



“Gheorghe Asachi” Technical University of Iasi, Romania



THE ROLE OF LONG TERMINAL REPEAT (LTR) RESPONSES TO DROUGHT IN SELENIUM-TREATED WHEAT

Seba Turhan¹, Mahmut Sinan Taspınar^{1*}, Esma Yigider¹, Murat Aydin¹, Guleray Agar²

¹Ataturk University, Faculty of Agriculture, Department of Agricultural Biotechnology, Erzurum 25240, Turkey

²Ataturk University, Faculty of Science, Department of Biology, Erzurum 25240, Turkey

Abstract

Wheat is one of the most significant food crops among cereals worldwide in terms of cultivation area and consumption. The reduction in wheat yield due to stress conditions has a major impact on the economy. Long Terminal Repeat (LTR) retrotransposons are considered to be one of the most important mobile elements, which are moved by the environmental alterations in the plant genome and are remarkable in the rearrangement of the genome. The research has been structured to elucidate the impact of selenium on DNA damage and LTR retro-transposition polymorphism in wheat subjected to drought stress. IRAP (Inter-Retrotransposon Amplified Polymorphism) and REMAP (Retrotransposon-Microsatellite Amplified Polymorphism) procedures were used to describe the DNA damage stages and retro-transposition polymorphism. The outcomes revealed that drought stress induced by polyethylene glycol (-4, -6, and -8 bar PEG 8000) led to a rise in retro-transposition polymorphism, and also a reduction in genomic template stability (GTS). However, DNA damage and retro-transposition polymorphism decreased by treatment with disodium selenite (6, 8, and 10 μM of $\text{Na}_2\text{O}_4\text{Se}$) co-treated with similar dosages of PEG 8000. These results suggest that drought-induced destructive impacts on wheat could be alleviated by exogenously applied disodium selenite.

Keywords: genomic template stability, IRAP, REMAP, retro-transposition polymorphism

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1. Introduction

Today, about 800 million people are exposed to malnutrition. The global population is estimated to spread 9.6 billion up to 2050. Thus, supplementary food necessary to nourish the growing population generates repression on present natural resources (McGuire, 2015). This rapid increase should be answered in the same way, and in the solution of nutritional problems, the production of herbal food sources in limited agricultural areas should be achieved with maximum efficiency. Plants are frequently subject to abiotic factors such as nutrient deficiency, salinity, drought, cold, temperature, and toxic metals (Zhu, 2016). Among these abiotic stresses, drought is a notable problem for crop production in the sub-arid and the arid area of the

world and these adverse impacts of drought are expected to rise further with global warming, which contributes in increasing average air temperatures (Ndehedehe et al., 2018). Recently, prolonged drought has given rise to serious damage to crops in most cultivation areas.

Drought stress is known that triggered biochemically, physiologically, and genetically changes, also causing many adverse impacts on plant growing parameters (Cho et al., 2009; Si et al., 2009). Prolonged exposure to oxidative stress such as drought, salinity, heavy metal, UV radiation, pathogens, ionic toxicity, mechanical and high-temperature stress, etc. lead to damage of the plant cells owing to the gathering of extreme reactive oxygen species (ROS) (Astaneh et al., 2019; Pandey and Gupta, 2015; Qing et al., 2015). Plants have

* Author to whom all correspondence should be addressed: e-mail: taspinar@atauni.edu.tr; Phone: +90 442 2312135; Fax: +90 442 2360948

antioxidant mechanisms to eliminate the negative effect of ROS. The imbalance between ROS production and antioxidants leads to damage of cellular components including lipids, nucleic acids, metabolites, and proteins (Foyer and Fletcher, 2001; Hasanuzzaman and Fujita, 2011).

Different exogenous applications such as putrescine (Sigmaz et al., 2015), humic acid (Yigider et al., 2016), silicon (Zhu, 2016), salicylic acid (Shaki et al., 2017), melatonin (Kul et al., 2019), and selenium (Agar and Taspinar, 2003; Agar et al., 2005; Filek et al., 2019; Taspinar et al., 2009) has been shown to be used to increase plant stress tolerance. Selenium is not a vital nutrient due to its natural structure for a plant, but recent researches have indicated in beneficial effects of low concentration of selenium which it is one of the most important antioxidant substances known in the world (Feng et al., 2013; Proietti et al., 2013).

Selenium may promote plant growth, increase the antioxidative ability of plants, and control the water case of plants in drought conditions and improves photosynthetic systems by rising chlorophyll content, transpiration efficiency, intercellular CO₂ concentration, and stomatal conductance (Astaneh et al., 2019; Djanaguiraman et al., 2005; Hasanuzzaman and Fujita, 2011; Jiang et al., 2015; Kuznetsov et al., 2006; Nawaz et al., 2013; Zhang et al., 2014). Moreover, selenium has been demonstrated to reduce the toxicity of several heavy metals to high plants, e.g. arsenic (As), chromium (Cr), lead (Pb), cadmium (Cd) (Shahid et al., 2019; Shekari et al., 2019; Zhao et al., 2019).

Numerous researches revealed that selenium may reduce the harmful impact of many stresses on plants such as drought (Aissa et al., 2018; Yao et al., 2012), salt (Astaneh et al., 2019; Elkelish et al., 2019; Lan et al., 2019), heat (Haghighi et al., 2019) and toxic metals (Shekari et al., 2019; Wan et al., 2019; Zhao et al., 2019).

It was demonstrated that environmental stresses (heavy metal, water, cold, drought, salt, and osmotic) alter gene expression by DNA methylation, histone modifications, and retrotransposons (RTNs) activities in recent researches (Grativol et al., 2012; Karan et al., 2012; Kumar et al., 2012; Tan, 2010). These epigenetic alterations may be linked to the capability to adapt to plants submitted to drought (Lu et al., 2007). Except for epigenetic mechanisms, various factors have been shown to modify these significant reactions of drought stress in plants (Hirayama and Shinozaki, 2010). These include vitamins, trace metals, and other compounds. Most researchers noticed that exogenous selenium implementation increased the osmoregulatory capacity, antioxidative, etc. (Astaneh et al., 2019; Hu et al., 2013; Nawaz et al., 2014). This protective impact was confirmed in several later studies with drought stress (Taspinar et al., 2009; Yao et al., 2009; 2012). The protective effect of selenium has been shown to depend on its concentration used in both plant and animal studies (Abul-Hassan et al., 2004;

Agar and Taspinar, 2003; Agar et al., 2005; El-Sharaky et al., 2007; Filek et al., 2008; Muñoz et al., 2007; Theodorakis et al., 2006). Besides, selenium has been found to stimulus the degree of DNA methylation in plants and animals (Davis et al., 2000; Filek et al., 2008; Takiguchi et al., 2003; Xu et al., 2000). Their outcomes show that selenium may be protecting the impact against stress by using biochemical and epigenetic mechanisms. However, the protecting impact of selenium against drought stress by inducing genetic and retrotransposition activity in the plant has not been clarified. Therefore, in this study our main aim was to examine DNA damage and the polymorphism of RTNs in wheat subjected to drought stress using IRAP and REMAP assay and whether selenium has any effect on polymorphisms.

2. Material and methods

Twenty wheat (*T. aestivum* L. cv. Kirik) seeds were sterilized with 70% ethanol for 1 min. and 10% commercial bleach for 15 min., respectively, and afterward washed twice with sterile dH₂O. 20 sterilized seeds for each treatment were sowing in small plastic pots which include hydrotones and afterward placed on a container containing Hoagland solution (pH=5.8) (Sigma H2395) (Hoagland and Arnon, 1950). Hydroponic containers with the nutrient solutions were covered with aluminum foil to prevent light. The air-pump system was used to provide oxygen into the solution. The seeds were germinated in 22±1°C (16 h light/8 h dark), 400 µmol m⁻² s⁻¹ light intensity, and 65% relative humidity for 14 days. After this period, plants were exposed to different concentrations of disodium selenite (0, 6, 8, and 10 µM Na₂O₄Se) with a foliar spray. The first container nutrient solutions were changed with prepared nutrient solution based on osmotic potentials (0, -4, -6 and -8 created with PEG 8000). 24 hours after Na₂O₄Se application, seedlings were cultured in the same condition for 14 days. Afterward 14 days, a total of 10 plant samples were collected for each treatment and were kept at -80°C. The strategy of bulk DNA sampling was applied in this study and total DNA was insulated from using the CTAB procedure of Sigmaz et al. (2015) with small alterations. Basic parameters for DNA such as the concentration and quantification were designated using a spectrophotometer and electrophoresis on a 0.8% agarose gel.

Nikita-E2647 (ACC CCT CTA GGC GAC ATC C), *Nikita-57* (N57) (CGC ATT TGT TCA AGC CTA AAC C), *Sukkula* (GAT AGG GTC GCA TCT TGG GCG TGA C), *BARE 1(0)* (CTA GGG CAT AAT TCC AAC A) and *WLTR2105* (ACT CCA TAG ATG GAT CTT GGT GA) primers were used in IRAP molecular analysis. IRAP-PCR reactions were achieved in 20 µl reaction mixture; including 50 ng DNA, 0.25 mM LTR primer, 2.5 mM MgCl₂, 10 × PCR buffer (without MgCl₂), 0.25 µM dNTP and 1.5 U *Taq* DNA polymerase (BioLabs M0267S). The PCR amplification program formed of 1 cycle at 95°C,

5 min; pursued by 42 cycles at 94°C, 1 min; 55°C to 63°C, 1 min; 72°C, 2 min, and the last extension at 72°C, 15 min. The reaction products were analyzed by electrophoresis on 1% agarose gel for 180 min at 90 volts; detected by ethidium bromide staining and snapped by gel photograph.

Giving the best performance in wheat the primers IRAP Sukkula, *Nikita*-E2647, BARE1 (0), and Stowaway were combined with two ISSR primers 8081/8082 ((GA)₉C/(CT)₉G). Five LTR-ISSR primer combinations were used as REMAP primers. The indicated methods in IRAP analysis were also used for REMAP analysis except for primers annealing temperature.

IRAP and REMAP designs were calculated using TotalLab TL120 software (Table 3 and Table 4). GTS was calculated by using the formula $100 - (100 - a / n)$ for each primary product according to Atienzar et al. (1999). "a" in the formula refers to the IRAP and REMAP polymorphic profiles determined for each sample, and "n" represents the total amount of DNA bands obtained in the negative control group with the respective primer.

3. Results

In total, out of 10 IRAP primers tested, 5 single primers (WLTR2105, Sukkula, N-57(*Nikita*), BARE 1(0), *Nikita*-E2647) produced distinguishable and polymorphic banding patterns. 5 different REMAP primer combinations were employed using 4 LTR primers and 2 ISSR primers for amplification of

REMAP resulted in particular and steady DNA profiles in the wheat genome. The disappearance of bands and appearance of novel bands and difference in band intensity is the clear changes in the IRAP and REMAP designs generated by PEG 8000 and/or Na₂O₄Se treatments in plants. The polymorphic bands that appeared for all the primers used in the study were determined by comparing control and plants exposed to PEG 8000 and Na₂O₄Se. The banding patterns of the E2647-IRAP primer are shown in Fig. 1. Amplified fragment lengths for IRAP and REMAP profiles ranged from 280 bp (N-57) to 2972 bp (*BARE 1(0)*) and from 227 bp (*Nikita*-E2647+ISSR 8081) to 1612 bp (N-57+ ISSR 8081), respectively (Table 1 and Table 2).

IRAP results showed that different PEG 8000 concentrations caused a rise (from 29.9% to 48.0%) in the rate of t retrotransposon-induced polymorphism. Also, two different doses of Na₂O₄Se (6 μM and 8 μM) combined with PEG 8000 decreased the polymorphism. According to IRAP results, increased PEG 8000 dose resulted in a decreasing GTS% ratio (from 70.1% to 52%). 6 μM and 8 μM doses of Na₂O₄Se against to PEG 8000 were increased GTS value (Table 3).

According to REMAP results, the highest polymorphism was calculated as 58.3% (-8 bar PEG 8000, 0 μM Na₂O₄Se) and the lowest polymorphism 31.0% (-4 bar PEG 8000, 6 μM Na₂O₄Se). When three doses of Na₂O₄Se (6 μM, 8 μM, 10 μM) were applied together with drought, the first two doses reduced the polymorphism caused by drought stress.

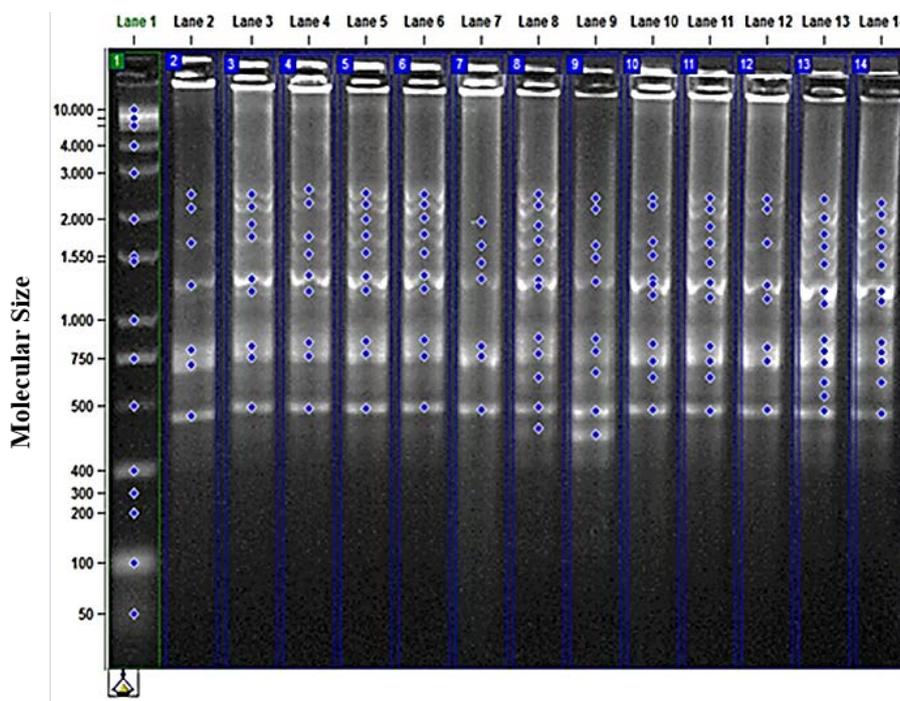


Fig. 1. The amplification products of E2647 - IRAP primer and arrows indicate appeared and disappeared bands L1:Marker, L2: Control, L3: -4 bar PEG 8000+0 μM Na₂O₄Se, Line4: -4 bar PEG 8000+6μM Na₂O₄Se, L5: -4 bar PEG 8000+ 8μM Na₂O₄Se, L6: -4 bar PEG 8000+10μM Na₂O₄Se, Line7: -6 bar PEG 8000+0μM Na₂O₄Se, L8: -6 bar PEG 8000+6μM Na₂O₄Se, L9: -6 bar PEG 8000+8μM Na₂O₄Se, L10: -6 bar PEG 8000+10μM Na₂O₄Se, L11: -8 bar PEG 8000+0μM Na₂O₄Se, L12: -8 bar PEG 8000+6μM Na₂O₄Se, L13: -8 bar PEG 8000+8μM Na₂O₄Se, L14:-8 bar PEG 8000+10μM Na₂O₄Se

Table 1. Molecular sizes (bp) of appeared/disappeared bands in IRAP profiles of Na₂O₄Se and/or PEG 8000 treatment vs. control in wheat seedlings

IRAP Primers	Control	+/-	-4 bar PEG 8000				-6 bar PEG 8000				-8 bar PEG 8000			
			Na ₂ O ₄ Se				Na ₂ O ₄ Se				Na ₂ O ₄ Se			
			0 μM	6 μM	8 μM	10 μM	0 μM	6 μM	8 μM	10 μM	0 μM	6 μM	8 μM	10 μM
Sukkula	8	+	-	-	-	720	1064	1172	1194	890	977 638	890 612	1677 638	1665 963 638
		-	1709 1117 950 921	1117	921	1117 863 451	1117 451	518 1117	1117 451	451	1117 921	518 771	518	518
WLTR2105	9	+	-	624	-	-	1105	1119	647	1105	893	1079	-	-
		-	928	912	989 870	928 829	989 969	989 969	989 928	989	989 912 789	989 912	989 928	989 928
Nikita-E2647	7	+	-	-	1500	-	2483 2210	1907 1027	1595 1027	2000 1675 1044 2413	1352 1990	2010 1675 1063 1925	1960 1352 953	1567 1449 1012 496
		-	2381 2120 1854	2381 2120 1854	-	2381 2120 1854	2381 2120	-	-	2381	2381 2120	1854	-	705
Nikita-57(N57)	6	+	-	-	-	-	-	2450 1813	-	-	-	-	2450 1550	-
		-	400	1121 400	1121 400	400	899 400	-	400	859 494 400	400	-	400	899 400
BARE1(0)	7	+	-	-	1050 989 702	-	702	722	-	696	1054 995 742	-	772	1050 995 442 690
		-	630 592	630 592	-	630 592	374	483	483 374	483	483 374	592 483 431	374	592 483

Table 2. Molecular sizes (bp) of appeared/disappeared bands in REMAP profiles of Na₂O₄Se and/or PEG 8000 treatment vs. control in *Triticum aestivum* Kirik seedlings

REMAP Primers	Control	+/-	-4 bar PEG 8000				-6 bar PEG 8000				-8 bar PEG 8000			
			Na ₂ O ₄ Se				Na ₂ O ₄ Se				Na ₂ O ₄ Se			
			0 μM	6 μM	8 μM	10 μM	0 μM	6 μM	8 μM	10 μM	0 μM	6 μM	8 μM	10 μM
WLTR2105+8082	6	+	1000	946	-	1064	1400	-	285	862 604	-	1020	565	-
		-	1159	1491 1159 750	-	1159 325	-	325	750	750 325	750 325	1159	325	-
Nikita-57(N57)+ 8081	7	+	1176	1071	-	-	1017	687	670	1071	-	1106	-	1089 670
		-	1612 1466 1258 896	1612 1466 1258 896	1612 1466 896	1612 1466 896	1612 1258 896	1612 896 400	896 551	1612 1258 896	1612 1466 896	1258 896	1612 1466 896	1612 1258 896 400
Sukkula+8081	5	+	-	-	1222 762	724	892 775 675	1000 663	1222 916	1222 1000 663	1222 699	854 675	775 608	1222 867 712
		-	-	-	432	-	550	479	1111	1111 479	479	479	479	1111 479
Nikita-E2647+8081	6	+	575 458	-	-	569 453	446 251	515	632 447	443	599 196 441	612 442	593 511	471
		-	275	741	848 275	227	848	-	848	848	848 275	848	848	848
Nikita-57(N57)+8082	7	+	-	-	1431	-	542	-	-	-	1442 1116	-	760	542
		-	1000	-	1315 400	867	663 400	663 244	663 244	663 244	1315 400 1000	663 244	663 867	1315 867 663 244

Table 3. Changes of polymorphism% values of all IRAP primers in wheat seedling exposed to different PEG 8000 and/or Na₂O₄Se concentrations

IRAP Primers	Control	- 4 bar PEG 8000				-6 bar PEG 8000				-8 bar PEG 8000			
		Na ₂ O ₄ Se				Na ₂ O ₄ Se				Na ₂ O ₄ Se			
		0μM	6μM	8μM	10μM	0μM	6μM	8μM	10μM	0μM	6μM	8μM	10μM
Sukkula	0	50	12.5	12.5	50	37.5	37.5	37.5	25	50	50	37.5	50
WLTR2105	0	11.2	22.3	22.3	22.3	33.4	33.4	33.4	22.3	44.5	33.4	22.3	22.3
Nikita-E2647	0	42.9	42.9	14.3	42.9	57.2	28.6	28.6	71.5	57.2	71.5	57.1	71.5
Nikita-57(N57)	0	16.7	33.4	33.4	16.7	33.4	33.4	16.7	50	16.7	0	50	33.4
BARE1(0)	0	28.6	28.6	42.9	28.6	28.6	28.6	28.6	28.6	71.5	42.9	28.6	85.8
Polymorphism (%)	0	29.9	28.0	25.4	32.1	38.1	32.3	29.0	39.5	48.0	39.6	36.3	52.6
GTS value (%)	100	70.1	72.0	74.6	68.9	62.9	67.7	71.0	60.5	52.0	60.4	63.7	47.4

Table 4. Changes of GTS% and polymorphism% values of all REMAP primers in wheat seedling exposed to different PEG 8000 and/or Na₂O₄Se concentrations

REMAP Primers	Control	-4 bar PEG 8000				-6 bar PEG 8000				-8 bar PEG 8000			
		Na ₂ O ₄ Se				Na ₂ O ₄ Se				Na ₂ O ₄ Se			
		0μM	6μM	8μM	10μM	0μM	6μM	8μM	10μM	0μM	6μM	8μM	10μM
WLTR2105+8082	100	100	33.3	66.6	50	83.3	83.3	66.6	33.3	66.6	66.6	66.6	100
Nikita-57(N57)+8081	100	57.1	28.5	28.5	57.1	42.8	42.8	57.1	42.8	57.1	57.1	57.1	14.2
Sukkula+8081	100	40	100	100	80	20	40	40	0	40	40	40	0
Nikita-E2647+8081	100	66.6	83.3	50	50	50	83.3	50	66.6	16.6	50	50	66.6
Nikita-57(N57)+8082	100	57.1	100	85.7	85.7	57.1	71.4	71.4	71.4	28.5	71.4	57.1	28.5
Polymorphism (%)	0	35.9	31.0	33.9	35.5	49.4	35.9	43.0	57.2	58.3	43.0	45.9	58.2
GTS (%)	100	64.1	69.0	66.1	64.5	50.6	64.1	57.0	42.8	41.7	57.0	54.1	41.8

Furthermore, REMAP results indicated that GTS was significantly affected depending on different PEG 8000 concentrations. Generally, increased PEG 8000 concentration caused in decreasing GTS rate (from 64.1% to 41.7%) in REMAP. However, after the application of Na₂O₄Se, the retrotransposon polymorphism caused by PEG 8000 was remarkably reduced (Table 4). Application of Na₂O₄Se against to PEG 8000 caused an increase in GTS rate. The results obtained in our study showed that a higher level of Na₂O₄Se (10 μM) has a toxic impact on plants in relation to both IRAP and REMAP results. When the GTS ratios given by REMAP and IRAP applications were compared, it was observed that the GTS ratio was lower and the polymorphism was higher in the REMAP technique. The reason for the high polymorphism in REMAP is due to both the movement of retrotransposons, the calculation of DNA damage, and the use of ISSR primers.

4. Discussion

Drought is a major stress factor that has a negative effect on plant growth and development by triggering alterations such as metabolism, oxidative activity, gene expression, and physiology (Ashraf et al., 2002; Zhu, 2016). Plants respond to stress conditions such as free radicals and abscisic acid (ABA) by causing various metabolic responses. ROS are normally synthesized in cellular events but are harmful to the detoxification mechanism under stress conditions (Halliwell and Gutteridge, 1995; Tripathy and Oelmüller, 2012). Nevertheless, drought stress disturbed this balance, and ROSs cause oxidative stress, because they are more than antioxidants. Oxidative stress may result in damage to DNA

resulting in mutation (Blokhina et al., 2003; Ge et al., 2002). When a plant is exposed to stress, its main purpose is to preserve the stability of the genome, because the stress causes a genotoxic effect on plant genome structures. This genotoxic effect may be related to the construction of free radicals. Drought stress has a negative effect on epigenetic phenomena such as histone modifications, DNA methylations, and retrotransposon polymorphism (Jaligot et al., 2004; Lu et al., 2007). It is known that DNA methylation is formed from epigenetic mechanisms due to the rise in ABA with oxidative stress in plant structures (Chinnusamy et al., 2008).

The transformation of RTNs is one of the epigenetic differences in the cell under drought stress (Sabot and Schulman, 2006). RTNs are mostly silent during plant growth, but various stresses increase retrotransposition activity using different molecular techniques (Bennetzen and Kumar, 1999; Finatto et al., 2015; Grandbastien 2004; Makarevitch et al., 2007; Picault et al., 2009). The expression of RTNs such as Tnt1 and Tto1 is raised in tobacco subject to diverse stresses (Hirochika and Otsuki, 1995; Pouteau et al., 1991; Sugimoto et al., 2000; Takeda et al., 1999). We have shown LTR retrotransposons polymorphism, stimulated Sukkula, WLTR2105, BARE 1(0), Nikita-57 (N57), and Nikita-E2647, in wheat subject to drought stress. Moreover, retrotransposon polymorphisms were detected to have a rise in IRAP profiles between the rates of 29.9% and 48.0% and REMAP profiles between the rates of 35.9% and 58.3% compared to control. RTNs most probably have many connections with the molecular mechanism of plant resistance genes and affect them directly. Some active RTNs such as Ttd1 are known to have like sequence to the motifs in the transcriptional

activation of defensive genes, which including the construction of secondary signaling molecules (Mhiri et al., 1999; Petersen, 2014; Tuteja, 2007). TLC1.1 RTNs are activated by many signaling molecules (synthetic auxin 2,4-D, MeJA, SA, H₂O₂, and ABA) (Salazar et al., 2007). Though the active RTNs were intended to protect plants, they could bring new properties by providing insertion-polymorphisms, changes in genome size, genomic instability and can also provide a contribution to genome evolution in high plants (Bennetzen, 2000; Grandbastien et al., 1997; Wessler et al., 1995). Some researches underlined the important protecting role of exogenous application of selenium against environmental many stress such as chilling, osmotic, heat, drought, paraquat, cadmium, lead, chromium, and fungal infection (Aggarwal et al., 2011; Cartes et al., 2005; Djanaguiraman et al., 2005; Hasanuzzaman et al., 2012; Shekari et al., 2019; Terry et al., 2000; Yao et al., 2009; Wan et al., 2019; Zhao et al., 2019). The present work examined the protecting impact of Se on PEG 8000 induced stress.

Selenium has served as a stress modulator and inhibits the gathering of ROS during stress by acting as a ROS repressive and as a pro-oxidant and antioxidant. Numerous reports have revealed a protecting impact of selenium against oxidative stress by swelling GSH-Px activity, by reducing lipid peroxidation generated by stress in high plants, stimulation of the spontaneous dismutation of O₂⁻ (superoxide) into H₂O₂ (hydrogen peroxide), organizing of enzymatic and non-enzymatic antioxidant systems and repressive of ROS through selenium types (Cartes et al., 2005; Chauhan et al., 2019; Hartikainen, 2005; Kuznetsov et al., 2006; Wan et al., 2019). Also, studies have reported reductions in H₂O₂ production due to the addition of selenium (Elkelish et al., 2019; Hawrylak-Nowak, 2013). Alyemeni et al. (2018) indicated that the treatment of selenium at 10 µM to cadmium-treated plants up-regulated the antioxidative defense mechanisms by raising the activity of glutathione reductase (GR), catalase (CAT), superoxide dismutase (SOD), ascorbate peroxidase (APX). Selenium-stimulate alterations in the actions of oxidoreductase enzymes were described in white clover (Wang, 2011), broad bean (Mroczek-Zdyrska and Wojcik, 2012), and lettuce (Ríos et al., 2009). Furthermore, studies showed that the anti-oxidative impact of selenium was related to α-tocopherol synthesis but not with rising enzyme activity (Hartikainen et al., 2000). Blokhina et al. (2003) have proposed the likely role of non-enzymatic reactions in eliminating free radicals. It is the first report focused on protecting the impact of selenium on genetic changes and on LTR retro-transposition polymorphism causing drought stress using IRAP and REMAP assay. The different polymorphic bands and GTS decreasing were obtained under the drought stress treatments compared with the control. After the selenium application, the polymorphism rate decreased and GTS increased.

The protecting impacts of selenium in the steadying of the DNA methylation design have been notified in plants (Filek et al., 2008; Taspinar et al., 2009). Selenium ions can change their methylation bounding DNA cytosine and creating methyl derivative. The protecting impacts of selenium in the variations in DNA methylation designs may also be linked to the elimination of free radicals in situ formed by stress (Filek et al., 2008). Based on these data, we suppose that the antioxidant possible activity of Se may contribute to reduce LTR activity by protecting plants from stress.

Therewithal, Se ions may eliminate epigenetic modifications such as DNA methylation formed by stress for mostly protection plants. However, the protecting role of selenium is related to its concentrations (Table 3 and Table 4). Since low concentrations of selenium are beneficial to the plant, they may show toxic effects when optimum conditions are exceeded. Many studies on different organisms have reported toxic effects of high concentrations (Agar et al., 2005; Agar and Taspinar 2003; El-Sharakly et al., 2007; Ohlendorf, 1989; Theodorakis et al., 2006; Wilber, 1980). Bai et al. (2019) reported that selenium doses above 20 mg kg⁻¹ were negatively affected plant growth, root activity, antioxidant enzyme activity, and P and K absorption.

4. Conclusions

The drought, which is caused by the lack of water resources, is one of the most major matters threatening world food security. Drought depends on factors such as precipitation formation and distribution, evaporation need, and moisture storage capacity of the soil.

Under varying conditions, it is necessary to rise the drought tolerance of crops. Recent studies have revealed that many substances exogenously increase drought tolerance. Selenium might show anti-stress impacts under drought stress conditions. In our study was determined that selenium application has suppressed the genetics and epigenetics changes such as LTR retro-transposition activity and caused drought stress and stimulate plant growth.

The application of selenium can be an effective approach to increase the drought tolerance of wheat. But, it was also found that this protective effect of selenium depends on its dose.

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