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RESEARCH ARTICLE

Conditional and unconditional QTLs mapping of gluten strength in common wheat (*Triticum aestivum* L.)

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Abstract

Dissecting the genetic relationships among gluten-related traits is important for high quality wheat breeding. Quantitative trait loci (QTLs) analysis for gluten strength, as measured by sedimentation volume (SV) and gluten index (GI), was performed using the QTLNetwork 2.0 software. Recombinant inbred lines (RILs) derived from the winter wheat varieties Shannong 01-35×Gaocheng 9411 were used for the study. A total of seven additive QTLs for gluten strength were identified using an unconditional analysis. *QGi1D-13* and *QSv1D-14* were detected through unconditional and conditional QTLs mapping, which explained 9.15–45.08% of the phenotypic variation. QTLs only identified under conditional QTL mapping were located in three marker intervals: *WPT-3743–GLU-D1* (*1D*), *WPT-7001–WMC258* (*1B*), and *WPT-8682–WPT-5562* (*1B*). Six pairs of epistatic QTLs distributed nine chromosomes were identified. Of these, two main effect QTLs (*QGi1D-13* and *QSv1D-14*) and 12 pairs of epistatic QTLs were involved in interactions with the environment. The results indicated that chromosomes 1B and 1D are important for the improvement of gluten strength in common wheat. The combination of conditional and unconditional QTLs mapping could be useful for a better understanding of the interdependence of different traits at the QTL molecular level.

Keywords: wheat (*Triticum aestivum* L.), gluten strength, gluten index, sedimentation volume, unconditional QTL mapping, conditional QTL mapping

1. Introduction

Wheat (*Triticum aestivum* L.) gluten gives elasticity to dough, helping it rise and maintain its shape, and often gives the final product a chewy texture. The quality of food products, such as baked bread, steamed bread, and noodles, is considerably influenced by wheat quality traits and is particularly determined by gluten strength. Therefore, improvement in gluten strength is emphasized in wheat breeding programs. Gluten strength is commonly measured by gluten index, sedimentation volume (SV), the dough rheology, such as

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mixing properties, alveograph, extensograph, and farinograph parameters (Huang *et al*. 2006; Elangovan *et al*. 2008; Li *et al*. 2009; Kerfal *et al*. 2010; Tsilo *et al*. 2011). However, SV, which is a composite reflection of protein content and quality, has been considered a useful indicator for not only detecting the gluten strength of wheat flour but also estimating the quality of the food made from wheat flour (He *et al*. 2004; Ozturks *et al*. 2008). And SV appears to be the most valuable method for predicting gluten strength because it significantly correlates with rheological properties (Clarke *et al*. 2000). Compared with the SV, gluten index (GI) is less dependent on the protein concentration (Clarke *et al*. 2010). Cubbada *et al*. (1992) found that GI was closely correlated with the SDS sedimentation volume (r=0.78–0.81). Edwards *et al*. (2007) demonstrated that GI was closely correlated with the alveograph W value and the mixograph mixing time. Therefore, the analysis of GI and SV is emphasized for improvement in gluten strength in wheat quality.

Gluten-related traits are quantitative traits that are difficult to assess because of the influences of genetics and environmental conditions. Quantitative trait locus (QTL) analysis has provided an effective approach for dissecting complicated traits into component loci to study their relative effects on a specific trait (Doerge 2002). Many studies have analysed QTLs for gluten strength measured by SV (Patil *et al*. 2009; Conti *et al*. 2011; Kumar *et al*. 2013). Patil *et al*. (2009) identified that in addition to the major QTL on chromosome 1B, regions on chromosomes 1A, 4A, 5B, 6A, and 7A were associated with SV. Conti *et al*. (2011) identified 11 QTLs for SV located on chromosomes 1A, 1B, 3B, 4A, 4B, 6A, 6B, and 7A, which contributed from 4.9 to 54.2% of the phenotypic variation. More recently, Kumar *et al*. (2013) identified five QTLs on chromosomes 1B, 3B, and 7B and the phenotypic variations explained by each QTL ranged from 2.6 to 11.6%. Regarding GI, five QTLs that mapped onto chromosomes 1A, 1B, 1D, and 6A were identified which explained 3.96 to 22.44% of the phenotypic variation (Deng *et al*. 2014).

However, most of the previously identified QTLs belonged to the class of unconditional QTLs. Zhu (1995) proposed conditional analysis methods that has been used to study developmental quantitative genetics. And conditional QTL mapping has been studied at different developmental stages for plant height, tiller number, and other phenotypic characteristics (Liu *et al*. 2005; Wang *et al*. 2010; Cui *et al*. 2011). Now the conditional QTL mapping method was developed to define the genetic relationship among different traits at the QTL level. This method serves to indicate whether the QTL of the target trait is associated with the components related to the trait (Deng *et al*. 2013). To date, however, only few studies have investigated conditional QTL mapping for wheat quality traits.

In the present study, we investigated the SV and GI associated with gluten strength in a RIL population. The objective of this work was to validate the QTLs controlling wheat gluten strength and the information obtained from the present study could contribute to marker-assisted breeding for wheat quality traits.

2. Materials and methods

2.1. Plant materials

The recombinant inbred line (RIL) population ($F_{8:9}$) contained 182 lines derived from a cross of common winter wheat Shannong 01-35 and Gaocheng 9411. The two parents greatly differ in quality traits. Shannong 01-35 created in our lab is a middle-gluten variety germplasm. Gaocheng 9411 is a strong-gluten variety from the Gaocheng Institute of Agricultural Sciences in Hebei Province, China.

2.2. Field trails

The RIL population was grown in Tai'an (116°36′E, 36°57′N) in 2008 (E1) and 2009 (E2) and in Suzhou (116°58′E, 33°38′N) in 2010 (E3). The pooled data were derived from the average of the three environments (AvE). The strains were planted in a randomized complete block with two replications in each environment. Each block consisted of three 2-m-long rows with a row to row distance of 21 cm. Crop management was performed according to local cultivation practices.

2.3. Measurement of gluten-related traits

Samples were milled using a Laboratory MLU202 (BUHLER, Jiangsu, China), as indicated in AACC26-21 (AACC International 2000). Flour protein content (FPC) and grain protein content (GPC) were measured using NIR DA7200 (Perten instruments 7200 type, Huddinge, Sweden). Wet gluten content (WGC), dry gluten content (DGC), and gluten index (GI) were measured with a gluten analysis instrument (Perten Instruments 2200 type, Huddinge, Sweden) according to AACC38-11 (AACC International 2000). Sedimentation volume (SV) was determined using the AACC method 56-61A (AACC International 2000).

2.4. Genetic linkage map construction

The linkage groups were constructed using MAPMAKER 3.0 (Lincoln *et al*. 1992). The linkage map was drawn using Mapchart 2.3 (Voorrips 2002), and the Kosambi mapping function was used to convert the recombination fractions into cM values as map distances (Kosambi 1944). The RIL