there should be some interactions among amylose, amylopectin and β-glucan metabolites.

**CANDIDATE GENES AND THEIR INTERACTIONS**

**β-glucan**

HvCslF6 located around 71 cM on chromosome 7H should be the major gene responsible for β-glucan. Similarly, in a GWAS of oat one significant DArT marker sequence associated with β-glucan content was located in rice and found adjacent to an OsCslF gene (Newell et al., 2012). HvCslF6 showed the highest transcript level throughout the endosperm development out of 7 HvCslF genes identified and characterized (Burton et al., 2006, 2008) and it was the key determinant for the biosynthesis of (1,3; 1,4)-β-D-glucan (Taketa et al., 2012). Over-expressing HvCslF6 oat lines showed 80% higher (1,3; 1,4)-β-D-glucan content (Burton et al., 2011) and genetic markers for this gene had been applied successfully in segregating individuals with different β-glucan content (Cory et al., 2012).

Besides HvCslF6, HvGSL3 located on chromosome 4H, were also detected in this study. The minor genes controlling β-glucan content seems to cluster together. As in the same syntenous region of Brachypodium, a cluster of genes involved in β-glucan synthesis including β-galactosidase (Bradi2g40450) and glucan synthase-like 11 (Bradi2g40437) can be found. Furthermore, downstream of HvGSL3, a glucan synthase-like gene HvGSL1 has been mapped on 107.7 cM (Schober et al., 2009), corresponding to about 130 cM in the SNP map of OPA 2009 (http://wheat.pw.usda.gov).

**Amylopectin**

In the present GWAS, we obtained several genes responsible for amylopectin content including waxy. The waxy gene is epistatic over the am01 gene and its mutation affected the activity of GBSSI greatly (Hylton et al., 1996), which means that the loss
or the reduced activity of GBSS1 can result in a waxy phenotype with high amylopectin content, while its mutation did not abolish amylase synthesis completely in the starchy endosperm but reduced the amylase content below 5% (Andersson et al., 1999).

PWD, one of the new genes identified for amylopectin in this study, exclusively phosphorylates the C-3 positions of starch (Kotting et al., 2009). Phosphorylation of starch disrupts the packing of amylopectin double helices and can render them accessible for the subsequent degradation by enzymes like isoamylase (ISA), pullulanase (PUL), and alpha-/beta- amylase (AMY, BMY) (Zeeman et al., 2010) (Figure 4) and influences amylopectin accumulation. Reduced PWD expression in transgenic Arabidopsis can result in excess starch phenotype (Kotting, 2005; Kotting et al., 2009).

β-fructofuranosidase might play an important role in starch synthesis especially in the amylopectin pathway because its orthologous SNP SCR1_RS_208186 had the highest P-value for amylopectin content (Table 1). Though the function of SRF6 remained elusive, it might act as the key protein kinase to catalyze the phosphorylation of those enzymes, like SS and SBE, participating in carbohydrate metabolism (Figure 4). It was found that enzymes for amylopectin synthesis were regulated by protein phosphorylation which played a wide role in controlling starch metabolism in wheat amyloplasts (Tetlow et al., 2004) and starch synthesis is regulated through the interactions of a number of genes and regulators, thus different combinations of mutants resulted in different amylase content and amylase to amylopectin ratio. As an example a double mutant amo1sex6 showed parallel increases in both amylase and amylopectin content (Li et al., 2011).

INTERACTIONS AMONG AMYLOSE, AMYLOPECTIN AND β-GLUCAN

In this study, several genes belonging to GT family were identified to be associated with amylase and amylopectin content. Members

FIGURE 4 | Putative functions of the candidate genes in the co-regulated metabolite network of starch and β-glucan. The candidate genes and their encoding protein were dashed circled. The cell wall components were marked by black box. The dash arrows indicated there were no a single step. EC3.2.1.73: (1,3; 1,4)-β-glucanase; EC3.2.1.21: β-1,4-glucosidase; EC3.2.1.39: glucan-1,3-β-glucosidase; EC3.2.1.6: glucan-1,3-β-glucosidase; EC2.4.1.12: Cellulose synthase; EC2.4.1.34: glucan synthase; EC2.4.1.117: dilichyl-phosphate-β-glycosyltransferase; EC2.4.1: galactosyl transferase; EC2.7.7.27: ADP-glucose pyrophosphorylase; EC3.2.1.23: β-galactosidase; EC2.2.1.26: β-fructofuranosidase; EC2.4.1.43: glucosyl transferase; EC3.2.1.15: polygalacturonase; EC2.7.9.5: phosphoglucom water dikinase; EC2.3.1.168:Isoamylase; EC2.2.2.1: amylase; EC3.2.1.41: Amylopullulanase.
of the GT family and glycoside hydrolase were also found to be responsible for resistant starch accumulation in a recent GWAS of barley (Shu et al., 2012). That indicated these genes might affect synthesis of starch molecular components indirectly by regulating other pathways in the metabolic network through the same substrates especially those depending on UDP-glucose (Figure 4). In cereals like barley, other major carbohydrates of endosperm are cell wall polysaccharides of which β-glucan is the primary component.

Chromosomes 5 and 7H contain major QTLs and genes controlling amylose, amylopectin and β-glucan in barley. The overlapping associations among these three traits might suggest that polysaccharides like starch and β-glucan in barley endosperm are correlated due to shared genetics and may have negative or positive pleiotropic effects. UDP-glucose is a central substrate in these metabolic pathways, the mutation of one single gene or in one single step may cause dramatic changes in the whole metabolic network a new area for pleiotropic mechanism (Stearns, 2010). Several minor genes might affect synthesis of starch fractions by regulating the formation of the cell wall polysaccharides constituents, while how they work and interact needs further studies. Chromosome 7H, on which several genes responsible for starch and β-glucan were closely located as an operon like structure, seems to be an important chromosome for barley grain quality. These results showed that, with GWAS, major genes or genetic regions as well as two new genes important for quality traits in cereal crops can be identified successfully. This approach can also help to dissect element in interaction network resulting in different traits, interactions that often has been said to be pleiotropic effects. The highly associated SNPs distributed one several chromosomes especially those within the candidate genes are a first choice for testing the power of genomic selection in barley.

ACKNOWLEDGMENTS
The grant j. nr 3304-ERA-0700752 from The Danish AGRifish Agency to Søren K. Rasmussen is acknowledged. Xiaoli Shu gratefully acknowledges financial support by the IAEA (CPR15422) and Research Projects 2013CBA01403 and 2012C12902-2.

SUPPLEMENTARY MATERIAL
The Supplementary Material for this article can be found online at: http://www.frontiersin.org/10.3389/fpls.2014.00197/abstract

Table S1 | The AAC, amylopectin and beta-glucan content in all analyzed 254 European spring barley varieties.

REFERENCES


Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 25 February 2014; accepted: 23 April 2014; published online: 15 May 2014. Citation: Shu X and Rasmussen GWAS for quality in barley *(Hordeum vulgare)*. *Frontiers in Plant Science*. Copyright © 2014 Shu and Rasmussen. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.