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The Effect of Rye Translocation on Grain Yield and Agronomic Properties in the Recombinant Inbred Line Population Developed in Bread Wheat

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Abstract: Tolerance to biotic and abiotic stress factors is an important issue in wheat breeding studies. Rye translocation is an important genetic resource used in wheat breeding for tolerance to stress conditions and grain yield. In this study, the rye translocation and *Glu-B3b* allele, which is one of the Low Molecular Weight Gluten Subunits (LMW-GS), were identified by Polymerase Chain Reaction (PCR) method in the population of 145 recombinant inbreed lines (RILs) developed by crossing Tahirova-2000 and Tosunbey cultivars. It was determined that 85 out of 145 RILs carried the *Glu-B3b* allele. Statistical differences were analysed between the lines containing rye translocation or not in terms of the grain yield, thousand kernel weight and heading time. Physiologically, it was observed that the *1BL.1RS* rye translocation affects the heading time. An increase in root biomass was observed in genotypes carrying the rye translocation. It was determined that the thousand kernel weights of the lines were negatively affected by the rye translocation. These results indicated that the lines in the population can be used as gene resources for wheat breeding program and agronomic researches.

Keywords: Wheat, Rye translocations, *Glu-B3b, RILs*

Ekmeklik Buğdayda Geliştirilen Rekombinant Kendilenmiş Hat Popülasyonunda Çavdar Translokasyonunun Tane Verimi ve Tarımsal Özellikler Üzerine Etkisi

Öz: Buğday ıslah çalışmalarında biyotik ve abiyotik stres faktörlerine tolerans önemli bir konudur. Çavdar translokasyonu, buğday ıslahında stres koşullarına tolerans ve tane verimi için kullanılan önemli bir genetik kaynaktır. Bu çalışmada, Tahirova-2000 ve Tosunbey çeşitlerinin melezlenmesiyle geliştirilmiş 145 adet rekombinant kendilenmiş hat (*RIL*) popülasyonunda çavdar translokasyonu ve Düşük Moleküler Ağırlıklı Gluten Alt Birimlerinden (LMW-GS) biri olan *Glu-B3b* alleli Polimeraz Zincir Reaksiyonu (PCR) yöntemi ile tanımlanmıştır. 145 *RIL*'den 85'inin *Glu-B3b* alleli taşıdığı belirlenmiştir. Çavdar translokasyonu içeren ve içermeyen hatlar arasında tane verimi, bin tane ağırlığı ve başaklanma zamanı açısından istatistiksel farklılıklar analiz edilmiştir. Fizyolojik olarak *1BL.1RS* çavdar translokasyonunun başaklanma süresini etkilediği belirlenmiştir. Çavdar translokasyonunu taşıyan genotiplerde kök biyokütlesinde artış gözlenmiştir. Hatların bin tane ağırlıklarının çavdar translokasyonundan olumsuz etkilendiği belirlenmiştir. Bu sonuçlar, popülasyondaki hatların buğday ıslah programı ve agronomik araştırmalar için gen kaynağı olarak kullanılabileceğini göstermiştir.

Anahtar Kelimeler: Buğday, Çavdar translokasyonu, *Glu-B3b, RILs*

1.Introduction

Wheat meets approximately 35% of the daily energy need, ranks first among the cereals cultivated in the World (Liu, 2007). While most of the wheat production in the world is consumed as a staple food, approximately 15% is used for animal feed (Shewry, 2009). Approximately 770 million tons of wheat was produced worldwide in 2020. According to the figures of 2020, approximately 20.5 million tons of wheat was produced on an area of 7.7 million hectares in Turkey (TUİK, 2020). According to these data, Turkey ranks 11th among wheat producing countries (TUİK, 2020).

While the increasing population in the world is rising the demand of grains, biotic and abiotic stress factors threaten wheat production and yield due to changing climatic conditions. The goal of many breeding studies in recent years is to develop varietiesa are tolerant to biotic and abiotic stress factors. In this context, rye translocations are important and widely used genetic resources in wheat breeding. The 1RS chromosome of rye, which can be located in different chromosomes of wheat, is frequently used by breeders (Graybosch, 2001). The 1RS rye chromosome carries genes that confer tolerance to diseases and insect pests. The 1RS chromosome arm of rye also contains genes that provide resistance to diseases such as *Puccinia recondita f. sp. tritici, Puccinia graminis f. sp. tritici, Puccinia striiformis f. sp. tritici* and *Blumeria graminus f. sp. tritici* (Hsam et al., 2000). There are also studies reporting that rye translocation increases the adaptability and yield potential of bread wheat and provides tolerance to drought stress (Feldman & Levy, 2015; Yang et al., 2016; Leonardo et al., 2017; Tunca et al., 2018).

1BL.1RS translocation is widely used in wheat breeding programs. In the study published by Kim et al. in 2004, they determined that *1BL.1RS* translocation provides high yield potential by increasing the number of seeds in wheat. In the literature, it has been reported that wheat with rye translocation under arid conditions has higher root development and root biomass compared to wheat do not. Due to these characteristics of rye translocation, drought tolerance of the plant increases (Schlegel & Meinel, 1994; Rajaram et al., 2003). The effect of rye translocation on the regeneration capacity of the plant is positive, and it has been stated that the genotypes carrying the translocation have twice the regeneration capacity compared to the genotypes that do not (Agache et al., 1989). McKendry et al. (1996) reported in their study that genotypes carrying the *1BL.1RS* translocation had shorter plant height and a later heading period. In some studies, no advantages related to grain yield were observed in some wheats with different genetic bases and *1BL.1RS* translocation (Xue et al., 2014). This is thought to be due to gene suppressors in wheat (Carver &Rayburn, 1995; Leonardo et al., 2017).

Rye translocation, which has a positive effect on agronomic characteristics, generally affects the bread quality of genotypes negatively. It has been reported that the *1BL.1RS* rye translocation causes a decrease in the sedimentation volume in wheat, an increase in dough hardness and a decrease in gluten strength, and thus a decrease in the bread quality of wheat (Graybosch, 1990; Lelleya et al., 2004). It has been reported that the unfavorable effects on bread quality are due to the fact that *Sec-1* locus on the 1R chromosome of rye produces w-secaline protein and these monomeric proteins make the dough sticky (Lee et al., 1995). Another reason for the undesired effect is the loss of glutenin (*Glu-B3*) and gliadin (*Gli-B1*) loci from LMW-GS, which have the effect of improving the rheological quality properties of dough in translocation genotypes (Singh & Shepherd, 1988). Loss of these alleles causes a decrease in disulfide bonds in the protein scaffold that forms the gluten protein and decreases the dough quality (Wieser, 2007).

Rye translocations can be detected by different morphological, biochemical and molecular methods such as C-banding (Rayburn & Carver, 1988), Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) method (Zeller & Fuchs, 1983; Koebner & Shepherd, 1986) and Enzyme-Linked Immunoabsorbent Analysis (ELISA) (Andrews et al., 1996). Polymerase Chain Reaction (PCR) method is one of the fast and cost-effective methods that has been widely used in recent years. Genotypes carrying 1RS rye translocation can be detected easily with this method. Therefore, molecular screenings are widely used by breeders to determine the *1BL.1RS* rye translocation (Yamamoto & Mukai 2005; Landjeva et al., 2006; Tunca et al., 2018).

Mapping populations are used to identify genes controlling phenotypic characters in molecular level (Assanga et al., 2017). Backcross, F2, double haploid and recombinant inbred populations are the populations that are widely used for molecular detection of genes. Recombinant inbred line populations can be used to determine genotype x environment interactions of vegetative traits because they have homozygous pure lines (Hu et al., 2020).

In this study, 145 recombinant inbred lines obtained by crossing Tosunbey and Tahirova-2000 cultivars and five control cultivars were screened using PCR method for rye translocation and *Glu-B3b* allele. The effects of rye translocation on thousand kernel weight, plant height, grain yield, grain number per square meter, spike number per square meter, harvest index and NDVI measurements of recombinant inbred lines were investigated.

2. Materials and Methods

2.1. Plant materials, location and trials

In this study, 145 homozygous inbred Tosunbey x Tahirova-2000 cross lines obtained in another study and five control genotypes were used as material. Tosunbey, Tahirova-2000, Adana99, Nevzatbey and Altay2000 cultivars were used as control cultivars in the experiments. The lines and controls are white grained. Tahirova-2000 cultivar carries *1BL.1RS* rye translocation, while Tosunbey cultivar does not carry rye translocation.

Experiments were conducted in three crop years (2012-2015) on the experimental fields of Eskisehir Transitional Zone Agricultural Research Institute (300 31'N, 390 46 E). The seed rate was 450 seeds m^{-2}. Plot dimensions were 1.2 m wide (6 rows with 20 cm row space) and 5 m long (Wintersteiger). Monthly precipitations for the experimental years of the research institute were provided in Table 1. The lowest precipitation was 254 mm in 2012-2013 and 319 mm in 2013-2014, below the long-term average. The highest precipitation was received in 2014-2015, and it was an extreme year with 125. 3 mm precipitation in June and total precipitation of 643 mm (Table 1). The experimental soils formed over deep alluvial sediment. The soils were high clay content, low organic matter (1.01-1.30%), medium in lime content and slightly alkaline character (pH=7.53-7.90) (Table 2). Depending on whether the growing season was rainy or not in Eskişehir conditions, 10 kg of pure nitrogen fertilizer (DAP and Amonyum Nitrat) was applied per decare. Fertilization was done as pure phosphorus at 6 kg/da in locations. Selective herbicide was used in weed control.

Table 1. Monthly precipitation of the experimental site at during 2013-2015growing seasons (mm).
Çizelge 1. *2013-2015 yetiştirme mevsimi boyunca deneme alanının aylık yağış miktarı (mm).*

Years	Sep.	Oct	Nov	Dec	Jan	Feb	Marc	April	May	June	July	Aug.	Annual Total
Long-Term	14.4	26.1	29.8	46.1	38.2	32.5	33.4	35.2	43.3	28.6	13.5	6.4	348
2012-13	0.0	16.1	14.5	78.2	18.5	36.5	33.2	37.8	9.5	14.0	0.8	0.0	254
2013-14	2.0	65.0	15	1.5	21.0	7	27.1	23.2	53.8	70.5	20.4	12.2	319
2014-15	41.4	66.1	26.2	72.1	39.0	60.9	46.0	41.3	61.2	125.3	0	63.5	643

Table 2. Soil chemical properties (0- to 30-cm soil layer).
Çizelge 2. *Toprak kimyasal özellikleri (0-30 cm toprak tabakası).*

Years	Texture	Potassium (K)	Phosphorus (P)	pH (1:2.5 Soil:Water)	Organic Matter	$CaCO_3$ (Lime)
		mg kg^{-1}	mg kg^{-1}		%	%
2013	C	107	3.58	7.90	1.10	9.27
2014	C	175	7.10	7,53	1,30	10,0
2015	C	142	7.40	7.80	1.01	10.28

C:Clay

2.2. DNA isolation and PCR analysis

DNA isolation was performed from 150 mg ground seeds of 145 recombinant inbred lines and five control lines using the ZR Plant/Seed DNA miniPrep™ Kit (Zymo, D6020). The *1BL.1RS* translocation (*Sec1Gene* primer*)* and the *Glu-B3b* allele were screened in 145 recombinant inbred lines and five control groups using the Biorad C1000 TouchThermalCycler device. PCR reaction conditions were described by Yamamoto and Mukai (2005) and Wang et al. (2010) was done as stated. PCR products were run on a 2% agarose gel for 1.5 hours and the gel was imaged using the BioradChemidoc MP gel imaging system.

2.3. Phenotypic measurements and observations

While determining the plant height, the distance from the tip of the last spikelet to the soil surface was measured and recorded in centimeters. During the measurements, attention was paid to ensure that the soil was not pits or bumps, and awn lengths were not included in the measurements (Torres & Pietragalla, 2012). As of January 1, the period in which approximately 50% of the plants in the plot were spiked has been determined as the number of days to heading (Tavella, 1978). From the seeds obtained from the wheat spikes in each line, 100 seeds were taken twice and counted with an automatic seed counting machine (Chopin-Numigral-I), and the weight of one thousand grains (g) was determined by taking the average and multiplying by 10, and this value was calculated according to the 14% moisture content. Harvest index was determined by Reynolds et al. (2001) according to the method used. According to this method; 50 spicate plants (Bb 50) were selected from among the plants cut from an area representing the plot and dried in paper bags at 75 °C for 48 hours (Ka 50). These plants were blended and their grains and stems were separated. In order to determine the grain yield, the parcel was harvested and the obtained product was weighed and converted to decare. 250 grains were counted and weighed to determine the grain weight.

NDVI values were determined using NTech, GreenSeeker Model 505 optical hand sensor in the first week of March, second week of April, last week of May and June to determine the early covering (NDVI) characteristics of the cultivars (Peňuelas et al., 1994). Measurements were taken when the light source (sensor) was 80 cm above the vegetation and walking at a constant speed along the five-meter plot. NVDI calculations were made according to the Equation 1.

$$\mathrm{NDVI} = (R_{900} - R_{680})/(R_{900} + R_{680}) \qquad (1)$$

R: indicates the reflection (Reflectance), while the subscript numbers indicate the wavelength (nm) of the rays.

2.4. Statistical analysis

The agronomic and physiological data obtained from the yield trials were analyzed in the JUMP statistical program, the effect of rye translocation according to the partial lattice trial design (Patterson & Hunter, 1983). Before the analysis of the data, the normal distribution was checked by performing the normality test. A very limited number of values (less than five) that did not fit the normal distribution were excluded. In the analyzes made according to the lattice trial design, the mean values of the genotypes were obtained as corrected values (Least Sq Mean). These values may differ from the arithmetic averages.

3. Results

3.1. Molecular scans of the *Glu-B3b* and *Sec-1* gene

The lines with and without the *Glu-B3b* allele as a result of molecular screenings for the *Glu-B3b* allele are given in Table 3 and Figure 1. As a result of molecular scanning by using *Glu-B3b* primers, bands with a length of 1570 bp (base pairs) were obtained in some lines which means *Glu-B3b* allele is included in these genotypes. Lines that did not carry the relevant allele did not produce bands. While 85 of the lines in its population carry the *Glu-B3b* allele, such as the Tosunbey variety, 60 lines do not carry the relevant allele (Table 3).

Table 3. Data on the *Glu-B3b* and *Sec-1* allele transport status of lines in the mapping population.
Çizelge 3. *Haritalama popülasyonundaki hatların Glu-B3b ve Sec-1 allel taşıma durumuna ilişkin veriler.*

Alleles	Lines Number
Genotypes carrying the *Glu-B3* allele	Tosunbey, 1, 2, 6, 11, 12, 13, 14, 15, 17, 18, 21, 23, 24, 25, 26, 27, 31, 33, 36, 38, 39, 40, 41, 45, 46, 47, 48, 49, 50, 51, 52, 56, 58, 60, 61, 63, 67, 69, 70, 71, 72, 73, 75, 76, 77, 79, 80, 81, 83, 84, 85, 86, 89, 93, 95, 96, 97, 99, 100, 108, 109, 112, 114, 116, 118, 119, 120, 126, 127, 129, 130, 131, 132, 134, 135, 136, 137, 138, 140, 144, 145, 146, 147, 148
Genotypes not carrying the *Glu-B3b* allele	Tahirova2000, 3, 4, 7, 8, 9, 10, 16, 19, 20, 22, 28, 29, 30, 32, 34, 35, 37, 42, 43, 44, 53, 54, 55, 57, 59, 62, 64, 65, 66, 68, 74, 78, 87, 88, 90, 91, 92, 94, 98, 101, 102, 103, 104, 105, 106, 107, 110, 111, 115, 117, 121, 122, 123, 124, 125, 128, 133, 139, 141, 141, 143, 149, 150
Genotypes carrying the *Sec1* allele	Tahirova2000, 3, 4, 7, 8, 9, 10, 16, 19, 20, 22, 28, 29, 30, 32, 34, 35, 37, 42, 43, 44, 53, 54, 55, 57, 59, 62, 64, 65, 66, 68, 74, 78, 87, 88, 90, 91, 92, 94, 98, 101, 102, 103, 104, 105, 106, 107, 110, 111, 115, 117, 121, 122, 123, 124, 125, 128, 133, 139, 141, 141, 143, 149, 150
Genotypes not carrying the *Sec1* allele	Tosunbey, 1, 2, 6, 11, 12, 13, 14, 15, 17, 18, 21, 23, 24, 25, 26, 27, 31, 33, 36, 38, 39, 40, 41, 45, 46, 47, 48, 49, 50, 51, 52, 56, 58, 60, 61, 63, 67, 69, 70, 71, 72, 73, 75, 76, 77, 79, 80, 81, 83, 84, 85, 86, 89, 93, 95, 96, 97, 99, 100, 108, 109, 112, 114, 116, 118, 119, 120, 126, 127, 129, 130, 131, 132, 134, 135, 136, 137, 138, 140, 144, 145, 146, 147, 148

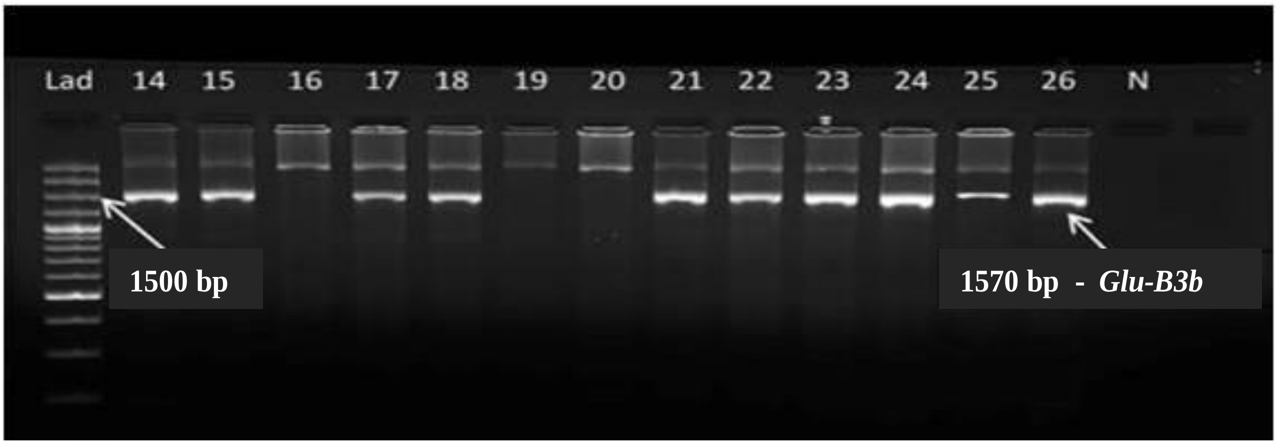

Figure 1. Results of PCR analysis using primers belonging to the *Glu-B3b* allele (Lad: Ladder, N: Negative control).
Şekil 1. *Glu-B3b alleli için kullanılan primerin PZR analiz sonuçları (Lad: Ladder, N: Negatif kontrol).*

The *Sec1Gene* primer was used to identify lines in the population carrying the *1BL.1RS* rye translocation. The agarose gel images of the lines in the mapping population are given in Figure 2, and the numbers of the lines with and without the rye translocation are given in Table 3. When the lines were screened using the *Sec1Gene* primer pair, 1216 base pairs (bp) long bands were obtained, but no bands were formed in the lines that did not carry the relevant allele. Among the lines in the recombinant inbred population, 60 lines carry the *Sec1Gene* allele such as Tahirova2000 variety, while 85 lines do not carry the relevant allele such as the Tosunbey variety. As a result, it was confirmed that genotypes carrying the *Glu-B3b* allele did not carry the rye translocation (Table 3).

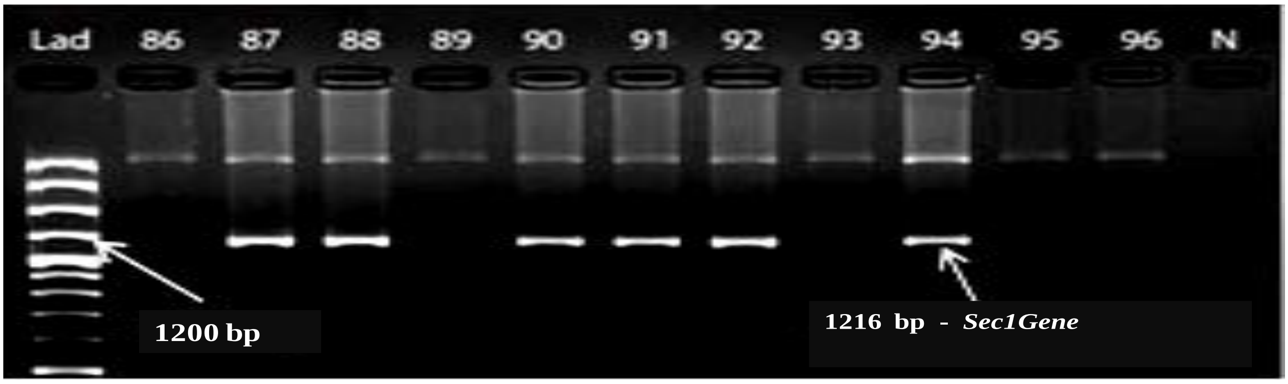

Figure. 2. Results of PCR analysis using primers of the *Sec-1* Gene (Lad: Ladder, N: Negative control).
Şekil 2. *Sec-1 Gene alleli için kullanılan primerin PZR analiz sonuçları (Lad: Ladder, N: Negatif kontrol).*

3.2. Effects of rye translocation on some agronomic traits

The average grain yield of the population used in the study was 473 kg/da (Table 5). The highest average grain yield was obtained in 2013 harvest year and the lowest grain yield was obtained in 2015 harvest year. The average grain yield in 2013, 2014 and 2015 was determined as 484, 486 and 443 kg/da, respectively (Table 4). The average thousand-grain weight of lines and control varieties in 2013, 2014 and 2015 was 45.3 g, 41.7 g and 38.3 g, respectively, and the average of these three years was 41.8 grams (Tables 4 and 5). The highest average in thousand kernel weight values was obtained in 2013, and the lowest average was obtained in 2015. As a result of the analyses, the average of the earliest heading was in 2014 and the average of the latest heading was in 2015. In the 2013, 2014 and 2015 harvest years in which the research was carried out, the average heading times were 135.8, 134.4 and 142.3 days, respectively, and the average of the three years was 137.4 days. (Tables 4 and 5). The average of plant heights were 89.9 cm in 2013, 87.1 cm in 2014 and 82.7 cm in 2015 (Table 4). When the average of three years is taken, the plant height is 86.6 cm (Table 5).

When the effects of lines with and without rye translocation on agronomic characteristics were examined, the difference between average grain yields was found to be 1% significant (Table 6). The average yields of lines carrying and not carrying rye translocation were determined as 459 and 482 kg/da, respectively. The average grain yield of lines carrying rye translocation was lower. It was determined that the thousand-grain weights of the lines were negatively affected by the rye translocation and the difference between the thousand kernel weights was significant at the 5% level (Table 6) The average thousand kernel weight of the lines with rye translocation was calculated 42 g, and the ones without rye translocation were 44 g. As a result of the analysis, it was determined that the difference between the average number of days of heading of genotypes and the interaction of genotype x environment were significant at the 1% level (Table 6). The mean heading times of the lines with and without the rye translocation were determined as 138 and 137.1 days, respectively (Table 5). It was determined that the heading occurred later in the lines carrying the rye translocation. No significant difference was observed between the mean plant heights of genotypes with and without rye translocation (Table 6). Similarly, it was determined that rye translocation did not cause a significant change on biomass (g/m^{2}), grain number per square meter, spike number and grain/head ratio, harvest index and NDVI analyzes (Tables 4, 5 and 6).

Table 4. Average values of agronomic traits by years.
Çizelge 4. *Agronomik özelliklerin yıllara göre ortalama değerleri.*

Sources of Variation	2013	2014	2015
Grain Yield (kg / da)	484^{a}	486^{a}	443^{b}
Biomass (g/ m^{2})	1120.7^{b}	1164.2^{a}	1023.8^{c}
Thousand kernel weight (g)	45.4^{a}	41.5^{b}	38.2^{c}
Number of Grains per Square Meter	10709.4^{b}	11769.5^{a}	11623.1^{a}
Spike Per Square Meter	339.2^{c}	513.4^{a}	463.8^{b}
Grain / Spike Ratio	32.1^{a}	23.3^{c}	25.4^{b}
Harvest Index	0.4^{a}	0.4^{b}	0.4^{a}
Heading Time (Days)	135.8^{b}	134.4^{c}	142.3^{a}
Plant Height (cm)	89.8^{a}	87.0^{b}	82.6^{c}
NDVI 6 March	0.2^{c}	0.3^{b}	0.3^{a}
NDVI 18 April	0.5^{a}	0.4^{c}	0.5^{b}
NDVI 28 May	0.5^{c}	0.6^{b}	0.7^{a}
NDVI 21 June	0.1^{c}	0.3^{a}	0.3^{b}

Table 5. Three-year average data of the whole population, average data of grains with and without rye translocation, standard error and coefficients of variation.
Çizelge 5. *Tüm popülasyonun üç yıllık ortalama verileri, çavdar translokasyonu olan ve olmayan tahılların ortalama verileri, standart hata ve varyasyon katsayıları.*

Sources of Variation	Average	RT (-)	RT (+)	SE	CV
Grain Yield (kg / da)	473	482.6^{a}	459.4^{b}	91.8	19.4
Biomass (g/ m^{2})	1104.3	1106.8	1099	220.6	20.0
Thousand kernel weight (g)	41.8	44.4b	42.1^{a}	3.7	8.9
Number of Grains per Square Meter	11406.6	11559.3	11175.4	2346.30	20.6
Spike Per Square Meter	439.6	443.2	434.4	99.8	22.7
Grain / Spike Ratio	26.9	27.0	27.0	3.82	14.2
Harvest Index	0.43	0.44^{a}	0.42^{b}	0.03	7.2
Heading Time (Days)	137.4	137.1^{b}	138.0^{a}	2.6	1.89
Plant Height (cm)	86.6	86.8	86.3	7.6	8.8
NDVI 6 March	0.3	0.3	0.3	0.05	16.7
NDVI 18 April	0.4	0.5	0.5	0.09	18.4
NDVI 28 May	0.6	0.6	0.6	0.06	9.09
NDVI 21 June	0.2	0.2	0.2	0.05	17.2

RT: Rye Translocation. S.E.: Standard Error. C.V.: Coefficient of Variation

Table 6. Analysis of variance for agronomic properties.
Çizelge 6. *Agronomik özellikler için varyans analizi.*

Sources of Variation	Degree of Freedom (D.F.) Mean of squares (M.S.)	Year	Recurrence (Year)	Block (Year. Recurrence)	Rye Translocation	Error
Grain Yield (kg / da)	D.F.	2	3	30	1	828
	M.S.	8.88	6.9	12.91	**109.139.5****	8.335.60
Biomass (g / m^{2})	D.F.	2	3	30	1	821
	M.S.	3.056.270	836.247	4.799.480	12.110	48.547
Thousand kernel weight	D.F.	2	3	30	1	827
	M.S.	7.663	757	1590	**80.12***	13.9
Grains per Square Meter	D.F.	2	3	30	1	822
	M.S.	197.607.058	40.506.979	522.302.398	29.581.114	5.480.723
Spike Per Square Meter	D.F.	2	3	30	1	822
	M.S.	4.829.728	52.371	442.333	15.573	9.971
Grain / Spike Ratio	D.F.	2	3	30	1	823
	M.S.	12.633	670	1.875	0.003	14.2
Harvest Index	D.F.	2	2	30	1	821
	M.S.	8.24	16.9	13.03	**0.065****	0.001
Heading Time	D.F.	2	3	30	1	828
	M.S.	5.344.30	159.69	14.56	**172.78****	6.64
Plant Height (cm)	D.F.	2	3	30	1	827
	M.S.	3.934.20	1.272.29	287.23	52.31	57.78
NDVI Mart (March)	D.F.	2	3	30	1	828
	M.S.	2.09	0.007	0.03	0.002	0.002
NDVI Nisan (Nisan)	D.F.	2	3	30	1	828
	M.S.	2.05	0.02	0.04	0.003	0.008
NDVI Mayıs (May)	D.F..	2	3	30	1	828
	M.S.	2.32	0.13	0.016	0.001	0.003
NDVI Haziran (June)	D.F.	2	3	30	1	828
	M.S.	3.14	0.02	0.02	0.006	0.003

** P <0.01 level. 0.01. * P <0.05 level of significance

4. Discussion and Conclusion

The *1BL.1RS* rye translocation is widely used in breeding programs because it provides resistance to biotic and abiotic stresses and drought tolerance. An increase in root biomass was observed in genotypes carrying the rye translocation. and the water use efficiency was higher than the genotypes carrying the rye translocation. The reason for including such important features in wheat is that the 1RS fragment of rye is translocated to wheat. In this study. RIL lines were screened with rye translocation *Sec1Gene* primers and 1216 bp long bands were observed in agarose gel images of PCR analysis results. Part of 1RS rye was translocated with part 1BL of Tahirova2000 rootstock.

Therefore. it has lost the *Glu-B3* locus. which is one of the low molecular weight glutenin subunits of gluten protein. which has an important quality enhancing feature in bread wheats. *Glu-B3b* allele was screened as a control in RIL lines using this information and the presence of genotypes without rye translocation was determined. In PCR scans were performed with *Glu-B3b* primer. bands with a length of 1570 bp were detected in the gel images of genotypes that did not have the rye translocation. Since this locus was absent in genotypes with rye translocation. no bands were observed. As a result of PCR analysis using *Sec1Gene* and *Glu-B3b* primers to determine the presence of rye translocation in genotypes. *1BL.1RS* rye translocation was detected in 60 of 145 RIL lines. while rye translocation was not observed in 85 genotypes. The Jump statistical program was employed for the reliability of the data and the analysis of the interaction of rye translocation and phenotypic characters to determine the effect of *1BL.1RS* translocation of the phenotypic characters of each line with the results obtained from molecular markers (Table 6).

The thousand kernel weight. which is an important quality component in bread wheat. increases in parallel with the increase in photosynthesis product. When environmentally suitable high yield conditions are provided. genotypes generally increase the thousand kernel weight and reflect this on yield. Studies conducted so far have also reported that the 1000 grains weight is an important feature affecting grain yield in cereals (Korkut et al.. 1993). Even Peterson et al. (1992) found that the effect of the environment on the thousand kernel weight was higher than the other quality criteria.

In this study. it was determined that the thousand-grain weights of the lines were negatively affected by the rye translocation. While the average thousand kernel weight of lines carrying rye translocation was 42.1 g. lines not carrying rye translocation were found to be 44.4 g (Table 5). The obtained result indicates that there may be decreases in thousand kernel weight of wheat with rye translocation in non-arid regions (Table 5). The *1BL.1RS* rye translocation in the lines decreased the 1000 grain yield. and in parallel. decreases in grain yield were observed. While the kilogram of wheat per decare was 459 kg/da on the lines carrying rye translocation. it was observed as 483 kg/da on the lines not carrying it. It is insufficient to argue that the result is only due to the rye translocation. Because grain yield is affected by both genetic structure and environmental factors. Peterson et al. (1992) reported that grain yield was affected by genotype x environment interaction. In this study. irrigation (35-40 mm) was applied to the trial material once in the summer of 2013 and 2014 in Eskişehir conditions. The relatively high yield potential in the studied location. as mentioned in the literature. did not show any improvement in the drought tolerance performance of the lines carrying rye translocation. and even had a negative effect (Xue et al.. 2014).

It was observed that the *1BL.1RS* rye translocation affects the heading time. The heading time is one of the most common features of transgressive expansion in wheat. The heading time is under the influence of many environmental factors besides the sensitivity to the photoperiod and vernalization genes (Shcherban et al.. 2015). The effect of rye translocation on *RIL* lines differed significantly at the 1% significance level. In addition to environmental factors affecting the heading time. translocation of rye also affects the duration of heading time and suggests that it is an important gene source that can be used in breeding later plants

The results obtained show that the recombinant inbred line population used in the research can be used in genetic resource development and in some physiological studies related to drought. especially in bread wheat.

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