THE EFFECT OF HMW-GS ON GLUT-A1, GLUT-B1, GLUT-D1 IN SOME LOCAL BREAD (Triticum aestivum L.) WHEAT GENOTYPES

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Abstract. Wheat gluten proteins are extremely important proteins in terms of quality. Glutenin from the sub-units of gluten, because of the multi-polymer structure is effective in the rheological properties of the dough. In the study, samples taken from the endosperm section of local bread wheat (Triticum aestivum L.) genotypes; The HMW-GS band patterns in the 1A, 1B, 1D genomes were determined, and the band patterns of the glutenin were determined using the vertical electrophoresis apparatus by SDS-PAGE. During the determination of HMW-GSs; Cheyenne, Gabo, Chinese Spring, Insignia genotypes were used as markers. According to the data obtained, some bread wheat genotypes carry high-quality glutenin bands found in the markers used in the study. As a result, in accordance with the data obtained from the study, the use of some bread wheat genotypes with high-quality scores in production will contribute to the development of high-quality products. However, a high-quality score with the improvement of genotypes used as parental lines, yield, and quality of high-new bread wheat cultivars will be developed.

Keywords: band, genotype, HMW-GS, local bread wheat, mobility, molecular weight, quality, score

Introduction

Wheat is a very important food material in terms of being the raw material of various nutrients. In order to meet the needs of the world population, the quality of flour should be increased due to wheat quality in order to meet the increasing demands along with the efficiency of the unit area. The quality of wheat produced in Turkey some years due to inadequate quality flour in some areas to meet the consumer demand is made by blending high-quality wheat. In addition, considering the self-sufficiency and the export of approximately 3.32 million tons of flour annually, it is essential to increase the flour quality of the bread wheat varieties (Anonymous, 2018). The most important parameter that determines the flour quality characteristics obtained from wheat is gluten proteins (Tatham and Shewry, 2000; Özberk, 2018). Gluten proteins are examined in two parts, gliadins and glutenins, and glutenin polymers form a multi-polymer structure by cross-linking of HMW-GS and LMW-GSs (Wrigley, 1996; D’Ovidio and Masci, 2004; Appelbee, 2006). Although HMW-GSs have a determinative role in dough basic properties, LMW-GSs also play an important factor (Cornish et al., 2001; D’Ovidio and Masci, 2004). Researchers also indicate that gluten proteins are highly effective in environmental factors as well as genetic factors (Payne et al., 1981; Troccoli et al., 2000). The use of sulfur fertilizers during wheat cultivation, in particular, increases the quality of gluten and thus increases the technological properties of flour (Zhao et al., 1999). HMW-GS is the bands that vary between I-5 in bread and durum wheat (Waines and Payne,
that number between 1-3 due to the absence in the durum wheat genome 1D, the glutenin banding varies from 3-5 and in bread wheat. In the studies carried out by the researchers, the sulfur-deficient omega-gliadin and HMW-GS proteins increased in the wheat grown in the areas where sulfur deficiency was observed, on the other hand, they reported that sulfur-rich proteins such as gamma and LMW-GS were reduced (Wieser et al., 2004). HMW-GS in the long arms of 1A, 1B, 1D genomes in bread wheat (Triticum aestivum L.) and gliadins found in short arms of 6A, 6B, 6D genomes are extremely important for the quality of the flour (Garg et al., 2006). In particular, HMW-GSs are effective on the baking quality of the products obtained from bread wheat (Shewry et al., 1995). In terms of gluten quality, in the grain filling process, the 1D genome HMW-GSs are more susceptible to the formation of poor gluten content with the high temperature occurring in the bread wheat (Deng et al., 2008) and this indicates the importance of environmental factors (Raza, et al., 2019). In this study, it was aimed to determine and score the HMW-GS protein bands in the 1A, 1B, 1D genomes of local bread wheat genotypes which have a significant effect on the quality and to determine the bread wheat genotypes with superior quality bands.

Review of literature

HMW-GSs are important parameters to determine gluten quality characteristics. Numerous studies have been conducted to determine the formation and functional relationships of gluten in many researchers and research groups (Payne et al., 1987; Lawrence et al., 1988; Popineau et al., 1994; Gupta et al., 1995; Yu et al., 2019). However, the effect of the Glu-1 locus allelic variations on dough formation and development was not fully characterized (Li et al., 2016a). Some researchers stated that hydrogen and disulfide bonds are important factors for gluten rheology during dough formation and development (Wang et al., 2013; Li et al., 2016b). According to Wang et al. (2003), the glutenin macropolymer structure and HMW-GS formations determine the rheological properties of dough and glutenin macropolymer structure with have found a close correlation between the end-use quality. Shewry and Halford (2003) stated that although HMW-GSs constitute approximately 20% of all glutenin proteins, they have a major effect on the viscoelastic properties of the dough. The number and distribution of cysteine residues in the 1A, 1B, 1D genomes found in HMW-GSs is important for the formation of proteins due to the di-sulfide bonds they contain. These structures are important factors related to the technological properties of the dough. HMW-GS cysteine residues are important in determining the elastic and polymeric structure of the dough (Tatham et al., 1985; Buonocore et al., 1998; Wang et al., 2016). Payne (1987) and Roy et al. (2018) Glu-1 locus allelic varieties have a significant effect on bread quality characteristics, especially in the end-use quality development has stated that a very high potential has been obtained. Zhang et al. (2018) HMW-GSs have been highly effective on dough elasticity and baking quality. Glu-B1 and Glu-D1 genomes were found in the study of different bread wheat genotypes, respectively; 17 + 18 and 5 + 10 bands have a high effect on the amount and quality of gluten (Gupta et al., 1994). The technological quality development of flour can be achieved by increasing the number of active HMW-GS in genomes or by regulation of allelic formation (Lafiandra et al., 1998).
Materials and methods

The research was conducted in Tokat Gaziosmanpaşa University Faculty of Agriculture, Grain Laboratory (Fig. 1). Gluten quality of bread wheat genotypes with HMW-GS bands (Gianibelli et al., 2002; Singh et al. 1991) were determined by using vertical electrophoresis device with a modified method of Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis (SDS-PAGE) (Koyuncu’s, 2009) (Fig. 2). The used of 21 bread wheat genotypes in the study was obtained from Turkey Seed Gene Bank. Six bread wheat varieties used in the study were obtained from the International Maize and Wheat Improvement Center and used as a marker (Table 1). The scoring of the bands in 1A, 1B, 1D genomes was determined by the method of scoring (Figs. 3 and 4) defined by Lasztity (2002), Lasztity and Abonyi (2009) and Payne (1987).

Figure 1. The study was carried out in Tokat province

Figure 2. Vertical electrophoresis device
The effect of HMW-GS on Glu-A1, Glu-B1, Glu-D1 in some local bread (Triticum aestivum L.) wheat genotypes

Figure 3. 1A, 1B, 1D genomes with the HMW-GS bands

Figure 4. 1A, 1B, 1D found in the genome of protein bands and scores

Table 1. Bread wheat varieties that are used as markers

| Varieties     | 1A genome bands | 1B genome bands | 1D genome bands |
|---------------|-----------------|-----------------|-----------------|
| Janz          | 1               | 7 + 8           | 2 + 12          |
| Gabo          | 2*/Null         | 17 + 18         | 2 + 12          |
| Chinese Spring| Null            | 7 + 8           | 2 + 12          |
| Cheyenne      | 2*              | 7 + 9           | 5 + 10          |
| Baxter        | Null            | 13 + 16         | Null            |
| Insignia      | 1               | 20              | 5 + 10          |
Results and discussion

Wheat breeders aim to ensure high gluten growth in genotypes where quality comes to the forefront with their yield characteristics (He et al., 2001). Studies conducted by researchers at Glu-1 locus 1A, 1B, 1D in wheat HMW-GS genome bands were detected in the relationship to between wheat quality (Payne et al., 1987; Vapa et al., 1996). Approximately 13-14%, 55-58% and 28-30% of HMW-GSs respectively; They were found in the 1A, 1B, 1D genomes (Li et al., 2016a). Larroque et al. (2004) stated that in terms of the functional properties of bands contained 1A, 1B, 1D genomes were found to be highly effective. In different studies examining the functional properties of HMW-GSs, they reported that it affects approximately 70% of the quality of bread, although it accounts for approximately 11% of the total protein content (Yu et al., 2019). In the study in which quality scoring was performed according to the protein bands found in the HMW-GS; 1A, 1B, 1D genomes, the genotypes examined were found to have 8, 7, 6, 5 (Table 2). TR63581, TGB000534 genotypes 2* in the 1A genome, TGB000526 genotypes in the 1, 1A genome in the other genotypes have a null band (Figs. 5 and 6). The 1A genome affects about 15% of the wheat quality changes according to the 1B and 1D genomes (Yu et al., 2019). One of the important quality parameters in terms of Farinograph values 1 and 2* bands in the genome 1A has a higher value than the genotypes contain null bands (Bagulho et al., 2004), especially the 2* band has been determined to have a high Farinograph-PSI value. The 2* band carrying TR63581, TGB000534 genotypes were determined to have a higher Farinograph-PSI (Table 2). 1B genome of 12 genotypes 7 + 8, 7 genotypes 7 + 9, 1 genotype 7, 1 genotype determined to carry the 20 bands (Fig. 3). 7 + 8 band of the other band (7 + 9, 7, 20) having a higher quality score (Fig. 4). In the studies performed, the researchers found that 1A genome 1, 2*, 1B genome 14 + 15, 13 + 16, 7 + 8 and 7 + 9 bands were positive for the quality of gluten and thus the quality of the products (Kaan et al., 1995). Other researchers reported that 20 and 6 + 8 bands have negative effects (Oak et al., 2004; Nachahi et al., 2009). According to the obtained results, it was determined that the examined genotype of TR44433 carrying 20 bands in the 1B genome was determined that could show negative quality characteristics (Table 2). The 1B genome of the TGB000534 genotype only carries bands with high scores in the 1A and 1D genomes, despite the presence of only 7 bands (Fig. 6). Examined other genotypes had 7 + 8 or 7 + 9 bands that had positive gluten quality in 1B genomes (Table 2). Branlard and Dardevet (1985) in the study; The dough elasticity of 17 + 18, 7 + 8 bands determined a positive effect on elasticity, Li et al. (2016b) reported that 17 + 18 > 14 + 15 > 7 + 8 > 7 + 9 sorting was performed between the bands in the 1B genome. In the 1D genome, 8 genotypes with a high HMW-GS band score (Fig. 4) carry 5 + 10, 13 genotypes 2 + 12 bands (Table 2). The bands found in the genome 1D affect the quality rather than the amount of protein. The 1A genome was found to be more effective on the dough strength and gluten quality compared with the 1D genome (Zhang et al., 2018). According to 1 and null bands, 2* in genome 1A and, particularly, 5 + 10 bands in the 1D genome had extra-strong flour and baking characteristics compared to the 2 + 12 band (Payne et al., 1981; Payne and Lawrence, 1983; Kolster et al., 1991; Lukow, 1991; Maruyama-Funatsuki et al., 2004). Altpeter et al. (1996) and Barro et al. (1997) examined the bands found in the 1D genome and stated that the 10 band has an important relationship with the dough strength and bread-making quality (Wang et al., 2016).
Table 2. Protein bands and quality scores of local bread wheat genomes

| No | Genotypes      | 1A | 1B | 1D | Score |
|----|----------------|----|----|----|-------|
| 1  | TGB003246      | Null | 7 + 9 | 2 + 12 | 5     |
| 2  | TR63575        | Null | 7 + 8 | 2 + 12 | 6     |
| 3  | TGB008249      | Null | 7 + 8 | 2 + 12 | 6     |
| 4  | ZERUN          | Null | 7 + 8 | 2 + 12 | 6     |
| 5  | TGB003247      | Null | 7 + 8 | 5 + 10 | 8     |
| 6  | ÇALIBASAN       | Null | 7 + 9 | 5 + 10 | 7     |
| 7  | TR63581        | 2*   | 7 + 8 | 2 + 12 | 8     |
| 8  | TGB000543      | Null | 7 + 8 | 5 + 10 | 8     |
| 9  | TR63501        | Null | 7 + 8 | 2 + 12 | 6     |
| 10 | TR48371        | Null | 7 + 8 | 2 + 12 | 6     |
| 11 | ÖRMECE         | Null | 7 + 8 | 2 + 12 | 6     |
| 12 | TGB003232      | Null | 7 + 9 | 5 + 10 | 7     |
| 13 | AKSUNTERİ      | Null | 7 + 8 | 2 + 12 | 6     |
| 14 | TR44433        | Null | 20   | 5 + 10 | 6     |
| 15 | TGB000526      | 1    | 7 + 9 | 2 + 12 | 7     |
| 16 | ÇAM BUĞDAYI    | Null | 7 + 9 | 2 + 12 | 5     |
| 17 | TGB000534      | 2*   | 7    | 5 + 10 | 8     |
| 18 | DIMENİT        | Null | 7 + 8 | 5 + 10 | 8     |
| 19 | TGB000521      | Null | 7 + 9 | 2 + 12 | 5     |
| 20 | TR63497        | Null | 7 + 8 | 5 + 10 | 8     |
| 21 | TR37373        | Null | 7 + 9 | 2 + 12 | 5     |

Figure 5. HMW-GS band models of local bread wheat genotypes (a)

Figure 6. HMW-GS band models of local bread wheat genotypes (b)
Conclusion

HMW-GS is an important parameter in terms of quality in wheat. TGB003247, TR63581, TGB000543, TGB000534, DİMENİT, TR63497 local bread wheat genotypes have high HMW-GS scores according to bands found in 1A, 1B, 1D genomes. TR63581, TGB000534, TGB000526 genotypes have come to the fore in some quality parameters with the bands they have in the genome 1A. In this research, the Glu-band pattern of 1A, 1B, 1D genomes of local bread wheat genotypes were determined and the effects of HMW-GS were explained in detail. Local bread wheat genotypes with high scores in terms of the parameters examined can be used as parental lines in breeding studies.

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