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Determination of Eggplant Pure Lines Suitable for Drying by Different Methods**

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ABSTRACT

In the gastronomic culture of certain geographical regions such as Southeastern Anatolia, the position of eggplant, both fresh and dried, is very important. Dried eggplant production is common in Türkiye, and the drying process is traditionally done outdoors and under the sun. However, there are technologically developed technical drying methods as an alternative to this traditional method. In this study, local eggplant populations were collected from the regions, and DH pure lines were obtained from them by androgenesis. By examining criteria such as yield, fruit characteristics and growth strengths, 44 eggplant pure lines were selected among more than 200. Harvesting was done three times during the growing period in 3 different locations, Adana, Antalya, and Manisa. Conventional drying method (under 50% shade net in sunny weather) and drying method in tunnel type ovens were used to determine the drying performance of DH eggplant lines whose pre-washing and filtration processes were completed. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. Various drying tests were applied to dried fruit samples such as moisture, ash, oil, pH, process efficiency, sensory evaluations and dry product shelf life were calculated separately for both sun drying and oven drying methods. On the 32nd, 48th and 64th days, the weights, color parameters, shape and taste characteristics of the products were evaluated as packed in vacuum and normal bags. Finally, four prominent dried eggplant DH lines were determined to be used for test hybridizations.

Keywords*:* Eggplant, pure line breeding, sun drying, oven drying

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Introduction

Eggplant (*Solanum melongena* L.), a member of the Solanaceae family, has a production value of 56.618.843 tons worldwide in 2020 (FAOSTAT 2020). China is the largest eggplant producer, providing about 65% of global eggplant production. Turkey is the 4th largest eggplant producer after India and Egypt with an annual eggplant production amount of 832.938 tons. In Türkiye, the provinces of Antalya (246.993 tons), Mersin (152.491 tons), Adana (43.270 tons), Mugla (35.120 tons) and Gaziantep (33.128 tons) had the largest production shares in 2021 (TUIK 2021).

Eggplant is among the vegetable types with a wide consumption range and economic value. In addition to being consumed by cooking, freezing and canning, eggplant is also consumed as dried slices and dried stuffed eggplants. In recent years, eggplant has been included in the product portfolio of businesses that commercially market dried food. In addition to being a newly developing sector commercially, eggplant has been dried for many years in order to meet the needs of families as family businesses and/or amateurs. Dried eggplant in Turkey has an important place in traditional Turkish cuisine. There is no statistical data about dried

eggplant cultivation in Turkey. In almost every region in Turkey, eggplant is dried and consumed in different ways as a dried product. Okra, pepper, eggplant and beans are the most dried vegetables among Turkish societies since Central Asia (Kosay and Ulkucan 1961). In addition to selling products for local consumption, dried peppers, chili peppers and dried eggplants are also exported abroad, primarily to European and Middle Eastern countries (Ozkan 2021). Considering the change in consumption habits in the world in recent years, it is seen that the interest in dried foods has increased gradually. This situation shows that the dried pepper and eggplant market abroad will also increase. The main shortcoming here is the lack of commercial varieties with sufficient number and product range in terms of suitability for drying in Turkey. In eggplant, fruits of varieties grown for fresh consumption or local populations with limited agronomic characteristics are used for drying. In eggplant, it is necessary to develop domestic hybrid varieties that are suitable for the drying sector, highly productive and resistant to diseases. It is known that open pollinated domestic and foreign hybrid varieties are used in the production of dried eggplant. In dried eggplant, many technical features such as the uniformity of the plant, homogeneous fruit structure, suitability for machine harvesting, nucleation, suitability for drying, shelf life, yield after drying, drying time and microbial status before and after drying come to the fore. There is a lack of commercial varieties with these characteristics in Turkey. With a study conducted by Antalya Agriculture Co., it was aimed to breed hybrid varieties (Sliced eggplant and stuffed eggplant) suitable for drying technology.

Mostly local genotypes and/or populations are used for drying. Although local genotypes are valuable materials, they are insufficient in terms of characteristics such as homogeneity, productivity, wide adaptability, suitability for machine harvesting, plant strength, and they also show variation. Therefore, they are not preferred in commercial production. Among the most important advantages of local genotypes are that they are suitable for local taste, local adaptation ability, aroma and quality characteristics are high. With breeding studies, it is generally preferred to develop dihaploid lines and hybrid varieties by preserving the characteristics of local populations and improving their deficiencies. Within the scope of our large project, dihaploid lines were obtained by androgenesis by using local genotypes in dried eggplant. Also in this study, the quality analyzes were made in terms of suitability for drying in these lines.

Eggplant is a vegetable that has taken its place in many cultures, as in the Mediterranean diet (Gallo et al., 2014). It is preferred for consumption due to its low calorie, low glycemic index (GI 15), low oil and low sodium content. Although the provitamin A and vitamin E content in eggplant seems low (fresh weight 27 IU/100 g vitamin A, 0.30 mg/100 g vitamin E), it is considered as one of the vegetable types rich in mineral substances such as ascorbic acid (Hanson et al., 2006) and phenolic compounds, phosphorus (P), potassium (K), calcium (Ca) and magnesium (Mg) (Stommel and Whitaker 2003). Depending on the genotype and locations, dry matter content in eggplant is 4.69-7.16 g/100 g, protein content is 0.41 – 0.68 g/100 g, phenolic content is 34.46 – 60.7 mg/100 g; P, K, Ca and Mg contents are up to 43.1 – 275.4 – 31.0 and 15.9 mg/100 g, respectively (Raigon et al., 2008; Michaloje and Buczkowska 2012).

Thanks to the drying method, which is the process of removing most of the existing moisture in the food from the product, the products to be processed or sold can be stored for a long time. Drying method is accepted as the oldest preservation method that people learned from nature and therefore has been applied since ancient times (Ayhan 2005; Er 2011; Alibas 2012). The drying method is the most suitable method in terms of preserving the vitamin values in the products, keeping the taste and appearance of the products, as well as the reduced mass amount and packaging, storage and transportation possibilities. (Ceylan et al., 2006; Kaya and Aydin 2008). Drying method is examined under two main headings as drying in “sun” or “artificial” dryers and these are grouped by considering various technical features. Drying in the sun is the traditional method applied to reduce the water content of the product by utilizing the heat of the sun. Artificial drying, on the other hand, can be defined as the process of performing the drying process in closed areas and under controllable standard conditions (Ayan 2010).

In our country, most of the products are still dried in the open air under the sun, which is the most economical and natural method. However, during the outdoor drying process under the sun, nutrient losses and deterioration can be seen due to the prolongation of the drying time of the product. Toxic risks due to air pollution such as exposure of the products to rain, wind, dust and soil, negative situations such as not drying the product uniformly and direct contact of the sun rays with the dried product may occur. Quality losses in the product cause commercial losses in the domestic and foreign markets economically (Ayhan 2005; Kocabiyik and Demirturk 2008). Considering the disadvantages of drying under the sun, various alternative drying methods such as contact, convective, radiation, dielectric, vacuum, freeze and osmotic drying have been developed.

Convective (hot air) drying process is one of the most used technical drying methods for drying fruits and vegetables. During drying, hot air is in direct contact with the product to be dried. Tunnel and cabinet dryers are the types of convective dryers in which air flow is most commonly applied during the drying of fruits and vegetables. This type of dryer is widely preferred due to the ease of application and low cost. Drying process has become widespread with the use of modern drying methods as well as the traditional sun drying method. In this way, dried products have become an effective alternative to the fresh product market (Hasturk-Sahin 2010).

In this study, DH eggplant lines obtained from local eggplant populations of Turkey were used as plant material. The aim of the study is to determine pure lines (containing different fruit types) for slice and stuffed eggplant product segments suitable for the drying industry. Another aim is to compare the quality characteristics of eggplant fruits dried by oven and sun drying methods.

Materials and Methods

This study covers a part of the hybrid variety breeding project of eggplant for drying. In the first phase of the project, eggplant genotypes with different drying characteristics were collected from the regions where dried eggplant cultivation is most common in Turkey (Southeast Anatolia and Mediterranean Regions). Seedlings grown from seeds of 35 local eggplant genotypes, 9 different F_1 and 2 standard eggplant varieties were examined for selection of donor parents to be used in anther culture studies.

During the selection stage, 30 different features were examined, including the suitability of the selected plants for drying work. At the end of this phase of project, 13 local eggplant genotypes were selected. After anther culture process, DH lines were obtained by using this local material as donor plants (Figure 1). The DH seedlings obtained from the seeds of pure lines were planted in the greenhouse located in the Antalya Tarım Research and Development Center. By examining 86 DH genotypes, 41 of them were selected for using quality analyses to obtain the prospective parents of eggplant hybrid varieties for dried fruits. This 41 eggplant DH lines and three OP varieties (as control) were grown together to be used in quality analysis in the study.

1. Prewash processes

Eggplant samples were immersed in 50 ppm sodium hypochlorite, 1% citric acid, 1.5% salt solution and distilled water for 10 minutes (Figure 2).

2. Drying processes in fruits

2.1. Traditional sun drying method

After the pre-washing processes were applied, the eggplants were cut as a whole in one piece and in longitudinal strips and lined up on the rope, then hung on the bunk bed system and left to dry in the sun under 50% shade tulle (Figure 3).

2.2. Oven drying method

Eggplant samples, which were pre-washed, were dried using a drying oven. The products are taken into trays specially produced for the use of the drying oven and after placing them on the carriage with shelves, the process is carried out in the drying room. There are special equipment in the system to circulate the air in the tray and the dryer. In this type of dryer, the air is heated by the heater in the device, no hot air is taken from outside (Badger and Banchero 1993).

The products are left to dry for 6-8 hours at 60-70°C. With the hot air flow that is continuously heated and introduced into the system, the formation of moisture is prevented and the problems that may occur in the quality of the products are minimized. During the drying process, the temperature is usually 60°C, but the temperature is increased to 70°C to stop the microbial activities in the products and this application continues for 10-15 minutes.

3. Quality analyzes

3.1 Amount of Water-Soluble Dry Matter

Before drying, the amount of water-soluble dry matter in fresh fruits was determined using the "Milwaukee MA871" digital refractometer device.

3.2. Determination of Moisture Content

In order to determine the moisture content, 3-5 g of dried products were weighed and moisture was determined in the samples with the 'Sartorius MA 45' device. For this, the Petri dish is placed in an oven at 100°C and brought to constant weight. It is then taken to a desiccator and waited for cooling. The Petri dish is weighed and the tare is noted. Approximately 5g of sample is weighed and added. Then it is placed in an oven at 100°C and waited for approximately 24 hours. The petri dish removed from the oven is taken to the desiccator and allowed to cool. Weighing is done and noted (TS EN ISO 712, 2012).

Calculation: % Humidity = [(M1-M2) / m] x 100

M1 = Sample weight + weight of the drier brought to constant weight

M2 = Dried sample + weight of the drying container brought to constant weighing

m = weight of sample taken

3.3 Determination of Ash Content

The crucibles are dried in a muffle furnace at 500-600°C. The crucibles are cooled in the desiccator and weighed (Y1). 3-4 gr sample is placed in the crucible and weighed (Y2). It is burned at 520°C until white ash is formed in the muffle furnace. After cooling in the desiccator, weighing is performed (Y3) (TS EN ISO 2171, 2010).

Calculation: Ash %=((Y3–Y1)/(Y2–Y1))×100

3.4 Determination of Oil Content

The Soxhelet extraction balloon is dried in an oven and brought to constant weight. It is noted by taking the tare. After the sample is dried and ground, approximately 5 g is weighed and put into the soxhelet cartridge. The cartridge is placed in the soxhelet extraction flask. About 140 ml Petroleum ether is added and placed in the device. After the water and pressure checks are made, the analysis is started. After the analysis is finished, the balloon is placed in the oven and kept in an oven at 100°C for approximately 1 hour. The balloon that is removed from the oven is placed in the desiccator and allowed to cool. The glass balloon is weighed and the amount is noted (TS EN ISO 11085, 2016).

Calculation: % oil = (M2-M1/m)*100

M1=Weight of balloon brought to constant weight (g).

M2=Total amount of oil in the balloon at the last weighing (g).

m=weight of the sample taken (g).

3.5 Determination of pH

To determine the pH ratio, 5 g of dried eggplant samples were ground and homogenized with 50 ml of distilled water. The pH of the resulting mixture is measured using a calibrated pH-meter with 4.0-7.0 buffer solutions.

3.6 Process Efficiency

It was calculated as % value using the formulation (Total dried fruit (kg) / Total fresh fruit (kg) x100) to determine the process efficiency.

3.7 Shape and Taste

In dry product shelf life studies, sensory evaluation analysis was made in terms of shape and taste on the 32., 48. and 64. days of the dried and stored samples. 10 trained panelists took part in the evaluation of these features. Scoring from 1 to 9 was made. 1 point was used as the worst value and 9 points as the best value.

3.8 Color Measurements

Color values were measured using a Spektropen hand-held colorimeter according to the CIE (International Commission on Illumination) color system. Luminosity value (L*); It ranges from 0-100, a value of 0 (black) and a value of 100 (white). Redness (a*) and greenness (-a) values; It varies between -90 and +90; A value of -90 (green) and a value of +90 (red). Yellowness (b*) and blueness (-b) values; It varies between -90 and +90; It is expressed as -90 value (blue) and +90 value (yellow) (McGuire 1992).

3.9 Sensory Evaluations

Finally, sensory evaluation tests were carried out in terms of color, juiciness, crispness, flavor and general acceptability of the dried products. In the sensory evaluation test studies, help was received from 10 panelists who were trained, experienced and knowledgeable on this subject. While evaluations were made on a 1-9 scale, the lowest score was scored as 1 point as the worst and 9 points as the best value.

Results and Discussion

In the study, populations were collected from the regions where dried local eggplant genotypes were grown in our country, and haploid pure lines folded by anther culture were obtained from them. More than 200 eggplant pure lines were examined in terms of yield, fruit characteristics and growth strengths and 44 of them were selected. Fruit samples dried on 44 DH eggplant lines were taken to drying tests. The values of parameters such as moisture, ash, oil, pH, process efficiency, sensory evaluations (color, juiciness, crispness, flavor, general acceptability) and dry product shelf life were calculated separately for both sun drying and oven drying methods. For evaluation in dry product shelf life studies, the samples dried in the sun and in the oven were stored in vacuum and non-vacuum packages and at room conditions (24°C). On the 32nd, 48th and 64th days, the weights, color parameters (L*(brightness), a*(redness), b*(blueness)), shape and taste properties of the products were evaluated. At the end of the study, the prominent dried eggplant DH lines were determined to be used in test hybridizations.

Post-Drying WSDM, Moisture, Ash, Oil, pH and Process Efficiency Parameters in Eggplant

Amount of Water-Soluble Dry Matter (%)

Before drying, the amount of water-soluble dry matter was determined with the “Milwaukee MA871” refractometer device. When the data obtained as a result of fruit observations were examined, the highest dry matter amount was obtained from the genotype D-650 with 4.9%. The lowest dry matter amount was determined as 3.2% in genotypes D-048 and D-580 (Table 1). The dry matter content of the eggplants to be used in the drying experiments was found to be 6.02% (wet) as a result of the dry matter determination (Doymaz and Aktas, 2018). There is a relatively low difference between the mean value reported by Doymaz and the data in this study.

Moisture

The lowest humidity rate was 4.83% (Topan 374) and the highest value was 7.93% (D-580) in the sun-dried samples (Table 1). The lowest moisture content of the samples dried in the oven was 5.93% (Adana dolma) and the highest humidity was 9.33% (D-590). When the drying methods are evaluated, it is seen that the samples dried in the oven contain an average of 21% higher moisture than those dried in the sun. The lowest increase was observed in the D580 genotype with 12%, and the highest difference was observed in the genotypes D-581 and D-655 with 36%. As the temperature increases during the drying process, the drying time of the samples becomes shorter. The reason for this is that as the temperature increases, the existing moisture in the eggplant samples is removed faster.

In the oven drying method, there is a higher temperature treatment compared to the sun drying method. Rozykulova (2021) determined the moisture values of eggplants dried at different temperature values in her study and she reported that the moisture content of eggplants dried at 60°C was 23.07%, and that of eggplant dried at 80°C as 17.07%.

Ash (%)

The highest ash values were 8.85% (D-580) and 8.55% (D-571, D-582) in sun-dried samples. The lowest value was determined in genotype D-048 with 5.48%. Among the samples dried by oven drying method, genotype D-571 increased by 17% compared to sun drying method. It contains the highest ash ratio with a value of 10.05%. Genotype D-048, which has the lowest ash ratio in the sun drying method, showed an increase of 46% in the oven drying method and the ash ratio was determined at the level of 8.05% (Table 1). According to the data in Table 1, the products dried with the oven drying method were represented with higher ash values than the sun drying method.

Oil (%)

The highest oil content was determined as 1.76% (D-654) and the lowest oil ratio was determined as 0.16% (D-051) in the sun-dried samples. The average oil content of products dried in the sun is 0.5%. D-654 and D-580 genotypes, which have the highest oil content in the sun drying method, showed a 3% decrease in oil ratios when they were dried in the oven (Table 1). Contrary to these two genotypes, an average increase of 17% was detected in the oil ratio of the other samples. Nisha et al., (2009) determined the oil content of eggplant as 0.88%, 0.66%, 0.50% and 0.72% in four different samples, respectively. These values were found to be compatible with the research results.

pH (%)

The average pH value of eggplant samples was 4.82 in the sun drying method, and this value was determined as 5.06 with an increase of 5% in the oven drying method. The highest pH value was 5.15 (D-580) and the lowest pH value was 4.47 (D-586) in the sun-dried samples. Genotype D-580 supports an average increase of 5% with a pH value of 5.42 in the oven drying method (Table 1). Akcelik et al., (2000) reported the pH value of eggplants as 4.5 in his study and this value supports our study data.

Process Efficiency (%)

To determine the process efficiency (Total dried fruit (kg) / Total fresh fruit (kg) x100) formulation was used. The most significant difference between the "post-drying processes" examined in sun and oven drying methods was observed in the process efficiency. It was determined that the process efficiency of the samples dried with the oven drying method was 93% higher on average compared to the sun drying method. In the samples dried in the oven, the lowest increase was observed in the genotype D-590 with 17% compared to the sun drying, and the value of 7.2% increased to 8.4% in the oven drying method. The highest increase was observed in the genotype D-584, which has 1.6% treatment efficiency, and the process efficiency was determined as 6.5% with an increase of 305% compared to the sun drying method (Table 1).

Dry Product Shelf Life Evaluations in Eggplant Weight

On the 32nd, 48th and 64th days of the dry product shelf life evaluations, the dried weights of the products were determined by weighing them with precision scales. The samples were dried using sun and oven drying methods, and in addition to this, the weight values were measured according to whether the products were stored in vacuum and non-vacuum packages (Table 2a, 2b and 2c).

In the weight measurements of both drying methods on the 32nd, 48th and 64th days, the weight values of the samples in non-vacuum packages were found to be lower than the samples in vacuum packages. According to the average of the values, it was found that the products that were dried in the sun and in vacuum packages had 70-75% higher weight than those in the non-vacuum package. This rate is 30-35% in oven drying method. These data show the importance of the experimental group using vacuum packs. Trials using both non-vacuum and vacuum packs were also evaluated among themselves. In the evaluations of the 32nd day, the weight values of the samples stored in non-vacuum packages were measured 80-90% higher in the oven-drying method compared to those

that were dried in the sun (Table 2a). Although this difference decreased relatively in the 48th and 64th day evaluations, it was determined that the samples dried in the oven had higher values. The products stored in vacuum packages were also evaluated according to the drying method, 20-30% higher values were observed in the oven drying method compared to the sun drying method. It was determined that the weight values on the 32nd day measured in all experimental groups (Sun-dried – vacuum/non-vacuum; Oven-dried – vacuum/non-vacuum) decreased by 5-8% in the measurements made on both 48th and 64th days. While the weight value of the genotype D-640, which was dried in the sun and stored in non-vacuum packages, was 0.044 on the 32nd day, this value was calculated as 0.040 on the 48th day and 0.034 on the 64th day (Table 2a, 2b and 2c). It is expected that the weight of the products will decrease depending on the parameters such as the time spent in the drying process, moisture loss and shrinkage.

Shape

In the evaluations made on day 32, samples dried in the sun and stored in non-vacuum packages had a lower score range. 16 samples kept in non-vacuum packages were evaluated in the range of 5-6 points, and 17 samples were evaluated in the range of 8-9 points. In the 48th and 64th day evaluations, it was determined that the sun-dried samples stored in vacuum packages had higher shape values compared to the ones without vacuum. In the oven drying method, both vacuum and non-vacuum experimental groups are represented by high shape values in general. Only 2-3 samples received 6 points.

Major changes occur in the structure of vegetables due to the removal of moisture during and after the drying process. This causes shrinkage and change in the porosity of the dried product (Jangam et al., 2010). The removal of the water content of the products during the drying process creates a pressure difference. This often causes cracking (also known as surface cracking) and shrinkage events inside and outside the product. Shrinkage increases in proportion to the volume of water removed during drying. When the internal volume of the product becomes smaller after removal of the moisture content, the outer surfaces of the product will cause shrinkage.

This situation negatively affects the quality of the product, increases the hardness of the product and adversely affects customer preferences due to shape and texture defects (Jangam et al., 2010).

Especially the genotypes D-582 and D-584 were scored in the range of 4-5 points in terms of shape characteristics after drying (Table 2b). These genotypes need to be evaluated for suitability for drying.

Taste

During the drying process, certain rates of deterioration occur in color, aroma and texture (Colak Gunes, 2009). Since volatile compounds that provide aroma and taste have a lower boiling point than water, they can be removed from the product by evaporation during drying (Bingol and Devres, 2010). Volatile compounds in foods can evaporate at high temperatures and long drying processes, and these losses, which occur together with water vapor, can cause significant losses in the taste and aroma of the dried product (Konak et al., 2009). In the taste evaluations on the 32nd day, only 2-3 genotypes were scored low in the samples that were dried in the sun and stored in both non-vacuum and vacuum packages. Sample D-584 received 6 points in both the vacuum and non-vacuum experimental groups in the taste evaluations. D-584 was represented by low scores in figure evaluations. The lowest score was 5 (D-582 and D-047) in the samples dried in the oven and stored in non-vacuum packages, and the value observed in the 10 samples was 6 (Table 2a).

Generally, high values (8-9) were observed in the samples stored in vacuum packages. In the 48th and 64th day evaluations, a significant decrease was observed in the taste values of the samples that were stored in non-vacuum packages, both in the sun and in the oven. Samples stored in vacuum packages were represented with high scores in terms of taste characteristics. In line with these data, we can said that in both drying methods, the taste properties of the samples stored in vacuum packages are preserved compared to the samples stored in non-vacuum packages, and there is no loss of value.

Color L*

Color values were measured using a Spectropen colorimeter. In the evaluations of the 32nd day, it was determined that the samples stored in vacuum packages in both drying methods had 5-8% higher L* values compared to those stored in non-vacuum packages (Table 3a). This situation is also valid in the analyzes performed on the 48th and 64th days. The L* values of the sun-dried samples were lower than the oven-dried samples in all three different evaluation stages. The decrease in the L* value is important as it indicates that the color of the product changes towards black. Bayraktaroglu (2015) found the lowest L values averages in eggplant samples dried by traditional sun drying method in his study. However, he reported that the L values of the samples dried by the convective and infrared-convective combined method were higher than the sun drying method. Bayraktaroglu's study and the findings of this study support each other.

Color (a*)

Samples dried in the sun and stored in vacuum packages have an average of 50-55% higher a* values than samples stored in non-vacuum packages. An average increase of 17-20% was observed in the oven drying method. D-650 genotype had the highest a* value with 14.70 on the 64th day evaluations (Table 3c). In addition, D-650 was represented with the highest average a* values in the measurements made in 3 different time periods in all variations. The average a* value of the genotype D-650, which was dried in the sun and stored in non-vacuum packages, measured at 3 different times, was calculated as 8.25, and this value was calculated as 10.60 in vacuum packages. While the a* value average was 10.71 in the oven-dried and non-vacuum packaged samples, this value was calculated as 12.60 in vacuum packages. The increase in a* values in the CIE color space represents the change from green to red (Anonymous 2002). In general, it was determined that a* values increased in all variations in the drying process, that is, a change towards red color occurred.

Bayraktaroglu (2015) reported that the a* values of the samples increased as the drying temperature increased in the products dried with hot air. It is thought that the oven drying method has higher a* values because it allows drying at a certain constant temperature value (60°C) and in more optimum conditions. The data in this study agree with the outputs of Bayraktaroglu's study in 2015.

Color (b*)

As with the other color parameters evaluated, higher values were observed in the oven-dried samples compared to the sun-dried samples in terms of b* value. When the 32nd day data were examined, the average color values of the samples dried in the oven were found to be 30-40% higher. This situation is also observed on the 48th and 64th days (Table 3b and 3c). On average, the lowest b* value was obtained in sun-dried samples (Bayraktaroglu 2015). However, when the 32, 48 and 64 days values were examined, a gradual decrease was observed in the average b* values. In Soltani and Kulcu, MB's study in 2021, an increase was observed in b* values, as well as L* and a* values, after drying processes. The observed and unexpected gradual decrease in b* values over time in this study needs to be evaluated and clarified.

Sensory Evaluations in Eggplant

Finally, sensory evaluation tests were carried out in terms of color, juiciness, crispness, flavor and general acceptability of the dried products. In the sensory evaluation test studies, assistance was received from 10 panelists who were trained and knowledgeable on this subject. While evaluations were made on a 1-9 scale, the lowest score was scored as 1 and the highest score as 9.

In terms of color, juiciness, crispness and general acceptability, a partial height was determined in the scores of the products dried in the oven compared to the sun drying method. Especially in the sun-dried genotypes D-582 and D584, low scores were made regarding these parameters and their suitability for drying was reviewed. Both genotypes were scored in the range of 5-6 points in sensory evaluations. Some eggplant samples dried by the sun drying method had higher or equivalent scores in terms of flavor compared to those dried in the oven. D-628 sample, which was dried in the oven, was determined as the genotype with the lowest value with 4 points in terms of flavor (Table 4).

Conclusions

In our country, most of the products are dried in the open air under the sun. Traditional sun drying method is an economical method, but it can cause negative situations such as toxic risks caused by air pollution, inability to dry the product homogeneously and direct contact of sun rays with the dried product. These negativities cause both the prolongation of the drying process and the loss of quality in the product and thus economic damage.

For these reasons, considering the need for alternative drying technologies and storage methods, the most suitable drying method for the energy consumption, nutritional value and quality characteristics of the eggplant samples dried with the traditional method and oven drying method was investigated. In addition, ideal genotypes suitable for the drying sector were determined based on the plant and fruit observations and analysis results after drying (high dry matter content in eggplant, low moisture, high ash, low oil, ideal dry product shelf life). D-644 and D-632 coded genotypes were found to be suitable for stuffed drying studies, and D-654 and D-581 coded genotypes were found to be suitable for slicing drying studies.

With this study, an important step has been achieved in the development of new qualified hybrid varieties by using accelerated breeding techniques from local Turkish eggplant populations. The data obtained reveal the importance of alternative drying technologies for the sector, the convenience and advantages they provide in practice compared to the sun drying method. In addition, the data obtained on the storage methods of dried products also show the advantages of the storage method in vacuum or non-vacuum packages.

We believe that the outputs of these studies will be an important source and guide for possible studies and researches on the drying sector in the future.

Figure 1. Examples of DH breeding lines used in the study. (Original)

Figure 2. Prewash process. (Original)

Figure 3. Sun drying process. (Original)

Figure 4. Oven and sun dried samples. Products stored in vacuum and non-vacuum packages were used in dry product shelf life analyses. (Original)

Figure 5. Equipment for analysis. A. used for oil determination; B. Spectropen colorimeter; C. Milwaukee MA871 refractometer device; D. Drying oven; E. pH meter. (Original)

Table 1. Post-Drying Water-Soluble Dry Matter, Moisture, Ash, Oil, pH and Process Efficiency Parameters.

Origin Location	Open Field Code	Water Soluble Dry Matter %	Moisture %		Ash %		Oil %		pH %		Process Efficiency %	
			Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying
O.P. Variety	Adana dolmalık	3,3	4,93	5,93	6,25	7,95	0,35	0,43	4,75	4,99	1,9	3,0
O.P. Variety	Topan 374	3,5	4,83	6,03	6,35	7,87	0,26	0,33	4,68	4,94	2,0	3,5
O.P. Variety	Antep Dolmalık	4,1	5,03	6,33	6,55	7,25	0,37	0,44	4,95	5,29	1,7	4,7
Manisa / Turgutlu	D-048	3,2	5,63	7,13	5,48	8,05	0,25	0,31	5,01	5,26	2,9	5,8
Manisa / Turgutlu	D-051	3,5	5,43	6,53	6,35	7,45	0,16	0,29	5,15	5,38	2,7	7,1
Manisa / Turgutlu	D-057	3,4	4,93	6,13	5,85	7,05	0,47	0,54	4,65	4,86	2,1	5,1
Manisa / Turgutlu	D-0146	3,9	5,93	7,13	6,85	8,05	0,35	0,41	4,58	4,84	2,9	6,5
Adana Topan Patlıcan	D-055A	3,7	5,43	6,93	6,35	7,85	0,36	0,46	4,89	5,13	2,5	6,0
Adana Topan Patlıcan	D-074A	4,2	5,63	6,53	6,55	7,45	0,37	0,49	4,52	4,77	2,9	6,7
Adana Topan Patlıcan	D-079A	4,3	5,23	6,23	6,15	7,25	0,45	0,46	5,14	5,37	2,7	6,1
Adana Topan Patlıcan	D-A89	4,5	5,43	6,63	6,35	7,55	0,36	0,38	4,78	4,92	2,2	4,3
Adana Topan Patlıcan	D-A90	3,5	6,03	7,33	6,95	8,25	0,37	0,45	4,69	4,93	2,7	4,5
Aydın / Nazilli	D-114	4,2	6,13	7,63	7,05	8,55	0,35	0,42	4,85	5,07	1,8	3,6
Aydın / Nazilli	D-234	4,5	6,53	7,63	7,45	8,55	0,46	0,53	4,79	5,00	5,7	7,3
Aydın / Nazilli	D-235	4,1	5,73	6,93	6,65	7,85	0,37	0,43	5,10	5,32	2,0	4,0
Manisa / Salihli	D-570	4,6	7,41	8,61	7,85	9,05	0,45	0,50	5,14	5,42	6,9	8,8
Manisa / Salihli	D-571	4,5	7,63	9,13	8,55	10,05	0,46	0,53	4,75	4,99	6,6	9,1
Manisa / Salihli	D-576	4,2	7,03	7,93	7,95	8,85	0,37	0,43	4,98	5,24	1,6	4,7
Burdur / Merkez	D-580	3,2	7,93	8,93	8,85	9,95	1,74	1,69	5,15	5,41	6,5	8,2
Burdur / Merkez	D-581	4,8	5,12	6,98	8,55	9,75	1,73	1,75	5,11	5,36	2,8	6,7
Gaziantep / Oğuzeli	D-582	3,6	7,63	8,93	8,55	9,85	0,37	0,38	4,78	5,12	1,7	4,4
Gaziantep / Oğuzeli	D-584	3,4	5,63	7,13	6,55	8,05	0,45	0,47	4,85	5,06	1,6	6,5
Gaziantep / Oğuzeli	D-586	4,2	5,63	6,73	6,55	7,65	1,62	1,74	4,47	4,73	4,5	6,9
Gaziantep / Oğuzeli	D-587	4,3	5,43	6,63	6,35	7,55	0,37	0,44	4,58	4,82	1,6	3,7
Gaziantep / Oğuzeli	D-588	4,1	5,73	6,93	6,65	7,85	0,35	0,42	4,67	4,92	1,8	3,0
Gaziantep / Oğuzeli	D-590	4,2	7,83	9,33	8,75	9,25	1,67	1,71	4,85	5,08	7,2	8,4
Artvin / Hopa	D-628	3,6	6,33	7,23	7,25	8,15	0,37	0,42	5,01	5,15	1,3	2,4
Artvin / Hopa	D-630	4,1	6,43	7,43	7,35	8,45	0,25	0,32	4,95	5,19	4,8	6,3
Adana / Akkapı	D-632	4,6	5,33	6,53	6,25	7,45	0,36	0,42	4,87	5,09	2,2	3,7
Adana / Akkapı	D-634	4,6	5,63	6,93	6,55	7,85	0,47	0,57	4,52	4,73	2,2	3,5
Doğal Topan Patlıcan	D-635	4,4	5,43	6,93	6,35	7,85	0,35	0,47	4,73	4,95	2,3	3,9
Doğal Topan Patlıcan	D-637	4,5	5,03	6,13	5,95	7,05	0,46	0,47	4,52	4,80	1,7	3,2
Doğal Topan Patlıcan	D-638	4,1	5,43	6,63	6,35	7,55	0,47	0,49	5,12	5,36	2,3	3,8
Doğal Topan Patlıcan	D-639	4,2	5,23	6,43	6,15	7,35	0,35	0,43	4,83	5,09	2,4	4,9
Adana / Sarıçam	D-640	4,6	5,33	6,83	6,25	7,75	0,21	0,28	4,76	5,10	1,7	3,5
Adana / Sarıçam	D-641	4,5	6,33	7,23	7,25	8,15	0,27	0,34	4,98	5,23	2,2	4,1
Adana / Sarıçam	D-644	4,2	5,33	6,33	6,25	7,35	0,35	0,41	4,91	5,25	2,0	2,8
Adana / Sarıçam	D-645	4,1	5,43	6,63	6,35	7,55	0,46	0,51	4,81	5,02	2,3	3,9
Adana / Sarıçam	D-646	3,7	5,83	7,13	6,75	8,05	0,37	0,44	4,76	5,02	2,3	4,1
Adana / Sarıçam	D-647	4,6	5,73	7,23	6,65	8,15	0,35	0,41	4,65	4,89	2,4	4,2
Adana / Sarıçam	D-648	4,8	5,63	6,73	6,55	7,65	0,36	0,46	4,66	4,91	2,3	4,2
Balıkesir / Bandırma	D-650	4,9	5,43	6,63	6,35	7,55	0,37	0,49	4,68	4,91	1,7	4,3
Urfa / Mezra	D-654	4,5	5,86	7,85	7,65	8,85	1,76	1,69	4,71	4,85	7,2	9,8
Urfa / Mezra	D-655	4,7	5,98	8,14	7,85	9,35	1,65	1,78	4,69	4,93	7,7	10,4

Table 2a. Shelf Life Evaluations of 32nd Days (Weight, Shape, Taste).

Origin Location	Open Field Code	Dry Product Shelf Life											
		32nd Day											
		Weight (kg)				Shape				Taste			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed
O.P. Variety	Adana Dolmalık	0,044	0,074	0,069	0,099	7	8	7	7	8	8	7	8
O.P. Variety	Topan 374	0,046	0,081	0,080	0,115	9	8	8	9	9	7	8	7
O.P. Variety	Antep Dolmalık	0,022	0,047	0,062	0,087	6	7	6	6	7	8	6	8
Manisa / Turgutlu	D-048	0,036	0,064	0,072	0,100	7	8	7	7	8	7	7	9
Manisa / Turgutlu	D-051	0,028	0,077	0,073	0,122	8	7	7	8	8	7	7	7
Manisa / Turgutlu	D-057	0,028	0,057	0,066	0,095	7	6	7	7	8	8	7	8
Manisa / Turgutlu	D-0146	0,031	0,069	0,070	0,108	8	9	8	8	9	8	8	9
Adana Topan Patlıcan	D-055A	0,034	0,083	0,081	0,130	8	9	6	8	7	8	6	7
Adana Topan Patlıcan	D-074A	0,038	0,099	0,089	0,150	7	6	5	7	6	8	5	9
Adana Topan Patlıcan	D-079A	0,048	0,064	0,109	0,125	6	7	6	6	7	7	6	8
Adana Topan Patlıcan	D-A89	0,048	0,078	0,095	0,125	9	8	7	9	8	8	7	7
Adana Topan Patlıcan	D-A90	0,066	0,101	0,111	0,146	6	7	6	6	7	7	6	8
Aydın / Nazilli	D-114	0,026	0,051	0,051	0,076	9	8	8	9	9	8	8	9
Aydın / Nazilli	D-234	0,122	0,150	0,156	0,184	8	7	7	8	8	7	7	7
Aydın / Nazilli	D-235	0,038	0,087	0,078	0,127	7	8	7	7	8	8	7	8
Manisa / Salihli	D-570	0,128	0,157	0,164	0,193	8	7	7	8	8	7	7	6
Manisa / Salihli	D-571	0,120	0,158	0,165	0,203	7	8	7	7	8	7	7	7
Manisa / Salihli	D-576	0,020	0,069	0,058	0,107	6	8	6	6	7	8	6	8
Burdur / Merkez	D-580	0,152	0,213	0,191	0,252	6	8	7	6	8	7	7	9
Burdur / Merkez	D-581	0,034	0,050	0,081	0,097	7	7	8	7	9	8	8	7
Gaziantep / Oğuzeli	D-582	0,032	0,062	0,083	0,113	5	7	6	5	7	9	6	7
Gaziantep / Oğuzeli	D-584	0,020	0,055	0,081	0,116	5	7	5	5	6	6	5	8
Gaziantep / Oğuzeli	D-586	0,088	0,113	0,135	0,160	6	7	7	6	8	7	7	8
Gaziantep / Oğuzeli	D-587	0,034	0,062	0,079	0,107	6	8	7	6	8	8	7	7
Gaziantep / Oğuzeli	D-588	0,040	0,089	0,065	0,114	6	8	6	6	7	6	6	7
Gaziantep / Oğuzeli	D-590	0,200	0,229	0,234	0,263	7	7	7	7	8	7	7	8
Artvin / Hopa	D-628	0,050	0,088	0,090	0,128	6	8	7	6	8	8	7	9
Artvin / Hopa	D-630	0,120	0,169	0,156	0,205	8	7	8	8	9	7	8	8
Adana / Akkapı	D-632	0,064	0,125	0,109	0,170	7	8	6	7	7	8	6	7
Adana / Akkapı	D-634	0,062	0,078	0,100	0,116	6	6	7	6	8	9	7	8
Doğal Topan Patlıcan	D-635	0,056	0,086	0,095	0,125	7	8	7	7	8	9	7	9
Doğal Topan Patlıcan	D-637	0,054	0,089	0,101	0,136	8	7	8	8	9	9	8	8
Doğal Topan Patlıcan	D-638	0,080	0,105	0,131	0,156	6	8	7	6	8	7	7	7
Doğal Topan Patlıcan	D-639	0,056	0,084	0,117	0,145	6	8	6	6	7	8	6	8
Adana / Sarıçam	D-640	0,044	0,093	0,091	0,140	8	6	7	8	8	7	7	9
Adana / Sarıçam	D-641	0,052	0,081	0,097	0,126	6	7	6	6	7	9	6	9
Adana / Sarıçam	D-644	0,064	0,102	0,089	0,127	8	6	8	8	9	7	8	8
Adana / Sarıçam	D-645	0,050	0,099	0,084	0,133	8	8	7	8	8	8	7	9
Adana / Sarıçam	D-646	0,052	0,113	0,092	0,153	9	8	8	9	9	9	8	9
Adana / Sarıçam	D-647	0,050	0,066	0,086	0,102	8	9	8	8	9	9	8	9
Adana / Sarıçam	D-648	0,054	0,084	0,099	0,129	7	8	7	7	8	7	7	8
Balıkesir / Bandırma	D-650	0,026	0,061	0,064	0,099	6	7	7	6	8	8	7	7
Urfa / Mezra	D-654	0,112	0,137	0,151	0,176	8	8	8	8	9	9	8	8
Urfa / Mezra	D-655	0,134	0,162	0,181	0,209	8	8	8	8	9	8	8	9

Table 2b. Shelf Life Evaluations of 48th Days (Weight, Shape, Taste).

Origin Location	Open Field Code	Dry Product Shelf Life											
		48th Day											
		Weight (kg)				Shape				Taste			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed
O.P. Variety	Adana Dolmalık	0,041	0,067	0,054	0,080	6	8	7	8	7	8	7	8
O.P. Variety	Topan 374	0,043	0,088	0,056	0,101	8	8	9	7	8	7	9	8
O.P. Variety	Antep Dolmalık	0,018	0,053	0,032	0,067	5	7	7	8	6	8	6	7
Manisa / Turgutlu	D-048	0,032	0,067	0,046	0,081	6	8	8	7	7	9	7	8
Manisa / Turgutlu	D-051	0,023	0,058	0,038	0,073	7	7	8	7	7	7	8	7
Manisa / Turgutlu	D-057	0,023	0,058	0,038	0,073	6	6	8	8	7	8	7	8
Manisa / Turgutlu	D-0146	0,025	0,060	0,041	0,076	7	9	9	8	8	9	8	8
Adana Topan Patlıcan	D-055A	0,028	0,075	0,044	0,091	7	9	7	8	6	7	8	8
Adana Topan Patlıcan	D-074A	0,035	0,084	0,048	0,097	6	7	6	8	5	9	7	8
Adana Topan Patlıcan	D-079A	0,045	0,102	0,058	0,115	5	7	7	7	6	8	6	7
Adana Topan Patlıcan	D-A89	0,044	0,112	0,058	0,126	8	8	8	8	7	7	9	8
Adana Topan Patlıcan	D-A90	0,062	0,088	0,076	0,102	5	7	7	7	6	8	6	8
Aydın / Nazilli	D-114	0,021	0,066	0,036	0,081	8	8	9	8	8	9	9	7
Aydın / Nazilli	D-234	0,117	0,152	0,132	0,167	7	7	8	7	7	7	8	8
Aydın / Nazilli	D-235	0,032	0,067	0,048	0,083	6	8	8	8	7	8	7	8
Manisa / Salihli	D-570	0,122	0,157	0,138	0,173	7	7	7	7	7	6	8	8
Manisa / Salihli	D-571	0,117	0,152	0,130	0,165	6	8	8	7	7	7	7	8
Manisa / Salihli	D-576	0,017	0,052	0,030	0,065	5	8	7	8	6	8	6	8
Burdur / Merkez	D-580	0,148	0,195	0,162	0,209	5	8	8	7	7	9	6	9
Burdur / Merkez	D-581	0,030	0,079	0,044	0,093	6	7	9	8	8	7	7	9
Gaziantep / Oğuzeli	D-582	0,027	0,084	0,042	0,099	4	7	6	9	6	7	5	9
Gaziantep / Oğuzeli	D-584	0,015	0,083	0,030	0,098	4	7	6	6	5	8	5	8
Gaziantep / Oğuzeli	D-586	0,082	0,108	0,098	0,124	5	7	7	6	7	8	6	8
Gaziantep / Oğuzeli	D-587	0,028	0,073	0,044	0,089	5	8	8	8	7	7	6	8
Gaziantep / Oğuzeli	D-588	0,037	0,072	0,050	0,085	5	8	7	7	6	7	6	7
Gaziantep / Oğuzeli	D-590	0,197	0,232	0,210	0,245	6	7	8	7	7	8	7	8
Artvin / Hopa	D-628	0,046	0,081	0,060	0,095	5	8	7	8	7	9	6	8
Artvin / Hopa	D-630	0,116	0,151	0,130	0,165	7	7	9	7	8	8	8	7
Adana / Akkapı	D-632	0,059	0,094	0,074	0,109	6	8	7	8	6	7	7	8
Adana / Akkapı	D-634	0,057	0,104	0,072	0,119	5	7	8	9	7	8	6	7
Doğal Topan Patlıcan	D-635	0,050	0,099	0,066	0,115	6	8	7	9	7	9	7	8
Doğal Topan Patlıcan	D-637	0,048	0,105	0,064	0,121	7	7	9	9	8	8	8	9
Doğal Topan Patlıcan	D-638	0,077	0,145	0,090	0,158	5	8	8	7	7	7	6	8
Doğal Topan Patlıcan	D-639	0,053	0,079	0,066	0,092	5	8	7	8	6	8	6	9
Adana / Sarıçam	D-640	0,040	0,085	0,054	0,099	7	6	9	7	7	9	8	8
Adana / Sarıçam	D-641	0,048	0,083	0,062	0,097	5	7	7	9	6	9	6	7
Adana / Sarıçam	D-644	0,059	0,094	0,074	0,109	7	6	9	7	8	8	8	8
Adana / Sarıçam	D-645	0,045	0,080	0,060	0,095	7	8	8	8	7	9	8	9
Adana / Sarıçam	D-646	0,046	0,081	0,062	0,097	8	8	9	9	8	9	9	8
Adana / Sarıçam	D-647	0,044	0,079	0,060	0,095	7	9	9	9	8	9	8	9
Adana / Sarıçam	D-648	0,051	0,098	0,064	0,111	6	8	7	7	7	8	7	9
Balıkesir / Bandırma	D-650	0,022	0,071	0,036	0,085	5	7	7	8	7	7	6	8
Urfa / Mezra	D-654	0,108	0,165	0,122	0,179	7	8	9	9	8	8	8	8
Urfa / Mezra	D-655	0,129	0,197	0,144	0,212	7	8	9	8	8	9	8	8

Table 2c. Shelf Life Evaluations of 64th Days (Weight, Shape, Taste).

Origin Location	Open Field Code	Dry Product Shelf Life											
		64th Day											
		Weight (kg)				Shape				Taste			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed
O.P. Variety	Adana Dolmalık	0,036	0,061	0,058	0,083	7	8	7	8	8	9	7	7
O.P. Variety	Topan 374	0,038	0,063	0,051	0,076	9	7	8	7	9	8	8	8
O.P. Variety	Antep Dolmalık	0,012	0,038	0,021	0,047	6	7	7	9	7	7	6	9
Manisa / Turgutlu	D-048	0,026	0,049	0,039	0,062	7	8	7	8	8	8	7	8
Manisa / Turgutlu	D-051	0,020	0,043	0,022	0,045	8	7	8	7	8	9	7	7
Manisa / Turgutlu	D-057	0,020	0,050	0,029	0,059	7	7	7	8	8	8	7	7
Manisa / Turgutlu	D-0146	0,021	0,048	0,031	0,058	8	7	7	9	9	7	8	7
Adana Topan Patlıcan	D-055A	0,024	0,049	0,026	0,051	7	7	8	7	7	8	6	8
Adana Topan Patlıcan	D-074A	0,030	0,054	0,026	0,050	6	8	7	8	6	9	5	7
Adana Topan Patlıcan	D-079A	0,040	0,061	0,026	0,047	6	6	7	7	7	8	6	8
Adana Topan Patlıcan	D-A89	0,038	0,063	0,040	0,065	8	8	8	8	8	8	7	8
Adana Topan Patlıcan	D-A90	0,056	0,082	0,060	0,086	6	7	7	9	7	8	6	8
Aydın / Nazilli	D-114	0,018	0,042	0,040	0,064	9	8	9	8	9	8	8	7
Aydın / Nazilli	D-234	0,114	0,135	0,127	0,148	8	9	8	7	8	8	7	8
Aydın / Nazilli	D-235	0,028	0,053	0,037	0,062	7	9	7	8	8	9	7	8
Manisa / Salihli	D-570	0,118	0,143	0,131	0,156	8	8	7	9	8	9	7	9
Manisa / Salihli	D-571	0,112	0,138	0,114	0,140	7	7	8	8	8	9	7	8
Manisa / Salihli	D-576	0,012	0,035	0,021	0,044	6	8	6	7	7	8	6	7
Burdur / Merkez	D-580	0,142	0,165	0,152	0,175	7	9	8	8	8	8	7	8
Burdur / Merkez	D-581	0,024	0,054	0,026	0,056	8	8	8	9	9	7	8	9
Gaziantep / Oğuzeli	D-582	0,024	0,051	0,020	0,047	6	7	6	7	7	8	6	8
Gaziantep / Oğuzeli	D-584	0,012	0,037	0,032	0,057	5	8	5	6	6	8	5	7
Gaziantep / Oğuzeli	D-586	0,078	0,102	0,080	0,104	7	9	7	7	8	9	7	7
Gaziantep / Oğuzeli	D-587	0,024	0,045	0,028	0,049	7	8	7	7	8	8	7	7
Gaziantep / Oğuzeli	D-588	0,032	0,057	0,054	0,079	6	8	7	8	7	7	6	8
Gaziantep / Oğuzeli	D-590	0,192	0,218	0,205	0,231	7	7	8	7	8	8	7	9
Artvin / Hopa	D-628	0,040	0,064	0,049	0,073	7	7	7	8	8	7	7	8
Artvin / Hopa	D-630	0,110	0,131	0,123	0,144	8	7	8	8	9	8	8	7
Adana / Akkapı	D-632	0,056	0,081	0,058	0,083	7	7	7	8	7	7	6	7
Adana / Akkapı	D-634	0,053	0,078	0,063	0,088	7	7	7	7	8	8	7	7
Doğal Topan Patlıcan	D-635	0,046	0,072	0,056	0,082	7	8	8	8	8	8	7	8
Doğal Topan Patlıcan	D-637	0,043	0,066	0,046	0,069	8	8	8	7	9	8	8	8
Doğal Topan Patlıcan	D-638	0,072	0,095	0,068	0,091	7	8	7	7	8	8	7	9
Doğal Topan Patlıcan	D-639	0,047	0,077	0,034	0,064	6	7	7	8	7	8	6	8
Adana / Sarıçam	D-640	0,034	0,061	0,036	0,063	8	7	8	7	8	8	7	7
Adana / Sarıçam	D-641	0,045	0,070	0,046	0,071	6	8	6	8	7	7	6	8
Adana / Sarıçam	D-644	0,056	0,080	0,078	0,102	8	8	8	9	9	7	8	8
Adana / Sarıçam	D-645	0,041	0,062	0,055	0,076	8	7	8	8	8	7	7	7
Adana / Sarıçam	D-646	0,042	0,067	0,051	0,076	9	8	8	7	9	7	8	8
Adana / Sarıçam	D-647	0,039	0,065	0,053	0,079	8	8	8	8	9	7	8	9
Adana / Sarıçam	D-648	0,046	0,070	0,048	0,072	7	8	8	9	8	7	7	7
Balıkesir / Bandırma	D-650	0,016	0,037	0,027	0,048	7	8	8	9	8	7	7	8
Urfa / Mezra	D-654	0,102	0,121	0,112	0,131	8	9	8	9	9	7	8	7
Urfa / Mezra	D-655	0,126	0,142	0,136	0,152	8	9	8	8	9	7	8	7

Table 3a. Dry Product Shelf Life Evaluations of 32nd Days (Color; L*, a*, b*).

Origin Location	Open Field Code	Dry Product Shelf Life											
		32nd Day											
		L*				a*				b*			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed
O.P. Variety	Adana Dolmalık	30,54	32,69	32,95	35,10	5,88	7,98	8,29	9,44	5,75	6,90	8,16	9,31
O.P. Variety	Topan 374	23,08	25,22	25,18	27,32	3,97	6,17	6,07	7,21	1,14	2,28	3,24	4,38
O.P. Variety	Antep Dolmalık	31,39	33,66	33,93	36,20	5,01	7,11	7,55	8,82	-0,06	1,21	2,48	3,75
Manisa / Turgutlu	D-048	22,82	24,92	25,43	27,53	6,54	8,84	9,15	10,25	8,95	10,05	11,56	12,66
Manisa / Turgutlu	D-051	28,00	30,10	30,71	32,81	5,87	7,87	8,58	9,68	1,81	2,91	4,52	5,62
Manisa / Turgutlu	D-057	31,05	33,35	33,16	35,46	5,61	7,61	7,72	9,02	1,48	2,78	3,59	4,89
Manisa / Turgutlu	D-0146	29,35	32,25	31,55	34,45	6,02	8,12	8,22	10,12	4,75	6,65	6,95	8,85
Adana Topan Patlıcan	D-055A	24,68	27,48	26,68	29,48	5,47	7,77	7,47	9,27	7,41	9,21	9,41	11,21
Adana Topan Patlıcan	D-074A	31,25	33,65	33,55	35,95	3,24	5,74	5,54	6,94	5,61	7,01	7,91	9,31
Adana Topan Patlıcan	D-079A	35,18	37,28	37,28	39,38	4,57	6,67	6,67	7,77	7,31	8,41	9,41	10,51
Adana Topan Patlıcan	D-A89	29,34	31,54	31,56	33,76	5,09	7,29	7,31	8,51	3,66	4,86	5,88	7,08
Adana Topan Patlıcan	D-A90	19,96	22,26	21,85	24,15	4,82	7,12	6,71	8,01	7,62	8,92	9,51	10,81
Aydın / Nazilli	D-114	26,84	29,04	28,62	30,82	4,46	6,78	6,24	7,44	-1,57	-0,37	0,21	1,41
Aydın / Nazilli	D-234	21,22	23,22	23,20	25,20	2,94	5,34	4,92	5,92	5,19	6,19	7,17	8,17
Aydın / Nazilli	D-235	32,89	35,09	35,30	37,50	3,78	6,18	6,19	7,39	4,79	5,99	7,20	8,40
Manisa / Salihli	D-570	47,60	49,80	49,70	51,90	5,47	8,01	7,57	8,77	16,20	17,40	18,30	19,50
Manisa / Salihli	D-571	49,05	51,35	51,59	53,89	4,40	7,09	6,94	8,24	15,70	17,00	18,24	19,54
Manisa / Salihli	D-576	34,78	37,08	37,39	39,69	2,81	5,35	5,42	6,72	4,76	6,06	7,37	8,67
Burdur / Merkez	D-580	19,47	21,62	22,18	24,33	2,94	5,45	5,65	6,80	5,19	6,34	7,90	9,05
Burdur / Merkez	D-581	25,41	27,55	27,52	29,66	3,78	5,88	5,89	7,03	4,79	5,93	6,90	8,04
Gaziantep / Oğuzeli	D-582	24,41	26,68	26,61	28,88	3,83	6,03	6,03	7,30	4,74	6,01	6,94	8,21
Gaziantep / Oğuzeli	D-584	25,81	27,91	27,81	29,91	6,21	8,31	8,21	9,31	1,24	2,34	3,24	4,34
Gaziantep / Oğuzeli	D-586	21,79	23,89	24,09	26,19	4,89	7,19	7,19	8,29	2,78	3,88	5,08	6,18
Gaziantep / Oğuzeli	D-587	34,21	36,51	36,31	38,61	5,78	7,78	7,88	9,18	-0,04	1,26	2,06	3,36
Gaziantep / Oğuzeli	D-588	27,24	30,14	29,46	32,36	4,98	6,98	7,20	9,10	0,98	2,88	3,20	5,10
Gaziantep / Oğuzeli	D-590	51,47	54,27	53,36	56,16	3,58	5,68	5,47	7,27	8,77	10,57	10,66	12,46
Artvin / Hopa	D-628	29,35	31,75	31,13	33,53	4,89	7,19	6,67	8,07	2,78	4,18	4,56	5,96
Artvin / Hopa	D-630	30,54	32,64	32,52	34,62	2,81	5,31	4,79	5,89	4,76	5,86	6,74	7,84
Adana / Akkapı	D-632	30,21	32,41	32,62	34,82	2,98	5,08	5,39	6,59	3,86	5,06	6,27	7,47
Adana / Akkapı	D-634	35,21	37,51	37,31	39,61	3,81	6,01	5,91	7,21	5,41	6,71	7,51	8,81
Doğal Topan Patlıcan	D-635	23,43	25,63	25,97	28,17	4,83	7,13	7,37	8,57	4,49	5,69	7,03	8,23
Doğal Topan Patlıcan	D-637	30,24	32,24	32,85	34,85	5,87	8,19	8,48	9,48	3,74	4,74	6,35	7,35
Doğal Topan Patlıcan	D-638	26,69	28,89	29,40	31,60	6,60	9,00	9,31	10,51	4,96	6,16	7,67	8,87
Doğal Topan Patlıcan	D-639	28,90	31,10	31,01	33,21	4,07	6,47	6,18	7,38	4,79	5,99	6,90	8,10
Adana / Sarıçam	D-640	31,39	33,69	33,59	35,89	3,47	6,01	5,67	6,97	2,78	4,08	4,98	6,28
Adana / Sarıçam	D-641	25,81	28,11	27,81	30,11	5,88	8,57	7,88	9,18	4,76	6,06	6,76	8,06
Adana / Sarıçam	D-644	24,57	26,72	26,87	29,02	4,07	6,61	6,37	7,52	6,98	8,13	9,28	10,43
Adana / Sarıçam	D-645	23,08	25,22	25,18	27,32	4,83	7,34	6,93	8,07	4,74	5,88	6,84	7,98
Adana / Sarıçam	D-646	20,13	22,40	22,35	24,62	3,06	5,46	5,28	6,55	7,72	8,99	9,94	11,21
Adana / Sarıçam	D-647	21,22	23,32	23,11	25,21	4,07	6,47	5,96	7,06	8,24	9,34	10,13	11,23
Adana / Sarıçam	D-648	32,89	34,99	34,67	36,77	3,47	6,01	5,25	6,35	8,52	9,62	10,30	11,40
Balıkesir / Bandırma	D-650	28,90	31,20	30,88	33,18	7,19	9,88	9,17	10,47	12,71	14,01	14,69	15,99
Urfa / Mezra	D-654	49,83	52,73	51,93	54,83	2,11	4,65	4,21	6,11	9,88	11,78	11,98	13,88
Urfa / Mezra	D-655	56,84	59,64	59,06	61,86	4,52	7,03	6,74	8,54	8,00	9,80	10,22	12,02

Table 3b. Dry Product Shelf Life Evaluations of 48th Days (Color; L*, a*, b*).

Origin Location	Open Field Code	Dry Product Shelf Life											
		48th Day											
		L*				a*				b*			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed
O.P. Variety	Adana Dolmalık	31,85	34,06	34,42	36,63	7,19	8,40	9,76	10,97	4,44	5,65	6,69	5,48
O.P. Variety	Topan 374	24,32	26,57	26,87	29,12	5,21	6,46	7,76	9,01	-0,10	1,15	1,55	0,30
O.P. Variety	Antep Dolmalık	32,76	34,76	35,80	37,80	6,38	7,38	9,42	10,42	-1,43	-0,43	0,61	-0,39
Manisa / Turgutlu	D-048	24,34	26,70	27,01	29,37	8,06	9,42	10,73	12,09	7,43	8,79	9,98	8,62
Manisa / Turgutlu	D-051	29,41	31,98	32,36	34,93	7,28	8,85	10,23	11,80	0,40	1,97	2,87	1,30
Manisa / Turgutlu	D-057	32,30	34,71	34,46	36,87	6,86	8,27	9,02	10,43	0,23	1,64	2,29	0,88
Manisa / Turgutlu	D-0146	30,59	33,13	33,05	35,59	7,26	8,80	9,72	11,26	3,51	5,05	5,45	3,91
Adana Topan Patlıcan	D-055A	25,93	28,51	28,18	30,76	6,72	8,30	8,97	10,55	6,16	7,74	7,91	6,33
Adana Topan Patlıcan	D-074A	32,86	35,55	35,20	37,89	4,85	6,54	7,19	8,88	4,00	5,69	6,26	4,57
Adana Topan Patlıcan	D-079A	36,49	38,96	39,07	41,54	5,88	7,35	8,46	9,93	6,00	7,47	7,62	6,15
Adana Topan Patlıcan	D-A89	30,58	32,73	33,43	35,58	6,33	7,48	9,18	10,33	2,42	3,57	4,01	2,86
Adana Topan Patlıcan	D-A90	21,33	23,47	23,21	25,35	6,19	7,33	8,07	9,21	6,25	7,39	8,15	7,01
Aydın / Nazilli	D-114	28,36	30,49	30,14	32,27	5,98	7,11	7,76	8,89	-3,09	-1,96	-1,31	-2,44
Aydın / Nazilli	D-234	22,63	24,78	24,67	26,82	4,35	5,50	6,39	7,54	3,78	4,93	5,70	4,55
Aydın / Nazilli	D-235	34,14	36,30	36,99	39,15	5,03	6,19	7,88	9,04	3,54	4,70	5,51	4,35
Manisa / Salihli	D-570	48,84	51,14	51,57	53,87	6,71	8,01	9,44	10,74	14,96	16,26	16,43	15,13
Manisa / Salihli	D-571	50,30	52,80	53,17	55,67	5,65	7,15	8,52	10,02	14,45	15,95	16,66	15,16
Manisa / Salihli	D-576	36,39	38,60	39,04	41,25	4,42	5,63	7,07	8,28	3,15	4,36	5,72	4,51
Burdur / Merkez	D-580	20,78	23,03	23,48	25,73	4,25	5,50	6,95	8,20	3,88	5,13	6,60	5,35
Burdur / Merkez	D-581	26,65	28,65	29,02	31,02	5,02	6,02	7,39	8,39	3,55	4,55	5,40	4,40
Gaziantep / Oğuzeli	D-582	25,78	28,14	28,11	30,47	5,20	6,56	7,53	8,89	3,37	4,73	5,44	4,08
Gaziantep / Oğuzeli	D-584	27,33	29,90	29,46	32,03	7,73	9,30	9,86	11,43	-0,28	1,29	1,59	0,02
Gaziantep / Oğuzeli	D-586	23,20	25,61	25,88	28,29	6,30	7,71	8,98	10,39	1,37	2,78	3,29	1,88
Gaziantep / Oğuzeli	D-587	35,46	38,00	38,18	40,72	7,03	8,57	9,75	11,29	-1,29	0,25	0,19	-1,35
Gaziantep / Oğuzeli	D-588	28,48	31,06	30,82	33,40	6,22	7,80	8,56	10,14	-0,26	1,32	1,84	0,26
Gaziantep / Oğuzeli	D-590	52,72	55,41	54,88	57,57	4,83	6,52	6,99	8,68	7,52	9,21	9,14	7,45
Artvin / Hopa	D-628	30,96	33,43	32,60	35,07	6,50	7,97	8,14	9,61	1,17	2,64	3,09	1,62
Artvin / Hopa	D-630	31,85	34,00	34,21	36,36	4,12	5,27	6,48	7,63	3,45	4,60	5,05	3,90
Adana / Akkapı	D-632	31,45	33,59	34,49	36,63	4,22	5,36	7,26	8,40	2,62	3,76	4,40	3,26
Adana / Akkapı	D-634	36,58	38,71	38,89	41,02	5,18	6,31	7,49	8,62	4,04	5,17	5,93	4,80
Doğal Topan Patlıcan	D-635	24,95	27,10	27,62	29,77	6,35	7,50	9,02	10,17	2,97	4,12	5,38	4,23
Doğal Topan Patlıcan	D-637	31,65	33,81	34,15	36,31	7,28	8,44	9,78	10,94	2,33	3,49	5,05	3,89
Doğal Topan Patlıcan	D-638	27,94	30,24	30,90	33,20	7,85	9,15	10,81	12,11	3,71	5,01	6,17	4,87
Doğal Topan Patlıcan	D-639	30,14	32,64	32,51	35,01	5,31	6,81	7,68	9,18	3,55	5,05	5,40	3,90
Adana / Sarıçam	D-640	32,64	34,85	35,24	37,45	4,72	5,93	7,32	8,53	1,53	2,74	3,33	2,12
Adana / Sarıçam	D-641	27,42	29,67	29,60	31,85	7,49	8,74	9,67	10,92	3,15	4,40	4,97	3,72
Adana / Sarıçam	D-644	25,88	27,88	28,74	30,74	5,38	6,38	8,24	9,24	5,67	6,67	7,41	6,41
Adana / Sarıçam	D-645	24,32	26,68	26,54	28,90	6,07	7,43	8,29	9,65	3,50	4,86	5,48	4,12
Adana / Sarıçam	D-646	21,50	24,07	23,87	26,44	4,43	6,00	6,80	8,37	6,35	7,92	8,42	6,85
Adana / Sarıçam	D-647	22,74	25,15	24,58	26,99	5,59	7,00	7,43	8,84	6,72	8,13	8,66	7,25
Adana / Sarıçam	D-648	34,30	36,84	36,36	38,90	4,88	6,42	6,94	8,48	7,11	8,65	8,61	7,07
Balıkesir / Bandırma	D-650	30,15	32,73	32,75	35,33	8,44	10,02	11,04	12,62	11,46	13,04	12,82	11,24
Urfa / Mezra	D-654	51,07	53,76	53,51	56,20	3,35	5,04	5,79	7,48	8,64	10,33	10,40	8,71
Urfa / Mezra	D-655	58,09	60,56	60,71	63,18	5,77	7,24	8,39	9,86	6,75	8,22	8,57	7,10

Table 3c. Dry Product Shelf Life Evaluations of 64th Days (Color; L*, a*, b*).

Origin Location	Open Field Code	Dry Product Shelf Life											
		64th Day											
		L*				a*				b*			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed	NonVacuum Packed	Vacuum Packed
O.P. Variety	Adana Dolmalık	32,59	42,67	35,89	45,97	7,93	10,08	10,23	12,38	5,18	6,13	6,22	5,27
O.P. Variety	Topan 374	24,96	33,07	28,56	36,67	5,85	8,11	8,45	10,71	0,54	1,60	0,86	-0,20
O.P. Variety	Antep Dolmalık	33,33	42,76	37,67	47,10	6,95	9,43	10,29	12,77	-0,86	0,42	-0,26	-1,54
Manisa / Turgutlu	D-048	25,02	36,61	28,59	40,18	8,74	11,59	11,31	14,16	8,11	9,76	9,40	7,75
Manisa / Turgutlu	D-051	30,09	40,42	34,01	44,34	7,96	10,33	10,88	13,25	1,08	2,25	2,22	1,05
Manisa / Turgutlu	D-057	32,54	42,11	35,76	45,33	7,10	9,57	9,32	11,79	0,47	1,74	1,99	0,72
Manisa / Turgutlu	D-0146	31,17	41,60	34,55	44,98	7,84	10,43	10,22	12,81	4,09	5,48	4,95	3,56
Adana Topan Patlıcan	D-055A	26,61	36,16	29,68	39,23	7,40	9,55	9,47	11,62	6,84	7,79	7,41	6,46
Adana Topan Patlıcan	D-074A	33,54	41,18	36,85	44,49	5,53	7,64	7,84	9,95	4,68	5,59	5,61	4,70
Adana Topan Patlıcan	D-079A	37,06	46,30	40,86	50,10	6,45	9,24	9,25	12,04	6,57	8,16	6,83	5,24
Adana Topan Patlıcan	D-A89	31,27	39,19	35,30	43,22	7,02	7,92	10,05	10,95	3,11	2,81	3,14	3,44
Adana Topan Patlıcan	D-A90	22,01	30,76	24,57	33,32	6,87	8,75	8,43	10,31	6,93	7,61	7,79	7,11
Aydın / Nazilli	D-114	28,93	37,36	31,66	40,09	6,55	8,43	8,28	10,16	-2,52	-1,84	-1,83	-2,51
Aydın / Nazilli	D-234	23,31	30,22	26,14	33,05	5,03	6,91	6,86	8,74	4,46	5,14	5,23	4,55
Aydın / Nazilli	D-235	34,88	42,44	38,68	46,24	5,77	7,56	8,57	10,36	4,28	4,87	4,82	4,23
Manisa / Salihli	D-570	49,48	59,07	53,44	63,03	7,35	9,59	10,31	12,55	15,60	16,64	15,56	14,52
Manisa / Salihli	D-571	50,87	59,24	54,75	63,12	6,22	8,37	9,10	11,25	15,02	15,97	16,08	15,13
Manisa / Salihli	D-576	37,07	44,43	40,69	48,05	5,10	7,36	7,72	9,98	3,83	4,89	5,07	4,01
Burdur / Merkez	D-580	21,46	28,87	24,78	32,19	4,93	7,41	7,25	9,73	4,56	5,84	6,30	5,02
Burdur / Merkez	D-581	26,89	35,00	30,52	38,63	5,26	8,11	7,89	10,74	3,79	5,44	4,90	3,25
Gaziantep / Oğuzeli	D-582	26,36	34,51	29,61	37,76	5,78	8,15	8,03	10,40	3,95	5,12	4,94	3,77
Gaziantep / Oğuzeli	D-584	28,01	38,89	31,11	41,99	8,41	10,88	10,51	12,98	0,40	1,67	0,94	-0,33
Gaziantep / Oğuzeli	D-586	23,88	33,45	27,67	37,24	6,98	9,57	9,77	12,36	2,05	3,44	2,50	1,11
Gaziantep / Oğuzeli	D-587	36,03	45,78	40,05	49,80	7,60	9,75	10,62	12,77	-0,72	0,23	-0,68	-1,63
Gaziantep / Oğuzeli	D-588	29,17	38,19	32,18	41,20	6,91	9,02	8,92	11,03	0,43	1,34	1,48	0,57
Gaziantep / Oğuzeli	D-590	53,40	61,70	56,40	64,70	5,51	8,30	7,51	10,30	8,20	9,79	8,62	7,03
Artvin / Hopa	D-628	31,53	39,50	34,07	42,04	7,07	7,97	8,61	9,51	1,74	1,44	2,62	2,92
Artvin / Hopa	D-630	32,53	39,21	35,90	42,58	4,80	6,68	7,17	9,05	4,13	4,81	4,36	3,68
Adana / Akkapı	D-632	32,19	39,03	36,36	43,20	4,96	6,84	8,13	10,01	3,36	4,04	3,53	2,85
Adana / Akkapı	D-634	37,22	44,92	40,47	48,17	5,82	7,70	8,07	9,95	4,68	5,36	5,35	4,67
Doğal Topan Patlıcan	D-635	25,52	34,23	29,27	37,98	6,92	8,71	9,67	11,46	3,54	4,13	4,73	4,14
Doğal Topan Patlıcan	D-637	32,33	42,53	35,45	45,65	7,96	10,20	10,08	12,32	3,01	4,05	4,75	3,71
Doğal Topan Patlıcan	D-638	28,62	39,30	32,40	43,08	8,53	10,68	11,31	13,46	4,39	5,34	5,67	4,72
Doğal Topan Patlıcan	D-639	30,38	38,19	34,01	41,82	5,55	7,81	8,18	10,44	3,79	4,85	4,90	3,84
Adana / Sarıçam	D-640	33,22	41,00	36,89	44,67	5,30	7,78	7,97	10,45	2,11	3,39	2,68	1,40
Adana / Sarıçam	D-641	28,10	39,12	31,39	42,41	8,17	11,02	10,46	13,31	3,83	5,48	4,18	2,53
Adana / Sarıçam	D-644	26,56	34,99	30,61	39,04	6,06	8,43	9,11	11,48	6,35	7,52	6,54	5,37
Adana / Sarıçam	D-645	24,89	34,00	27,90	37,01	6,64	9,11	8,65	11,12	4,07	5,34	5,12	3,85
Adana / Sarıçam	D-646	22,19	29,90	25,39	33,10	5,12	7,71	7,32	9,91	7,04	8,43	7,90	6,51
Adana / Sarıçam	D-647	23,42	31,84	26,05	34,47	6,27	8,42	7,90	10,05	7,40	8,35	8,19	7,24
Adana / Sarıçam	D-648	34,87	42,43	38,05	45,61	5,45	7,56	7,63	9,74	7,68	8,59	7,92	7,01
Balıkesir / Bandırma	D-650	30,83	42,74	34,62	46,53	9,12	11,91	11,91	14,70	12,14	13,73	11,95	10,36
Urfa / Mezra	D-654	51,64	56,46	55,09	59,91	3,92	4,82	6,37	7,27	9,21	8,91	9,82	10,12
Urfa / Mezra	D-655	58,77	67,10	62,36	70,69	6,45	8,33	9,04	10,92	7,43	8,11	7,92	7,24

Table 4. Sensory evaluations (Scored from 1 to 9; 1: lowest score, 9: highest score).

Origin Location	Open Field Code	Sensory Evaluation (1-9) points									
		Colour		Juiciness		Crispness		Taste		General Acceptability	
		Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying
O.P. Variety	Adana dolmalık	7	8	7	8	7	8	8	8	7	8
O.P. Variety	Topan 374	9	8	8	9	9	9	9	8	9	9
O.P. Variety	Antep Dolmalık	6	7	7	8	7	8	7	7	7	8
Manisa / Turgutlu	D-048	7	8	7	9	8	8	8	8	8	8
Manisa / Turgutlu	D-051	8	8	8	8	8	8	8	8	8	8
Manisa / Turgutlu	D-057	7	7	7	7	8	9	8	7	8	8
Manisa / Turgutlu	D-0146	8	8	7	8	9	9	9	8	8	8
Adana Topan Patlıcan	D-055A	8	9	8	9	7	8	7	9	8	9
Adana Topan Patlıcan	D-074A	7	8	7	8	6	8	6	8	7	8
Adana Topan Patlıcan	D-079A	6	8	7	7	7	9	7	8	7	8
Adana Topan Patlıcan	D-A89	9	8	8	8	8	8	8	8	8	8
Adana Topan Patlıcan	D-A90	6	7	7	9	7	9	7	7	7	8
Aydın / Nazilli	D-114	9	8	9	8	9	9	9	8	9	8
Aydın / Nazilli	D-234	8	9	8	7	8	8	8	9	8	8
Aydın / Nazilli	D-235	7	8	7	8	8	8	8	8	8	8
Manisa / Salihli	D-570	8	7	7	9	7	9	8	7	8	8
Manisa / Salihli	D-571	7	9	8	8	8	8	8	9	8	9
Manisa / Salihli	D-576	6	8	6	7	7	9	7	8	7	8
Burdur / Merkez	D-580	6	7	8	8	8	8	8	7	8	8
Burdur / Merkez	D-581	7	8	8	9	9	9	9	8	8	9
Gaziantep / Oğuzeli	D-582	5	7	6	8	6	8	7	7	6	8
Gaziantep / Oğuzeli	D-584	5	6	5	8	6	7	6	6	6	7
Gaziantep / Oğuzeli	D-586	6	7	7	9	7	9	8	7	7	8
Gaziantep / Oğuzeli	D-587	6	7	7	9	8	8	8	7	7	8
Gaziantep / Oğuzeli	D-588	6	8	7	9	7	7	7	8	7	8
Gaziantep / Oğuzeli	D-590	7	7	8	8	8	8	8	7	8	8
Artvin / Hopa	D-628	6	4	7	7	7	9	8	4	7	6
Artvin / Hopa	D-630	8	7	8	8	9	8	9	7	9	8
Adana / Akkapı	D-632	7	8	7	9	7	7	7	8	7	8
Adana / Akkapı	D-634	6	7	7	8	8	8	8	7	7	8
Doğal Topan Patlıcan	D-635	7	9	8	7	7	7	8	9	8	8
Doğal Topan Patlıcan	D-637	8	9	8	8	9	8	9	9	9	9
Doğal Topan Patlıcan	D-638	6	8	7	9	8	8	8	8	7	8
Doğal Topan Patlıcan	D-639	6	8	7	8	7	8	7	8	7	8
Adana / Sarıçam	D-640	8	7	8	7	9	7	8	7	8	7
Adana / Sarıçam	D-641	6	8	6	9	7	8	7	8	7	8
Adana / Sarıçam	D-644	8	7	8	8	9	7	9	7	9	7
Adana / Sarıçam	D-645	8	8	8	7	8	9	8	8	8	8
Adana / Sarıçam	D-646	9	9	8	8	9	8	9	9	9	9
Adana / Sarıçam	D-647	8	8	8	9	9	7	9	8	9	8
Adana / Sarıçam	D-648	7	7	8	8	7	8	8	7	8	8
Balıkesir / Bandırma	D-650	6	8	8	7	7	9	8	8	7	8
Urfa / Mezra	D-654	8	7	8	8	9	8	9	7	9	8
Urfa / Mezra	D-655	8	8	8	9	9	9	9	8	9	9

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Cytoplasmic Genome Prediction in Cucumber (*Cucumis sativus* L.) Hybrid Variety Breeding**

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ABSTRACT

Breeding studies in Cucurbitaceae species take a long time. It has become necessary to shorten the time and support traditional breeding methods with modern biotechnological methods to get qualified domestic cucumber varieties. Cytoplasmic genome prediction within the scope of molecular-based breeding is a very important application. To increase heterosis in test crosses, reciprocal 'double way' crosses can be made as well as single crosses. Cytoplasmic organelles 'plastid and mitochondria' are considered to be different from each other between individuals and reciprocal crosses are made based on this idea. However it significantly increases the labor. In this study, 4 plastid genome regions (rbcL, psb-trnS, trnHK, trnSt) located within non-conserved regions therefore expected to be variable of 50 donor genotypes were sequenced, analyzed and their cytoplasmic genome prediction was estimated. A total of 6300 bp including four plastid regions indicated no polyfmorphism and all sequences were identical among the 50 donor genotypes analyzed. This may imply no cytoplasmic organelle variation. In conclusion, reciprocal crosses were excluded from our breeding studies. So cytoplasmic genome prediction can provide rapidity and savings in breeding by eliminating unnecessary reciprocal test crosses.

Keywords **:** Breeding, cucumber, *Cucumis sativus* L., cytoplasmic genome prediction, double haploid, hybrid variety breeding

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Introduction

Cucumber (*Cucumis sativus* L.) belongs to the family of Cucurbitaceae which is one of the largest vegetable families with 117 genera and 825 species (Gopalakrishnan 2007). It is the top of 10 most cultivated products among fruits and vegetables. Cucumber is a warm-season vegetable crop and grows best at temperatures above 20°C. It consists of 95% water, 4% carbohydrates, 1% protein and negligible fat. It has a production value of 91 million tons in the world according to the latest statistics and Turkey ranks second after China with 1.9 million tons of production. (FAO 2020). It is necessary to carry out effective and rapid breeding studies in order to develop domestic hybrid varieties with high yielding and resistance to both abiotic and biotic stress factors in cucumber cultivation. Cucumber breeding with classical methods take too much time and effort. It has become necessary to shorten the time and support traditional breeding methods with modern biotechnological methods to get qualified domestic cucumber varieties. Cucumber has a small chromosome complement with n=x=7 and a small haploid genome of 367 Mbp/C (Huang et al., 2009) and genetic base of cultivated cucumber is narrow with 3–8% polymorphism within the cultivated genotypes (Behera et al., 2011). This narrow genetic

diversity makes breeding of this species is more difficult (Acquaah 2012). Obtaining haploid plants by double haploid techniuqe and make selection after hybridization with molecular markers is one of the supportive methods for shorten time. Many important horticultural traits such as size/shape of fruits and flowering time are quantitatively inherited and related genes have been recently identified and reported (Pan et al., 2020). Complex genetic variances can be captured with genomic prediction models by using genomic-coverage molecular markers to achieve more accuracy in the selection process (Liu et al., 2021). The genomic prediction has also become more practical in cucumber with the release of the full cucumber genome (Huang et al., 2009; Yang et al., 2012). Chloroplast and mitochondria genomes of plant cell are usually inherited from maternal parent, with rare exceptions (Park et al., 2021). In cucumber, previous studies indicated that chloroplast genome is maternally inherited whereas the large cucumber mitochondrial genome is paternally inherited (Park et al., 2021). To get heterosis in test crosses, reciprocal crosses can be applied as well as single crosses. Reciprocal crosses which are made based on the idea that the cytoplasmic organelles 'plastid and mitochondria' between individuals are different from each other, significantly increases the labor. So cytoplasmic genome prediction within the scope of molecular-based breeding is a very important application. In case where the origins of individuals whose cytoplasm can be estimated by molecular methods are not different, the need for reciprocal crosses will be eliminated, and a significant labor and time savings will be provided. In crop breeding genomic prediction method has been widely used such as rice (Xu et al., 2016), maize (Riedelsheimer et al., 2012) and potato (Sverrisdottir et al., 2018). However, in horticultural crops there are relatively fewer studies such as in pea (Tayeh et al., 2015), strawberry (Gezan et al., 2017) and tomato (Duangjit et al., 2016) while there are no related reports in cucumber. In this study, we tried to figure out our parental lines reciprocal need by cytoplasmic genome prediction for accelerate breeding.

Materials and Methods

Plant materials

The plant material used in this study was consisted of 44 cucumber parental donor lines and 6 selected promising lines from Antalya Tarım Seed Company's cucumber gene pool (Table 1). These total 50 donor lines were germinated in controlled conditions for DNA isolation.

Molecular Marker analysis

Single fresh leaf was used for DNA extraction. Total DNA was extracted from 100 mg fresh leaf tissue according to a modified CTAB DNA extraction procedure (Doyle and Doyle 1990). DNA pellets were diluted with 100 uL of TE (10 mM Tris, 0.1 mM EDTA, pH 7.4) and their concentrations were measured with Qubit fluoremeter. 10 ng ul^{-1} DNA templates for PCR amplifications were made using with distilled water. Four plastid genome regions (rbcL, psb-trnS, trnHK, trnST) of 50 donor genotypes were sequenced. Region spesific polymorphic universal primers were used for PCR assays (Gulsen and Ceylan 2011) (Table 1). Regions were amplified by using specific primers designed for this purpose at 60°C annealing temperature in a 50-uL reaction and 15 ul of PCR-amplified products were separated by agarose gel electrophoresis for control. These marker analyses were done by Agromar Seed Company. Remaining 35 ul of PCR products, which has seen as a single band, were analysed with MEGA Genetic Analysis Program by MASGEN Ar-Ge Ltd.Sti for statistical analyses.

Results and Discussion

Molecular Marker Analysis

Four plastid genome regions which are assumed to be non-conserved due to their intergenic location were amplified with polymorphic universal primers targeting rbcL, psb-trns, trnHK and trnST regions. Primer pairs produced non-polymorphic, size expected fragments and those fragments are 100% reproducible. (Fig.1). The resulting band sizes are approximately about 900, 1500, 3000 and 1400 base pairs. Obtained results are consistent with previous studies (Gulsen and Ceylan 2011).

Statistical Analysis

Illumina DNA libraries of the PCR products were prepared and barcoded ('indexed') for sequencing by MASGEN Ar-Ge Ltd.Ş., Antalya. The bioinformatics processes (quality filtering processes, demultiplex processes and assembly processes) of each of the PCR products to be obtained as a result of sequencing, were carried out by the company. According to alignment results which achieved by using MEGA Genetic Analysis Program, there were no cytoplasmic genome difference among 50 donor genotypes although these regions are assumed to be non-conserved due to their intergenic locations.

In a previous study the chloroplast genomes of some cucumber lines were fully assembled however the mitochondria genomes could not which also same in our study (Park et al., 2021). In this study, the plastid genomes of the 50 cucumber lines were checked, however, the mitochondria genomes were not because generally chloroplast copy number is much higher than that of the mitochondria (Alverson et al., 2011).

Conclusions

The plastid genome length of cucumber is 150,501 base pairs, and its length of about 6300 base pairs was analyzed and estimation done for the rest according to these results in this study. It is found that four intergenic plastid regions, which were known to be polymorphic in previous studies, were exactly the same for 50 genotypes so all came from same maternal origin. Only plastid specific primers were used in this study, therefore our results indicate only maternal origins not paternal origins. Therefore combined use of plastid and mitochondria specific primers may produce more comprehensive results about need of reciprocal crosses. Since these results were assumed that there was no cytoplasmic genome difference between the hundreds of inbred lines obtained from 50 genotypes, reciprocal crosses were excluded. This analysis can provide rapidity and savings in breeding by eliminating unnecessary reciprocal test crosses.

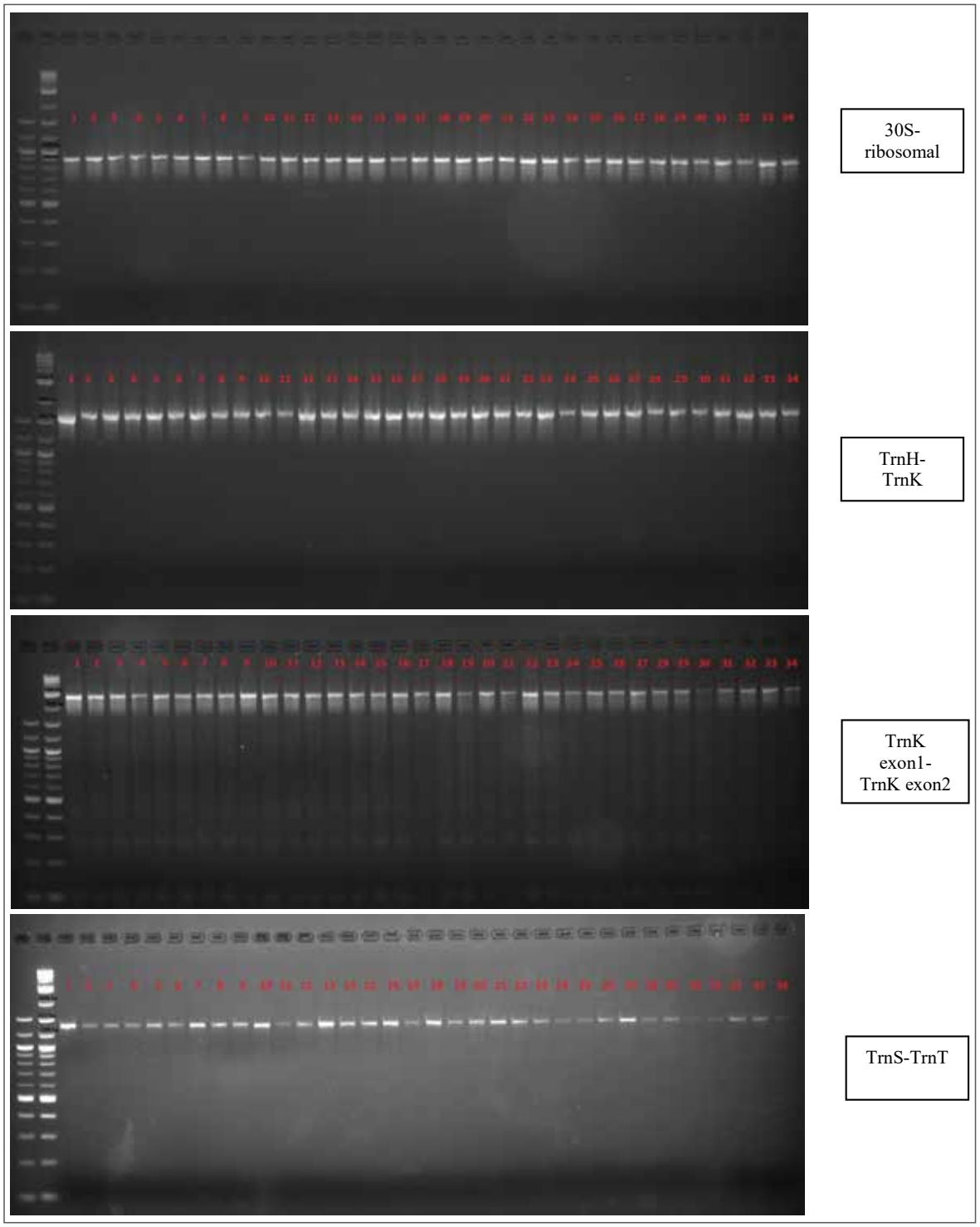

Figure 1. Gel images of uncut PCR products with primers which targets four plastid genome regions.

Table 1. Genotypes and sources used in this study.

Genotype	Source	Genotype	Source	Genotype	Source
Baby F_1	Multi Tohum	Petek Çıtır	Petek Tarım	Kıtır F_1	Yüksel Tohum
Çaka F_1	Antalya Tarım	Emek F_1	Antema Tarım	Yazel 801	Remitto
Umur F_1	Antalya Tarım	Tofida F_1	Teksin	Seçkin F_1	Multi Tohum
Ayda F_1	Takii Seed	Zincir F_1	Mars	Egemen F_1	Seminis
Multistar	Rıjk Zwaan	Uçar F_1	Yüksel Tohum	SV2709 CB	Seminis
PTK40	Petek Tarım	Captainstar	Rıjk Zwaan	Faris F_1	Gavrish
Senyal F_1	Rıjk Zwaan	Kıvılcım F_1	Tasaco	Gözde F_1	Multi Tohum
Süvari F_1	Seminis	Assos F_1	Seminis	Solo F_1	Yüksel Tohum
Çakıl F_1	Axia	Zirve F_1	Yüksel Tohum	Y*225 F_1	Yüksel Tohum
Efsane F_1	AG Tohum	Amisos F_1	Altın Tohumculuk	Tenedos F_1	Seminis
Şampiyon	Altın Tohumculuk	Malazgirt	Altın Tohumculuk	Gordion F_1	Seminis
Nur F_1	Eastern Seed	Özde F_1	Yüksel Tohum	PS 64 F_1	Seminis
Sardes F_1	Seminis	Falconstar	Rıjk Zwaan	Bellastar F_1	Rıjk Zwaan
Titanik F_1	Yüksel Tohum	Çılgın F_1	Vilmorin	Tribün F_1	AG Tohum
Haylaz F_1	Vilmorin	Carrera F_1	Fito		

Table 2. Region specific universal primer list.

Primer Name	Forward Primer	Reverse Primer
rbcl	TAGTTTCTGTTTGTGGTGACAT	AAGTAGTAGGATTGGTTCTCAT
psb-trns	GGTCGTGACCAAGAAACCAC	GGTTCGAATCCCTCTCTCTC
trnHK	ACGGGAATTGAACCCGCGCA	CCGACTAGTTCCGGGTTCGA
trnST	CGAGGGTTCGAATCCCTCTC	AGAGCATCGCATTTGTAATG

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Variability for Drought Stress Effects on Seedling Growth in Bread Wheat (*Triticum aestivum* L.) Genotypes**

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ABSTRACT

The study was carried out under different drought/osmotic stresses (0.00 MPa-control, 0.25 MPa, 0.50 MPa, 0.75 MPa and 1.00 MPa applications) created by using PEG 6000 with 43 genotypes under laboratory, with 5 replications according to a split-plot experiment design. The genotypes constituted the main plots, and the drought/osmotic stress applications constituted the sub-plots.

In the study, seedling weight, root number, root length, root weight, shoot length, and shoot weight characters were determined. It was determined that drought stress applications caused statistically significant decreases in root and shoot characters. Osmotic stress of, 1.00 MPa and 0.75 MPa caused statistically significant reductions in root and shoot characters. The results indicated that early and mid-early varieties were more tolerant to drought than the late varieties. Although Aglika, Anapo, Enola and Hamza varieties were outstanding for their root properties, while Maden, NKU Ergene and Bezostaja-1 cultivars showed more appropriate shoot characteristics than other cultivars. Enola, Aglika, Bezostaja-1, NKU Ergene, Anapo, Hamza and Maden bread wheat varieties showed better growth characteristics under drought stress conditions in the study.

Keywords: Bread wheat, seedling, drought, PEG, root, shoot

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Introduction

World wheat production in 2020 was 780 million tons, and in Turkey, it was 20.5 million tons (FAO, 2021). Along with the increasing population around the world, it is necessary to consider the quality and yield factors as well as the varieties that have adapted to abiotic and biotic stresses in the regions where the food demand is increasing (Güngör and Dumlupınar, 2019). Drought which is one of the most common abiotic stress factors is the most important factor limiting crop production in most agricultural areas. Wheat production is generally carried out in dry agricultural areas and drought often causes serious problems in wheat production in these areas.

The decrease in productivity under drought stress conditions is one of the most important factors threatening global food production (Fahad et al., 2017). High temperatures occurring due to global climate change increase the drying rate of agricultural soils and cause higher drought stress to occur (Fischer and Knutti, 2015). Therefore, it is important for plants to withstand long-term water deficiencies, adapt to these environments, and improve the plants' ability to recover from water deficiencies. Stress tolerance of plants and the ability of plants to maintain productivity during stress periods is a complex phenotypic trait (Ngumbi and Kloepper, 2016). Plants have numerous mechanisms to tolerate drought stress down to cellular levels, such as root structure, above-ground growth, osmotic adjustment, water use optimization, and management of reactive

oxygen species (Meena et al., 2017). With regard to plant growth and development, changes in root system architecture, especially the proliferation of high-grade roots, are known to be beneficial in short-term adaptation to water deficiency (Xu et al., 2015).

Drought is one of the most important environmental stress factors limiting crop production in many countries of the world. Insufficient/irregular precipitation and high temperature during the year are the main factors causing drought. One of the most important research approaches to minimize the effects of drought is the breeding of drought-resistant varieties. However, it is difficult to develop studies on this subject unless the mechanism of drought resistance and the parameters that reflect it are well understood. In arid conditions, plants reduce all enzyme activity, slow down their growth, cause the closure of stomata, causing a decrease in CO_2 assimilation (Baranyiova et al., 2014). More than 50% of wheat growing areas are affected by periodic drought. Although drought affects wheat development in all phenological periods, its greatest negative effect occurs during pollination and grain filling periods. While mild drought after pollination reduces wheat yield by 1-30%, mild drought during flowering and grain filling period reduces grain yield up to 58-92% (Farooq et al., 2014). Grain yield is affected by the interaction of genetic and environmental factors. Soil type, sowing time, sowing method, sowing frequency, fertilization and irrigation time, spacing between rows have an important role in obtaining high yields. Water stress significantly affects yield components such as the number of grains per spike and the number of spikes per plant (Aghanejad et al., 2015).

The study was carried out to identify drought resistant genotypes, which is one of the most important problems in cereal production in our country. In the study, a total of 43 genotypes, including thirty nine bread wheat, one rye, one emmer and two einkorn wheat genotypes with different growth characteristics, were used as material. Seedling and root development characteristics of these genotypes were investigated in a drought environment created with polyethylene glycol (PEG) in the laboratory.

Materials and Methods

In the study, thirty nine bread wheat, one rye, one emmer and two einkorn varieties were used as material. The research was carried out according to split-plot design in 5 different drought conditions (0.00 MPa, 0.25 MPa, 0.50 MPa, 0.75 MPa and 1.00 MPa applications) created with PEG 6000 in laboratory conditions. For sterilization, seeds were kept in 80% alcohol for 1 minute, then put into a mixture of 2% sodium hypochlorite with 2-3 drops of tween, shaken for 20 minutes and then washed 4-5 times in autoclaved sterile water. Sterile filter paper was placed in the petri dish sterilized in autoclave under a sterile cabinet and 10 ml of PEG solution was applied to the filter paper. Fifteen sterilized seeds were placed on the filter papers to which PEG solution was added. After the seeds were placed in the petri dishes, filter paper was placed on the seeds and the lid of the petri dish was closed. Petri dishes with closed lids were wrapped with cling film. Then the petri dishes were placed in the climate chamber. After 3 weeks, the seedling weight, root number, root length, root weight, shoot length and shoot weight values were determined in the germinated seedlings under stress created by PEG in each petri dish.

Results and Discussion

In the present study, seedling weight, root number, root length, root weight, shoot length and shoot weight values were measured in plants growing in 5 different drought conditions created with PEG 6000 in forty-three genotypes. Differences between genotypes were determined by performing analysis of variance and significance testing on the values obtained. As a result of the analysis of variance, the effect of PEG application on the examined characters was found to be statistically significant.

Seedling Weight, Root Number and Root Length

As a result of the analysis of variance, the effects of genotype and PEG application on seedling weight, root number and root length were found to be statistically significant. The results of the significance test (Tukey) performed revealed the differences between the applications are given in Table 1.

As a result of the significance test (Table 1), the highest value for seedling weight was found in Enola cultivar with 0.343 g. Aglika, NKU Ergene, Bezostaja-1, Falado, Anopa, Maden, NKU Lider, Ambrosia, Hamza, Bora, Anica and Selimiye statistically at par. Similar Enola. Pannonia, Quality, Hakan, Mihelca, Refikbey and Adelaide varieties were grouped together. The lowest value for seedling weight was obtained from Siyez-1 with 0.161 g. Siyez-2, Maya, Rebelde, Emmer colour, Esperia, Golia and Başkan varieties were in the same statistical group as Siyez-1.

According to the significance test, when the number of roots was examined, the highest value was found in Aglika genotypes with 5.4 unit and Quality genotypes with 5.3 unit, followed by Esperia and NKU Lider. Aglika and Quality genotypes. The lowest value for root number was seen in the Başkan variety with 3.0 unit. Emmer colour, NKU Ergene,

Misiia Odes'ka, Rumeli, Masaccio, Adelaide, Ducato, Krasunia Odes'ka, Genesi varieties were in the same statistical group with the Başkan.

According to the results of the significance test, the genotype with the longest root with a root length of 24.80 cm was NKU Ergene. Hakan, Falado and Kaan varieties followed and ranked subsequent for root length. While the genotype with the lowest value for root length was Emmer colour with 5.867 cm. Siyez-2, Siyez-1 and Aldane followed this variety.

Average values and important groups for seedling weight, root number and root length obtained in PEG dose applications are given in Table 2.

When the effects of different PEG applications on the seedling weight were examined, the seedling weight varied between 0.280 - 0.230 g. The highest seedling weight was obtained in the control application with 0.280 g, followed by 0.25 MPa PEG application (0.265 g). The lowest seedling weight value of 0.230 g was obtained in the highest PEG application. This was followed by seedling weight obtained in 0.75 MPa PEG application. The results revealed that PEG application slowed down the water uptake of the plants and caused significant reductions in plant weight. It has been determined that root properties are affected significantly under water stress and decreases in characters such as root length and root dry matter ratio (Adda et al., 2005; Öztürk and Korkut, 2018).

When the effect of different PEG doses on the root length of the genotypes was examined, it was observed that the root length varied between 16.62 and 13.59 cm. The maximum root length was seen in the 0.25 MPa dose application with 16.62 cm. The control application with 16.031 cm and the 0.50 MPa dose application with 15.895 cm were in the same statistical group with the 0.25 MPa dose application. The lowest root lengths were obtained with 13.59 cm and 14.11 cm in 0.75 and 1.0 MPa applications.

It was observed that there was a change between 0.0710 g and 0.0516 g for root weight in different doses of PEG applications. The highest value was obtained in the control application with 0.071 g. The data obtained on root weight in different PEG applications revealed that there was a decrease in root weight as the PEG dose increased, but the differences were statistically insignificant. There was a significant decrease in the characters examined after the drought stress level of 5.0 bar in wheat varieties (Dolgun and Çiftçi, 2018).

Root Weight, Shoot Weight and Shoot Length

According to the variance analysis results, the effects of genotype and PEG applications on root weight, shoot length and shoot weight were statistically significant. Tukey test results, which were performed to see the significance between applications are given in Table 3.

According to the significance test, the highest root weight was from Enola genotype with 0.0862 g. Bora, Anopa, Ambrosia and Iveta varieties were found in the same statistical group as Enola. While the lowest root weight was 0.0210 g in Emmer colour genotype, Siyez-1, Siyez-2, Ducato, Enargo and Maya were followed by this genotype. In the significance test, it was observed that the highest shoot length was from Maden variety with 20,067 cm. Bezostaja-1, NKU Ergene, Hakan, Selimiye, Sarı Mustafa, Enargo and Prima varieties were in the same statistical group with this genotype. The lowest shoot length was found in Emmer colored genotype with 11,400 cm. Ambrosia, NKU Asiya, Iveta and Siyez-2 genotypes were ranked after Emmer colored genotype. In bread wheat cultivars, osmotic stress significantly reduced root length, seedling length and root fresh weight during germination and early seedling development (Balkan and Gençtan, 2013)

In the significance test, the highest value in terms of shoot weight was in Selimiye variety with 0.1554 g, Maden, Enola, Bezostaja-1, NKU Ergene, Prima and TT601 genotypes were calculated in the same statistical group with Selimiye genotype. The lowest value for shoot weight was determined in Siyez-2 with 0.0665 g. Siyez-1, Emmer colored, Maya, Rebelde, NKU Asiya, Başkan, Almeria and Masaccio genotypes were in the same statistical group as Siyez-2. Average values of root weight, shoot length and shoot weight and importance groups in PEG dose applications were given in Table 4.

When the effects of different PEG applications on root weight were examined, it was seen that root weights varied between 0.0710-0.0516 g. The highest root weight was obtained with 0.0710 in 0.00 MPa PEG application. The lowest root weight was obtained with 0.534 g and 0.0516 g in the highest applications, 0.75 and 1.0 MPa PEG applications. Obtained results showed that root weight decreased with increasing PEG dose.

It is seen that shoot length varied between 15.632 cm and 13.760 cm in different PEG applications. The highest shoot length was obtained with 15.632 cm in 0.25 MPa PEG application and 15.392 cm in plants without PEG application. The lowest shoot length was obtained with 13.760 cm from 0.75 MPa PEG application, followed by the highest dose of 1.00 MPA PEG application with 14.240 cm. The results showed that the shoot length decreased as the PEG dose increased.

When the data on shoot weight of different PEG applications were examined, the highest values were 0.1358 g in 0.25 MPa PEG application and 0.1334 g in

0.00 MPa PEG application respectively. The lowest shoot weight was 0.1072 g and 0.1079 g in 0.75 and 1.00 MPa PEG applications were obtained. In wheat, germination rate, root length and shoot length were significantly decreased in drought stress as a result of increase in PEG 6000 concentration (Hossein Pour et al., 2013).

Conclusions

In this study, seedling weight, root number, root length, root weight, shoot length and shoot weight characters were determined in the drought stress created with different PEG doses. In this study carried out with 43 genotypes, 1.00 MPa and 0.75 MPa applications of PEG 6000 caused statistically significant reductions in root and shoot characters. The results indicated that early and mid-early varieties were more tolerant to drought than the late varieties. Although Aglika, Anapo, Enola and Hamza varieties were outstanding for their root properties, while Maden, NKU Ergene and Bezostaja-1 cultivars showed more appropriate shoot characteristics than other cultivars. Enola, Aglika, Bezostaja-1, NKU Ergene, Anapo, Hamza and Maden bread wheat varieties showed better growth characteristics under drought stress conditions in the study.

Table 1. Average values and importance groups for seedling weight, root number and root length.

Genotypes	Seedling Weight (g)	Genotypes	Root Number (Unit)	Genotypes	Root Length (cm)
Enola	0.343 a	Aglika	5.400 a	Hakan	24.800 a
Aglika	0.306 ab	Quality	5.333 a	Falado	21.533 ab
NKU Ergene	0.296 abc	Esperia	5.200 ab	Kaan	21.067 abc
Bezostaja-1	0.293 a-d	NKU Lider	5.133 abc	Mihelca	20.667 a-d
Falado	0.284 a-e	Bora	5.067 a-d	Adelaide	18.267 b-e
Anopa	0.282 a-e	Anopa	5.067 a-d	Refikbey	18.233 b-e
Maden	0.282 a-e	Rebelde	5.000 a-e	Misiia Odes.	18.100 b-f
NKU Lider	0.280 a-e	TT 601	4.867 a-f	Golia	17.833 b-g
Ambrosia	0.278 a-e	Enola	4.867 a-f	Krasunia Odes.	17.567 b-h
Hamza	0.277 a-e	Hamza	4.667 a-g	Enola	17.133 b-ı
Bora	0.277 a-e	Almeria	4.667 a-g	Pannonia	17.033 b-ı
Anica	0.276 a-f	Golia	4.667 a-g	Rumeli	17.000 b-ı
Selimiye	0.274 a-f	Anica	4.667 a-g	Maden	16.900 c-ı
Pannonia	0.271 b-f	Bezostaja-1	4.600 a-h	Rebelde	16.900 c-ı
Quality	0.268 b-f	Prima	4.600 a-h	Quality	16.800 c-ı
Hakan	0.266 b-f	Selimiye	4.467 a-ı	Sarı Mustafa	16.700 c-j
Mihelca	0.266 b-f	Siyez-1	4.467 a-ı	NKU Asiya	16.533 c-j
Refikbey	0.265 b-f	Iveta	4.400 a-j	Prima	16.333 d-k
Adelaide	0.262 b-f	LG59	4.400 a-j	Iveta	16.067 e-l
TT 601	0.258 b-f	NKU Asiya	4.267 b-j	Selimiye	15.667 e-l
LG59	0.256 b-f	Maya	4.267 b-j	Başkan	15.467 e-m
Iveta	0.253 b-f	Aldane	4.200 b-j	Hamza	15.067 e-m

Continuing table 1

Genotypes	Seedling Weight (g)	Genotypes	Root Number (Unit)	Genotypes	Root Length (cm)
Ducato	0.253 b-f	Refikbey	4.200 b-j	Bezostaja-1	14.800 e-m
Aldane	0.250 b-f	Ambrosia	4.200 b-j	Almeria	14.633 e-n
Misiia Odes.	0.246 b-f	Siyez-2	4.133 c-k	Bora	14.433 e-n
Masaccio	0.246 b-f	Enargo	4.067 d-k	Aglika	14.200 e-n
Prima	0.245 b-f	Pannonia	4.000 e-l	LG59	13.933 e-n
NKU Asiya	0.244 b-f	Falado	3.933 f-l	Genesi	13.867 e-n
Enargo	0.240 b-f	Kaan	3.800 g-l	Anica	13.700 e-n
Sarı Mustafa	0.238 b-f	Mihelca	3.800 g-l	Anopa	13.633 f-n
Almeria	0.236 b-g	Sarı Mustafa	3.800 g-l	Maya	13.467 g-n
Genesi	0.234 c-g	Maden	3.733 g-l	TT601	13.233 h-n
Kaan	0.233 c-g	Hakan	3.600 h-l	Ambrosia	12.733 ı-n
Rumeli	0.233 c-g	Genesi	3.600 h-l	Ducato	12.700 ı-n
Krasunia Odes.	0.232 c-g	Krasnia Odes.	3.600 h-l	Masaccio	12.600 ı-o
Başkan	0.227 c-h	Ducato	3.533 ı-l	Esperia	12.200 j-o
Golia	0.225 c-h	Adelaide	3.533 ı-l	Enargo	11.833 k-o
Esperia	0.223 d-h	Masaccio	3.467 ı-l	NKU Lider	11.667 l-o
Emmer c.	0.213 e-h	Rumeli	3.467 ı-l	Aldane	10.967 mno
Rebelde	0.205 fgh	Misiia Odes.	3.400 jkl	Siyez-1	10.067 nop
Maya	0.205 fgh	NKU Ergene	3.400 jkl	Siyez-2	8.033 op
Siyez-2	0.165 gh	Emmer c.	3.133 kl	Emmer c.	5.867 p
Siyez-1	0.161 h	Başkan	3.000 l		

The identical letters indicate statistical groups of identical values with a 99.0% confidence level by the Student-Newman-Keul Test (SNKT)

Table 2. Average values and importance groups of seedling weight, root number and root length.

PEG Doses (MPa)	Seedling Weight (g)	PEG Doses (MPa)	Root Number (Unit)	PEG Doses (MPa)	Root Length (cm)
0.00	0.280 a	0.75	4.473 a	0.25	16.620 a
0.25	0.265 ab	0.50	4.302 a	0.00	16.031 a
0.50	0.252 bc	1.00	4.271 ab	0.50	15.895 a
0.75	0.237 cd	0.00	4.054 bc	1.00	14.109 b
1.00	0.230 d	0.25	4.023 c	0.75	13.589 b

Table 3. Average values and importance groups of root weight, shoot length and weight in genotypes.

Genotypes	Root Weight (g)	Genotypes	Shoot Length (cm)	Genotypes	Shoot Weight (g)
Enola	0.0862 a	Maden	20.067 a	Selimiye	0.1554 a
Bora	0.0799 ab	Bezostaja-1	18.833 ab	Maden	0.1538 ab
Anopa	0.0771 abc	NKU Ergene	18.633 abc	Enola	0.1531 a-c
Ambrosia	0.0765 abc	Hakan	18.100 a-d	Bezostaja-1	0.1511 a-d
Iveta	0.0762 abc	Selimiye	17.800 a-e	NKU Ergene	0.1507 a-d
Pannonia	0.0716 a-d	Sarı Mustafa	17.333 a-f	Prima	0.1433 a-e
Aglika	0.0714 a-d	Enargo	16.667 a-g	TT601	0.1423 a-e
Hamza	0.0699 a-e	Prima	16.600 a-h	Refikbey	0.1351 a-f
Mihelca	0.0691 a-f	Falado	16.233 b-ı	Aglika	0.1345 a-f
NKU Asiya	0.0691 a-f	Kaan	16.167 b-ı	Hakan	0.1331 a-f
Falado	0.0689 a-f	Anica	15.733 b-j	Falado	0.1329 a-f
Adelaide	0.0672 a-g	Rumeli	15.733 b-j	Enargo	0.1309 a-f
Quality	0.0669 a-g	Aglika	15.667 b-j	Anopa	0.1305 a-f
LG 59	0.0668 a-h	Refikbey	15.600 b-k	Hamza	0.1292 a-f
Bezostaja-1	0.0647 a-h	Enola	15.600 b-k	Golia	0.1274 a-f
Misiia Odes.	0.0637 a-h	Hamza	15.233 c-k	Aldane	0.1271 a-f
NKU Lider	0.0634 a-h	TT601	14.867 d-l	Mihelca	0.1263 a-f
Masaccio	0.0631 a-h	Misiia Odes.	14.767 d-l	Sarı Mustafa	0.1258 a-f
Hakan	0.0628 a-h	Esperia	14.667 d-l	Bora	0.1256 a-f
Kaan	0.0614 a-h	Masaccio	14.433 e-l	NKU Lider	0.1247 a-f
Krasunia Odes.	0.0607 a-h	Golia	14.400 e-l	Quality	0.1229 a-f
NKU Ergene	0.0603 b-h	Krasunia Odes.	14.267 f-l	Anica	0.1225 a-f
Anica	0.0601 b-h	Almeria	14.167 f-l	Ambrosia	0.1218 a-f
TT 601	0.0596 b-h	Quality	14.167 f-l	Pannonia	0.1197 a-f
Refikbey	0.0579 b-h	NKU Lider	14.067 f-l	Adelaide	0.1170 a-g
Esperia	0.0575 b-h	Pannonia	13.900 f-l	LG 59	0.1170 a-g
Rumeli	0.0575 b-h	Anopa	13.767 g-l	Ducato	0.1169 a-g
Almeria	0.0571 b-h	Aldane	13.700 g-l	Misiia Odes.	0.1154 a-g
Rebelde	0.0539 c-ı	Rebelde	13.633 g-l	Kaan	0.1146 a-g
Başkan	0.0520 c-ı	Genesi	13.467 g-l	Genesi	0.1139 a-g

Continuing table 3

Genotypes	Root Weight (g)	Genotypes	Shoot Length (cm)	Genotypes	Shoot Weight (g)
Aldane	0.0487 d-j	Bora	13.433 g-l	Krasunia Odes.	0.1135 a-g
Golia	0.0475 d-j	Mihelca	13.400 g-l	Rumeli	0.1117 b-g
Genesi	0.0472 d-j	Siyez-1	13.300 g-l	Iveta	0.1097 c-h
Prima	0.0451 e-k	Adelaide	13.300 g-l	Esperia	0.1085 d-h
Selimiye	0.0447 e-k	Başkan	13.267 g-l	Masaccio	0.1060 e-h
Maden	0.0443 e-k	Maya	13.133 h-l	Almeria	0.1044 e-h
Sarı Mustafa	0.0441 f-k	LG 59	12.967 ı-l	Başkan	0.1040 e-h
Maya	0.0429 g-k	Ducato	12.933 ı-l	NKU Asiya	0.1034 e-h
Enargo	0.0421 g-k	Siyez-2	12.600 jkl	Rebelde	0.1031 e-h
Ducato	0.0411 h-k	Iveta	12.467 jkl	Maya	0.1009 e-h
Siyez-2	0.0307 ıjk	NKU Asiya	12.267 jkl	Emmer c.	0.0949 fgh
Siyez-1	0.0246 jk	Ambrosia	12.167 kl	Siyez-1	0.0749 gh
Emmer c.	0.0210 k	Emmer c.	11.400 l	Siyez-2	0.0665 h

The identical letters indicate statistical groups of identical values with a 99.0% confidence level by the Student-Newman-Keul Test (SNKT)

Table 4. Average values and significance groups of root weight, shoot length and weight.

PEG Doses (MPa)	Seedling Weight (g)	PEG Doses (MPa)	Shoot Length (cm)	PEG Doses (MPa)	Shoot Length (cm)
0.00	0.0710 a	0.25	15.632 a	0.25	0.1358 a
0.25	0.0574 b	0.00	15.392 ab	0.00	0.1334 a
0.50	0.0569 b	0.50	14.802 bc	0.50	0.1222 b
0.75	0.0534 b	1.00	14.240 cd	0.75	0.1079 c
1.00	0.0516 b	0.75	13.760 d	1.00	0.1072 c

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Effect of Temperature on Yield and Quality Parameters of Bread Wheat Cultivars at Different Growth Stages under Rainfed Conditions

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ABSTRACT

High temperature and its fluctuation influence bread wheat (*Triticum aestivum* L.) yield and quality before and after the grain filling stage in the Trakya region of Türkiye. Effect of the temperature between the Z24 and Z89 growth stages on yield, quality and some agronomic characters in bread wheat cultivars were investigated. This research was established with 25 genotypes in a randomised complete block design (RCBD) with 4 replications in Edirne and Tekirdağ locations, from 2010-2011 (E1) to 2015-2016 (E6) growing seasons. 5 common checks varieties were examined for their grain yield (GY), 1000-kernel weight (TKW), test weight (TW), protein ratio (PRT), wet gluten content (GLT), gluten index (IND), grain hardness (HARD), sedimentation value (SED), plant height (PH) and days of heading (DH). There were various relationships among environment, cultivar and temperature. The mean grain yield was in the range of 4454-8158 kg/ha^{-1} across six environments, in the Edirne location and E4 was the highest yielding environment while E6 was the lowest. As a result of the environmental effect, there was a 83.2% difference between the highest and lowest yield. The highest TKW (47.2 g) was in E4 and the lowest (34.3 g) was in E1. Test weight varied across six environments the lowest was in E3 and the highest in E2. Environment E1 had a higher protein ratio and wet gluten content, and E4 had the lowest protein ratio and wet gluten content. The gluten index varied from the lowest in E6 (71.3%), and the highest was 93.3 in E4. There was high variation in sedimentation value across six environments. The lowest value was in E4 (40.0 ml) and the highest was in 64.8 ml in E1. In the Tekirdağ location, the mean grain yield was in the range of 5485-8283 kg/ha^{-1}, so there was a 51.0% difference between the highest and lowest yield. The highest (46.6 g) and lowest (39.5 g) TKW were in environments E2 and E1. Test weight varied across six environments the lowest was 81.1 kg in E4 and the highest was 85.2 kg in E2. Environment E3 had the lowest protein ratio, E1 had the lowest wet gluten content and E2 had the highest protein ratio and wet gluten content. Across six environments, the gluten index varied from the lowest in E2 (74.8%), and the highest was 94.5 in E1. The lowest sedimentation was in E4 (42.2 ml) and the highest was in 47.0 ml in E5.

***Keywords*:** Bread wheat, environment, temperature, yield, quality characters

Introduction

Global climate change is one of the most important factors threatening world food security. The weakest aspect of agricultural production is that it is very susceptible to the effects of changes in climate factors. At the beginning of climate change in the world and in our country, increasing air temperatures and drought generated attention. Wheat has the maximum cultivated area among cereals and is mostly grown in rain-fed areas. Global climate change and consequent environmental stress factors cause significant yield losses in wheat (Ayrancı and Bağcı, 2020). Wheat is one of the most important cereal crops in the world. The widespread cultivation of the crop all along the globe is mainly due to the high versatility of evolution, which enables its adaptation to different agro-climatic conditions and the unique property of wheat flour and dough which allows its processing into a range of food products (Kant et al., 2014).

Improving crop yields is essential to meet the increasing pressure of global food demands. The loss of high-quality land, the slowing in annual yield increases of major cereals, increasing fertilizer use, and the effect of this on the environment all indicate that we need to develop new strategies to increase grain yields with less impact on the environment (Chapagain and Good, 2015). Environmental factors play a main role in the expression of genotype characteristics (Peterson et al., 1998). In wheat, grain yield and baking quality are dependent on the environment, genetic factors and the interaction between them (Yan and Holland, 2010; Coventry et al., 2011). Environmental factors, such as nitrogen fertilization, water and temperature, influence protein content (Sissons et al., 2005). In contrast, the protein quality is largely under genetic control (Lerner et al., 2006; Rogers et al., 2006). The physical characteristics of grain are important as they are indicative of potential processing quality. Grain hardness, which is largely genetically determined (Pena, 2008). Grain protein content in the mature grain is largely determined by environmental and farm management factors, with genetics playing a minor role in being either low or high in protein content. By contrast, the protein quality is determined by the genetic composition of the wheat variety and also how the environment influences genetic expression (Blakeney et al., 2009). Heat and drought stress are currently the leading threat to the world's food supply, limiting wheat yield. The extent and severity of stress-affected agricultural land are predicted to worsen as a result of inadequate irrigation resources, declining water tables and global warming. Drought/heat tolerance is crucial to stabilize and increase food production since domestication has limited the genetic diversity of crops including wild wheat, leading to cultivated species, adapted to artificial environments, and losing tolerance to stress episodes (Arya et al., 2012; Kaur et al., 2016). Climate change threatens to impact wheat productivity, quality and global food security. Heat stress events at the post-anthesis stage impacted wheat grain yield mostly at the grain filling stage, whilst the effect on physical and chemical quality was varied. The overall effect of post-anthesis heat on wheat yield and quality was genotype-specific (Fernie et al., 2022).

The knowledge about the nature and extent of genotype × environment interaction can help the plant breeders a great deal in formulating their breeding plans in the selection of varieties for location-specific responses and general adaptation. Consistently good performance over a range of environments (phenotypically stable) must be one of the important criteria while evaluating any wheat genotype or variety, where great variations occur in environmental conditions, locations and seasons. Besides this identification of phenotypical stable genotypes, it is also essential to identify genotypes suitable for the specific favourable and unfavourable environments for commercial production. Thus, the identification of stable genotypes, adaptable to a wide range of environments has considerable significance in bread wheat improvements (Kant et al., 2014). The success of a wheat breeding program depends on the regional adaptability of the cultivars improved and the adaptability of such cultivars in the target environments determined by their tolerance to biotic and abiotic stresses (Altay, 2012). Therefore the aim of this study was revealing the effects of genotype, environment, and GE interaction on yield, and quality parameters under different environmental conditions.

Materials and Methods

The experiment was carried out in the Trakya region of Türkiye from 2010-2011 to 2015-2016 growing cycles. Twenty-five winter wheat genotypes were examined under rainfed conditions with a randomized complete block design (RCBD) with four replications at 2 locations in Edirne (latitude 41° 38' 57'' N, longitude 26° 35' 59'' E and altitude 41 m), and Tekirdağ (latitude 40° 58' 27'' N, longitude 27° 27' 58'' E and altitude 43 m) provinces. Each plot had 6 meters length, in 6 rows, spaced 0.17 meters apart. A seed rate of 500 seeds m^2 was used. In this study, five commonly cultivated bread wheat cultivars Pehlivan, Gelibolu, Aldane, Selimiye and Bereket were evaluated. Grain yield, 1000-kernel and test weights, protein ratio, gluten, gluten index, hardness, sedimentation, plant height and days of heading were investigated (Perten, 1990; Anonymous, 2002; Anonymous, 1990)

The quality analysis of the Zeleny sedimentation test and wet gluten content were determined according to ICC standard methods No. 116/1 and 106/2, respectively (Anonymous, 1972; Anonymous, 1984).

The mean and maximum temperature in Edirne and Tekirdağ locations in March (Z24-30), April (Z31-49), May (Z51-75), and June (Z77-Z89) from shooting up to ripening period were taken from 2011 up to 2016 growing cycles in experimental field area (Table 1 and 2). The Zadoks Decimal Code (Z) was used to describe the plant growth stages of cereals. There were significant differences in average and maximum temperatures over the years. Due to this difference, there were significant differences in the parameters examined.

To determination of the regression equations R^2 were calculated (Finlay and Wilkinson, 1963; Eberhart and Russell, 1969). Data were analysed statistically for

analysis of variance the method described by Gomez and Gomez (1984). The significance of differences among means was compared by using Least Significant Difference (L.S.D. at a 5%). Stability analysis of 5 wheat cultivars for all traits was also done using the model proposed by Eberhart and Russel (1966).

Results and Discussion

Combined analysis of variance (ANOVA) across the 6 environments revealed highly significant variation among growing cycles and wheat cultivars for yield, days of heading, plant height and quality characters in the Edirne location (Table 3). Grain yield, 1000-kernels weight, test weight, protein and gluten value, gluten index, hardiness, sedimentation days of heading and plant height of wheat genotypes grown in two different environments and during 6 growing cycles are shown in Tables 3 and 4. At the Edirne location, across the 6 years environments, the mean grain yield was in the range of 4454- 8158 kg/ha^{-1}, and the mean grain yield was 6525 and 2013-2014 was the highest yielding growing cycle. Across 6 environments, the highest mean 1000-kernel weight (TKW) and test weight (TW) for all genotypes were in 2013-2014 and 2011-2012 while the lowest values were in 2010-2011 and 2012-2013 cycles, respectively. Test weight is the weight of a specific volume of grain and is an indication of the bulk density of the grain. It reflects the extent of grain filling and the potential for flour yield (Blakeney et al., 2009). The results revealed significant differences ($P<0.01$) in the protein content among growing cycles. The crude protein ratio was found to be in the range of 9.6-14.6% for the growing environments in 2013-2014 and 2010-2011, respectively. Mean values of wet gluten of wheat genotypes grown in six environments were significantly varied ($P<0.01$) depending on the differences in the genotypes and environments as well as the protein content. The highest wet gluten was determined in the 2010-2011 cycles and the lowest was in the 2013-2014 cycle. Across six environments minimum, sedimentation value was 40.0 ml in 2013-2014, and the maximum was 64.8 ml in the 2010-2011 cycles (Table 3).

According to cultivars, at the Edirne location, Gelibolu had the highest yielding cultivar. The highest TKW and TW were observed for Pehlivan and Selimiye, while the lowest values were obtained for Bereket, respectively. The highest protein ratio and sedimentation value were determined in cultivar Aldane. The highest mean value for wet gluten was obtained for Selimiye (36.9%) and Aldane (36.7%) grown at the Edirne location, while the lowest value was recorded for Gelibolu (27.3%) cultivated at Edirne location.

In the research carried out in six varies environments, Aldane was determined to be the best quality variety (Table 4).

A combined analysis of variance across the six environments in the Tekirdağ location revealed highly significant variation among years and cultivars for yield, days of heading, plant height and quality parameters (Table 5). At the Tekirdağ location, across six environments, the mean grain yield was in the range of 5485 – 8283 kg/ha^{-1}, and the mean grain yield was 6837 kg/ha^{-1}. The highest yielding cycle was 2011-2012. Based on years, the highest mean values of TKW, TW, protein ratio and gluten value for all genotypes were in 2011-2012. Across six environments minimum, sedimentation value was 42.2 ml in 2013-2014, and the maximum was 47.0 ml in the 2014-2015 cycles (Table 5).

At the Tekirdağ location, the minimum grain yield of 6415 kg/ha^{-1} was produced by the wheat cultivar Aldane. In contrast, a maximum grain yield of 7142 kg/ha^{-1} was produced by the cultivar Gelibolu, both varieties released by Trakya Agriculture Research Institute (Table 6). In the study, the TKW of wheat cultivars ranged from 40.2 g (cv Bereket) to 46.2 g (cv Pehlivan). Across six environments cultivar Selimiye had the highest test weight (84.1 kg). Cultivar Aldane had the highest protein ratio (12.4%), gluten index (93.0%), and sedimentation value (58.2 ml). The highest wet gluten content (34.5%) was determined in cv Pehlivan (Table 5). The highest mean value for wet gluten was obtained for Pehlivan (34.5%) and Aldane (33.2%) grown at Tekirdağ, while the lowest value was recorded for Gelibolu (26.2%) cultivated at the Tekirdağ location.

Correlation coefficients among temperature and the tested characters in the Edirne location were given in Table 7. Various relations among investigated parameters were found based on temperature with yield and quality parameters. The effect of the mean and maximum temperature on the quality parameters and yield of the correlations parameters were determined by Pearson's correlation analysis (Table 7). The results of the Edirne location showed that higher temperature from shooting up to the grain filling stage negatively affected protein ratio, gluten value, hardness and sedimentation in cultivars. Also, 1000-kernel weight was positively affected by mean and maximum temperature from shooting to the maturating stage in Edirne. Increasing in mean and maximum temperature during Z24 and Z89 reduced plant height and shortened in days of heading (Table 7).

Mean temperature during the Z51-75 growth stage had a significant effect and increased grain yield ($r=0.492$). An increase in maximum temperature during

the shooting and grain filling period more negatively affected grain yield than the heading stage. So, there was a negative relation between grain yield with maximum temperature during Z31-49 (r=-0.390), and Z77-89 (r=-0.753) growth stage. Thousand kernel weight was positively affected by increasing in mean temperature during Z24-30 (r=0.473), Z31-49 (r=0.445), Z51-75 (r=0.594), and Z77-89 (r=0.459) growth stage. The mean and maximum temperature during the Z51-75 growth stage had a significant effect and reduced test weight (r=-0.479 and r=-0.618). During the grain-filling period, the mean and maximum temperature had a significant effect on test weight (r=0.667; r=0.597). The higher mean and maximum temperature during the Z24 up to Z89 growth stage led to various levels of reductions in protein ratio and gluten value. The mean temperature during Z24-30 (r=-0.955**), Z31-49 (r=-0.615), Z51-75 (r=-0.311), and Z77-89 (r=-0.298) growth stage had negatively effect and caused various level of decline on protein ratio. An increase in maximum temperature during Z31-49 and Z51-75 negatively affected protein ratio and gluten value. The mean temperature during Z24-30 (r=-0.931**), Z31-49 (r=-0.546), Z51-75 (r=-0.325), and Z77-89 (r=-0.142) growth stage had a negative effect and caused a various level of decline on gluten value. The higher temperature during Z31-49 (r=-0.827*) and Z77-89 (r=-0.979**) growth stage had significant reductions in gluten index. Grain hardness and sedimentation in cultivars were negatively affected by mean and maximum temperature during the Z24 and Z89 growth stages. Hardness in cultivars was negatively affected by increasing in mean temperature during Z24-30 (r=-0.955**), Z31-49 (r=-0.575), Z51-75 (r=-0.342), and Z77-89 (r=-0.129) growth stage. Also, the mean temperature negatively affected sedimentation value of cultivars during Z24-30 (r=-0.861**), Z31-49 (r=-0.676), and Z77-89 (r=-0.670) growth stage. Maximum temperature had negatively effect during Z24-30 (r=-0.489), Z31-49 (r=-0.699), and Z77-89 (r=-0.405) growth stage (Table 7).

The correlation coefficients between the quality parameters in the Edirne location are given in Table 8. Grain yield was positively correlated (r=0.739) with 1000-kernel weight, and gluten index (r=0.805) but negatively correlated with test weight (r=-0.481). Protein content was significantly positively correlated with wet gluten content (r=0.987, $p<0.01$), grain hardness (r=0.970, $p<0.01$), and sedimentation value (r=0.862, $p<0.05$). TKW showed a negative correlation with protein ratio, wet gluten content, grain hardness, and sedimentation value. Test weight was positively correlated with protein ratio, wet gluten content and grain hardness, negatively correlated with gluten index (Table 8).

Correlation coefficients among temperature and the tested characters in the Tekirdağ location were given in Table 9. There were various relations among investigated parameters based on mean and maximum temperature. Increasing in mean temperature during Z24-30 (r=-0.517) negatively affected grain yield but positively affected during Z31-49 (r=0.559) and Z51-75 (r=0.648) growth stage. An increase in maximum temperature during Z77-89 (r=-0.651) growth stages negatively affected grain yield. In the study, 1000-kernel weight was positively affected by increasing in mean temperature during Z31-49 (r=0.912*), Z51-75 (r=0.672), and Z77-89 (r=0.369) growth stage. Mean and maximum temperature during Z31-49 (r=0.638), Z51-75 (r=0.545), and (r=0.818*) growth stage had positive effect and increased test weight. The results of Tekirdağ location showed that mean temperature from Z31 up to Z89 growth stage had a positive effect on grain yield, 1000-kernel weight, and test weight. But, increasing in maximum temperature during Z77-89 reduced grain yield, 1000-kernel weight, and test weight. The gluten index in cultivars was negatively affected by mean and maximum temperature from shooting up to the physiological maturating stage. Protein ratio, hardness and gluten value was positively affected by mean temperature during the Z31-49 and Z77-89 stage.

During Z31-49 growth stage mean temperature had significant effect protein ratio (r=0.572), wet gluten value (r=0.582) and grain hardness (r=0.566). Also, there was a positive relationship between mean temperature with protein ratio (r=0.450), gluten value (r=0.601) and hardness (r=0.474) during the Z77-89 growth stage. Gluten index was negatively affected by mean and maximum temperature during all growth stages investigated in the study. The higher mean and maximum temperature during Z24-30, Z31-49 (r=-0.538), and Z89-89 (r=-0.457), growth stage caused various levels of reductions in sedimentation value. The maximum temperature during Z24-30 (r=-0.906*) growth stage caused a significant effect and reduced sedimentation in cultivars. Increases in mean and maximum temperature during Z24 and Z89 caused various effects and reduced plant height and shortened days of heading to the Tekirdağ location (Table 9).

The correlation coefficients between the quality parameters in the Tekirdağ location are given in Table 10. Grain yield was significantly positively correlated (r=0.839*, $p<0.05$) with 1000-kernel weight, and positively correlated with TW, grain hardness. Protein content was significantly positively correlated

with wet gluten content (r=0.917, p<0.01), grain hardness (r=0.861, p<0.05), and negatively correlated with sedimentation value (r=0.588). TKW had a positive effect on TW, protein ratio, wet gluten content, and hardness. Test weight was positively correlated with protein ratio, wet gluten content and grain hardness, and negatively correlated with gluten index. It was found highly significant negative correlation between wet gluten content and gluten index (r=-0.939, p<0.01) (Table 10).

Conclusions

According to the results there were various relations between environment, cultivar and temperature. In the Edirne location, environment E4 was the highest yielding environment and E6 was the lowest. There was a 45.4% difference between the highest and lowest yield for the environmental effect. The highest TKW was in E4 and the lowest was in E1. Test weight varied across six environments the lowest was in E3 and the highest in E2. Environment E1 had a higher protein ratio and wet gluten content, and E4 had the lowest protein ratio and wet gluten content. The gluten index varied from the lowest in E6 and the highest in E4. There was high variation in sedimentation value across six environments. The lowest value was in E4 and the highest was in E1. The Edirne location showed that higher temperature from tillering up to the grain filling phase had a negatively effect on protein ratio, gluten value, hardness and sedimentation. Also, 1000-kernel weight was positively affected by mean and maximum temperature from the shooting to the maturating stage. An increase in mean and maximum temperature during Z24 and Z89 reduced plant height and shortened in days of heading.

In the Tekirdağ location, there was a 33.8% difference between the highest and lowest yield. The highest and lowest TKW was in environments E2 and E1. Test weight varied across six environments the lowest was in E4 and the highest in E2. Environment E3 had lowest protein ratio, E1 had lowest wet gluten content, E2 had the highest protein ratio and wet gluten content. Across six environments, the gluten index varied from the lowest in E2, and the highest in E1. The lowest sedimentation was in E4 and the highest was in E5. The Tekirdağ location mean temperature during Z31-75 positively affected and increased grain yield. Increasing in maximum temperature negatively affected and decreased grain yield during Z77-89 growth phase. The Tekirdağ location showed that higher temperature grain filling phase had a negatively effect on TKW, TW and sedimentation value. An increase in mean and maximum temperature during Z24 and Z89 reduced plant height and shortened in days of heading.

Table 1. The mean and maximum temperature from Zadoks 24 to Zadoks 89 growth stages (in March, April, May and June) in the Edirne location.

Year	Mean Temperature (°C)				Maximum Temperature (°C)			
	Z24-30	Z31-49	Z51-75	Z77-Z89	Z24-30	Z31-49	Z51-75	Z77-Z89
2011 (E1)	7.4	10.5	17.4	21.9	23.7	24.1	31.8	34.4
2012 (E2)	8.9	15.5	19.1	25.3	24.4	30.2	31.7	36.9
2013 (E3)	9.8	20.3	20.8	23.3	23.6	32.0	32.9	36.2
2014 (E4)	10.1	13.6	18.6	22.9	23.7	25.5	32.1	33.6
2015 (E5)	9.0	13.1	20.4	22.5	19.9	25.7	33.3	35.3
2016 (E6)	10.2	15.5	17.4	23.9	23.3	31.8	32.2	38.4
Mean	9.2	14.8	19.0	23.3	23.1	28.2	32.3	35.8

Table 2. The mean and maximum temperature from Zadoks 24 to Zadoks 89 growth stages (in March, April, May and June) in the Tekirdağ location.

Year	Mean Temperature (°C)				Maximum Temperature (°C)			
	Z24-30	Z31-49	Z51-75	Z77-Z89	Z24-30	Z31-49	Z51-75	Z77-Z89
2011 (E1)	8.1	10.5	16.5	21.9	22.3	24.1	26.1	34.0
2012 (E2)	7.9	14.1	18.1	24.1	21.6	25.0	28.1	33.5
2013 (E3)	9.6	13.5	19.5	22.4	21.6	23.5	33.6	32.6
2014 (E4)	9.9	13.4	17.5	21.8	24.0	22.8	27.0	36.9
2015 (E5)	8.5	11.4	18.2	21.3	18.3	24.6	28.0	33.3
2016 (E6)	10.4	11.4	17.9	23.6	20.7	26.3	31.7	34.4
Mean	9.1	12.4	18.0	22.5	21.4	24.4	29.1	34.1

Table 3. Mean yield and quality parameters across six environments in Edirne location.

Environments	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH	PH
2010-2011 (E1)	6552^{b}	34.3^{c}	82.5^{bc}	14.6^{a}	43.4^{a}	86.7^{ab}	54.6^{a}	64.8^{a}	131.2^{a}	117.8^{a}
2011-2012 (E2)	7149^{b}	46.4^{a}	85.2^{a}	12.2^{b}	37.2^{b}	79.5^{bc}	51.6^{ab}	43.4^{b}	121.0^{b}	87.0^{d}
2012-2013 (E3)	7272^{b}	44.2^{ab}	80.1^{d}	10.5^{cd}	29.3^{de}	80.8^{abc}	47.0^{cd}	42.6^{b}	115.4^{c}	117.4^{a}
2013-2014 (E4)	8158^{a}	47.2^{a}	80.4^{d}	9.6^{d}	25.4^{e}	93.3^{a}	45.8^{d}	40.0^{b}	109.2^{d}	114.8^{a}
2014-2015 (E5)	6766^{b}	41.6^{b}	81.3^{cd}	12.3^{b}	34.7^{bc}	87.2^{ab}	49.4^{bc}	59.8^{a}	122.2^{b}	92.4^{c}
2015-2016 (E6)	4454^{c}	36.5^{c}	83.7^{b}	11.0^{c}	31.5^{cd}	71.3^{c}	47.6^{cd}	40.6^{b}	103.8^{e}	98.6^{b}
Mean	6725	41.7	82.2	11.7	33.6	83.1	49.3	48.5	117.1	104.7
LSD (0.05)	75.9^{**}	3.9^{**}	1.3^{**}	1.0^{**}	4.0^{**}	12.3^{**}	2.9^{**}	6.3^{**}	2.3^{**}	4.8^{**}

Significance at **: P<0.01; *: P<0.05; GY: Grain yield (kg/ha^{-1}), TKW: 1000-kernel weight (g), TW: Test weight (kg), PRT: Protein ratio (%), GLT: Wet gluten value (%), IND: Gluten index (%), HARD: Hardness (PSI), SED: Sedimentation value (ml)

Table 4. Mean yield and quality characters in genotypes in Edirne location.

Cultivars	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH	PH
Pehlivan	6649^{ab}	44.7^{a}	82.7^{ab}	11.3^{bc}	35.3^{ab}	60.3^{b}	50.5^{a}	41.8^{c}	118.7^{a}	108.0^{a}
Gelibolu	7116^{a}	39.6^{ab}	81.7^{ab}	10.8^{c}	27.3^{c}	92.2^{a}	48.8^{a}	43.5^{c}	117.3^{a}	100.3^{b}
Aldane	6394^{b}	42.9^{ab}	82.1^{ab}	13.0^{a}	36.7^{a}	92.4^{a}	48.7^{a}	61.0^{a}	114.5^{b}	104.5^{ab}
Selimiye	6800^{ab}	41.9^{ab}	82.9^{a}	12.1^{ab}	36.9^{a}	82.5^{a}	50.3^{a}	50.5^{b}	117.2^{a}	101.5^{b}
Bereket	6668^{ab}	39.4^{b}	81.5^{b}	11.3^{bc}	31.6^{b}	88.2^{a}	48.3^{a}	45.8^{bc}	118.0^{a}	109.0^{a}
Mean	6725	41.7	82.2	11.7	33.6	83.1	49.3	48.5	117.1	104.7
LSD $_{(0.05)}$	66.4ns	3.6^{*}	1.2ns	0.9^{**}	3.7^{**}	11.2^{*}	2.6ns	5.8^{**}	2.0^{**}	4.4^{**}

Significance at **: P<0.01; * :P<0.05; GY: Grain yield (kg/h^{-1}), TKW: 1000-kernel weight (g), TW: Test weight (kg), PRT: Protein ratio (%), GLT: Wet gluten content (%), IND: Gluten index (%), HARD: Hardness (PSI), SED: Sedimentation value (ml)

Table 5. Mean yield and quality parameters across six environments in Tekirdağ location.

Environments	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH	PH
2010-2011 (E1)	5852^{b}	39.5^{c}	81.4^{d}	10.5^{b}	26.0^{e}	94.5^{a}	47.6^{b}	44.2^{ab}	137.6^{a}	111.0^{a}
2011-2012 (E2)	8283^{a}	48.0^{a}	85.2^{a}	12.1^{a}	36.6^{a}	74.8^{c}	53.6^{a}	43.0^{ab}	124.2^{b}	102.0^{c}
2012-2013 (E3)	7821^{a}	46.6^{a}	83.8^{b}	10.1^{b}	26.6^{de}	87.7^{abc}	46.2^{b}	44.4^{ab}	125.4^{b}	105.6^{bc}
2013-2014 (E4)	5902^{b}	43.2^{b}	81.1^{d}	11.5^{a}	32.9^{b}	81.1^{bc}	48.0^{b}	42.2^{b}	109.4^{c}	109.8^{ab}
2014-2015 (E5)	7678^{a}	42.4^{b}	81.4^{d}	10.6^{b}	29.6^{cd}	88.1^{ab}	46.8^{b}	47.0^{a}	125.8^{b}	102.4^{c}
2015-2016 (E6)	5485^{b}	40.0^{c}	82.7^{c}	10.6^{b}	31.4^{bc}	80.3^{bc}	45.2^{b}	44.0^{ab}	106.2^{d}	100.8^{c}
Mean	6837	43.3	82.6	10.9	30.5	84.4	47.9	44.1	121.4	105.3
LSD (0.05)	60.2**	2.2**	1.0**	0.9**	2.9**	12.9**	4.2**	4.8ns	1.8**	4.9**

Significance at **: P<0.01; * :P<0.05; GY: Grain yield (kg/h^{-1}), TKW: 1000-kernel weight (g), TW: Test weight (kg), PRT: Protein ratio (%), GLT: Wet gluten content (%), IND: Gluten index (%), HARD: Hardness (PSI), SED: Sedimentation value (ml)

Table 6. Mean yield and investigated characters in cultivars in Tekirdağ location.

Cultivars	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH	PH
Pehlivan	6729^{ab}	46.2^{a}	82.6^{b}	10.9^{b}	34.5^{a}	64.4^{b}	47.8^{a}	37.8^{c}	123.0^{a}	111.5^{a}
Gelibolu	7142^{a}	40.7^{b}	82.9^{b}	10.2^{cd}	26.2^{c}	90.8^{a}	47.8^{a}	40.0^{c}	121.5^{ab}	100.3^{b}
Aldane	6415^{b}	44.9^{a}	82.1^{bc}	12.4^{a}	33.2^{ab}	93.0^{a}	45.7^{a}	58.2^{a}	119.7^{c}	100.7^{b}
Selimiye	7023^{a}	44.6^{a}	84.1^{a}	10.9^{bc}	31.3^{b}	87.8^{a}	49.5^{a}	44.8^{b}	121.0^{bc}	102.8^{b}
Bereket	6876^{ab}	40.2^{b}	81.3^{c}	10.1^{d}	27.3^{c}	86.1^{a}	48.7^{a}	39.8^{c}	122.0^{ab}	111.0^{a}
Mean	6837	43.3	82.6	10.9	30.5	84.4	47.9	44.1	121.4	105.3
LSD (0.05)	55.0ns	2.0**	0.9**	0.6**	2.7**	11.8ns	3.9ns	4.3**	1.6**	4.3**

Significance at **: P<0.01; * :P<0.05; GY: Grain yield (kg/h^{-1}), TKW: 1000-kernel weight (g), TW: Test weight (kg), PRT: Protein ratio (%), GLT: Wet gluten content (%), IND: Gluten index (%), HARD: Hardness (PSI), SED: Sedimentation value (ml)

Table 7. Correlation coefficients among investigated parameters and mean-max temperature in Edirne location.

Parameter	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH	PH
MT (Z24-30)	-0.073	0.473	-0.252	-0.955**	-0.931**	-0.255	-0.955**	-0.861*	-0.949**	-0.072
MT (Z31-49)	0.033	0.445	-0.183	-0.615	-0.546	-0.463	-0.575	-0.676	-0.469	0.025
MT (Z51-75)	0.492	0.594	-0.479	-0.311	-0.325	0.186	-0.342	-0.068	0.090	-0.115
MT (Z77-89)	-0.119	0.459	0.667	-0.298	-0.142	-0.586	-0.129	-0.670	-0.356	-0.632
MXT(Z24-30)	0.100	0.129	0.321	-0.109	-0.009	-0.212	0.086	-0.489	-0.140	0.322
MXT(Z31-49)	-0.390	0.171	0.266	-0.448	-0.337	-0.827*	-0.395	-0.699	-0.555	-0.247
MXT(Z51-75)	0.036	0.101	-0.618	-0.248	-0.333	0.091	-0.427	0.150	-0.077	-0.046
MXT(Z77-89)	-0.753	-0.196	0.597	-0.098	0.010	-0.979**	-0.090	-0.405	-0.419	-0.542

Significance at **: P<0.01 and * :P<0.05; GY: Grain yield, TKW: 1000-kernel weight, TW: Test weight, PRT: Protein ratio, GLT: Wet gluten content, IND: Gluten index, HARD: Hardiness, SED: Sedimentation value, DH: Days of heading, PH: Plant height, MT: Mean Temperature, MXT: Maximum Temperature, Z: Zadoks

Table 8. Correlation coefficients among yield quality characters in Edirne location.

Traits	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH
TKW	0.739								
TW	-0.481	-0.208							
PRT	-0.215	-0.648	0.406						
GLT	-0.241	-0.600	0.530	0.987**					
IND	0.805	0.335	-0.588	0.011	-0.092				
HARD	-0.115	-0.513	0.520	0.970**	0.987**	0.007			
SED	-0.030	-0.578	-0.044	0.862*	0.773	0.346	0.745		
DH	0.285	-0.250	0.094	0.858*	0.830*	0.368	0.859*	0.844*	
PH	0.294	-0.165	-0.676	-0.087	-0.170	0.395	-0.119	0.070	0.049

Significance at **: P<0.01 and *: P<0.05; GY: Grain yield, TKW: 1000-kernel weight, TW: Test weight, PRT: Protein, GLT: Wet gluten content, IND: Gluten index, HARD: Hardiness, SED: Sedimentation, DH: Days of heading, PH: Plant height

Table 9. Correlation coefficients among investigated parameters and mean-max temperature in Tekirdağ location.

Traits	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH	PH
MT (Z24-30)	-0.517	-0.226	-0.197	-0.303	-0.055	-0.196	-0.661	-0.238	-0.819*	-0.095
MT (Z31-49)	0.559	0.912*	0.638	0.572	0.582	-0.677	0.566	-0.538	-0.267	-0.134
MT (Z51-75)	0.648	0.672	0.545	-0.222	0.002	-0.243	-0.105	0.218	-0.168	-0.514
MT (Z77-89)	0.144	0.369	0.818*	0.450	0.601	-0.734	0.474	-0.457	-0.299	-0.564
MXT(Z24-30)	-0.391	0.093	-0.037	0.345	0.127	-0.141	0.218	-0.906*	-0.166	0.701
MXT(Z31-49)	-0.084	-0.252	0.320	-0.007	0.254	-0.315	-0.026	0.248	-0.219	-0.773
MXT(Z51-75)	0.194	0.282	0.467	-0.488	-0.203	-0.133	-0.427	0.113	-0.309	-0.485
MXT(Z77-89)	-0.651	-0.309	-0.528	0.421	0.346	-0.260	-0.022	-0.612	-0.584	0.452

Significance at **: P<0.01 and * :P<0.05; GY: Grain yield, TKW: 1000-kernel weight, TW: Test weight, PRT: Protein, GLT: Wet gluten content, IND: Gluten index, HARD: Hardiness, SED: Sedimentation, DH: Days of heading, PH: Plant height, MT: Mean Temperature MXT: Maximum Temperature, Z: Zadoks

Table 10. Correlation coefficients among yield quality characters in Tekirdağ location.

Traits	GY	TKW	TW	PRT	GLT	IND	HARD	SED	DH
TKW	0.839*								
TW	0.641	0.771							
PRT	0.206	0.446	0.340						
GLT	0.213	0.443	0.433	0.917**					
IND	-0.207	-0.514	-0.576	-0.766	-0.939**				
HARD	0.525	0.632	0.580	0.861*	0.700	-0.545			
SED	0.297	-0.237	-0.244	-0.588	-0.477	0.523	-0.410		
DH	0.386	0.061	0.040	-0.236	-0.505	0.655	0.227	0.386	
PH	-0.406	-0.259	-0.535	-0.097	-0.437	0.551	-0.082	-0.348	0.343

Significance at **: P<0.01 and *: P<0.05; GY: Grain yield, TKW: 1000-kernel weight, TW: Test weight, PRT: Protein, GLT: Wet gluten content, IND: Gluten index, HARD: Hardiness, SED: Sedimentation, DH: Days of heading, PH: Plant height

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Breeding Potentials of Durum Wheat Landraces for Yield and Quality Traits

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ABSTRACT

The study was carried out to evaluate yield components and some physiological quality traits for 30 durum wheat landraces (native and foreign originated) and 5 obsolete cultivars in Thrace ecological conditions. Experiments were set up in randomized block design in 3 replicated during the 3 consecutive growing seasons. As a result of the analysis of variance, the differences between the averages of the genotypes for the traits were found to be statistically significant. This indicated that there may be enough variation for traits within landraces. The mean values of genotypes ranged between 2238 kg/ha^{-1} and 3749 kg/ha^{-1} for grain yield, 98.8 cm and 135.3 cm for plant height, 6.04 cm and 8.88 cm for spike length, 26.6 and 35.3 for the number of grains per spike, 0.988 g and 1.494 g for grain weight per spike, 36.1 g and 42.7 g for thousand grain weight, 74.4 kg/hl^{-1} and 79.4 kg/hl^{-1} for test weight and 82.1% and 94.6% for vitreous grain percentage. Although Kahramanmaraş, Dicle, Boğacak, Sorgül, Ionia, Cyprus and Haurani were determined as promising populations for yield and yield components, Siverek, Çanakkale, Tokat, Gaziantep, Yozgat and Urfa landraces had better physical quality. The estimated coefficient of variation and broad sense heritability shifted from 3.9% to 24.52% and from 7.91% to 72.44% for the traits, respectively. Moderately high coefficient of variation, broad sense heritability a genetic advance for plant height, spike length and vitreous grain percentage indicated that selection based on these traits will be more effective and accomplished in the genetic material.

***Keywords*:** Durum wheat, landraces, obsolete cultivar, yield components, physical quality traits

Introduction

Durum wheat is an important raw material in the world food industry, especially in pasta and bulgur. 20% of the world's durum wheat production takes place in Middle East countries, including Turkey. As a result of climate change, it is estimated that the production areas of durum wheat (*Triticum durum* Desf.) will decrease by 19% by 2050 and 48% at the end of the century (Ceglar et al., 2021). This means that production decreases, dependence increases and may cause a threat to food safety for millions of people due to increasing temperatures in the areas where wheat production is made (Tesfaye, 2021). Turkey is one of the most important producer countries in the world in durum wheat production and is also the "gene" centre of durum wheat.

In our country, 15-20% of durum wheat production is carried out on the coast, 25-30% is made in Southeastern Anatolia, and 50-55% is carried out in Central Anatolia and passage zones (Alp and Kün, 1999). Due to its ecological feature, the South-eastern Anatolia Region in Turkey is known as the durum wheat zone of our country. In our country, the share of durum wheat areas in wheat sowing areas is at the level of 8-10% (Anonymous, 2008). While durum wheat production was 60% in previous years in the Thrace region, it has decreased to a level that will be none at today's level (Anonymous, 2009). This is due to the low number of varieties in durum wheat breeding and the inadequacy of variation sources used in breeding. For this reason, it is important to use new genetic resources that have the desired

characteristics in the breeding of durum wheat and are well compatible with each other in crossing (Alp, 2005). One of the easiest and most effective ways to develop genetic varieties by expanding the genetic variation is the use of landraces (Gollin et al., 2000; Sönmezoğlu, 2006; Coşkun et al., 2019; Demirel et al., 2019).

As a result of plant breeding activities, although it makes a significant positive contribution to the increase in wheat production depending on the increase in field yield, it also causes the increase and extinction of direct and indirect use of genetic resources (landraces or local wheat population, etc.). It is stated by many researchers that landraces (Mazid et al., 2009) grown on less than 1% of the total wheat cultivation area of Turkey have significant potential in breeding studies (Dotlacil et al., 2010; Jaradat, 2012).

It is important to take advantage of landraces and wild forms to increase variation in breeding studies. They are at risk of extinction due to the development of a large number of high-yielding commercial varieties, the development of technology and the ease of transportation everywhere (Karagöz and Zencirci, 2005). There is a need to protect landraces with genetic diversity and use them as parents in breeding programs (Özberk, 2018).

Landraces are considered to be important genetic sources in increasing genetic diversity for the varieties to be developed by showing better adaptation in regions where abiotic and biotic stress factors are located (Soriano et al., 2018; Maccaferri et al., 2019). To increase the effectiveness of continuity and plant breeding programs in plant production, the protection of landraces and the prevention of genetic erosion are of great importance (Kabbaj et al., 2017). It is known that wheat landraces grown in different regions of Turkey have high adaptation capabilities and good quality characteristics. In the studies, it has been shown that there are very useful sources in the breeding studies of landraces because of their significant diversity among populations (Aoun et al., 2019; Chacon et al., 2020). When landraces are comprehensively characterized for genetic diversity and population structure, it has great potential to identify new resources of resistance against biotic and/or abiotic stresses (Marone, 2021). Wild relatives, landraces and other germplasms are important genetic sources in determining new sources of genetic resistance against diseases (Grandillo et al., 2007).

It is of great importance to give priority to the breeding of high-quality varieties for the increase in wheat production (Sözen and Yağdı, 2005; Tekdal et al., 2011). Wheat landraces have very good performance for quality characteristics in our country. However, to benefit from following the purpose and to use it as a gene source in breeding studies, its genetic structures must be determined well (Tanksley and McCouch, 1997; Eserkaya, 2010). Some of the landraces can reveal hopeful performances under modern production conditions for grain yield and quality characteristics (Brush, 1995; Karakaxas et al., 1998). In addition to being the preferred material in breeding programs, the increase in the use of nutritional values increases the importance of durum wheat landraces day by day (Trad et al., 2022). This study, it is aimed to investigate the usability of native and foreign landraces in agronomic performance and variability levels and wheat breeding programs.

Materials and Methods

In the study, 5 foreign origins (Myrina, Limnos, Cyprus, Ionia and Haurani), 25 native origins (Manisa, İzmir, Bursa, Çanakkale, Denizli, Mersiniye, Sorgül, Menceki, Urfa, Han 27, Siverek, Şırnak Akkaya, Dicle, Devedişi, Boğacak, İskenderun, Kahramanmaraş, Mardin, Adıyaman, Gaziantep, Tokat, Erzincan, Akbuğday, Amasya and Yozgat) durum wheat landraces and 5 obsolete durum wheat varieties (Beyaziye, Gökgöl 79, Berkmen 469, Japiga and Mondur) were used as genetic material. Landraces and obsolete durum wheat varieties were provided from the genetic stock from native and foreign sources of Tekirdag Faculty of Agriculture, Department of Field Crops.

The trials were carried out in Tekirdağ ecological conditions in 2006-2007, 2007-2008 and 2008-2009 growing periods according to the randomized blocks experimental design with 3 replications. Each genotype was sown in 5 m^2 plots with 500 plants per square meter. 20 kg/da^{-1} 20.20.0 fertilizer before planting sowing, 10 kg/da^{-1} urea (46%) during the tillering period, 15 kg ammonium nitrate during the booting period and 15 kg/da^{-1} ammonium nitrate (26%) fertilizer in the pre-heading period were given as fertilizer in the study. In the study, grain yield, plant height, spike length, number of grains per spike, grain weight per spike, thousand grain weight, test weight and vitreous grain percentages were investigated.

The data obtained from the landrace and obsolete cultivar were analysed according to the randomized blocks experimental design, and the differences between the means were determined by the DUNCAN (0.05) significance test (SAS Institute, 1999). In the estimation of variance components, Johnson et al., (1955) mean square values were used according to the

method described. Coefficient of variation (Burton, 1952), coefficient of genetic and phenotypic variation (Singh and Choudhury, 1985), heritability broad sense (Falconer and Mackay, 1996) and genetic progress (Allard, 1960) values were estimated.

Results and Discussion

As a result of the analysis of variance, the differences between the averages of the durum wheat landraces and obsolete cultivars for the grain yield, yield components and some physical quality characteristics were found to be statistically significant (Table 1).

The plant height in the landraces and obsolete cultivar varied between 98.8 cm and 135.3 cm. It is seen that landraces have taller plant heights with an average plant height of 119.6 cm. It is seen that especially Kahramanmaraş landrace with 98.8 cm plant height and Dicle, Han 27, Siverek, Ionia and Cyprus durum wheat landraces with short plant heights can be a material that has the potential to be used in direct and indirect breeding studies for plant height.

The spike length varied between 6.04 cm and 8.88 cm in landraces, and there were populations with longer spikes than the average of 6.77 cm obsolete cultivars. It is understood that the populations of İskenderun, Erzincan, Ionia, Boğacak, Dicle and Menceki which have longer spikes than the obsolete variety Berkmen 469 (7.78 cm), may be the right material to be used in direct and indirect breeding studies for spike length.

While the number of grains per spike in the landraces and obsolete varieties of durum wheat varied between 26.6 and 35.3 units in the experiment, the grain weights per spike were between 0.988 g and 1.494 g. Devedişi, Boğacak, İskenderun, Tokat and Yozgat populations, which give higher values than the obsolete variety Berkmen 469 (32.9 units), which has the highest value for grain number in spike, are the prominent populations.

The thousand kernel weight was changed between 36.10 and 42.70 g for the landraces and varied from 38.2 to 42.7 g for the obsolete cultivars. Among the 35 genotypes in the study, Sorgül and Dicle populations, Gökgöl 79 and Berkmen 469 obsolete cultivars gave higher thousand kernel weight over 42 g. Han 27 (36.1 g), Limnos (36.5 g) and Japiga (38.2 g) were the genotypes that gave the lowest thousand kernel weight. It is understood that the landraces and most of the obsolete cultivars gave close averages for thousand grain weight in the study.

It is seen that the test weights of the landraces and the majority of the obsolete cultivars are below the desired values (Table 1). Test weight values varied between 74.4 kg/hl^{-1} and 79.4 kg/hl^{-1} for the genotypes. Gökgöl 79 (78.7 kg/hl^{-1}) variety gave the highest test weight and Dicle, Siverek and Menceki landraces gave similar values.

In the study, vitreous grain percentages ranged from 82.1% to 94.6% for landraces. The vitreous grain average of obsolete cultivars was 91.5%. Similar values were determined for vitreous grain percentage in the obsolete variety Beyaziye (94.3%), which gave the highest vitreous grain percentage, and in Çanakkale, Urfa, Gaziantep and Yozgat populations.

While the grain yield means of landraces varied between 2238-3749 kg/ha^{-1}, obsolete cultivars gave average yields ranging from 2437 to 3639 kg/ha^{-1}. While Gökgöl 79 had the highest grain yield with 3639 kg/ha^{-1} among the obsolete varieties, the durum wheat landrace Dicle took place on this variety with a yield of 3749 kg/ha^{-1}. İzmir, Bursa, Denizli, Sorgül, Boğacak, Amasya, Cyprus and Haurani landraces gave statistically similar results with Gökgöl 79. The estimated parameters to determine the variability level of the genetic material in the research are given in Table 2.

The presence of a sufficiently large variation in a population indicated that the population has suitable genotypes that can be used successfully in breeding programs. Dotlacil et al., (2000) explained that a minimum coefficient of variation of 10% can be considered a sign of wide variation. The coefficients of variation for the examined characters ranged from 3.9% to 24.52%. As seen in Table 2, the high coefficients of variation for grain weight per spike, grain number per spike, grain yield, spike length, plant height and thousand grain weight indicated that there may be sufficient variation for breeding studies in existing populations. On the other hand, it is seen that there is not enough variation for test weight and vitreous grain percentage in landraces. In addition, it is seen that the estimated phenotypic variation coefficients for the examined traits are larger than the genotypic variation coefficients. This shows that environmental factors have a higher effect than genotypic factors in the emergence of these traits. The phenotypic and genotypic coefficients of variation were close values for ear length, grain weight per spike, thousand grain weight and vitreous grain percentage traits.

Heritability estimates indicate the response to selection based on the phenotype of different traits. Johnson et al., (1955) stated that using heritability

values together with genetic advance estimates is more beneficial than using heritability values alone in estimating the effect of selection.

The estimated broad-sense heritability for the traits examined in the study ranged from 7.91% to 72.44%. The highest heritability values were estimated for plant height (72.44%), vitreous grain percentage (61.73%), and spike length (61.43%), respectively. Generally, low and moderate heritability may be due to the type of genetic material and the environment of the growing region. In addition, high heritability estimated for plant height, spike length and vitreous grain percentage and high genetic advance values show that the genotypic effect is higher in the formation of these traits, and the selection to be made can be more effective and successful.

When populations are evaluated according to the data obtained, Kahramanmaraş, Dicle, Siverek, Ionia, Cyprus and Han 27 for plant height; Menceki, Dicle, Devedişi, Boğacak, İskenderun, Erzincan, Ionia and Cyprus for the number of grains per spike; Çanakkale, Denizli, Devedisi for the number of grains per spike; Boğacak, İskenderun, Ionia, Tokat, Adıyaman and Yozgat for grain weight per spike; Menceki, Çanakkale, Denizli, Sorgül, Dicle, Gaziantep and Tokat for test weight; Çanakkale, Gaziantep, Urfa and Yozgat for vitreous grain percentage and Dicle, İzmir, Bursa, Denizli, Sorgül, Amasya and Boğacak for grain yield were determined as beneficial populations for breeding studies.

The fact that grain weight per spike, number of grains per spike, grain yield, spike length, plant height and thousand grain weight characteristics have high coefficients of variation indicates that there is sufficient variation in these characteristics in populations. The calculated high heritability for plant height, spike length and vitreous grain percentage, and high genetic advance values show that parents and genotype selections based on these characteristics can be more effective and successful.

As result, Dicle, Boğacak, Cyprus, Haurani, Amasya and Denizli populations showed superior characteristics for grain yield and yield characteristics, and Çanakkale, İzmir, Sorgül, Menceki, Dicle, Amasya, Gaziantep and Yozgat populations showed superior characteristics for quality characteristics. It is seen that these populations are potential populations to obtain new varieties as a generator in crossbreeding in durum wheat breeding studies or directly by pure line selection.

Table 1. Average values of genotypes in the traits examined.

Genotypes	Plant Height	Spike Length	Number of Grains per Spike	Grain Weight per Spike	Thousand Grain Weight	Test Weight	Vitreous Grain Percent	Grain Yield
Beyaziye	115.1 d-h	6.86 g-l	32.2 a-d	1.328 a-f	40.3 abc	76.1 c-h	94.3 a	2887 d-l
Gökgöl 79	103.6 abc	6.80 h-m	30.2 a-d	1.419 a-d	42.2 a	78.7 ab	90.0 d-i	3639 ab
Berkmen 469	107.9 b-e	7.78 b-e	32.9 abc	1.476 ab	42.7 a	78.2 a-d	94.0 ab	3504 abc
Japiga	115.9 d-i	6.34 j-m	30.2 a-d	0.988 j	38.2 abc	76.1 c-h	90.1 c-i	2437 lm
Mondur	111.1 c-f	6.06 lm	28.2 cd	1.200 d-j	40.7 abc	76.3 b-h	89.2 f-i	2494 klm
Average	**110.7**	**6.77**	**30.7**	**1.282**	**40.8**	**77.1**	**91.5**	**2992**
Manisa	129.5 lmn	6.97 e-k	28.0 cd	1.039 hij	40.6 abc	76.4 b-h	82.1 l	2949 c-l
İzmir	126.6 k-n	7.37 b-h	30.4 a-d	1.206 c-j	41.3 ab	77.7 a-f	92.9 a-e	3384 a-d
Bursa	119.9 f-k	7.09 d-j	31.0 a-d	1.202 d-j	39.5 abc	76.8 a-h	91.4 a-g	3106 a-j
Çanakkale	124.8 i-m	7.21 b-i	35.3 a	1.454 abc	41.6 a	75.4 fgh	94.6 a	2681 f-m
Denizli	127.8 k-n	7.74 b-e	33.0 abc	1.292 a-g	41.1 ab	77.0 a-g	90.7 b-h	3120 a-i
Mersiniye	115.8 d-i	6.54 i-m	26.6 d	1.123 f-j	40.7 abc	76.8 b-h	92.9 a-e	2842 d-l
Sorgül	114.6 d-h	7.59 b-h	31.6 a-d	1.231 b-i	42.7 a	77.6 a-f	89.8 e-i	3323 a-e
Menceki	128.0 k-n	7.81 a-d	28.4 cd	1.198 d-j	41.2 ab	78.0 a-e	87.2 ij	2959 c-l
Urfa	121.1 g-l	7.70 b-f	29.6 a-d	1.200 d-j	40.4 abc	76.1 c-h	93.3 abc	2574 h-m
Han 27	109.8 b-e	6.90 f-k	31.7 a-d	1.190 d-j	36.1 c	74.4 h	89.9 e-i	2529 j-m
Siverek	107.3 a-d	7.73 b-e	32.6 abc	1.312 a-g	41.4 a	78.6 abc	83.7 kl	2960 c-l
Şırnak Akkaya	119.6 f-k	7.03 d-k	32.6 abc	1.186 d-j	41.2 ab	75.4 fgh	92.2 a-f	2575 h-m
Dicle	101.3 ab	7.82 a-d	31.9 a-d	1.494 a	42.0 a	79.4 a	85.2 jkl	3749 a
Devedişi	127.2 k-n	7.14 c-j	34.3 ab	1.163 e-j	41.3 ab	77.7 a-f	92.6 a-e	2238 m
Boğacak	112.8 d-g	7.84 a-d	33.3 abc	1.361 a-f	40.8 abc	77.3 a-g	93.0 a-e	3140 a-h
İskenderun	124.8 i-m	8.88 a	33.4 abc	1.283 a-g	40.8 abc	74.4 h	92.4 a-f	2596 g-m
Kahramanmaraş	98.8 a	7.02 d-k	31.1 a-d	1.277 a-h	39.2 abc	76.3 b-h	93.2 a-d	3039 b-k
Mardin	123.6 h-m	6.27 klm	29.9 a-d	1.001 ij	39.3 abc	76.8 b-h	87.4 hij	2805 d-m
Adıyaman	128.1 k-n	7.20 b-i	30.4 a-d	1.351 a-f	40.5 abc	76.3 b-h	91.8 a-f	2681 f-m
Gaziantep	122.0 h-l	7.39 b-h	32.2 a-d	1.078 g-j	39.8 abc	77.1 a-g	94.2 a	2993 c-l
Tokat	125.8 j-n	7.28 b-i	33.1 abc	1.304 a-g	41.4 a	76.2 b-h	92.1 a-f	2777 e-m
Erzincan	131.7 mn	8.01 ab	31.1 a-d	1.206 c-j	40.8 abc	75.8 d-h	92.0 a-f	2552 i-m
Akbuğday	124.9 i-n	7.47 b-h	29.2 bcd	1.322 a-f	39.5 abc	77.4 a-f	92.2 a-f	3030 b-k
Amasya	121.8 g-l	7.72 b-e	29.1 bcd	1.251 a-h	40.7 abc	77.0 a-g	91.6 a-g	3170 a-g
Yozgat	124.2 i-m	7.52 b-h	33.1 abc	1.348 a-f	41.1 ab	74.4 h	94.0 ab	2939 c-l
Myrina	116.8 e-j	7.36 b-h	27.9 cd	1.216 c-j	39.1 abc	77.2 a-g	90.2 c-i	2668 f-m
Limnos	135.3 n	6.86 g-l	29.0 bcd	1.269 a-h	36.5 bc	75.7 e-h	85.3 jk	2648 g-m
Cyprus	107.2 a-d	7.66 b-g	29.9 a-d	1.201 d-j	38.5 abc	75.2 fgh	83.1 kl	3239 a-f
Ionia	102.2 ab	7.96 abc	31.8 a-d	1.378 a-e	39.2 abc	76.4 b-h	88.3 g-j	2789 d-m
Haurani	115.0 d-h	6.04 m	29.8 a-d	1.304 a-g	39.7 abc	74.9 gh	82.8 kl	3123 a-i
Average	**119.6**	**7.37**	**31.0**	**1.248**	**40.3**	**76.6**	**90.1**	**2906**

Table 2. Estimated phenotypic and genotypic coefficients of variation, components of variance, heritability in broad sense (h^2BS), genetic advance (GI) and genetic advance as % of the mean for the traits examined.

	Ave.	Min.	Max.	CV (%)	PVC (%)	GVC (%)	Variance components			h^2BS (%)	GA*	GA (%)
							σ^2_{ph}	σ^2_g	σ^2_e/r			
PH	118.343	84.2	150.1	11.30	74.72	54.13	88.424	64.054	39.447	72.44	14.03	11.86
SL	7.284	5.0	10.3	12.78	4.98	3.06	0.363	0.223	0.243	61.43	5.94	81.55
SGN	31.006	16.0	53.0	20.80	13.17	1.04	4.083	0.323	10.337	7.91	0.33	1.11
SGW	1.256	0.5	2.04	24.52	1.19	1.004	0.015	0.005	0.420	33.33	0.08	6.37
TCW	40.385	27.9	52.2	9.15	10.93	5.06	4.413	2.045	13.460	46.34	2.01	4.98
TW	76.613	67.0	83.0	3.97	1.93	0.004	1.482	0.265	25.540	17.88	0.45	0.59
GVP	90.283	66.0	98.0	5.62	14.24	8.79	12.854	7.935	30.093	61.73	4.56	5.05
GY	2918.3	1578	4946	20.80	41.40	17.50	120818.2	51058.0	972.800	42.26	195.50	6.70

PH: Plant height, SP: Spike length, SGN: Grain number per spike, SGW: Grain weight per spike, TCW: Thousand grain weight, TW: Test weight, PGV: Vitreous grain percentage, GY: Grain yield.

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Host and Pathogen Factors Determining Yellow Rust Reaction in Wheat- An Overview

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ABSTRACT

Among cereals, wheat is one of the most important crop globally, being a major component of food security. Among rust diseases of wheat, yellow rust is an important which result in considerable losses in normal and colossal losses in epidemic conditions. The disease-causing organism *Puccinia striiformis* is an obligate pathogen with diverse pathotypes which have the ability to invade resistance of the wheat varieties due to prevalence of new pathotypes. It is therefore, important to understand the virulence patterns of pathotypes and host resistant genes to create a mismatch for sustainable production. This review paper examines the losses due to yellow rust, variability in pathogen for virulence, migration of pathogen, meteorological pre-disposing factors, types and number of resistant genes governing yellow rust resistance at various plant growth stages, identification of resistant genes through conventional and molecular markers, conventional and biotechnological methods for developing yellow rust resistant wheat varieties and futuristic outlook to tackle yellow rust epidemic under climate change regime through breeding and management strategies.

Keywords: Wheat, yellow rust, *Puccinia striiformis*, virulence, resistance genes, breeding methods

Introduction

Among cereals, wheat is one of the most important crops worldwide ranking second after rice (Bouvet et al., 2022). Wheat is majorly cultivated since ages to provide caloric and nutritive needs of the people through its biochemical constituents that includes starch, proteins, lipids, fiber and minerals. About 35% people worldwide in developing and developed countries depend on wheat as a staple food besides rice and maize (Pooja et al., 2019). To ensure world food security, sustainably increased wheat production is required. As per FAO, statistic, it is expected that the world population will be around 8 billion by 2025 and around 10 billion by 2050 (Reema et al., 2019). Such a huge increase in population would also result in increase in demand for wheat. Wheat production needs to be increasing sustainability by 50% by 2025 and about 4% annually (Yadav et al., 2017). Wheat production is subjected to risk due to abiotic stresses on account of climate change and biotic stresses on account of prevalence of mutated insect pests and pathotypes. Biotic stresses mainly foliar diseases may reduce wheat yield by 15-20% (Bouvet et al., 2022). Of these foliar diseases, rusts and mildews are more harmful. Among rust diseases, considerable losses are caused in grain yield and quality by yellow rust (*P. striiformis*), stem rust (*P. graminis*) and leaf rust (*P. recondita*) (Ali et al., 2017). Stripe rust also known as yellow rust possess a serious challenge to the wheat growers as well as wheat breeders due to its negative impact both on grain yield and its quality. Several yellow rust epidemics have been documented (Sanders, 2018) from middle East countries and Mediterranean countries during 2009-2010 leading to colossal losses.

Epiphytotic conditions due to yellow rust have been reported from all continents including Americas

(North and South) (Line, 2002), Africa, Asia (Ali et al., 2014a), Australia (Wellings et al., 2003) and Oceania (Chen et al., 2009), the moderate to high losses have been reported due to yellow rust over the years (Ali et al., 2014b). Therefore, yellow rust resistance in wheat has been a cherished goal, both for agronomist and plant breeders (Sharma et al., 2016). As a tangible solution, the resistant varieties are continuously looked upon as cost effective and environment friendly option to cope up with menace caused by yellow rust.

Yellow Rust Losses

Among most important rust diseases of wheat, yellow rust is the cause of concern globally due to losses caused by it as it infects wheat leaves during early growth phases including seedling stage as well as subsequent plant growth stage. The yellow rust infected plants are stunted and weak leading to considerable losses up to 70%. Yellow rust also reduces grain quality including size of the grains and its milling and food product quality. Chen, (2005) reported that development of yellow rust at seedling stage can cause higher or total yield loss in susceptible varieties. Pooja et al., (2021) reported that the yellow rust infection and disease severity is influenced by several plant factors like resistant genes offering host resistance, climatic conditions at initial infection as well as its time, prevailing meteorological conditions before or during infection, duration and progress of development of disease.

Wheat genotypes possessing different *Yr* genes grown in the specific wheat producing regions globally witnessed yield losses over decades of varying intensity ranging from 20-75% leading to huge economic losses subjected to environment during crop growth (Roelfs 1978; Saari et al., 1985; McIntosh et al., 2009; Bouvet et al., 2022). The control of yellow rust using fungicide is environmentally not benign, economically costly and damaging the food safety network (Khanfri et al., 2018). Under such situations, understanding of host pathogen interaction and deployment of resistant genes is the most important management strategy to avoid yield losses. The yellow rust resistant varieties have registered much less yield losses compare to the susceptible varieties as experienced by researchers and farmers in different countries (Sharma et al., 2015). However, the pathogenic races are continuously changing through environmental selection pressure affecting durability of resistance and thus regularly changing the yield loss scenario over the years in different countries (Bouvet et al., 2022).

Pathogen As Causal Organism

Yellow rust causing organism being an obligate parasite necessitate presence of a living host to complete its life cycle. It is caused by a fungal pathogen, *Puccinia striiformis* Westend. f.sp. *tritici* which belongs to order Pucciniales and family Basidiomycota. There has been several nomenclatures for this fungal pathogen since eighteenth century, however Hylander et al., (1953) recoined the name of yellow rust causing pathogen as *Puccinia striiformis* and later reviewed by several researchers over the decades (Rahmatov, 2016). Yellow spots or flecks are evident on wheat leaves after one week of infection as first symptoms of yellow rust. (Fig. 1). Thereafter, disease development progresses and spots or flecks appear in the form of stripes on leaves and sometimes on leaf sheath, awns and glumes. The Incubation period of pathogen ranged from 10-17 days, 11-21 days and 9-19 days whereas yellow rust latent period spanned over 10-23 days, 11-21 days and 11-22 days (Kashyap et al., 2018). As the disease progresses, the small yellow spots become bigger pustules which upon maturity release yellow-orange masses of urediospores. With senescence of wheat plant, the yellow spots and stripes become brown before the maturity of the plant. Yellow rust pathogen reduces plant growth and vigour by removing wheat plant nutrients and water and therefore, reduces grain yield as well (Line, 2002; Chen, 2005; Singh et al., 2017). Poor plant growth is the major reason for loss in grain yield. The other parameters determining yield losses are dry matter, low test weight, reduced kernel number and grain size as evidenced by number of researchers (Wellings, 2011; Mabrouk et al., 2022).

Centre of Diversity for *Puccinia striiformis*

Rusts are most serious concern in wheat production world over as they can cause colossal losses (Singh et al., 2004). In most wheat production areas globally, yellow rust is prevalent (Chen, 2005). Yellow rust was observed in wheat fields in USA as early as 1915, however it was not a devastating disease and no outbreaks were recorded till 1960's which were first recorded in some states of USA mainly in the western states (Line, 2002). Ali et al., (2014) and Thach et al., (2016) recorded high genetic diversity and recombinant races of *Pst* populations in Himalayan region and its vicinity. They postulated that these regions could be centre of origin and diversity for yellow rust causing pathogen *P. striiformis.* In 1979, yellow rust was reported first time in eastern Australia which subsequently spread to New Zealand in 1980 as reported by Wellings et al., (1987). Yellow rust was reported in the beginning from South Africa and in 2004 in Western Australia. Boyd, (2005) based on phyto-pathological analysis suggested that presumably the new yellow rust pathotype emerged in East

Africa. Singh et al., (2004) summarized that yellow rust appeared in different parts of the world despite diversity in cropping systems, germplasm traits and environmental conditions. A new level of adaptation in rust races is postulated due to outbreak of rusts in countries closer to equators. *Puccinia striiformis* has been witnessed from most of the wheat growing countries from all the continents with an exception of Antarctica. Many countries in north and south America including USA, Canada, Mexico, Bolivia, Cerrebians, Canada, Oceania including Australia, Europe including Germany, France, UK, Asia including India, Pakistan and Africa including south Africa, Kenya have witnessed serious outbreaks of yellow rust over different years.

Pre-disposing Meteorological Factors

Yellow rust occurrence in wheat is mainly governed by prevailing environmental conditions and rust resistance genes in host plant. The observations gathered world over have revealed that both occurrence and severity of rust diseases are associated with changes in major meteorological parameters including maximum and minimum temperature, high and low relative humidity, soil moisture, temperature of soil, photoperiod, velocity of wind, rainfall and cloud cover (Pooja et al., 2021). In general, the temperature ranges from 0-23°C mark the congenial temperature, being minimum at 0°C, optimal at 11-12°C and maximum at 23-24°C (Curtis et al., 2002). The cooler (0-12 °C) and humid nights (RH>70) favour the onset of disease and its progression (Chen et al., 2014). In recent years, yellow rust has predominated the other rusts due to climate change (Jevtić et al., 2017). Pandey et al., (2017) described that the yellow rust severity is determined by favorable pre-disposing meteorological factors and plant water relations along with genetic factors. Therefore, in order to develop pragmatic management strategy for control of yellow rust, it is worthwhile to characterize and modulate key pre-disposing factors governing initiation and progression of disease. In order to develop reliable prediction models for occurrence and severity of yellow rust infection in wheat, it would be necessary to understand meteorological parameters as baseline information to develop disease prediction system. As the wheat can grow in diverse environment, the incidence of yellow rust infection occurs only in cooler and humid environmental conditions. Pooja et al., (2021) elaborated that temperature (max. and min.), relative humidity (morning and evening), rainfall, sunshine hours, cloud cover are associated with infection and progression of yellow rust in wheat. Based on meteorological parameters and using step-wise regression, Pooja et al., (2021) suggested a prediction model that is based on meteorological parameters and their potential contribution in determining disease severity.

In general, the disease progression was slow in cooler months of December and January and faster in moderately cool, February in north-western plain zone of india. As the temperature grows and plant attains senescence in March-April, the pathogen *P. striiformis* is also affected and the disease progression declines due to senescence (Asseng et al., 2011). Also, high temperature, >34°C hampers the growth of *P. striiformis* and hence restrict disease development (Juroszek et al., 2013). Predisposing factors favoring yellow rust incidence are also changing under global climate change regime. In short span of time, the yellow rust occurrence is supposed to be lower in north western plain zone of India as the day and night temperature are rising during and beyond February month which is supposedly the time for progression. However, in longer run, it is expected that new pathotypes of yellow rust adaptable to high temperature conditions will emerge and cause losses due to yellow rust resistance even at higher temperature than the congenial temperature known for yellow rust initiation and progression (Kaur et al., 2008). Yellow rust was reported to be prevalent in wetter and temperate regions with different altitude and latitude Chen et al., (2014).

Introduction and Migration of *Puccinia striiformis*

Since, the inoculum of yellow rust resistance needs an obligate host for its perpetuation over seasons, after wheat season, it grows on its alternative collateral host, *i.e.*, grasses growing in cooler areas of hills. The spores migrate from the centre of origin to new localities with monsoon clouds and rains and are distributed over different geographical regions through rains. This fact can be ascertained through spore trap methods (Rogers et al., 2009). After falling on growing wheat plants in winter season, the yellow rust spores can have one of the following consequences: It may germinate on leaf sheath of wheat plant (Jin et al., 2010), form conidia, puncture leaf tissue and establish itself and draw nutrition from wheat leaves through formation of haustoria (Ma et al., 2009; Sorensen, 2012) and finally establish full grown mycelia from which urediospores will be produced and released in the air for secondary infection (Chen, 2005; Sorensen, 2012). During wheat growth, 2-3 such cycles may happen which is responsible for disease progression and in some cases epiphytotic conditions. The congeniality of climatic conditions, virulence of the pathotypes and resistance of the host will determine the number of reproductive cycles of fungal pathogen and hence disease severity.

Variability in Pathogen Virulence

The mother nature gives mechanisms to all living beings to adapt to changed habitat, natural selection pressures particularly to lower organisms through mutations which are building blocks of variations and recombination can further expand such variations. Yellow rust pathogen, being an obligate parasite, thrives on living host of crop plants and collateral host in off-season mostly weeds. During this phase, the rust causing pathotypes acquire variations. The awareness about the variations in yellow rust races were experienced in early fourtees when the yellow rust races 31,13 and 20 were identified from northern and southern hills. Likewise, race A was identified from Punjab (Gurdaspur) (Bhardwaj, 2011). Since then, about 28 pathotypes are known to occur from India (Bhardwaj et al., 2012). Tracing the variation in rust races revealed that Kalyansona, the first green revolution wheat variety sown in 1967 first time as rust resistant variety became susceptible to yellow rust races 14A, 20A and 38A within a span of three years by 1970 (Sharma et al., 1972). It is presumed that widespread cultivation of two green revolution varieties; Kalyansona (*Yr2*) and Sonalika (*Yr2*) were exposed to new races I, K, N which might have evolved in the region or migrated from other adjacent regions (Nagarajan et al., 1984). Since then, many evidences have been documented to register occurrence of new pathotypes like race L, P-1 and CIII-1 virulent to *Yr9* (Kumar et al., 1994; Nayar et al., 1996). In the same analogy, popular wheat cultivars PBW343 and PBW-373 possessing *Yr27* became susceptible to stripe rust as its resistance was overcome by virulent race 78S84 (Prasher et al., 2007).

Somatic recombination, sexual recombination and mutations during natural reproduction have been suggested as possible mechanisms for emergence of new pathotypes. Genomic diversification of pathogenic races has been attributed to genetic recombination in recent studies. Zheng et al., (2013) reported high levels of genetic recombination which were consequently found in *Pst* population in countries where *Berbery* species are widely distributed, for example, Western China and Central Asia. Variation in yellow rust pathogen should be correctly accessed for effective deployment of resistant genes to develop rust resistant wheat cultivars. It is therefore essential to identify virulent and avirulent races of *P. striiformis* as part of the management strategy of maximizing wheat production. In recent years, emergence of new virulent races of yellow rust have been identified which have caused yellow rust disease; these virulent races are identified as *PstS1, PstS2*, *PstS4*, *PstS5*, *PstS6 PstS7, PstS8*, *PstS9* and *PstS10* (Ali et al., 2017). The characteristic differences between virulence and avirulent race are related to initial inoculum, rate and time of reproduction. In virulent races, the rate as well as time of reproduction is high where as in avirulent strains, initial inoculum may be high but it does not explode due to low reproduction rate. The virulent races cause losses due to the fungal growth on wheat host depriving it for nutrients and water. Moreover, leaf area covered with fungal spores hampers photosynthesis and hence biomass in sink and source affecting grain yield adversely. These diverse races have been identified by differential host methods (Bhardwaj et al., 2012), morpho-pathotypes and molecular markers (Pooja et al., 2019). Molecular markers offer potential approach to tag genes for pathogenicity in pathogen and genes for resistance in plant host.

DNA /gene markers are DNA polypeptides coding for the particular trait like virulence and can be easily accessed for much higher reliable results both about number of genes and type of genes governing virulence in yellow rust pathotypes, with much higher reliability than conventional methods (Aktar-Uz-Zaman et al., 2017). Molecular markers like RFLP, AFLP, RAPD, SSR, SNPs etc. have been used for characterization of virulent pathotypes for yellow rust (Chen, 2005). Randhawa et al., (2019) reported the molecular markers are available to tag various *Yr* genes including *Yr5, Yr9, Yr10, Yr15, Yr18, Yr24, Yr26, Yr28, Yr32-Yr36, YrH52* and *Yrns-B1* as well as gene analog for *Yr17*. According to Wan et al., (2017) a *Pst* is a highly variable pathogen due to its unique attributes including high reproduction rate, ability to disseminate and its adaptation in various environments and to different host species. Liu et al., (2012) and Zheng et al., (2013) opined that sequencing technologies can facilitate to study variation in virulence and evolution of emerging pathotypes in yellow rust. Waqar et al., (2018) suggested that different mechanisms are involved in evolution of new virulent races, of which mutations are most important. In Turkey, the *Pst* named as "Warrior" was reported from RRS, Izmir and CRI, Ankara in 2014. This race became widespread in subsequent years as the resistant varieties in Turkey became susceptible to this *Pst* race (Warrior). Prevalence of Warrior race in high frequency in Morocco and Algeria (Rust Tracker, 2011) as well as North Africa and many European countries was reported by Mert et al., (2016). This new race was grossly different from the previously existing races in Europe and exhibited high diversity in pathogenesis (Hovmøller et al., 2016). Pooja et al., 2018 reported variability for rust infection among 210 RILs, of which 156 RILs showed 0-traces infection, 10 RILs depicted

0-5% infection, 6 RILs showed 5.1-10% infection, 15 RILs showed 10.1-20% infection, 6 RILs showed 20.1- 30% infection, 14 showed 30.1- 40% and 4 RILs showed 60% severity.

Morpho-Pathological Symptoms, Disease Severity and Incidence of Progression

Flor (1964 and 1971) propounded gene-for-gene hypothesis which elaborates that for each resistant gene (R) in host whereas corresponding gene for virulence/ avirulence (vr/avr) in pathogen. This hypothesis warrants a basic compatibility between host for *Yr* genes and pathogen for virulent genes is required for development of disease. In incompatible systems of *Yr* genes offering resistance is not overcome by virulence of pathogenic race and host expresses resistance to yellow rust. The severity as well as pattern of disease also varies depending on *Yr* gene (s) and virulence genes (vr). Some races of pathogen cause enormous number of pustules while in other races the number of pustules is less but the size of pustule is large and yet in other types the number of stripes is more covering major area of leaves. Some races show symptoms on glumes (Marsalis and Goldberg et al., 2016) while the others confined to leaves only.

There are some genes in pathogen which can set infection but not the disease, such genes are known as avirulent races (Surico, 2013). There are some races which lead to hypersensitive reaction in which the host cell immediately dies upon interaction which leads to incompatibility (Higgins et al., 1998; Hysing, 2007).

Plant Resistance to Yellow Rust

Resistance against fungal diseases is generally defined as plants ability to resist invasion by pathogen that includes infection by pathogen, its entry into plant tissues, development of haustoria for driving nutrition and water by pathogen and development of mycelia for further reproduction and uredospore production. This implies that development of disease is less in resistant genotypes possessing *Yr* genes in case of yellow rust than the susceptible genotypes.

Vertical or horizontal resistance or combination of both governs resistance against pathogen in plant host (Vander Plank, 1963; Miedaner, 2016). Vertical resistance is governed by one or more genes which are race specific and the resistance is qualitative meaning either the genotype is resistant or susceptible. Vertical resistance offers resistance against pathogen species-specific or pathogen strain-specific causal organisms whereas it is susceptible against matching races of pathogen. Several workers have reported race specific resistance by *Yr* genes in wheat. Also, it has been observed that low infection rate characterizes vertical resistance (Rajaram et al., 2002). Vertical resistance may be operative during all plant growth stages spanning from seedling to successive plant growth stages and thus may offer holistic durable resistance for some time. It is subjected to boom (resistance) and bust (breakdown of resistance) cycles with the occurrence of new pathotypes either through mutation or recombination (McDonald et al., 2002; Knott, 2008). When differential interaction is absent, it is called as horizontal resistance (Brar, 2015).

Horizontal resistance is governed by polygenes with small to intermediate additive effects. This is also known as race non-specific resistance as HR offers some resistance to all races of the pathogen. Inheritance of HR is usually complex as environmental factors have greater influence on HR than VR (Francisco., 2001). Sometimes the plant host possess both vertical and horizontal resistance combining synergy of both the systems in case of rusts which results in 'slow rusting'. In such a system of slow rusting, disease develop slowly against all pathotypes resulting into low levels of disease over longer period due to longer latent period of pathogen, low initial inoculum as well as low reproduction. Horizontal resistance slows down the disease progression due to smaller spore and uredial size and longer duration for sporulation (Kumar et al., 2015; Ellis et al., 2014).

Johnson (1988) described durable resistance as long lasting which remains effective over a longer period in environments favoring the disease development. This type of resistance is characterized by known race specific resistance operative at seedling and adult plant stages where resistant polygenes are effective additively to determine non-hypersensitive reaction. Race specific partial resistance against pathotypes is offered by some APR genes but offers tangible resistance over longer period. One such example is reported by Mallard et al., (2005) regarding resistance offered by APR genes in bread wheat variety "Camp remy" in France for more than 20 years.

'Vertfolia effect' (Vander Plank, 1963) is a condition where the oligogenes mask the expression of HR genes and/or VR genes are combined with low levels of HR offering low levels of resistance and the strong resistance offered by VR is overcome by virulent pathotypes leading to higher susceptibility of a genotype to rust pathotypes.

Resistance to yellow rust is also named as per the stage of plant at which it is expressed under controlled inoculated experiments. Chen (2005) and Bulli et al., (2016) opined that such resistance against specific races may be operative at seedling as well as Adult Plant stages as per expression of resistant stages. Some researchers like Chen (2005); Jin et al., (2010) and

Wellings (2011) reported that mostly, the seedling and in some cases adult plant resistance is race-specific which are subjected to emergence of new pathotypes due to natural selection pressure in favor of pathogen. In some genotypes, the adult plant resistance remains operative even at higher temperature particularly when plant grow old and progresses towards maturity. (Chen (2005) reported that high temperature adult plant resistance (HTAP) is durable against non-specific races and therefore, durable than seedling resistance, even though HTAP resistance is susceptible to all races of *Pst* at seedling stages.

In monocropping system, high yielding yellow rust resistant wheat varieties are grown over large areas year after year, this situation leads to enormous selection pressure on pathotypes for survival. Due to this reason, the prevailing pathotypes, both avirulent as well as virulent not able to cause disease due to host resistance undergo mutation to develop new pathotypes capable of overcoming host resistance. This determines potential of host resistant genes to offer resistance against race-specific pathogens for a specific period only. Pooja et al., (2019) investigated 210 recombinant inbred lines to conduct diversity and spatial analysis for different *Yr* genes for example 4 *Yr* genes in RILs *Yr7, Yr36, Yr47, Yr53* and 2 *Yr* genes in RILs *Yr18, Yr26* and *Yr7, Yr47* and 1 *Yr* gene in RILs *Yr26, Yr29, Yr26, Yr29, Yr18, Yr36, Yr7, Yr47.*

Genetic Variability for Plant Resistance Against Yellow Rust

Aktar-Uz-Zaman et al., (2017) reported more than 187 rust resistance putative genes were described of which 78 yellow rust resistance genes (*Yr1-Yr78*) were catalogued (This number of *Yr* genes is increasing with intensification of research on yellow rust resistance genes and about 83 yellow rust resistance genes have been described). The acronym '*Yr*' is used to specify strains for specific yellow rust resistance genes. In wheat germplasm these *Yr* genes have been introduced either from primary gene pool, *i.e.*, extant varieties of wheat through recombination or through secondary and tertiary gene pools through introgression. Sharma (2012) found that *Yr9* is linked to *Lr26* offering resistance to leaf rust, *Sr31* offering resistance to stem rust and *Pm8* offering resistance to powdery mildew. likewise *Yr17* was found to be linked to *Lr37* as well as *Sr38* offering resistance to leaf rust and stem rust respectively. Aktar-Uz-Zaman et al., (2017) suggested that *Yr* genes in *Triticum aestivum* were introgressed from its cultivated and wild relative species and genera namely, *T. spelta, T. album*, *T. dicoccoides, T. tauschii, Aegilops comosa, Aegilops ventricosa, Secale cereale* and *Haynaldia villosa.*

Wheat Breeding for Resistance to Yellow Rust

Wheat, being a predominantly self-pollinated hexaploid species have relatives in primary, secondary and tertiary gene pool. On the other hand, genes of interest like yellow rust resistance in present case are scattered over a number of purelines. Keeping in view, the prevalence of virulent pathotypes, a wheat breeder has to deploy yellow rust resistant genes in good agronomic backgrounds for sustainable wheat production. Several breeding techniques like pedigree, back cross, and single seed descent and biotechnological approaches like Marker Assisted Selection in segregating populations through genomic characterization of *Yr* genes and transgenics are effective to achieve tangible improvement in wheat for yellow rust resistance. Therefore, selection of purelines possessing different *Yr* genes is a pre-requisite for recombination breeding. Normally, good agronomic background purelines susceptible to yellow rust are crossed to donors of resistance '*Yr*' genes and then from segregating populations, high yielding stripe rust resistant plants are selected in each segregating generation of self-plants/lines till they become homozygous/pure line to be a new high yielding yellow rust resistant variety.

Disease resistance is mainly governed by one or more oligogenes in case of race-specific resistance. In such cases, gene deployment over space and time of major genes is important strategy to breed high yielding rust resistant variety for different wheat growing regions. Marker Assisted Selection (MAS) could also be effective in breeding yellow rust resistant wheat genotypes (Reema et al., 2019). Sometimes, more number of resistant genes are involved in determining resistance along with a threshold level. Under such situation, gene pyramiding is required approach in conventional plant breeding and accumulation of QTLs in biotechnological approaches.

In horizontal resistance, each gene of polygenic system contributes to rust resistance and sum total of polygenes are thus responsible for expression of yellow rust resistance. Such genes are highly sensitive to environmental effects and therefore exhibit low heritability, the judicious approaches to accumulate polygenes governing resistance through selection over generations in a selfing and selection series experiments in different environments. In view of these peculiarities, following breeding approaches may be explored to develop yellow rust resistant varieties.

Conventional Plant Breeding Methods

Recombination breeding including pedigree method for transgressive segregants and pyramiding

of genes through gene transfer and backcross method for transferring resistance gene only without disturbing genetic architecture of recipient parent as well as for breaking negative linkages. While pedigree method is a progressive method to expand genetic variability, the backcross method is genetically conservative as it allows transfer of donor genes. The conventional breeding includes initial wheat germplasm screening for yellow rust resistance under epiphytotic conditions created artificially followed by selection of resistant genotypes expressing resistant at seedling stage or adult plant stage or both. Such lines are involved in hybridization programme as one of the parents in pedigree, single seed descent and backcross to transfer genes as per breeding objective. Combining grain yield potential and resistance to yellow rust have been developed using these methods. However, the shuttle breeding method may nicely complement these conventional methods to select the potential resistant and high yielding lines in different environments by growing segregating generations in off-season nursery differing in environmental conditions and prevalence of virulent pathotypes of yellow rust. This will enable identification of wheat genotypes resistant to a mixture of yellow rust races across the years and locations. Both the nature of plant resistance against yellow rust (seedling or adult) and mode of inheritance of rust resistance genes (qualitative or quantitative) will determine the breeding strategy to be employed for desired improvement. Pureline selection in pedigree and modified pedigree method, bulk breeding, recurrent selection, single seed descent method and back cross breeding methods have been most sought-after method to develop high yielding yellow rust resistance cultivars. However, in some cases, gene mutations have also paid dividend. Earlier studies provide adequate evidence that these methods were used in red to amber color wheat namely, *Chandausi, White Pissi*, *Sharbati* and *Lal Kanak* in India. A cross between Indian wheat variety Hard Red Calcutta X Common Fife followed by pedigree selection led to the development of famous wheat variety 'Marquis' in 1909 which offered effective resistance against yellow. Marquis, being an early maturing escaped abiotic and biotic stress and become a prominent variety in yellow rust in the region of Western North Dakota (Stoa, 1945). When the major genes govern the yellow rust resistance, usually modified pedigree method is more effective in breeding yellow rust resistance cultivar. Back cross breeding method is more successful either to transfer single dominant gene (dominant and recessive) through crossing back F_1 with recipient parents recurrently followed by selection of homozygous phenotype. In case of resistance governed by recessive alleles, each backcross population needs to be selfed and selection is made in selfed population so that resistant types are phenotypically recognizable. Bulk breeding method is useful in both major and minor genes which are involved in governing yellow rust resistance (Singh and Trethowan, 2007; Singh *et al*., 2014).

Gene Deployment:

In order to ensure a mis-match between *Yr* resistant genes in wheat host and *Pst* effectors in field conditions, it is priori consideration to deploy resistant gene in wheat variety against specific races of yellow rust in different wheat growing regions to develop a mosaic canvass of resistance. Therefore, allocating wheat varieties possessing resistance against specific races in specific region is an effective approach of gene deployment to thwart yellow rust epidemics. In Indian sub-continent, the existence of *Puccinia* path is different in agro-ecological zones. The diversity of prevalence of races for yellow rust pathogen and the genes offering resistance to such races need a coherent strategy to deploy specific gene or gene combination in each agro-ecological zone. Therefore, strategy for the gene deployment would also differ from one region to the other (Nagarajan and Joshi, 1980). Nagarajan et al., (1986) and Bahadur and Nagarajan (1984) have suggested strategy for gene deployment in view of effectiveness of rust resistance genes and distribution of pathotypes and yellow rust races. Bahadur et al., (1985) reported that the deployment of *Yr*9 remain effective against stripe rust for many years which now has been ineffective whereas deployment of *Yr5*, *Yr10* and *Yr15* are still effective collectively or individually against prevailing races of yellow rust. They advocated that gene deployment is an effective strategy to avoid epidemics and hence losses. *Yr5* deployed in Australia (Wellings and McIntosh 1990) and *Yr10* have been defeated by a virulent strain emerged in Canada (Randhawa et al., 2011) but no virulence against *Yr5* was detected in india (Nagarajan et al., 1986). In some instances, unintentional deployment for *Sr* genes also resulted in a deployment of gene complex carrying *Sr57*/*Lr34*/*Yr18* besides other *Sr* genes. Diversity for oligogenes conferring resistance against yellow rust (*Yr*) in any geographical region or even in a wheat field is an effective strategy for resistance breeding in wheat (Simmonds, 1985). McIntosh, (1985) suggested that deployment of overlapping oligo-genes or combination of oligogenes resulted in low severity of rust infection coefficient. It could be pertinent to know as to which *Yr* genes are effective for rust resistance at what stage of plant growth whether it is seedling stage or adult plant stage. The deployment strategy should be judiciously

planned to ensure that at least one or more oligo-genes have been deployed for an effective resistance level at each stage of plant growth to minimize yield losses.

Gene Pyramiding:

In gene pyramiding, the objective is to assemble and reassemble multiple yellow rust resistant genes with additive effects in a certain genetic background of proven agronomic superiority. The care must be taken that all the multiple resistant genes are complementing each other and not antagonizing their effects to prevent breakdown of resistance in host against *Pst* strains under field conditions. Normally gene pyramiding is achieved by pair-wise crosses among various pure lines possessing different *Yr* genes followed by crossing of F_1 obtained from single crosses, double crosses and multiple crosses to pyramid all *Yr* genes in a pure line achieved through selection from segregating population of multiple crosses. However, this approach is time consuming which calls for employing speed breeding techniques (Watson et al., 2018) or growing segregating population in offseason nursery to advance generation. The first gene pyramiding experiments were conducted at CIMMYT where *Yr8* complex providing durable resistance was explored (Singh et al., 2005). Gene pyramiding can involve primary gene pool through intervarietal crosses for transfer of *Yr* genes to different genetic backgrounds or secondary or tertiary gene pool through interspecific and inter-generic crosses for achieving introgression of *Yr* genes present in associated progenitors, wild or cultivated relatives of bread wheat (Aktar-Uz-Zaman et al., 2017). However, it is difficult and time consuming to pyramid unlinked genes *via* crossing without their proper identification and characterization. In fact, linkage of *Yr* genes may create problems associated with 'linkage drag'. Hafeez et al., (2021) reported that incorporation of 12 resistant genes *via* crossing in a single recipient background needed 20 generation. This holds true even in interspecific and intergeneric crosses where the introgressed genes may also carry linked genes with deleterious effects on grain quality for grain size and texture through production of PUROINDOLINE genes and other genes for different rust diseases like *Sr*60 from *T. monococcum* in to bread wheat (Chen et al., 2020). Further, it is tedious to maintain different resistant genes together under selection, in fact some of the genes due to their over-expression may be selected preferably and such genes may be exposed to new pathotypes which can overcome the resistance of such genes. Therefore, it is important to identify natural occurring multigenic resistant varieties to mimic gene cassette for faster gene flow and quick incorporation of resistant genes (Luo et al., 2021). Gene pyramiding approach is not without challenges, though it offers tangible solution for durable resistance. Effects of different *Yr* genes incorporation through linkage drag may create new problems of consumer acceptance which need to be minimized by transfer of single resistant genes through back crosses to break negative linkages and then reassemble *Yr* genes to multiple crosses. Hafeez et al., (2021) has suggested some solutions to tackle such problems by generating R gene atlas for major wheat diseases and genes offering resistance. Corredor Moreno et al., (2021) suggested that gene identification will help in achieving *Yr* resistant genes *vis-à-vis Pst* effectors over different environments to eliminate *Yr* susceptibility increasing genes and eliminate other unwanted genes.

Introgression for yellow rust resistance

Identification and transfer of novel genes from interspecific crosses is also important to thwart the chances of moving and spreading races of yellow rust in wheat growing regions worldwide to cause disease epidemics. Yellow rust resistant wheat lines from inters-generic crosses such as wheat, *wheat-leymus,* rye and *wheat-thinopyrum* have been developed through transferred genetic material in the form of translocations/substitutions (Chen et al., 2020). The incorporation of resistance to yellow rust from associated species and genera growing in different environments also infuse environmental resilience in wheat variety developed in this way.

Multiline varieties:

Multiline varieties are a group of isogenic lines developed by convergence of donor genes in a common genetic background (pureline variety) through backcrossing to different donor varieties for resistance genes. Individual back crosses are needed to transfer one resistant gene each time. Therefore, multiline varieties involved simultaneous backcrossing programme to transfer rust resistant genes from different sources. The multilines are agronomically same except they differ for rust resistant genes. Collectively, these multilines mimic multigenic lines. The advantage of multiline is that various components are showing different pathogen host interaction and if one component line become susceptible to a new pathotype, all other components remain resistant. Therefore, different component lines preclude the possibility of epiphytotic conditions and allows sustainable wheat production. Several researchers have developed multilines like KSML3, (Gill et al., 1980) MLKS 11 and KML 7404 (Rao et al., 1981). There are two approaches for developing multilines, one is known as clean cut approach where dominant race-specific resistant genes are involved in transfer through series of backcrosses, allowing no

disease development till the resistance offered by genes is effective. In dirty approach, the component carrying major and minor genes offering partial resistance are transferred through backcross and in such lines some disease always prevails. Both types have their own advantages and limitations, the first approach multilines are subjected to emergence of new pathotypes and therefore, boom and bust cycle (Priestly, 1978) whereas in dirty approach, possibility of emergence of new races is low.

Biotechnological/Genomic approaches

The conventional plant breeding approaches for developing yellow rust resistant variety are time consuming and sometimes the environmental effects on expression of resistance gene may jeopardize whole hybridization and selection programmes. Moreover, gene transfer from interspecific and intergeneric gene pool is cumbersome and seldom possible. Due to these reasons, use of biotechnological methods called for. The new genomic techniques are more quick, reliable, targeted, independent of environmental effects and offer effective tool for characterizing wheat germplasm for rust resistant genes effective against different pathotypes as well as their transfer to desired wheat genotypes through complementing classical map-based technologies (Adamski et al., 2020).

Pooja, (2018) embarked on use of SSR markers for characterizing parental stocks for polymorphism to identify presence of *Yr* genes (Fig.2).

DNA molecular marker associated with rust resistant genes can be identified through association mapping and thus can be selectively identified in segregating populations of wheat crosses involving susceptible and resistant parents. In this analogy, 'RenSeq' method (Jupe et. al., 2013) for identification of stem rust resistance can also be used for detection of yellow rust resistant genes (Arora et al., 2019). Gardiner et al., (2019) and Walkowiak et al., (2021) reported More technology variants for association mapping such as capture arrays or whole genome sequencing, haplotyping, SNPs and use of reference genome assemblies which can be can be employed for identification of yellow rust resistant gene in wheat. Pooja et al., (2021) identified several *Yr* genes using SSR markers in recombinant inbred lines (F_6) obtained from cross between WH542 (resistant) X WH711 (susceptible) and developed using Single Seed Descent method. SSR markers were effective in deciphering *Yr5, Yr10, Yr13, Yr14Yr15, Yr17, Yr26, Yr28, Yr29, Yr34, YrH52, YrSp, YrSk* and *Yrns-B1* genes conferring resistance against yellow rust. In recombinant inbred lines and thus identified resistant stocks within a population. Likewise, molecular markers are also effective in identifying the *Pst* genome assemblies in pathotypes (Cantu *et al*., 2013; Zheng *et al*., 2013; Schwessinger et al., 2020). These molecular markers tools are effective in tracing pathogen effectors based on pathotype in to varietal interactions (Adams et al., 2021). For example, knowledge about the interactions between R genes (host) and corresponding *Pst* effectors (pathogen) can be precisely recognized to determine the contribution of each component. This will help in designing synthetic R genes which would offer resistance against multiple races of pathogen. Marker assisted selection also effective in allowing selection of *Yr* genes offering resistance and elimination of genes which are non-effective for rust resistance. Based on molecular markers and marker assisted selection, many resistant genes have been cloned and listed (Reema et al., 2019). Pooja et al., (2019) reported that out of 70 SSR markers, only 8 were found polymorphic (*Xgwm46*, *Xgwm95, Xgwm146, Xgwm296, Xgwm302, Xgwm334, Xgwm408, Xgwm68)* on parents and RILs. Out of these, seven *Yr* specific markers *Xgwm130* linked to *Yr7, Xbarc 352* linked to *Yr18, Xgwm 11* linked to *Yr26, Xwmc 44* linked to *Yr29, Xwmc 149* linked to *Yr53, WKS1_I* linked to *Yr36 and Xcfb309* linked to *Yr47* were evident and linked to yellow rust resistance in bread wheat (Table.1).

Therefore, attempt should be made to use disease resistance specific markers to save time, material and cost.

Future Outlook and Conclusion

Cultivation of yellow rust resistant cultivars has been the most commonly adopted strategy to manage successful wheat production globally. However, emergence of new pathogen races necessitates to continuously monitor for shifts in pathogenic races due to mutations on account of selection pressure to develop resistant wheat genotypes which would offer resistance against emerging pathotypes. Several approaches like pedigree, backcross, single seed descent, recurrent selection, gene pyramiding, gene deployment have been used to accumulate yellow rust resistance gene in good agronomic background. Both race specific, host resistant major genes as well as race-nonspecific polygenes have been capitalized to incorporate durable resistance. however, emergence of new pathotypes against race specific host resistance have caused disease problems and even epidemics in many instances world over. This would call for regular monitoring of emergence of new virulent races in the region or migration of virulent races from across the borders of other regions. The incorporation of resistant genes from primary gene pool is easier provided the

genes of interest offering yellow rust resistance are available in diversified varieties. The transfer of genes from allied wild progenitors or genera is cumbersome, yet it is bit feasible through embryo rescue technology followed by chromosome doubling. Many effective rust resistant genes have been transferred this way in to cultivated varieties of wheat. Climate change in relation to new pathotypes possessing virulence under high temperature and low humidity conditions have further cause complexity for developing yellow rust resistant varieties. Climate change is associated with shifts in meteorological parameters and also evolution of new races which are more virulent and can persist in diverse environment.

Breeding for yellow rust resistance in climate change regime requires further strengthening. The germplasm exchange among various countries should be encouraged to expand the genetic variability which would enable selection of potential resistant genes among accessions. In view of climate change, emphasis should be there on selection of high yielding genotypes possessing high level of yellow rust resistance. For that matter, diverse wheat genotypes possessing different *Yr* should be deployed in different agro-ecological zones and development of multigenic resistant varieties through gene pyramiding are promising strategy to increase the durability of resistance. In turn, cultivation of yellow resistant high yielding cultivars would offer more favourable option to the farmers. Both HR (Horizontal Resistance) and VR (Vertical Resistance) resistance genes should be combined to accomplish minimum selection pressure against pathotypes for durable resistance. Also, continuous search for resistant genes in gene pools should be continued and intensified.

The change in climate and consequent emergence of new pathotypes would need to employ biotechnological tools for diagnostics of pathogenic races, resistant gene, interaction between pathogen race and wheat variety using molecular markers. The use of genomics will help in tracing new pathotypes as well as new resistant genes across varieties, species, genera and also the incorporation of resistant genes through marker assisted selection (MAS). Molecular markers will also facilitate speed breeding to cut short time period either in selecting resistant genotype or designing of genes. Biotechnological tools would pay dividend in developing double haploid from high yielding rust resistant crosses to establish homozygous lines in quick succession. Molecular markers can be employed in identifying rust resistant genes from different genera and species for selective transfer as transgenes or through appropriate breeding methods assisted by biotechnological methods.

Finally, it is important to share data about emergence of new virulence globally so that appropriate strategy could be in place to control yellow rust and manage sustainable wheat production through international cooperation research and development.

Figure 1. Yellow rust symptoms in wheat. (Original)

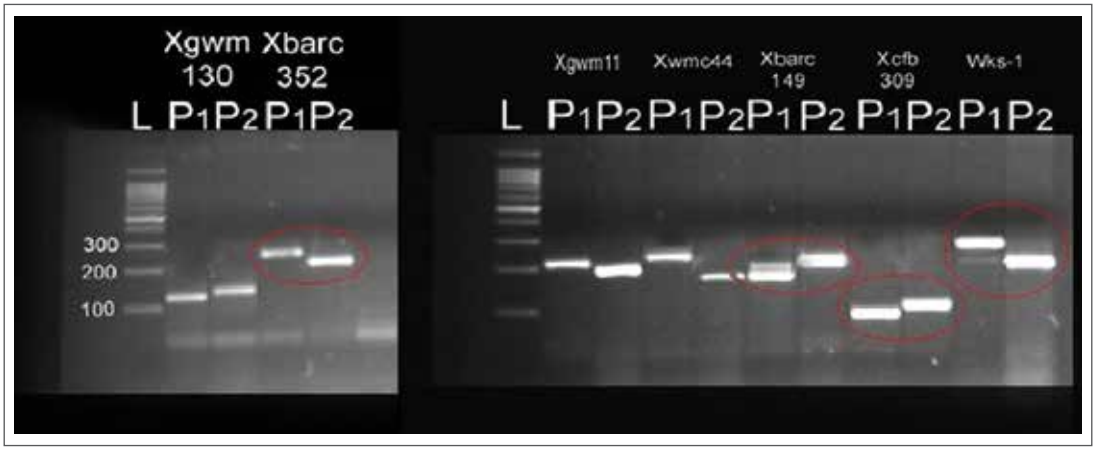

Figure 2. Parental polymorphism for seven *Yr* specific SSRs (Pooja et al., 2019).

Table 1. Identification of *Yr* genes in Recombinant inbred lines of bread wheat .

Recombinant Inbred Lines-210	
60 RILs (6, 8, 9, 10, 13, 17, 22, 26, 28, 30, 31, 32, 33, 35, 38, 43, 45, 48, 54, 56, 62, 65, 70, 71, 72, 75, 76, 79, 85, 89, 91, 92, 94, 103, 107, 110, 112, 113,114, 118, 119, 120, 123, 126, 128, 134, 140, 141, 170, 171, 180, 183, 190, 191, 195, 196, 198, 201, 207, 208)	RILs with 1 *Yr* gene
25 RILs (3, 7, 12, 15, 18, 19, 24, 25, 27, 40, 46, 63, 64, 66, 67, 73, 74, 82, 93, 115, 117, 121, 124, 133, 135)	RILs with 2 *Yr* gene
6 RILs (20, 21, 23, 29, 39, 53)	RILs with 3 *Yr* gene
3 RILs (51, 52, 55)	RILs with 4 *Yr* gene

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Development of Onion Hybrids using Cytoplasmic Genetic Male Sterility**

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ABSTRACT

Onion (*Allium cepa*) is an important vegetable/spice crop worldwide. It is an open pollinated crop; therefore, development of onion hybrids is most sought out option to boost onion productivity. Use of cytoplasmic genetic male sterility (CGMS) is most pragmatic method ofonion hybrid development. This includes use of three lines, *i.e.,* cytoplasmic male sterile line (A), its isogenic fertile maintainer line (B) and fertility restorer line (R). The conventional method of hybrid development is less efficient as compared to molecular marker assisted methods for identification of S, T, N cytoplasm, maintainer lines and fertility restorer genes with high heterosis. Various molecular marker systems have been established for commercial hybrid seed production. This review examines the development and identification of male sterile and its maintainer lines as well as restorer lines for hybrid seed production using conventional and molecular marker assisted methods.

Keywords**:** *Allium cepa*, hybrids, cytoplasmic genetic male sterility, molecular marker, restorer lines

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Introduction

Onion is one of the most important vegetable/spice crop worldwide used in vegetarian and non-vegetarian culinary. There are different types of onion depending on shape, size and colour. Onion is rich in fibre, Vitamin E, mineral matter and bioactive compounds and antioxidant properties (Ren and Zhou, 2021). Onion originated in Central Asia, Near- East and Mediterranean regions is a diploid species (2n = 16), belonging to family Alliaceae (Vavilov, 1951). Onion is grown mainly in countries of Asia, Middle east, Europe and North America. Onion is also an important vegetable crop in Eurasia including Turkey, Tajikistan, Kyrgyzstan and Uzbekistan. The major onion producing states in India are Maharashtra, Karnataka, Madhya Pradesh, Gujarat, Bihar, Andhra Pradesh, Rajasthan, Haryana, and Tamil Nadu. In India it is grown over 16.24 million hectare area with production 26.6 million tonnes and productivity 1.64 mt/ha in 2020-21(Agricultural Statistics at a Glance 2021).

Onion is a cross pollinated crop. In such crop, heterozygosity *per se* has to be maintained for better performance as selfing will lead to inbreeding depression and decreased performance. Therefore, the germplasm in onion is available in the form of open pollinated population and hybrids. Onion hybrids are known for their higher bulb yield potential as well as bulb quality. Flower of onion is perfect and tiny with 6 stamens and many flowers are arranged in umbel shaped inflorescence. Heterosis has been commercially exploited in onion since male sterility is available. The male sterility was reported in this crop long back in 1936 (cf Sidhu et al*.,* 2005). Honeybees are used for necessary transfer of pollen from male parent to female parent (Sidhu et al*.,* 2005). In conventional onion breeding, hand emasculation of onion flowers by removal of stamens is inefficient, time consuming,

labour intensive and costly proposition posing strong restriction on development of hybrid seeds to meet the demands of onion growers. Therefore, male sterility systems in onion are called for development of onion hybrids in an efficient manner. There are two strong possibility of male sterility system in onion: **1) Genetic male sterility-** This kind of male sterility is governed by dominant nuclear genes (Liu et al., 2019), which would segregate in cross population producing male fertile and male sterile plants. In such systems, male fertile plants need to be rouged out to develop onion hybrids using male sterile plant in the population. Rouging of male fertile plants essentially need markers, which are stable distinct and conspicuous to facilitate identification of male fertile plants before flowering. Due to this restriction genetic male sterility is hardly used in commercial onion hybrid seed production.

The 2nd option is based on cytoplasmic genetic male sterility systems which involve three lines *i.e.* cytoplasmic male sterile lines (A line), itsisogenic maintainer line (B line) and fertility restorer line (R line) yielding maximum heterosis/hybrid vigour in F_1 generation of crosses. This is most commonly used method for production of onion hybrid seeds. The future scope of commercial onion hybrids needs to be focused comprehensively for the identification of male sterile lines from onion open pollinated population by utilizing modern biotechnological tools. Molecular markers distinguishing sterile/fertile cytoplasm (N, S, T) linked to restorer (Rf) of male sterility locus (*Ms*) are important. Release of commercial hybrids from public/private sector would play a great role for breaking yield barriers and significant enhancement of productivity of onion under changing climate scenario and to meet increasing domestic demand (Singh and Khar, 2021). This review paper examines the important aspects of cytoplasmic male sterility system, procedure for development of onion hybrid and production of hybrid seeds using conventional and molecular marker assisted methods.

Cytoplasmic-Genetic Male Sterility System:

Male sterility is defined as a conditions of the flower where the anthers' are either missing or the pollen grains are non viable. Therefore, self pollination in complete male sterile lines is ruled out. Sidhu et al., (2005) reviewed male sterility in onion. According tothem it was discovered as early as1925 from Italian Red-13- 53, the causes of male sterility in this selection were investigated in 1926 and the use of male sterility systems for hybrid seed production were reported in 1943. Davis (1957) accounted the distribution of male sterility gene in different onion varieties. Banga and Petiet (1958) pointed that Dutch cms-T line had been isolated as point mutation from the line containing N-cytoplasm. Peterson (1970) utilized cytoplasmic male sterility (CMS) in the development of hybrid onion and suggested that recycling of selected onion inbreds' and selection for combining ability and quality be undertaken early. He isolated an open-pollinated single plant progeny with 21% higher yield than original cultivar. Gikalo (1972) noted morphological differences in umbels and flowers of normal and male sterile plants. He described a method of overcoming inbreeding depression in normal and male-sterile inbreds' by pollination with self-pollen from normal plants of same variety and multiplied them further.

Kazakova and Yakovlev (1973) developed 20 male sterile lines and 98 hybrid combinations with male sterile line Oriental S57, Oriental S61, Golden Globe S1 Valencia S1, Bessonovka S36 and Poyar, which exhibited heterosis for earliness, storage quality and yield of marketable quality onion. Dyki (1973) studied CMS in onion varieties Wolska and Rawska and noted abnormalities in male-sterile plants as withered stamens couples with long pistils, glossy looking green anther containing only watery fluid. Microscopic investigation confirmed 100% male sterility in lines. In fertile hard, brown anther supported on normal filaments produced fertile pollen grains. Holford et al., (1991a; b) observed difference in both chloroplast and mitochondrial genomes of N and S cytoplasm. However, no differences were detected in organellar genomes of N and cms-T onions suggesting different auto- and allo-plasmic origins of cms-T and cms S cytoplasms. Havey (1993) reported five polymorphisms between S sterile and N fertile cytoplasms where former was different form *Allium* species closely related to bulb onion. Havey (2000, 2004) studied diversity among CMS that provides an expedient mechanism to produce large population of male sterile plants for commercial F_1 hybrid seed production.

Melo and Boiteux (2001) attempted molecular identification of male-sterile line (line A) and maintainer (line B) but found only fertile cytoplasm in the Alfa Tropical population (Leite, 1999). However, lines A and B within the BaiaPeriforme derived onion population, Alfa Sao Francisco, based on a PCR marker system monitoring cytoplasm type, and by random field pairing of fertile plants with selected sterile plants, appeared important to develop tropical onion hybrid well-adapted to Brazilian low latitudes.

Yamashita and Tashiro (2004) developed male-sterile lines of Japanese bunching onion (*A. fistulosum*) possessing the cytoplasm of wild species, *A. galanthum*, by backcrossing. Yamashita et al., (2005) confirmed that the fertility-restoring gene (Rf) for

cytoplasmic male-sterility (CMS) in *A. fistulosum* from segregation of pollen fertility of backcross generation of *A. galanthum* is located on the 5F chromosome of the male fertile plants.

Work on hybrid seed production of onion using cytoplasmic male sterility was examined and the problem of protecting lines from genetic contamination and maintaining their high values for useful characters was described Khaisin (1988). Pathak and Gowda (1994) inferred that one of the main components for the exploitation of heterosis was the availability of male sterility. Indigenous male sterility was found in *cv.* Nasik white globe at Bangalore, having strong cytoplasmic factor for male sterility. It was successfully transferred to six different genotypes which were used to exploit heterosis. From 75 test crosses evaluated for bulb yield and quality, two were promising, Hybrids (Ms 65 x Sel.13) and hybrid–5 (MS-48 X Sel.14) for commercial use, with high bulb yields (45-50t/ha) and good quality bulbs. Pathak (1997) identified a second source of cytoplasmic male sterility (T-cytoplasm) with complex inheritance which was different form Jones's line with three independent segregating restorers. Havey (2006) reported two different sources of CMS (S and T cytoplasms). Test crosses of N-cytoplasmic maintaining and restoring genotypes to S and T cytoplasmic lines demonstrated that different alleles, or loci, restore male fertility for these two male-sterile cytoplasms. Other sources of CMS have been used or reported in Europe, Japan and India, and their relationships to S and T cytoplasms are still not clear. Restriction fragment length polymorphisms were identified in the organellar genomes among commercially used male-sterile cytoplasms from Holland, Japan and India, and were compared to S and T cytoplasms. Mitochondrial DNA diversity among 58 non-S-cytoplasmic open pollinated onion populations was also assessed. All five putative CMS lines selected from the Indian population Nasik White Globe were identical to S cytoplasm for all polymorphisms in the chloroplast genome, and always possessed the same-sized mitochondrial fragments as S cytoplasm. T cytoplasm, the male-sterile cytoplasm used to produce the Dutch hybrid Hygro F_1, and two sources of CMS from Japan, were similar and showed numbers of mitochondrial polymorphisms similar to those observed among the 58 non-S-cytoplasmic open-pollinated populations. This research demonstrated that the same, or very similar, male-sterile cytoplasms have been independently isolated and exploited for hybrid-seed production in onion.

Haishan et al., (2006) reviewed characterization and utilization of the S and T types of male sterile cytoplasm of onion. Netrapal et al., (1986) screened large number of onion lines to isolate the male sterile lines from a popular short day variety 'Pusa Red'. The maintainer lines were developed by backcrossing. Sharma (2018) reported isolation and identification of male sterile line from variety Hisar onion 2. He reported two methods for identification and validation of male sterility which included the touching sense of onion flowers at full bloom. The male sterile plants were oppressed as the anthers' were shrunken being devoid of pollen grains. The second method was based on pollen staining with acetocarmine stain and the stained pollen grains were observed under microscope. The flowers giving pink coloured pollen grain were considered to be male fertile and non-coloured hayeline pollen grains were non-fertile. Sharma (2022) reported 8 male sterile lines isolated from Hisar onion 2 and used these lines to produce F_1 hybrids.

Molecular basis of Cytoplasmic-Genetic Male Sterility System:

Cytoplasmic Genetic Male Sterility is governed by genetic mechanisms, which are influenced by the environment for its final expression. The ambiguity caused by environmental factors may sometimes jeopardise the whole effort of developing onion hybrids based on male sterility. Therefore, it is essential to target genetic mechanisms determining male sterility then the phenotypic expression for precision and efficiency.

Three commercially used sources of onion CMS can be distinguished by markers in the cp and mt DNAs. S and R cytoplasms which were commonly used sources of onion CMS; T cytoplasm as described by Berninger (1965) were rarely used commercially. N and T cytoplasms could be distinguished by mitochondrial polymorphisms cob and orfA501 developed by Engelke et al., (2003). Cho et al., (2005) selected N- cytoplasm plants using sequence characterized amplified region (SCAR) marker from 'Manchuhwang' (open-pollinated cultivar). Selected N-cytoplasm plants were crossed with male sterile inbred line (W202A, Wisconsin Univ., USA). A total of 66 crosses were accomplished, and 34 crosses could be analysed for the nuclear restore allele. Among 34 combinations, the offspring's of one combination showed all male sterility and this line was selected as the maintainer line in the 'Manchuhwang'

Kim et al., (2007) applied the PCR-marker (orfA-501) to identify the cytoplasmic genotypes of collected 100 accessions of bulb onion. Among accessions, S-cytoplasm was found in 57 accessions. Nineteen accessions possessed only N-cytoplasm and twenty

four accessions possessed both S- and N-cytoplasm. Two sets of cytoplasmic male sterile lines from two different onion cultivars (*Allium cepa* L.), were investigated by molecular method, and discussed about their polymorphisms with corresponding maintainers. The results showed that the cytoplasms of male sterile lines originated from 'ShagouHongpi' and 'ShuozhouZipi' were T and S, respectively. RAPD amplification showed that the S cytoplasm had more polymorphism than T cytoplasm compared to their maintainer lines (Jingfan, 2009).

R cytoplasm could be distinguished from the other cytoplasms by the presence of both 628- and 833-bp amplicons of mitochondrial orf725 (Kim et al*.,* 2009a). S cytoplasm could be distinguished from N, R, and T cytoplasms by chloroplast markers (as reviewed by Kim et al., 2015b). With these cytoplasmic markers, onion breeders should be able to confidently determine cytoplasms in commercial use. Although they did not score male fertility *vs.*sterility across the onion inbreds used in their study, genotypes at *Ms* as predicted by the AcPMS1 marker (Kim et al*.,* 2015a) were consistent with previous reports of male-fertility restoration by dominant allele(s) at the *Ms*locus for S and R cytoplasms Kim (2014), both of which produce the orf725 amplicon.

Ferreira et al., (2017) used molecular marker to identify the cytoplasmic types and the genotyping for the fertility restoration nuclear locus (*Ms*) in 59 onion accessions, aiming at the selection of 'A' and 'B' lines. Three markers were used to identify the cytoplasm 5' *cob*, *orf*A501, and *orf*725, and two were used for the *Ms* locus (AcSKP1 and AcPMS1). The two types of male-sterile cytoplasm ('S' and 'T'), as well as fertile cytoplasm ('N'), and the *Ms* and *ms* alleles in both homozygosity and heterozygosity were detected in the 59 genotypes. The frequencies of the 5' *cob*/*orf*A501 and *orf*725 markers, as well as of the markers AcSKP1 and AcPMS1, were close in the onion accessions. In the Brazilian germplasm, the frequencies of the 'N', 'S', and 'T' cytoplasm were approximately 0.47, 0.28 and 0.25, respectively, whereas the allele frequencies of *Ms* and *ms* were 0.52 and 0.48, respectively.

Identification of male sterile lines through conventional methods require 4-8 years of progeny testing before the cytoplasm type can be determined. Gazendam et al., (2018) analyzed five cytoplasmic (5'cob, orfA501, orf725, IGS and cob-type 2) and four nuclear markers (jnurF13, isotig34671_610, isotig30856_1351 and isotig29186_1830). Real-time polymerase chain reaction (PCR) was performed with custom TaqMan® SNP genotyping assays containing primer/probe pairs designed to detect single nucleotide polymorphisms (SNPs) linked to the nuclear *Ms* locus. OrfA501 proved useful as a presence/absence marker for cytoplasmic male sterility, while TaqMan® SNP genotyping assays were superior to the jnurF13 nuclear marker in terms of rapid throughput. PCR molecular markers and custom TaqMan® SNP genotyping assays were efficient in screening the onion lines rapidly and accurately for their cytoplasmic and nuclear male sterility genotype. These methods reduced the time to identify the correct genotype of male sterile and maintainer lines and also gave accurate information for larger scale use.

Numerous studies have documented polymorphisms in the organellar DNAs differentiating S and T cytoplasms from the normal male-fertile cytoplasm of onion. There may be additional source(s) of onion CMS that had been described as "T-like" and appear to bemore similar to N and T cytoplasms than S cytoplasm. He also evaluated commercial identities of onion breeding lines using, molecular markers distinguishing sources of onion CMS. He reported that bona fide T cytoplasm is rarely used commercially to produce hybrid-onion seed, and both S cytoplasm and "T-like" cytoplasm were widely used. Dehghani et al*.,* (2021) evaluated the effectiveness of marker-assisted selection (MAS) in identification of the cytoplasmic types and male sterility (*Ms*) locus in 123 onion accessions. Three cytoplasmic markers cob, accD and MK were used to identify the sterility (S) from the fertility (N) cytoplasm and four nuclear molecular markers (OPT, PsaO, Jnurf-13 and AcSKP1) were used for genotyping of *Ms* alleles. The results showed that the two accD and cob markers were quite similar in the detection of the type of cytoplasm with 100% male sterility for male sterile lines and 100% fertility for maintainer lines. Also, the MK marker was able to distinguish T-type cytoplasm. The frequency of fertile (N) was much more than the frequency of sterile (S and T) cytoplasm found to be 90% in Dorche (pop.1), 100% in Dorche (pop.2) and Kashan based on marker cob and accD. With MK marker, it was found to be 80, 90 and 82% in Dorche (pop.1), Dorche (pop.2) and Kashan, respectively. Molecular markers were very suitable for the identification of S or N lines. Cytotype (N/S) determination of plants by using molecular markers (cob, accD and MK) and it could reduce the population size required for the production of onion hybrid seeds.

A process for identification of specific onion cytotypes was recently proposed by Havey and Kim (2021). They replaced the orfA501 marker (Engelke et al., 2003) with a new molecular marker, orf219, to improve the robustness of onion cytotype screening. The orfA501 marker is a dominant marker whose

genotypes are determined based on the presence or absence of PCR products. Kim et al., (2009b) reported that CMS-R and CM-S were widely used in onion hybrid breeding in Korea. In contrast, only two Korean breeding lines possessing CMS-T cytotype were identified. In the case of CMS-Y, only two accessions (PI273626 and PI236025) were shown to contain this cytotype. Progenies is derived from PI273626 showed unstable male sterility when this cytoplasm was combined with a dominant *Ms2* allele (Kim et al., 2019; Yu and Kim, 2021), breeding materials containing the CMS-Y cytotype may not be suitable for hybrid breeding. The CMS-T cytotype was identified in a limited number of accessions, which were mostly introduced from European countries Likewise, the CMS-T cytotype was identified from a single breeding line in a previous study (Havey and Kim, 2021), indicating that the CMS-T cytotype is rarely used in hybrid breeding. Given that inheritance of fertility restoration of CMS-T cytotype is relatively complicated, breeding materials containing this cytotype may be undesirable in hybrid breeding programs. The improved process developed in this study can be used to identify accessions containing CMS-T cytotypes. In contrast, male sterility conferred by CMS-S and CMS-R can be restored by a dominant allele at a single nuclear locus, Ms (Jones and Clarke, 1943; Kim, 2014), and molecular markers tightly linked to the Ms locus have been developed (Kim et al., 2015a; Kim and Kim, 2019). Therefore, breeding lines containing either CMS-S or CMS-R may be most beneficial for efficient development of hybrid onions.

Heterosis

The term heterosis was first coined by Shull (1914) as the developmental stimulus resulting from the union of different gametes, whereas, hybrid vigour referred to the manifest effect of heterosis (Whaley, 1944). Singh, 2021 has extensively reviewed the various aspects of heterosis including genetic mechanisms, dominance and super dominance theory of heterosis, heterozygosity advantage, hybrid vigour, prediction of heterosis in hybrids and inbreeding depression.

Kozlova (1963) noticed considerable increase in yield of some F_1 hybrids; out of 11 hybrids tested, yield increases ranged from 71 to 158 per cent over the female parent and 53 to 153 per cent over the pollen parent. Out of the 85 F_1 hybrids studied by Poljanstrij (1963) only three produced heterosis for yield. The F_1 hybrids from inter varietal yellow x purple crosses were intermediate in dry matter content, monosaccharides, polysaccharides and the ratio between disaccharides and monosaccharide's. The results of observation by Orlova (1969) revealed that among 60 F_1 hybrids, 22 exceeded the better parent, 10 were worse than both the parents and 28 were intermediate for yield. The most hybrid combinations were more vigorous and had larger number of leaves than the parents. Heterosis for dry matter content and sugars exceeded the better parent in two out of three F_1 hybrids studied by Genejdi (1970). Out of the 28 F_1 hybrids evaluated by Doruchowski (1971), four exceeded the Polish cultivars Wolska and Rawaska and the American hybrid Elite significantly in the yield of marketable bulbs by up to 40 per cent. Dry matter content was highest in hybrid with the highest yields, which gave 410.7 q/ha of marketable bulbs with 13.73 per cent dry matter. The F_1 hybrids also proved superiorin respect of yield, bulb size, plant survival, earliness, uniformity and yield of soluble dry matter in the direct seeded crop (Andrasfalvy, 1971). Total soluble solid is an important quality attribute of onion genotypes with high solids store better. McCollum (1968) and Padda et al., (1973) obtained high heterosis for total soluble solids in onions.

Joshi and Tandon (1976) showed a wide range of heterotic values for bulb yield (ranging from -22.1 to 72.3 percent over the average of the parents and from -42.8 to 36.7 percent over better parent) in crosses of four male sterile lines with five selections.

Hosfield et al., (1977) observed significant heterosis for bulb weight over mid parent. However, the heterosis over better parent was significant, but comparatively low. The work of Ershov and Vorobeva (1979) revealed that the F_1 hybrids using a cytoplasmic male sterile parent out yielded the standard by up to 55 per cent in ware (total) yields and by up to 109 per cent in the marketable yields. They further noted that the male sterile line 1 x 8 derived from Mstera, when used in the F_1 hybrid production, resulted in heterotic effect of 164 to 173 per cent regardless of pollinators used. Pandian and Muthukrishnan (1979) recorded heterosis for plant height, number of leaver, bulb weight, dry matter and total soluble solids, especially in crosses C8 856-8 x CO 1 and C8 665-51 x CO 1 of aggregation onion (*Allium cepa* L. var. *aggregation* Don.). In a diallel cross of onion at Indian Agricultural Research Institute, New Delhi, Netrapal (1980) reported up to 28.8 per cent of heterosis for yield over best parent. He also found that these F_1 hybrids were also superior for processing and storage qualities. Vadivel et al., (1981) observed fourteen hybrids over the mid parent and twelve hybrids over the better parent heterosis for plant height and high heterosis for bulb weight in onion.

Vadivel et al., (1982) evaluated 30 hybrids and their parents. The results showed both positive and negative heterosis for bulb weight, whereas, one cross recorded significant heterosis for yield and yield components.

Doruchowsk (1986) crossed eight male sterile lines with 8 pollen parents and heterosis was observed for bulb weight only. Madalagiri (1983) recorded significant positive heterosis over mid parent in six crosses and two crosses have exceeded their better parental value in a 9 × 9 diallel analysis for number of leaves and negative significance for TSS. Netrapal et al., (1988) observed only one hybrid with heterosis over both the better and best parent out of 29 crosses.

Aghora (1985) reported that study on heterosis using 20 lines and 3 male sterile lines as testers. Heterosis over the best parent was observed for all the characters except dry weight of leaves. Thirty five hybrids were heterobeltiotic for total bulb yield with highest heterosis of 89.56 per cent in the cross MS 39 x IHR 78. Positive heterosis was observed in nine hybrid over better parent for total bulb yield and it ranged from 47.9 to 89.5 per cent while heterosis over best parent for marketable bulb was over 35 per cent in three hybrid *viz*., MS-1 x NEK-1, MS-1 x IIHR-21-1 and MS-8 x IIHR-52-1(Pathak et al., 1987). Netrapal and Singh (1986) through a diallel analysis, recommended heterosis breeding for improvement of number of leaves, plant height, bulb-yield, bulb weight, bulb diameter (both polar and equatorial) and maturity.

Netrapal (1988) observed significant heterosis over better parent for number of leaves, plant height, maturity, yield, bulb weight, bulb diameter (horizontal and vertical), total insoluble solids, total soluble solids, total solids, drying ratio, pyruvic acid, reducing sugar, total sugars, non-reducing sugar and storage losses. Number of leaves, plant height, yield, bulb weight, bulb diameter, total soluble solids and storage losses showed heterosis over the best parent. Netrapal et al., (1988) reported that heterosis for plant height in 30 hybrids significantly exceeded the better parent, 18 exceeded the top parent and 44 exceeded the standard control. However, 8 hybrids were significantly superior to the better parent and 11 to the standard control. Gowda (1988) concluded that the extent of heterosis estimated over mid, better and best parents revealed superiority of some outstanding F_1 hybrids over best parent; for equatorial and polar diameter of the bulb. There were 16 crosses that exceed in heterotic effects over best parent for dry weight of the bulb.

Kumar and Dhaliwal (1990) described heterosis over mid and better parent value as well as standard check variety. Aghora and Pathak (1991) reported significant positive heterosis for number of leaves over mid parent in five crosses, whereas only one F_1 recorded significant positive heterosis over the better parent.

Sayed et al., (1999) evaluated the parents and F_1 hybrids from half diallel cross of onion for earliness, bulb ratio (neck diameter or bulb diameter), number of leaves per plant and bulb height. They observed highly significant additive and non-additive gene effects, which were involved in the inheritance of all the characters. Divakar (2001) reported positive heterosis in 12 crosses for total soluble solid over better parent and 10 crosses exhibited heterosis over standard check. Shashikanth et al., (2007) reported appreciable amount of heterobeltiosis and standard heterosis for marketable bulb yield. Satyanarayan (2014) reported heterosis for plant height, number of leaves, bulb weight, total bulb yield, bulb diameter (polar and equatorial) and TSS.

Sharma (2018) made a series of crosses between male sterile and restorer lines and found that the extent of heterosis over mid and better parent was variable from cross to cross and hybrid to hybrid. Sharma (2022) reported that the cross MS 35 x Hisar- 3, MS 37 x Hisar-3, MS 22 x Agrifound Dark Red, MS 40 x Pusa Red and MS 21 x Pusa Red exhibited high SCA as well as heterosis, hence, these crosses can be utilized for breeding heterotic hybrids.

Development of onion hybrids using CMS

1) Conventional methods

Sharma (2018, 2022) out lined the procedure for developing onion hybrids in field condition of Northern India. The development of hybrid involved mainly three phases, *i.e.,* selfing of open pollinated population to develop both cytoplasmic male sterile line and their maintainer as well as potential restorer lines to develop F_1 hybrids through crossing. These are detailed below:

Selfing: Selfing in onion is done only on a limited scale as it becomes difficult to maintain the inbred lines beyond S_2 generation due to drastic inbreeding depression. Selfing is done by putting individual cages over the plants. Flies were used to ensure pollination within cages. 2-3 umbels of the same plant were caged muslin cloth bag before anthesis. After anthesis, the umbels were rubbed against each other daily for a few days to ensure self-pollination.

Crossing: As soon as few buds in an umbel opened, the whole umbel of the female parent was bagged with muslin cloth bag. The opened flowers were removed daily for a few days to avoid selfing. The emasculated buds were retained for crossing. The umbel of pollen parent covered with muslin cloth bagswere cut off and its stalk were placed in a glass bottle filled with water and fastened to a bamboo/ wooden stake fixed in soil close to the female parent. Female parent umbel (emasculated one) and the pollen parent umbels are now enclosed in to each of the same common bag. Within a few days in the morning, male

umbel was gently rubbed over the emasculated umbel to ensure pollen shedding and cross pollination.

Use of male sterility:

The variety used for selecting male sterile line was Hisar Onion 2. Hisar Onion 3, Pusa Red, and Agri-found Dark Red used as tester line for hybrid development. Selfing and inter crossing activities were carried out in seed to seed planted crop following Jones and Mann (1963). The procedure of development of onion hybrid seed included following steps:

A. Isolation and maintenance of male-sterile line

1. Screening for male sterile plant in Onion Hisar-2 variety was planted in one acre area. Screening was done through morphologicalexamination with hand touching method.
2. Plants were categorized based on presence/ absence of pollen for occurrence of male sterility.
3. Pollen viability of twenty sampled male fertile plants were accounted under microscope with the help of acetocarmine 0.5% solution. Viable/fertile pollen showed pink colour and vigorous.
4. Pollen sterility of identified male sterile plant was accounted and confirmed under microscope with the help of acetocarmine solution 0.5% solution. Sterile pollen showed colourless and shrinked.
5. Flower umbels of selected *MS* (male sterile) plants were paired tied with umbels from fertile pollen donor plants.

i. 60 male sterile plant was isolated from Onion Hisar-2 and these male sterile plant pair tied with fertile (pollen donor) plants.

ii. All possible crosses (95 crosses) made with sterile and fertile plant.

6. Flower umbels of *MS* plants were paired tied with umbels of male fertile for hybrid development.
7. Basal ends of pair tied fertile umbels were placed in water filled bottles with close to *MS* plants.
8. Pair tied umbels, protected by muslin cloth bags, were shaked each morning for pollination.
9. Umbel spikes of fertile pollinator plants were covered in netted cages or muslin cloth bags for self-seed production.
10. Seed from male sterile and male fertile plants were harvested separately for next planting.

B. Identification and maintenance of maintainer line

1. Plant progenies raised from seed harvested in previous year were screened to confirm male sterility. F_1 progenies and their pollen parent raised separately in nursery during last week of July and seedling are transplanted in October with spacing of 45 x 45 cm row to row and plant to plant distance. Pollen donor parent transplanted in pair with their progenies and the recommended package of practices was followed to raise a healthy crop. During initiation of bolting plants were covered with netted cages or muslin cloth bags. At the time of dehiscence each plant was morphologically scored for sterile check and fertile status on the basis of pollen present in the anther by hand touching. Plant showing the presence of greenish yellow or yellowish brown or yellow pollen were designated as fertile and those without pollen as male sterile. After that, pollen sterility was accounted and confirmed under microscope with the help of acetocarmine solution.
2. Plant progenies were categorized based on proportion of male sterile and fertile segregants. Among 95 crosses only 8 crosses (MS20 x pollinator 5, MS21 x pollinator 5, MS22 x pollinator 5, MS23 x pollinator 5, MS34 x pollinator 11, MS35 x pollinator 11, MS37 x pollinator 11, MS40 x pollinator 11) showed 100% sterile plant.
3. Pollen donating plants showing cross progenies as 100% sterile were marked as maintainers.
4. Seed of maintainer, fertility restorer and parental line of hybrids were taken separately and saved.

Mohsin et al., (2016) in a field experiment identified one cytoplasmic genetic male sterile line (Smsms) and two fertile lines as maintainer lines (Nmsms). These two crossed materials namely 004 (Shallot x Red creole) and 008 (Shallot x Red pinoy) produced 100 per cent male sterile progeny infull sib and backcross generations. The Shallot x Taherpuri/ Suksagor and Shallot x Hazera-202/Hazera-203 cultivar produced both male fertile and male sterile segregating progenies. It indicated that these materials areprobably determined by dominant and recessive independently acting genes, which was resulting the genetically impure lines. All other crossed materials produced 100 per cent male fertile progeny upon crossing with shallot. Thus, the materials Red creole and Red pinoy could be used as maintainer line for "Shallot". The performance of 904 F_1 and 905 F_1 hybrids over check (Taherpuri) and better parent was found to be preferably better using these CMS system. They also outlined procedure for developing onion hybrids in field conditions which is detailed below in Figure 1.

2) Development of onion hybrids using molecular marker assisted selection for CMS, maintainer and restorer lines

Now a day molecular marker facilitated methods for identification of cytoplasmic male sterile lines (A line, CMS), their maintainer lines (B line) and fertility restorer line (R line) to be involved in crossing programmes to developed commercial onion hybrid (F_1) seeds.

Manjunathagowda (2021), reviewed use of molecular markers for identification of male sterile line, maintainer lines (N smsm) and homozygous fertility restorer line (NMsMs) as well as male sterile line (S msms) from various populations. He demonstrated use of cytochrome-b(cob) protein mitochondrial DNA marker as well asphenotypic examination to validate isolation of male-sterileand maintainer lines from open pollinated population. Malik et al., (2017) reported that the frequencies of male-sterile plants (Smsms) were 0.015 in Punjab Naroya, 0.020 in Punjab Selection and 0.006 in Punjab White. Whereas frequencies for the male sterility maintainer plants (Nmsms) were 0.133 in Punjab Naroya, 0.231 in Punjab Selection and 0.182 in Punjab. These frequencies were determined using cob marker. Ferreira et al., (2017) determined in Brazilian onion germplasm, frequencies of CMS-S, CMS-T and N cytoplasms which were found to be 0.47, 0.28 and 0.25 whereas, the Ms and ms allele frequencies were 0.52 and 0.48, respectively, using cob, orfA501 and orf725 genes-specific markers, and Ms/ms allelic markers of AcSKP1 and AcPMS1 genes for MAS. The frequency of male-sterile plants ranged from 0.77 to 0.80 across the open-pollinated populations, the significant number of male-sterile lines was noted in the genotypes COHBONC03 (6.5%), COHBONC05 (8.5%), COHBONC17 (4.0%) and COHBONC25 (5.5%) and thus identified male-sterile plants were confirmed by orf725 gene molecular marker (Manjunathagowda and Anjanappa, 2020).

Ahmad et al., (2020) identified the fertility-restorer locus (Ms) using two sets of nuclear markers (novel chimeric gene, orf725 gene (N/S) MK marker) and SCAR markers (FN1, RN1, F3S2 and R3S2) for Ms and ms allelic plants among the open-pollinated varieties (OPVs). It was found that, 70% of OPVs have male-sterile cytoplasm with recessive alleles at restorer-of- fertility (Ms) locus are male sterile (A-line), and nearly 20% of plants with normal (N) cytoplasm have recessive alleles (ms) at Ms locus (male sterility maintainer, B-line). Thus, the identification of A-, -B and R/C (restorer line) lines from OPVs aids for development for high-yielding F_1 hybrids in onion with the low production cost of hybrid seed. A schematic presentation of MAS based identification of three lines involved in hybrid seed production in onion is given below in Figure 2.

Future Out Look

Male sterility facilitated development of onion hybrid is both economical as well as quick method. Molecular markers have further accelerated the development onion hybrids over space and time in different country globally by precise identification of cytoplasmic male sterile line (CMS-S and CMS-T) male fertile maintainer line (Nmsms) and nuclear-male- fertility restorers (NMSMS) lines.

Discovery of these markers have opened up new avenues to harness hybrid vigour/heterosis through marker assisted selection (MAS) in onion. Various studies (Manjunathagowda, 2021) have revealed that molecular markers can be usedeffectively and profitably to speed up development of F_1 hybrids and production of pure hybrid seeds through MAS. Identification of male sterility locus (*Ms* locus) in background of different cytoplasms (S, T) is cumbersome and ambiguous is short day onion population. This can be achieved effectively through use of molecular markers to supplement and speedup conventional way of onion hybrid development methods particularly for selection of three lines in open pollinated populations with linkage disequilibrium for *Ms* locus. Onion breeders in future would be required to develop polymorphic codominant molecular markers (SSR, SNPs) for mapping genetic variation in base population and identification of potential lines for further breeding programme. Although, onion is one of the most important vegetable/spice crops worldwide with great economic end use significant, yet the pace of progress in developing MAS is far behind the cereal, pulses and other vegetable crops like potato and tomato. Onion breeders should conversion on use of modern *Omic* methods including genomics, transcriptomics, proteomics and metabolomics for precise and quicker identification of A, B and R lines at molecular levels to resolve various complexities in view of socio-economic importance of *Allium* crop. Germplasm collection from different onion production locations worldwide and its characterization through genetic analysis and molecular markers is imperative to speed up the genetic improvement in this crop for sustainable production under climate change to meet the growing demand of consumers at national and international levels.

The most fascinating feature of onion hybrid breeding programme would be targeted to development of inbred lines through haploid induction as well as to fix heterosis in onion hybrids using double haploid approaches. Use of apomixes can also be explored for achieving this objective.

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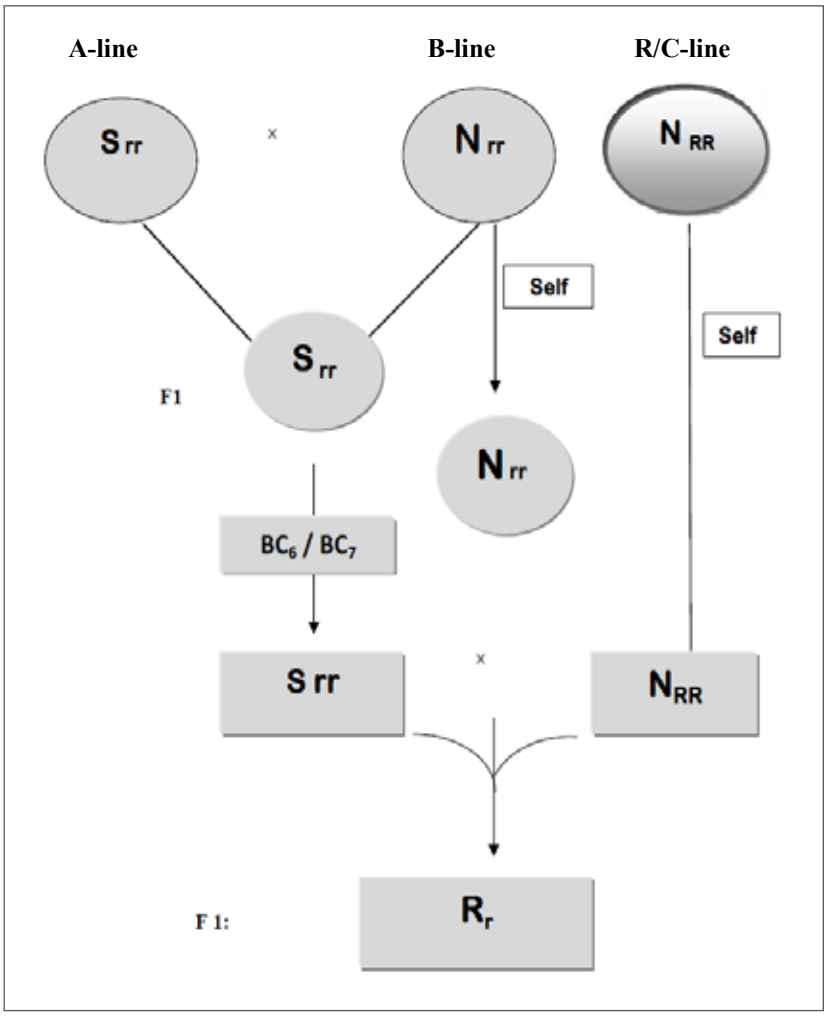

Figure 1. Flow diagram of various steps involved in development of onion hybrids using CMS system (Mohsin et al., 2016).

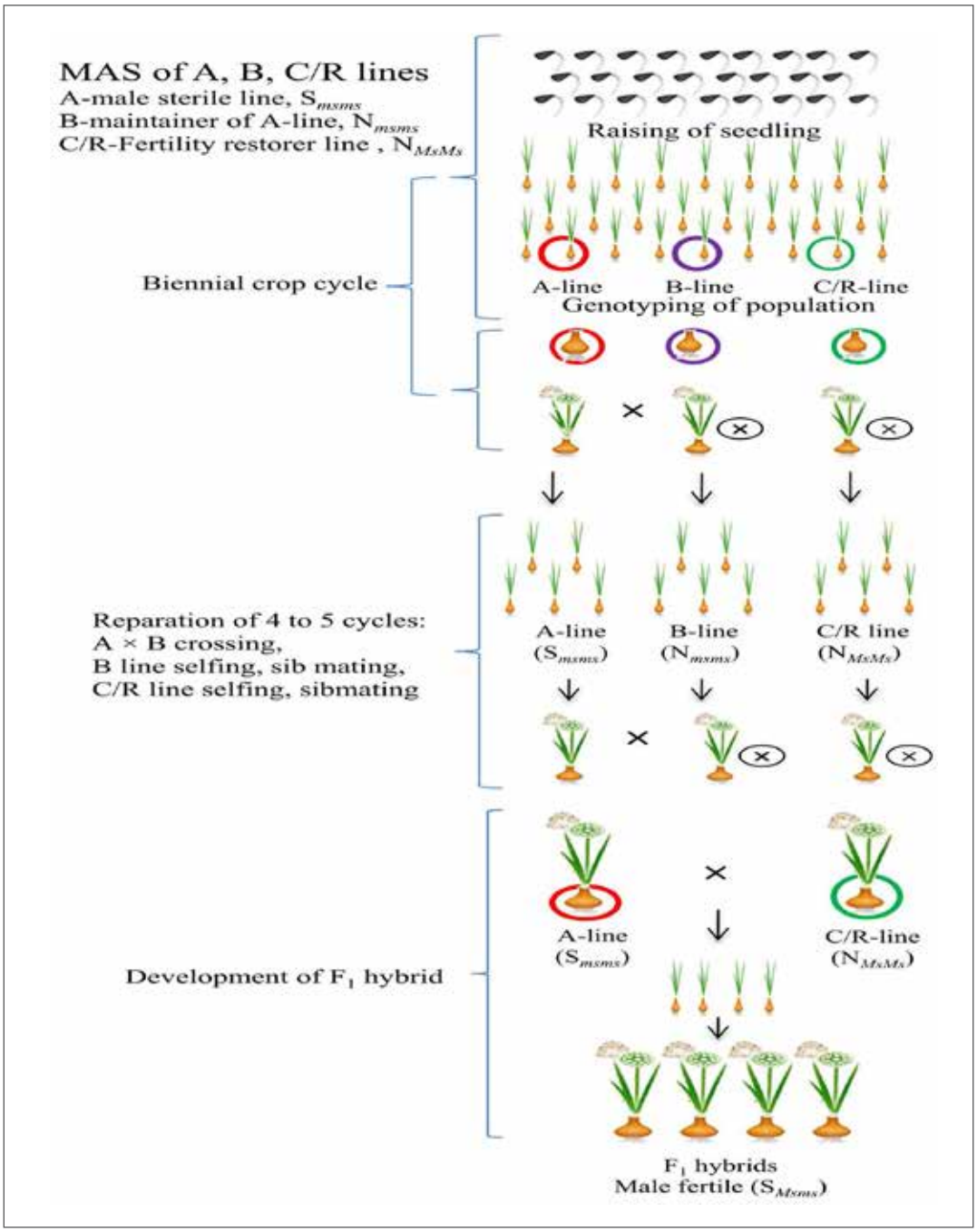

Figure 2. A schematic presentation of MAS based identification of three lines involved in hybrid seed production in onion (Manjunathagowda, 2021).

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Released Varieties

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Registration of "Sultan 1919" Red Clover (*Trifolium pratense* L.) Variety

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Sultan 1919 (*Trifolium pratense* L.) is short-lived perennial forage legume developed and registered by the Black Sea Agricultural Research Institute in 2019. In addition to being used primarily as a pasture crop for animal feeding, it is also used as green manure for increasing soil fertility and soil improvement due to its nitrogen fixation character. Sultan 1919 is developed through within-half sibling family selection as a medium-late flowering and diploid variety during 2016-2019 growing seasons. Sultan 1919 (*Trifolium pratense* L.) is a high quality cool season forage plant with an average plant height of 86.9 cm, green stem and leaf color with purple flowers.

It is a mid-late, diploid variety that can be taken in 3 cuttings under suitable precipitation, climate and soil conditions. The plant can give an average of 68820 kg/ha^{-1} of green herbage yield and 17420 kg/ha^{-1} of dry herbage yield in different climatic and regional conditions. The average physiological maturity period in the use of the plant as silage, grass and hay is 200-220 days; for the use of seeds, it was determined that it reached harvest maturity between 230-250 days on average.

The average 1000-seed weight is 2 g. The planting and harvesting of the variety is suitable for machine farming. Appropriate sowing time is recommended from October 15-November 15 in places with mild winters, and after late spring frosts in places with harsh winters. Although sowing with seeder is preferred, sowing can be done with broadcasting or seeder. Sowing depth is 1-2 cm, suitable row spacing for sowing with seeder is 20-40 cm, the amount of seed to be sown is 500-750 g per decare. Depending on factors such as climate, soil conditions, irrigation status, yield per unit area, 2.5-3.0 kg N should be given per decare by sowing, and 15-20 kg of P_2O_5 every 2-3 years. Although our soils are generally considered sufficient in terms of potassium, potassium fertilization must be applied to sandy and poor soils. According to the results of soil analysis, if the available amounts of macro and micro nutrients in the soil do not meet the needs of pasture clover, this deficiency must be eliminated in order to obtain high yields. In addition, if the soil pH is low (pH<6.5), the pH should be increased to the appropriate level by liming.

As a results of the quality analyses of hay samples taken from the plant, crude protein rate is 21.48%, crude fiber is 26.24%, dry matter is 92.09%, crude oil is 1.81%, NDF 46.28%, ADF 39.39% and RFV 117.

Although it depends on the environmental conditions in which it grows, rust and powdery mildew disease are generally seen in Sultan 1919.

Figure 1. (a) Flower (b) Plant (c) Seeds of *T. pratense*. (Original)

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Released Varieties

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Registration of "Ayzek 595" Cotton (*Gossypium hirsutum* L.) Variety

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Ayzek 595 is upland cotton (*Gossypium hirsutum* L.) variety developed by Eastern Mediterrenian Agricultural Research Institute (EMARI) in 2021. Ayzek 595 is developed by three way crossing as GS 71/GS 51// Cloudia in pedigree method. Crossing was made in 2010 in Adana. F_1 generation was grown in Adana and all individual plant selections, progeny rows and line selections were made in Harran/Şanlıurfa. Elite line performance tests were carried out in Adana, Hatay and Şanlıurfa in 2017-2018.

Ayzek 595 is in the medium-early maturity group, besides having a semi-pyramidal plant form and medium tall cultivar. Petal colour is cream and pollen colour yellow. Leaf and stem pubescence is moderate.

Ayzek 595 variety has high seedcotton yield, lint yield and adaptability as well as superior fiber quality properties according to upland cotton. Avarage of % Lint is 48. Some important fiber qualities are fiber fineness : 4.8 micronaire (units), fiber length 31-32 (mm), fiber strength 33 (g/tex),fiber reflectance : 79 (units) and Trash ID: 4 (units).

Plant height is between 120 and 140 cm depending on the growing conditions in cotton regions. It is medium early and as it has very good adaptation ability, it has been grown throughout Çukurova, Aegean and South eastern Anatolia regions of Turkey. It gives high seedcotton yield both on different soil and high temperature conditions. It has tolerance to verticillium wilt and is tolerant to medium drought conditions. Its yield potential is high however, high yield can be obtained if good agronomic practices and environmental conditions are provided by farmers. In the trials conducted by TTSM in the Aegean-Mediterranean regions in 2019 and 2020, Ayzek 595 variety ranked second in terms of seedcotton yield and first in terms of lint yield.

The highest seedcotton yield obtained was 6500 kg/ha^{-1} in Adana and Şanlıurfa in 2017-2018 growing years. Average of Mean yield of the variety testing experiment was 6250 kg ha^{-1} in all cotton regions and growing conditions.

Pre-Basic seeds of the Ayzek 595 cultivar have been produced by Eastern Mediterrenian Agricultural Research Institute (EMARI). Seed sales and marketing rights of Ayzek 595 variety were transferred to Atlas Tohum Industry company from Adana for 10 year period in March 2021, Seed lots are currently produced and marketed by the Atlas Seed company.

Figure 1. Before blooming (a), blooming (b) and harvesting stage (c) of the Ayzek 595 variety. (Original)

References and Notes

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Released Varieties

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Registration of "Karmen" Bread Wheat (*Triticum aestivum* L.) Variety

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Karmen is a spring bread wheat (*Triticum aestivum* L.) variety, developed by East Mediterranean Agricultural Research Institute and registered in 2020. Karmen is a commercial name given for a newly released bread wheat variety with the pedigree name BABAX/LR42//BABAX*2/3/KUKUNA/4/BACEU #1/5/BECARD which originated from CIMMYT.

The spike of the Karmen variety is long and dense, white, and awned. Grain is semi hard, large and reddish color. Karmen is a medium-tall cultivar, similar to Ceyhan 99 and Gökkan. Plant height is between 82 and 102 cm depending on the growing conditions. Karmen is erect during the juvenile plant growth stage and is green at the boot stage. Heading date of Karmen variety is medium-early.

It has medium resistance to cold and drought. Karmen variety is recommended for the all coastal area and South-Eastern Anatolia. It has medium resistant to Septoria. Karmen has excellent grain yield potential, good resistance to foliar diseases, particularly leaf rust (caused by *Puccinia triticina* Eriks.), stripe rust (caused by *Puccinia striiformis* Westend.) and powdery mildew (caused by *Erysiphe graminis* f. sp. *tritici*).

The variety showed higher grain yield performance than the check (Ceyhan 99, Adana 99) and it has good agronomic characteristics. Combined analysis over years and locations revealed that it had produced an average yield of 7500 kg/ha^{-1} and has wide adaptability. Suggested planting rate is between 450-500 seeds/m^2. Karmen has red grain color and it has good general acceptance for bread with high quality. Its grain feeding quality is good. Considering the quality analysis values of this variety in 2018 and 2019, the test weight, a thousand grain weight, protein content, gluten content, alveograph energy values and zeleny sedimantation were determined respectively 79.0-82.1 kg/hl^{-1}, 45-50 g, 12.5-14.8%, 25.0-36.5%, 274-358 W and 33-45 (ml). Royality negotiations with private companies continue to cover the production and sales of seeds of Karmen variety.

Figure 1. Spikes (a), Field view (b) and Seeds of Karmen (c) variety. (Original)

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Anonymous, (2020). Akdeniz Bölgesi Bölgesi ekmeklik buğday tescil raporu, TTSM, Ankara. (in Turkish)

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In Turkey, wheat was produced 10 million tons in 1923 (Gokgol 1939).

This result was in agreement with result of Sahin and Yildirim (2004).

Similar effect has been widely studied prior to this study (Eser 1991; Bagci et al. 1995; Uzun and Yol 2013).

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Journal article:

Toker C (1998). Adaptation of kabuli chickpeas (*Cicer arietinum* L.) to the low and high lands in the West Mediterranean region of Turkey. Turk J Field Crop 3:10-15.

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Article by Digital Object Identifier (DOI) number:

Yasar M, Ceylan FO, Ikten C and Toker C (2013). Comparison of expressivity and penetrance of the double podding trait and yield components based on reciprocal crosses of kabuli and desi chickpeas (*Cicer arietinum* L.). Euphyticadoi:10.1007/s001090000086

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FAOSTAT J (2013) http://faostat.fao.org/site/567/default.aspx# anchor. Accessed 15 May 2013.

Dissertation (Thesis):

Yasar M (2012). Penetrance and expressivity of double podding characteristic in chickpea (*Cicer arietinum* L.). Dissertation, Akdeniz University, Antalya.

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Abbreviations

Abbreviations should be defined at first mention and used consistently.

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