

Mechanisms of inheritance in durum wheat genotypes

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Abstract

Taneva, K., Dragov, R., Nedyalkova, S. & Bozhanova, V. (2023). Mechanisms of inheritance in durum wheat genotypes. *Bulg., J. Agric. Sci.*, 29(6), 1112–1119

Creating high-yielding cultivars with improved grain quality is a major priority in durum wheat breeding. Variability, heritability and genetic advance were studied for the following traits: grain yield, plant height, productive tillering, spike length, number of spikelets per spike, number of kernels per spike, kernels weight per spike, thousand kernel weight, protein content, wet gluten content, SDS–sedimentation value, yellow pigments content, vitreousness and test weight of 90 durum wheat genotypes of different origins. The phenotypic coefficient of variation (PCV) was established to be higher than the genotypic coefficient of variation (GCV) for all studied traits, which reflects the impact of the environmental conditions on the variation of these traits. The highest phenotypic (PCV-41.66%) and genotypic (GCV-41.39%) coefficients of variation were established for sedimentation value. High broad-sense heritability coefficients (h^2_{BS}) were established for almost all studied traits. The heritability for these traits ranged from 54.74% for number of kernels per spike to 98.72% for SDS-sedimentation value. The lowest coefficient of heritability was established for kernels weight per spike – 5.5%. High genetic advance as a percentage of the mean was calculated for the following traits: SDS-sedimentation value (84.71%) and grain yield (20.95%). A high heritability coefficient combined with high genetic advance was found for the following traits: SDS-sedimentation value and grain yield. This shows the presence of additive gene effects in the expression of these traits and therefore direct selection by these traits is possible under our conditions.

Keywords: qualitative traits of grain; phenotypic coefficient of variation; genotypic coefficient of variation; heritability; genetic advance

Introduction

Durum wheat (*Triticum durum* Desf.) is an important cereal crop used by man mostly for food. Due to its specific characteristics such as hard and compact endosperm, high vitreousness, high protein and carotenoid content, high-quality gluten with high extensibility and low elasticity, it is extremely suitable for processing into pasta products (Sissons, 2016).

The ultimate goal of any breeding program is the creation of high-yielding varieties in different environments. Phenotypic diversity analysis is useful to determine the genetic diversity of crop genetic resources, which is necessary for

successful crossing (Dagnaw et al., 2022). Hybridization is an important source for creating diversity. The study of genetic diversity is the basis for plant breeding improvement. An effective plant breeding strategy uses genetic diversity as a source of new alleles for crop improvement. Essential to the success of recombination breeding is the appropriate selection of genotypes as parents to produce highly heterosis crosses and the presence of genetic diversity in the source population (Bello et al., 2012). Modern breeding programs for durum wheat are aimed at improving the agronomic and qualitative traits of the grain.

Breeding based on phenotypic variation is not efficient, and therefore selection based on the evaluation and use of

genetic diversity in the desired direction is extremely important for the breed-improvement programs of durum wheat. Accordingly, information on genetic variation, heritability, genetic advance, and correlational relationships is necessary for a successful parental selection in breeding programs (Adhikari et al., 2018).

Genetic studies provide information on the extent of genetic control, particularly trait expression and phenotypic reliability in predicting breeding outcomes. Heritability is an indicator for transmission of desired traits from parents to offspring that is widely used in breeding programs (Lipi et al., 2020). The heritability assessment is a useful parameter for breeders because it allows the prediction of possibilities for successful breeding, as it reflects the correlation between phenotypic variation that can be inherited, in other words the heritability coefficient measures the reliability of the phenotypic value as an indicator of the genotypic value. The heritability assessment facilitates the selection of methods and traits used in the initial and advanced phases of breed-improvement programs, allowing the study of the mechanisms, genetic values and variation of each trait (Al-Naggar et al., 2022). Genetic advance (GA) is another important parameter that serves to determine the expected response of the breeding process. The combination of high genetic advance with high heritability predicts the most effective breeding conditions (Terfa, Gurnu, 2020) and indicates the presence of additive genes in the inheritance of the trait. Phenotypic and genotypic coefficients of variation, heritability and genetic advance are widely used to determine the amount of variation in breeding materials, to determine appropriate selection procedures and to predict breeding progress in the improvement of important traits (Clarke et al., 2010). A high to moderate range of coefficients of variation provides greater opportunities for selection of desired genotypes (Sravani et al., 2021).

The assessment of heritability and genetic advance is used in breeding numerous crops. There are popular publications of genetic studies on rice (Demekke et al., 2023), maize (Asare et al., 2022), sorghum (Sawadogo et al., 2023) and others.

The aim of this study was to determine the degree of variation, heritability, genetic advance and environmental impact in a sample of 90 durum wheat genotypes of diverse origins.

This research will enable the prediction of possible breeding advance in improving grain yield and quality in the breed-improvement program for durum wheat.

Material and Methods

The study included 90 modern durum wheat (*Triticum durum* Desf.) genotypes - varieties from all over the world

and breeding lines. The Bulgarian durum wheat is presented by 26 modern varieties and 36 breeding lines developed in the Institute of Field Crops (IFC, former Cotton and Durum Wheat Research Institute), Chirpan and Dobrudzha Agricultural Institute, Northern Bulgaria. The foreign germplasm introduced in Bulgaria is presented by the varieties from several European countries, including Italy, France, Austria, Hungary, Germany, Russia and Ukraine, and the USA. All the genotypes were grown under field conditions for three years 2020–2022. A randomised block method was used in four replications with an experimental plot size of 15 m². The accepted technology for growing durum wheat was used.

The following traits were monitored: grain yield (Y) – t/ha, plant height (H) – cm, productive tillering (PT) – number, spike length (SL) – cm, number of spikelets per spike (NSS) – number, number of kernels per spike (NKS) – number, kernels weight per spike (KWS) – g, grain protein content (GPC) – percentage, wet gluten content in grain (GWG) – percentage, SDS-sedimentation value (SDS) – cm³, vitreousness (VIT) – %, test weight (TW) – kg/hl, thousand kernel weight (TKW) – g, Minolta yellow index b* (MK).

The grain protein content was determined by the Kjeldahl method (N x 5.7) according to BNS EN ISO 20483: 2014, and wet gluten – according to BNS EN ISO 21415-2: 2008. The gluten strength was evaluated by measuring the sedimentation value of wholemeal flour in a lactic acid - sodium dodecyl sulfate (SDS) solution at a standard sedimentation time (ICC 151: 1990). Vitreousness was determined according to BNS EN 15585: 2008. Thousand kernel weight was determined according to BNS EN ISO 520: 2010. Test weight was determined according to BNS EN ISO 7971-1: 2009. The values of yellow colour b* were measured according to CIE L*a*b* cubic colour space, which is considered the most operational and informative one. The measurement was made per grain using a Minolta CR-410 chroma meter. The higher the b* value, the greater the amount of carotenoids. The chroma meter was calibrated with a standard calibration plate.

The total heritability (h^2) for the studied traits was calculated by the variance components method based on the results from the three years of cultivation. Primary data were processed with analysis of variance (ANOVA). The variance components were calculated according to Snedecor and Cochran (1980). All the studied genetic parameters, formulas for their calculation and designations are presented below (Table 1).

The results were processed statistically with a two-way analysis of variance (ANOVA) by means of Statistica, version 13.0 (TIBCO Software).

Table 1. Genetic parameters and formulas for their calculation

$\sigma_g^2 = (MS_g - MS_{gy})/yr$	Genotypic variance
$\sigma_{gy}^2 = (MS_{gy} - MS_e)/r$	Variance of interaction between G and Y
$\sigma_e^2 = MS_e$	Error variance
$\sigma_{ph}^2 = \sigma_g^2 + \sigma_{gy}^2/y + \sigma_e^2/ry$	Phenotypic variance
$h_{BS}^2 = (\sigma_g^2 / \sigma_{ph}^2) \times 100$	Broad-sense heritability
$GA = k \times (\sigma_{ph}^2)^{0.5} \times h_{BS}^2 / (100/\bar{x})$	Genetic advance K – selection intensity – 2.06
$PCV = \sqrt{\sigma_{ph}^2} / \bar{x} \times 100$	Phenotypic coefficient of variation
$GCV = \sqrt{\sigma_g^2} / \bar{x} \times 100$	Genotypic coefficient of variation
MS_g	Mean squares of genotype (g)
MS_{gy}	Mean squares of interaction (gxy)
MS_e	Mean squares of error
y	Number of years of cultivation
r	Number of repetitions
\bar{x}	Mean value

Results and Discussion

Heritability is an indicator of phenotypic variance, which is due to genetic reasons and has predictive function in plant breeding (Eid, 2009). According to Khan et al. (2009), the higher the heritability coefficient, the simpler the selection procedures. Broad-sense heritability only shows whether there is sufficient genetic variation in a population and how the population will respond to the selection pressure (Mila-tović et al., 2010).

Based on the collected data from the conducted 3-year experiment with the set of 90 genotypes of diverse origin the variation, broad-sense inheritance and genetic advance were determined for the following traits: grain yield, plant height, productive tillering, spike length, number of spikelets per spike, number of kernels per spike, kernels weight per spike, thousand kernel weight, protein content, wet gluten content, SDS-sedimentation value, yellow pigments content, vitreousness and test weight.

The performed analysis of variance shows that the mean squares, the years of cultivation and the interaction between them are significant for all studied traits (Table 2).

The mean values, the range of variation and the phenotypic and genotypic coefficients of variation of all investigated traits for the 90 durum wheat genotypes for the growing years are shown in Table 3.

The PCV was higher than the GCV for all studied traits and reflects the impact of environmental conditions (year of

Table 2. Mean squares value from ANOVA for 14 quantitative traits of 90 durum wheat genotypes

Traits	Genotype (G)	Environment (E) (year)	G × E	Error
Grain yield	5.31***	362.31***	1.6***	0.18
Plant height	450***	20980.86***	65***	0.2
Productivity tillering	2.685***	32.9***	2.4***	1.7
Spike length	2.74***	117.5***	0.8***	0.02
Number of spikelets per spike	13.2***	114.6***	4.5***	0.01
Number of kernels per spike	150***	902***	67.9***	1.1
Kernels weight per spike	0.495***	2.4***	0.2***	0.003
Thousand kernel weight	64***	772***	11.7***	0.03
Grain protein content	3.4***	362.6***	1.0***	0.01
Sedimentation value	1121.9***	249***	14.4***	0.9
Grain wet gluten content	14.9***	1593.5***	4.6***	0.02
Minolta kernel	2.1***	53.3***	0.5***	0.04
Vitreousness	286***	6350***	69.6***	0.02
Test weight	40***	670***	6.6***	0.02

*** – significant at $p < 0.001$

Table 3. Variation coefficient, means values and its ranges for 14 quantitative traits of 90 durum wheat genotypes

Traits	Min	Max	Mean	PCV%	GCV%
Grain yield	3.3	6.8	5.3	14.5	12.1
Plant height	71.1	110.3	90.2	7.84	7.25
Productivity tillering	2.7	4.1	3.4	16.0	5.3
Spike length	5.8	8.7	7.3	7.65	6.43
Number of spikelets per spike	18.3	23.9	21.4	5.66	4.59
Number of kernels per spike	36.4	54.8	43.7	9.34	6.91
Kernels weight per spike	1.5	2.7	1.9	12.89	9.56
Thousand kernel weight	36.6	50.3	43.0	6.20	5.61
Grain protein content	12.9	16.3	14.8	4.15	3.48
Sedimentation value	16.8	57.9	26.8	41.66	41.39
Grain wet gluten content	27.1	34.2	31.2	4.12	3.43
Minolta kernel	15.6	17.8	16.6	2.90	2.53
Vitreousness	67.9	95.6	86.8	6.49	5.65
Test weight	68.8	78.0	74.7	2.82	2.58

cultivation) on the variation of these traits. The highest PCV was established for sedimentation value (SDS – 41.66%) and productive tillering (YPG – 16.0%). The highest GCV was established for SDS-sedimentation value (41.39%). A smaller difference between the PCV and GCV was observed for traits: yield, grain protein content, wet gluten content in grain, yellow pigment content and test weight, indicating less environmental impact on the phenotypic expression of the respective trait.

The greatest difference between the PCV and GCV was established for the traits of productive tillering and kernels weight per spike, which is an indicator of a greater impact of the environmental than of genotype on the variation of these traits. On the other hand, the coefficient of variation is used to determine the diversity that exists in each population. A coefficient of variation (CV) above 20% is considered an indicator of high diversity, a CV value between 10 and 20% - moderate diversity, and less than 10% - low diversity (Deshmukh et al., 1992). In our study, high diversity was observed for trait SDS-sedimentation value (CV-41.66%). Moderate diversity was established for traits: grain yield (14.5%) and productive tillering (16.0%). The lowest PCV was found for test weight (2.82%), yellow pigment content (2.90%), wet gluten content in grain (4.12%), protein content (4.15%), number of spikelets per spike (5.66%), thousand kernel weight (6.20%), vitreousness (6.49%), spike length (7.65%), plant height (7.84%) and number of kernels per spike (9.34%).

The phenotypic variance of all studied traits and its two main components: genotypic variance and environmental variance, are presented in Table 4. The value of genotypic variance was higher than the one of environmental variance

(years of cultivation) for traits: plant height, thousand kernel weight, sedimentation value, yellow pigment content, vitreousness, and test weight. It comes to show that the genotypic component of variation is a major contributor to the overall phenotypic variation of these traits. The environmental variance was higher than the genotypic variance for traits: grain yield, productive tillering, spike length, number of spikelets per spike, number of kernels per spike, kernels weight per spike, protein content, wet gluten content in grain and therefore means that the environment is a major contributor to the whole phenotypic variation of these traits.

In our study, very high heritability coefficients (h^2_{BS}) were established for all the traits except for productive tillering and kernels weight per spike (Table 4). The heritability for these traits ranged from 54.74% for number of kernels per spike to 98.72% for SDS-sedimentation value. In support of our results, Muhammad et al. (2017) reported high broad-sense heritability coefficient for the traits: spike length, thousand kernel weight and grain yield. According to Kumar et al. (2014) high heritability is an indication that the traits are much less affected by environmental conditions. The lowest coefficient of heritability was found for productive tillering – 11.0% and kernels weight per spike – 5.5%.

Genetic advance is an important breeding parameter in addition to heritability by which the degree of improvement of desired traits can be predicted. Genetic advance, expressed as a percentage, is categorized as low (0-10%), moderate (10-20%) and high ($\geq 20\%$) (Johnson et al., 1955; Falconer, Mackay, 1996).

High genetic advance as a percentage of the mean was calculated for the following traits: SDS-sedimentation value (84.71%) and grain yield (20.95%). Moderate genetic advance

Table 4. Component of variance (σ^2), broad-sense heritability (h^2_{BS} %) and genetic advance (GA) for 90 durum wheat genotypes

Traits	Variance σ^2				h^2_{BS} %	GA as % of mean
	σ^2_{ph}	σ^2_g	σ^2_y	σ^2_{g/σ^2_y}		
Grain yield	0.59	0.412	0.473	0.87	70	20.95
Plant height	50.02	42.8	21.6	1.98	86	13.90
Productivity tillering	0.302	0.032	0.233	0.14	11	3.67
Spike length	0.312	0.22	0.26	0.85	70.5	11.14
Number of spikelets per spike	1.466	0.966	1.0496	0.65	65.9	7.68
Number of kernels per spike	16.66	9.12	22.27	0.41	54.74	10.53
Kernels weight per spike	0.06	0.033	0.066	0.5	5.5	1.46
Thousand kernel weight	7.11	5.81	3.89	1.49	81.7	10.44
Grain protein content	0.377	0.266	0.33	0.81	70.56	6.03
Sedimentation value	124.66	123.06	4.5	27.35	98.72	84.71
Grain wet gluten content	1.655	1.144	1.526	0.75	69.12	5.87
Minolta kernel	0.232	0.177	0.153	1.157	76.29	4.56
Vitreousness	31.77	24.04	23.19	1.04	75.67	10.12
Test weight	4.444	3.711	2.193	1.69	83.51	4.85

was calculated for three of the studied traits: plant height (13.90%), spike length (11.14%), number of kernels per spike (10.53%), thousand kernel weight (10.44%) and vitreousness (10.12%). Low genetic advance was found for the traits: kernels weight per spike (1.46%), productive tillering (3.67%), yellow pigment content (4.56%), test weight (4.85%), grain wet gluten content (5.87%), grain protein content (6.03%) and number of spikelets per spike (7.68%). High heritability combined with high genetic advance is considered to indicate the presence of additive gene effects, while high heritability combined with low genetic advance is an indicator of non-additive gene effects on the control of the respective trait. In the present study, additive gene effects were found for the following traits: SDS-sedimentation value and grain yield. This indicates the possibility of conducting efficient selection of genotypes by phenotype in early generations and achieving rapid selection progress on these traits.

Broad-sense heritability for SDS-sedimentation value in wheat was found to range from moderate to high in previous studies, which was also confirmed by our results (Clarke et al., 2010). High heritability and high genetic advance for this trait were also reported by Choudhary et al. (2020). There is information about low heritability of this trait in Turkish breeding lines of winter durum wheat (Akcura, 2009).

Some authors reported low heritability of grain yield (Alemu et al., 2020) and others – low heritability combined with high genetic advance (Wolde et al., 2016; Dagnaw et al., 2022), while still others found high heritability of this trait in durum wheat under various environmental conditions (Rapp et al., 2018). Kumar et al. (2014) reported high her-

itability and high genetic advance for biological plant yield and the presence of additive gene effects. There is also conflicting information regarding the heritability of vitreousness in durum wheat (Branković et al., 2014; Branković et al., 2018). Branković et al. (2014) reported moderately high the broad sense heritability for grain vitreousness (71%). In our study, high heritability combined with high genetic advance were found for trait grain yield and high heritability combined with moderate genetic advance for vitreousness.

High heritability combined with high genetic advance for grain yield, thousand kernel weight, number of kernels per spike, spike length and plant height were also reported by other authors (Wolde, et al., 2016; Nishant et al., 2018; Bendjama, Ramdani, 2022). Devesh et al. (2018) in their study reported high heritability and high genetic advance for thousand kernel weight. Thapa et al. (2019) reported high heritability and high genetic advance for the following traits: kernels weight per spike, thousand kernel weight, grain yield, number of kernels per spike as well as low to moderate high genetic advance for plant height. Additive gene effects for number of kernels per spike and kernels weight per spike under irrigated conditions were reported by Morteza et al. (2018).

Regarding protein and gluten content, a high heritability coefficient was combined with low genetic advance. This indicates the presence of non-additive gene effect and significant environmental impact on the expression of these traits. Protein content is one of the most important quality parameters of durum wheat. Breeding for increasing protein content is known to be complicated due to the existing negative cor-

relation with grain yield and the significant environmental impact on the variation of this trait (Würschum et al. 2016). There is conflicting information regarding the heritability of protein content in the different growing conditions and genotype groups used. Akcura (2009) reported low to moderate heritability coefficient for these traits. Rapp et al. (2018) used two different groups of durum wheat containing 159 and 189 genotypes tested at multiple locations across Europe and determined a relatively high heritability value for protein content of around 75% for both groups of genotypes used. Our results with a significantly smaller number but diverse genotypes support the findings of the latter authors. Under our conditions, high heritability coefficients were found for both traits: 70.56% for protein content and 69.12% for wet gluten content. Genetic advance was low for both indicators - 6.03% and 5.87%, which shows the presence of non-additive gene effects. Consistent with our results, Bayisa et al. (2020) reported a low genetic advance and high heritability for test weight and correspondingly the presence of non-additive gene effects in the expression of this trait. Other authors reported high heritability moderately high genetic advance for this trait and correspondingly the presence of both additive and non-additive gene effects (Rajput, 2018).

Numerous studies have been conducted related to establishing the heritability of yellow pigment content in durum wheat under different conditions and genotypes and with different methods (Clarke, 2005; Clarke et al., 2008; Roncallo et al., 2012; Gautam et al., 2023). Clarke (2005), analysing the existing studies, concluded that the heritability of pigment concentration is high and this allows selection for this trait in early generations. Clarke et al. (2008) found that yellow pigment content was controlled by several genes with an additive effect, influenced by environmental factors and epistatic interactions (Roncallo et al., 2012). Our results indicate the presence of non-additive gene effects, as the estimated genetic advance is low. Therefore, under our conditions, an effective selection for this trait is impossible.

The lowest heritability coefficient combined with the lowest genetic advance in our study was established for kernels weight per spike and productive tillering. This comes to indicate that non-additive gene effects prevail in the inheritance of this traits and efficient genotype selection by phenotype in early generations is not possible under our conditions. Thapa et al. (2019) reported high heritability and high genetic advance for productive tillering.

Conclusions

The analysis of variance performed shows that the mean squares, the years of cultivation and the interaction between

them are significant for all studied traits.

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all studied traits and reflected the impact of environmental conditions (year of cultivation) on the variation of these traits. The highest PCV (41.66%) and GCV (41.39%) were established for sedimentation value.

The greatest difference between the PVC and GVC was established for the traits of productive tillering and kernels weight per spike, which is an indicator of a greater impact of the environmental than of genotype on the variation of these traits.

High diversity was observed for trait SDS-sedimentation value (CV-41.66%). Moderate diversity was established for traits: grain yield (14.5%) and productive tillering (16.0%). The lowest PCV was found for test weight (2.82%), yellow pigment content (2.90%), wet gluten content in grain (4.12%), protein content (4.15%), number of spikelets per spike (5.66%), thousand kernel weight (6.20%), vitreousness (6.49%), spike length (7.65%), plant height (7.84%) and number of kernels per spike (9.34%).

Very high heritability coefficients (h^2_{BS}) were established for all the traits except for productive tillering and kernels weight per spike. A high heritability coefficient combined with high genetic advance was found in our study for the following traits: SDS-sedimentation value and grain yield. This indicates the presence of additive gene effects in the expression of these traits and therefore direct selection for these traits is possible under our conditions. High heritability combined with moderately high genetic advance was found for the following traits: plant height, spike length, number of kernels per spike, thousand kernel weight and vitreousness. This indicates the presence of additive and non-additive gene effects and therefore selection for these traits under our conditions would be difficult. A low heritability coefficient and low genetic advance was found for kernels weight per spike and productive tillering in our study. Therefore, this trait is controlled by non-additive genes and direct selection is impossible.

Acknowledgements

This work was supported by the Bulgarian Ministry of Education and Science under the National Research Programme „Healthy Foods for a Strong Bio-Economy and Quality of Life” approved by DCM # 577 / 17.08.2018”.

References

- Adhikari, B. N., Joshi, B. P., Shrestha, J. & Bhatta, N. R. (2018). Genetic variability, heritability, genetic advance and correlation

- among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*, 1(1), 149–160. DOI: <https://doi.org/10.3126/janr.v1i1.22230>.
- Akcura, M.** (2009). Genetic variability and interrelationship among grain yield and some quality traits in Turkish winter durum wheat landraces. *Turkish Journal of Agriculture and Forestry*, 33(6), 547–556. DOI: <https://doi.org/10.3906/tar-0903-5>.
- Alemu, Y. A., Anley, A. M. & Abebe, T. D.** (2020). Genetic variability and association of traits in Ethiopian durum wheat (*Triticum turgidum* L. var. *durum*) landraces at Dabat Research Station, North Gondar. *Cogent Food & Agriculture*, 6, 1778604. DOI: <https://doi.org/10.1080/23311932.2020.1778604>.
- Al-Naggar, A. M. M., Atta, M. M., El-Moneim, M. L. A. B. D. & Al-Metwally, M. S.** (2022). Heritability, genetic advance and trait interrelationships of *Chenopodium quinoa* under low, medium and high n organic and mineral fertilizer conditions. *Plant Cell Biotechnology and Molecular Biology*, 23(5–6), 52–73. DOI: 10.56557/pcbmb/2022/v23i5-67426.
- Asare, C., Akromah, R., Osekre, E.A., Kena, A., Amoah, S. & Annor, B.** (2022). Heritability and genetic advance estimates among some selected morphological traits and fall armyworm resistance in double cross hybrid maize (*Zea mays* L.). *Journal of Plant Biology and Crop Research*, 5(2), 1069.
- Bayisa, T., Tefera, H. & Letta, T.** (2020). Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. *Agriculture, Forestry and Fisheries*, 9(4), 128–134. DOI: 10.11648/j.aff.20200904.15.
- Bello, O. B., Ige, S. A., Azeez, M. A., Afolabi, M. S., Abdulmalik, S. Y. & Mahamood, J.** (2012). Heritability and genetic advance for grain yield and its component characters in maize (*Zea Mays* L.). *International Journal of Plant Research*, 2(5), 138–145. DOI: <https://doi.org/10.5923/j.plant.20120205.01>.
- Bendjama, A. & Ramdani, C.** (2022). Genetic variability of some agronomic traits in a collection of wheat (*Triticum turgidum* L. sp. pl.) genotypes under South Mediterranean growth conditions. *Italian Journal of Agronomy*, 17, 1976. DOI: <https://doi.org/10.4081/ija.2021.1976>.
- Branković G. R., Dodig D., Zorić M. Z., Knežević D., Šurlan-Momirović G. G., Dragičević V. & Đurić N.** (2014). Effects of climatic factors on grain vitreousness stability and heritability in durum wheat. *Turkish Journal of Agriculture and Forestry*, 38(4), 429–440. DOI: <https://doi.org/10.3906/tar-1308-51>.
- Branković, G., Dodig, D., Pajić, V., Kandić, V., Knežević, D., Đurić, N. & Živanović, T.** (2018). Genetic parameters of *Triticum aestivum* and *Triticum durum* for technological quality properties in Serbia. *Zemdirbyste-Agriculture*, 105(1), 39–48. DOI: <https://doi.org/10.13080/z-a.2018.105.006>.
- Choudhary, L., Goyal, V. K., Pandey, S., Moitra, P. K. & Shukla, R. S.** (2020). Assessment of genetic variability in advance breeding lines of wheat. *The Pharma Innovation Journal*, 9(5), 239–244.
- Clarke, J. M.** (2005). Durum wheat improvement in Canada. *Durum Wheat Breeding*, 2(30), 921–938.
- Clarke, B., Liang, R., Morell, M. K., Bird, A. R., Jenkins, C. L. D. & Li, Z.** (2008). Gene expression in a starch synthase IIa mutant of barley: changes in the level of gene transcription and grain composition. *Functional & Integrative Genomics*, 8, 211–221. DOI: <https://doi.org/10.1007/s10142-007-0070-7>.
- Clarke, F. R., Clarke, J. M., Ames, N. A., Knox, R. E. & Ross, R. J.** (2010). Gluten index compared with SDS-sedimentation volume for early generation selection for gluten strength in durum wheat. *Canadian Journal of Plant Science*, 90(1), 1–11. DOI: <https://doi.org/10.4141/CJPS09035>.
- Dagnaw, T., Mulugeta, B., Haileselassie, T., Geleta, M. & Tesfaye, K.** (2022). Phenotypic variability, heritability and associations of agronomic and quality traits in cultivated Ethiopian durum wheat (*Triticum turgidum* L. ssp. *durum* Desf.). *Agronomy*, 12(7), 1714. DOI: <https://doi.org/10.3390/agronomy12071714>.
- Demeke, B., Dejene, T. & Abebe, D.** (2023). Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza sativa* L.) genotypes at pawe, northwestern Ethiopia. *Cogent Food and Agriculture*, 9, 2157099. DOI: <https://doi.org/10.1080/23311932.2022.2157099>.
- Deshmukh, S. N., Basu, M. S. & Reddy, P. S.** (1992). Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. *Indian Journal of Agricultural Sciences*, 56, 516–521.
- Devesh, P., Moitra, P. K., Shukla, R. S., Shukla, S. S., Pandey, S. & Arya, G.** (2018). Analysis of variability, heritability and genetic advance of yield, its components and quality traits in wheat. *International Journal of Agriculture, Environment and Biotechnology*, spec. iss, 855–859.
- Eid, M. H.** (2009). Estimation of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought condition. *International Journal of Genetics and Molecular Biology*, 1(7), 115–120.
- Gautam, A., Prasad, S. V. S., Jajoo, A. & Bassi, F. M.** (2023). Evaluation of Indian Durum Wheat Genotypes for Yield and Quality Traits Using Additive Main Effects and Multiplicative Interaction (AMMI) Biplot Analysis under Terminal Heat Stress Conditions. *Crop Breeding, Genetics and Genomics*, 5(3), e230004. DOI: <https://doi.org/10.20900/cbagg20230004>.
- Falconer, D. S. & Mackay, T. F. C.** (1996). Introduction to Quantitative Genetics, fourth ed. Longman, Burnt Mill, England, 464.
- Johnson, H. W., Robinson, H. F. & Comstock, R. E.** (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47(7), 314–318. DOI: <https://doi.org/10.2134/agronj1955.00021962004700070009x>.
- Khan, A. S. M. M. R., Kabir, M. Y. & Alam, M. M.** (2009). Variability, correlation path analysis of yield and yield components of pointed gourd. *Journal of Agriculture and Rural Development*, 93–98. DOI: <https://doi.org/10.3329/JARD.V7I1.4427>.
- Kumar, N., Markar, S. & Kumar, V.** (2014). Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). *Bioscience Discovery*, 5(1), 64–69.
- Lipi, L.F., Hasan, M.J., Akter, A., Quddus, M.R., Biswas, P.L., Ansari, A. & Akter, S.** (2020). Genetic variation, heritability and genetic advance in some promising rice hybrids. *SAARC Journal of Agriculture*, 18(2), 39–49. DOI: <http://doi.org/10.3329/sja.v8i2.51107>.
- Milatović, D., Nikolić, D. & Đurović, D.** (2010). Variability, heritability and correlations of some factors affecting productivity in peach. *Horticultural Science*, 37(3), 79–87. DOI:

- 10.17221/63/2009-HORTSCI.
- Morteza, K., Ebadi, A. & Shiri, M.** (2018). Heritability, expected genetic advance, and genotype by trait analysis for grain yield and agronomic traits in durum wheat under irrigated and rainfed conditions. *Albanian Journal of Agricultural Sciences*, 17(3), 150-159.
- Muhammad, A., Mohammad, F., Hussain, Q. & Hussain, I.A.F.** (2017). Heritability estimates and correlation analysis in bread wheat (*Triticum aestivum* L.) under normal and late plantings. *Pure and Applied Biology*, 6: 1151-60. DOI: <http://dx.doi.org/10.19045/bspab.2017.600123>.
- Nishant, A. B., Arun, B. & Mishra, V. K.** (2018). Genetic variability, heritability and correlation study of physiological and yield traits in relation to heat tolerance in wheat (*Triticum aestivum* L.). *Biomedical Journal of Scientific and Technical Research*, 2, 000636. DOI: <https://doi.org/10.26717/BJSTR.2018.02.000636>.
- Rajput, R. S.** (2018). Correlation, path analysis, heritability and genetic advance for morpho-physiological character on bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(2), 107-112.
- Rapp, M., Lein, V., Lacoudre, F., Lafferty, J., Muller, E., Vida, G., Bozhanova, V., Ibraliu, A., Thorwarth, P., Piepho, H. P., Leiser, W. L., Wurschum, T. & Longin, C. F. H.** (2018). Simultaneous improvement of grain yield and protein content in durum wheat by different phenotypic indices and genomic selection. *Theoretical and Applied Genetics*, 131(6), 1315-1329. DOI: [10.1007/s00122-018-3080-z](https://doi.org/10.1007/s00122-018-3080-z).
- Roncallo, P. F., Gerardo, L., Cervigni, G. L., Jensen, C., Miranda, R. & Helguera, M.** (2012). QTL analysis of main and epistatic effects for flour color traits in durum wheat. *Euphytica*, 185, 77-92. DOI: <https://doi.org/10.1007/s10681-012-0628-x>.
- Sissons, M.** (2016). Pasta. *Encyclopedia of Food Grains (2nd ed.)*, 3, 79-89. DOI: <https://doi.org/10.1016/B978-0-12-394437-5.00123-6>.
- Snedecor, G. W. & Cochran, W. G.** (1980). *Statistical methods* (7th ed.). Iowa State University Press.
- Sravani, D., Bharathi, D., Reddi, S. M. & Kumar, A. R.** (2021). Estimation of genetic parameters for quantitative traits in maize (*Zea mays* L.) inbred lines. *The Pharm Innovation Journal*, 10(8), 501-503.
- Sawadogo, N., Drabo, I., Ouédraogo, N., Tondé, W. H., Béré, T. L. K., Tiendrébéogo, J., Compaoré, G., Ouédraogo, M. H., Nanema, K. R. & Bationo-Kando, P.** (2023). Heritability, genetic advance, and correlation studies of morpho-agronomic traits and brix in Burkina Faso sweet stalk sorghum genotypes. *Journal of Applied Biology and Biotechnology*, 11(4), 50-57. DOI: [10.7324/JABB.2023.110325](https://doi.org/10.7324/JABB.2023.110325).
- Terfa, G. N. & Gurmu, G. N.** (2020). Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) genotypes for seed yield and other agronomic traits. *Oil Crop Science*, 5, 156-160. DOI: <https://doi.org/10.1016/j.ocsci.2020.08.002>.
- Thapa, R. S., Sharma, K. P., Pratap, Dh., Singh, T. & Kumar, A.** (2019). Assessment of genetic variability, heritability and genetic advance in wheat (*Triticum aestivum* L.) genotypes under normal and heat stress environment. *Indian Journal of Agricultural Research*, 53(1), 51-56. DOI: <https://doi.org/10.18805/IJAR.A-5095>.
- Wolde, T., Eticha, F., Alamerew, S., Assefa, E. & Dutamo, D.** (2016). Genetic variability, heritability and genetic advance for yield and yield related traits in Durum wheat (*Triticum durum* L.) accessions. *Sky Journal of Agricultural Research*, 5(3), 42-47.
- Würschum, T., Leiser, W. L., Kazman, E. & Longin, C. F. H.** (2016). Genetic control of protein content and sedimentation volume in European winter wheat cultivars. *Theoretical and Applied Genetics*, 129(9), 1685-1696. DOI: [10.1007/s00122-016-2732-0](https://doi.org/10.1007/s00122-016-2732-0).

Received: October, 20, 2023; Approved: November, 13, 2023; Published: December, 2023