Department of Genetics and Plant Breeding
School of Agriculture

Heterosis and combining ability analysis for grain yield and quality traits in bread wheat (Triticum aestivum L. em Thell.)

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By

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Synopsis

Title:

Heterosis and combining ability analysis for grain yield and quality traits in bread wheat (Triticum aestivum L. em Thell.)

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CERTIFICATE

This is certified that this synopsis entitled "**Heterosis and combining ability analysis for grain yield and quality traits in bread wheat (Triticum aestivum L. em Thell.)**" submitted in partial fulfilment of requirements for degree – **Master of Science in Genetics and Plant Breeding** by **Mandeep Kumar**, Registration no. **11709359** to **Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University**, has been formulated and finalized by the student himself on the subject.

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DECLARATION

I hereby declare that the project work entitled — "**Heterosis and combining ability analysis for grain yield and quality traits in bread wheat (Triticum aestivum L. em Thell.)**" is an authentic record of my work carried at **Lovely Professional University** as requirements of Project work for the award of degree -**Master of Science in Genetics and Plant Breeding**, under the guidance of **Dr. Harshal Ashok Avinashe, Assistant Professor, School of Agriculture, Lovely Professional University, Phagwara, Punjab**

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Content

1. Introduction

Wheat variety is a self-pollination annual plant in the true grass family Gramineae (Poaceae). There are many type of wheat. These are Emmer wheat (Triticum dicoccum), Macaroni wheat (Triticum durum), Common bread wheat (Triticum vulgare), Indian dwarf wheat (Triticum spherococcum) and last one is Bread Wheat (Triticum aestivum). Triticum aestivumis heaxalpoid (2n=6x=42). Wheat is a very popular and highly demandable cereal crop in the world. It provides 20 percent food resources of the world (Farzi et al., 2010). Wheat is one of the cereal crop, highly grown in all over the world and it has 1strank in world crop production. Wheat is the National stable food of 43 countries. Wheat is the leading food crop in world farming. It is main food crop of temperate zone. It is a plastic crop. It is also extended to warm regions of temperate and sub tropics to tropical low lands. It is one of the most ancient crops of the world. Its cultivation began in the Neolithic period. Bread wheat is known to have been grown in the Nile valley by 5000 B.C., and its apparently later cultivation in other regions (e.g., the Indus and Euphrates valleys by 4000 B.C., China by 2500 B.C. and England by 2000 B.C.) indicate that it spread from Mediterranean centers of domestication. The civilizations of West Asia and of the European peoples have been largely based on wheat, while rice has been more important in East Asia. Since agriculture began, wheat has been the chief source of bread for Europe and the Middle East. It was introduced into Mexico by the Spaniards c.1520 and into Virginia by English colonists early in the 17th cent.

Wheat was grown an area 302.27 lakh hectarewith the production 93.50 million tonnes in India during 2016-17 (practices package by PAU, 2017). In Punjab, it was grown an area 35.06 lac tonnes with the production 160.08 lac tonnes and productivity is 45.83 quintals per hectare during 2015-16 (practices package by PAU, 2017). Since 2000, India has struggled to match the record production figure and thus faces a critical challenge in maintaining food security in the faces of its growing population. The current major challenges facing future wheat production in India are increasing heat stress, dwindling water supplies for irrigation etc (Joshi et al., 2007). Damage caused by temperature extremes and drought could be minimized or eliminated by framing strategy to develop thermo tolerance genotypes during early growth period and heat stress tolerance genotypes during grain filling stages. There is continuous increase in demand of wheat grain to feed the increasing population of about 109 million tonnes of wheat is to be needed to feed its projected population of 1.4 billion by 2020 AD. However to fulfill the task of meeting the increasing demand of wheat there is an urgent need to bread the high yielding wheat genotypes tolerant to high temperature and low moisture stress coupled with quality and suitable under semi irrigation.

Yield is a complex quantitative trait and under pleiotropic gene control at the same time it is highly influenced by environment and contributed by many other traits. Furthermore, selection based on only yield is misleading. Thus, for effective selection, information on nature and magnitude of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary (Yagdi 2009; Tsegaye et al., 2012). High magnitude of variability in a population provides the opportunity for the selection to evolve a variety having desirable characters.

Heterosis and combining ability analysis were studied in a 8 × 8 half diallel set of bread wheat. Analysis of variance (ANOVA) revealed the presence of significant variance due to general combining ability (GCA) among the parents for all the traits, and due to specific combining ability (SCA) among the crosses· Combining ability analysis is the best technique for the proper choice of the parents for improving specific traits as well as the

breeding value of the genetic variability which can be successfully used in future hybridization programs. Significant levels of heterosis have been reported in a number of self-pollinated crops, and were first observed in wheat by Freeman (1919). In wheat there are several reports on combining ability and heterosis (%) using F_1 generation.

Keeping in view the aforesaid problems, the present investigation has been planned with the following objectives:

Objectives:

1. To study *per se* performance of parents and hybrids
2. To estimate heterosis over mid parent (%), better parent (%) and standard parent (%) for yield and quality traits.
3. To assess the general combining ability effects of the parents and specific combining ability effects of crosses for yield and its component.
4. To judge the nature and magnitude of the gene action involved in the inheritance of the traits.
5. Authentication of F_1 hybrid by using SSR markers

2. Review of Literature

The success of any plant improvement programme mainly depends on the right selection of material and its skillful management. It is only possible when we possess knowledge of previous work done in the concerned field. In wheat substantial contribution has been made to the literature regarding its genetics and breeding in the recent years. The literature pertaining to the various aspect of the present study has been reviewed under the following heads:

2.1 Heterosis analysis

2.2 Estimation of combining ability

2.3 Gene action in plant population

2.4 SSR markers

2.1 Heterosis Analysis

The term heterosis given by Shull 1914. It may be defined as superiority of the F_1 hybrid over its both parent in term of yield or some other characters.

Ali and Ali (2015). six possible cross combinations (*F*1*s*) were obtained (Imdad × TD-1, Imdad × SKD-1, Imdad × Moomal, TD-1 × SKD-1, TD-1 × Moomal, and SKD-1 × Moomal). A three-replicated RCB Design was used. The mean squares corresponding to different traits of various hexaploid wheat genotypes indicated significant (P < 0.01) GCA (parents) and SCA (*F*1 hybrids) effects for the characters (plant height, tillers plant−1, spike length, spikelets spike−1, seeds spike−1, seed index, and grain yield plant−1). The mean performance of *F*1 hybrids differed significantly (P < 0.01) for all the traits studied. Among the parents, Imdad and TD-1 proved to be better general combiners for almost all the studied traits. In regards to SCA effects, the *F*1 hybrids Imdad × TD-1 and Imdad × SKD-1 expressed higher SCA and heterotic effects for most of the studied traits.

Kumaret al., (2011). revealed that crosses for the all the traits except for number of tillers per plant, plant height and number of spikelets per spike. Combining ability analysis revealed the involvement of both additive and non-additive gene action in the inheritance of most of the traits. On the basis of GCA, SCA effects and per se performance, parents K 9107 for 6 traits, K 9162 for 4 traits and GW 373 for 3 traits and crosses K 9107 × K 7903 for 2 traits, K 68 × K 7903 for 2 traits were found good general and specific combiners, respectively. Significant heterosis over economic parent and mid parent was observed for almost all the traits studied. The magnitude of heterosis was highest (21.74%) for number of spikelets per spike over economic parentand for number of tillers per plant (13.73%) over mid parent.

Singhet al., (2012). reported that analyses of combining ability and heterosis over mid parent (MP) as well as economic parent (HD 2733) were undertaken for yield and its component traits. The results revealed that non-additive genetic variance played a predominant role in the inheritance of most of the traits. The best combinations mostly involved high × low and low × low general combiners for the characters under study. There was very rare case in which high × high general combiners were involved for best combinations. On the basis of *gca*and *sca*effects, 3 parents (i e K 7903, K 9465 and HUW 234) and 14 cross combinations (i.e. 5 top crosses namely HD 2733 × K 7903, HUW 234 × K 9423, HD 2285 × K 2021, HUW 234 × K 2021 and K 9423 × K 2021) were found good

general and specific combiners for higher grain yield and also for various yield contributing traits, respectively.

Jainet al., (2012). revealed that among the selected hybrids WH-542 x Raj-3077 and WH 542 x K-65 were effect with highest magnitude of heterobeltiosis and per se performance for grain yield.

2.2 Combining Ability Analysis

Kandil et al., (2016). Revealed thatnumber of spikes/plant, spike length, number of grains/spike, 1000-grain weight and grain yield/plant, were studied using 8×8 diallel crosses, excluding reciprocals. The studied genotypes were; *i.e.* Sides 12, Gemmiza 11, Miser 1, Miser 2, Shandaweel 1, Giza 168, Sakha 93 and Sakha 94. In the second season 2013/2014, the eight parental and28 F1's was evaluated. Obtained results are great interest for bread wheat breeder to improve grain yield through its components.

Kumar et al., (2015). reported that the basis of gca and sca effects, two parents (i.e. PBW 373 and RAJ 3765) and 17 cross combinations (i.e. five best crosses namely, K 9423 x NW 1014, UnnatHalna x HUW 560, K 9423 x UnnatHalna, K 9162 x NW 1014, K 7903 x HUW 560), were found good general and specific combiners for higher grain yield and also for other yield contributing traits, respectively. These crosses may be used in heterosis breeding programme for developing new wheat genotype with broad genetic base by multiple crossing programmes. Therefore, crosses involving high x low general combiners in respect of different characters in the present study may be utilized for obtaining transgressivesegregants in the next generation resulting from dominance gene interaction.

Khodadadiet al., (2012). reported thatthe grain protein content, Zeleny sedimentation volume, loaf volume, grain moisture content, grain hardness, water absorption, SDS-sedimentation volume, wet gluten content, thousand kernel mass and hectoliter mass were measured. The result of combined analysis of variance (in two environments) showed that there are significant differences among genotypes for all of the traits excepts for Zeleny sedimentation volume, grain moisture content and wet gluten content, indicating the presence of enough genetic availability among genotypes and as a result genotype mean square can be further separated to general and specific combining ability mean squares.

Akbaret al., (2009). revealed that grain yield per plant, tillers per plant, spikelets per spike, 1000 grain weight, spike length, days to 50 percent heading, days to 50 percent maturity and plant height were evaluated. Among lines, Faisalabad 83 and Faisalabad-85 were good general combiners for most of the agronomic traits including grain yield per plant. The tester PBW65 / ROER /3/ PB6 // MIRLOW / BUC followed by PBW502 was found good general combiner for grain yield and some other traits studied. Faisalabad-85 □ PBW502 and Faisalabad-83 □ PBW65 / ROER /3/ PB6 // MIRLOW / BUC performed better for grain yield and most of other traits studied. GCA to SCA variances ratio revealed predominantly non-additive gene action for these traits. Development of new varieties with improved agronomic traits is, therefore, suggested through selection in late segregation generations of these cross.

2.3 Gene Action Analysis

Gene action refers to the behavior or mode of expression of genes in a genetic population, knowledge of gene action helps in the selection of parents for use in the hybridization programmes and also choice of appropriate breeding procedure for the genetic improvement of various quantitative characters.

Ahmad et al., (2016). revealed thatsix wheat genotypes and their F1 diallel hybrids were evaluated for gene action of yield and related attributes. Highlysignificant differences were detected amongst the genotypes for all the traits under study. Components of geneticvariation highlighted the importance of both additive and non-additive gene effects for the inheritance of studied traits.Graphical representation displayed additive gene action with partial dominance for tillers per plant, grain yield per plant,1000-grain weight and plant height and over dominance for flag leaf area. High narrow senseheritability was observed for majority traits except flag leaf area. Grain yield had strong correlation with tillers per plant.

Ibrahimet al., (2016). reported that the analysis of the F_1 generations and their parents revealed that additive gene effects was manifested for all traits studies in the first sowing date, but the reverse was true in the second sowing date. However, over-dominance type of gene action was recorded for grain yield in the first sowing date and partial dominance in the second sowing date. As to the number of kernels/spike partial dominance was displayed in the first sowing date and over dominance in the second sowing date. Narrow sense heritability estimates ranged from 0.49 in the first sowing date to 0.69 in the second sowing date for grain yield. Meanwhile, narrow sense heritability was 0.58 for 1000-grain weight and 0.69 for grain yield in the second sowing date.

Kandilet al., (2016). revealed thatthe genotypeswere Sides 12, Gemmiza 11, Maser 1, Maser 2, Shandaweel 1, Giza 168, Sakha 93, and Sakha 94. Results revealedthat both additive (D) and dominance (H1 and H2) genetic variance were significant for flagleaf length and flag leaf area, extrusion length, number of tillers/plant number of spikes/plant, number ofgrains/spike and 1000- grain weight. The overall dominance effects of heterozygous loci h2, indicated directional dominance forheading date, flag leaf length, flag leaf area, spike length, extrusion length, spike density, grain yield/spike,number of tillers/plant number of spikes/plant, number of grains/ spike and grain yield/plant. Proportion ofgenes with positive and negative effects in the parent (H2/4H1) was deviated from 0.25 for all studied charactersHeritability in narrow sense was moderate (0.369) for grain yield/plant.

Jadoonet al., (2012). reported thatplant height, days to heading, spike length, grains spike21 andbiological yield traits in 8 £ 8 half diallel F2 wheat populations was studied at Agricultural University,Peshawar, Pakistan, during 2006-07. Diallel analyses reflected significance of both additive and non-additive components in theinheritance of these traits, however, genetic components revealed the importance of a non-additivecomponent. The average degree of dominance being greater than unity indicated involvement ofover-dominance for phenotypic expression of all traits studied. Broad-sense heritability values weremuch higher than narrow-sense and thus delayed selection till advance generations are suggested.

Hussainet al., (2008). revealed that grain yield per plant, tillers per plant, numberof grains per spike, 100-grain weight and number of spikelets per spike, spike length, and peduncle length. Analysis for genetic components indicated that additive (d) and dominant (h) were significant for all the traits.However, un-equal distribution of dominant alleles was present in the traits except spikelets per spike. The genetic informationobtained would be utilized in wheat breeding program for the development of leaf rust resistant wheat varieties with higheryield potential.

Kutluet al., (2015). Results revealed that significant variance among the genotypes to make diallel analyses for all traits and the scaling test suggested that the additive-dominance model was adequate for data analysis for all characters except for maturing date, spike length and grain weight per spike. Additive (a and d) and non-additive (b and H1, H2) gen effects

were involved in the heritance of all traits according to diallel variance analyses and estimation of genetic parameters. The Wr/Vr graphs and (H1/D)0,5 value revealed that partial dominance for plant height, peduncle length, spikelet and grain number per spike, while over dominance for harvest index and grain yield per plant.

2.4 SSR Markers

Simple sequence repeats (Ssrs) or Short Tandem Repeats (Strs), are rehashing sequences of 2-5 base sets of Dna.it is a sort of Variable Number Tandem Repeat (VNTR). Microsatellites are commonly co-prevailing. They are utilized as atomic markers as a part of STR dissection, for connection, populace and different studies. They can additionally be utilized for investigations of gene duplication or erasure, marker aided determination, and fingerprinting.

Ahmed et al., (2011). studied 15 SSR primers of Xgwm series and 5 of X series to find out the codominant loci in the hybrid and single dominant loci in parents. Three primers from X series, namely, X66-5b, X-135-1a, and X-129-2b, gave the polymorphic band in hybrids but no single banding pattern in the parent, so it was concluded that these primers can be used to confirm the hybrids under study. Out of 15 primers, Xgwm-314 and Xgwm-311 gave the polymorphic banding pattern. The primer Xgwm-314 gave ambiguous polymorphic banding pattern that was not used to confirm the hybrids, while the primer Xgwm-311 showed the polymorphic dominant loci in the parents (LU26S, Mehraj 9272 and 9381) and codominant loci midway between these Parents. Therefore, this SSR primer was used to confirm the two best performing hybrids (LU26S x 9272 and Mehraj x 9381).

Hipi et al., (2013). revealed that the assessment of genetic purity of two hybrid varieties namely cv. Bima-3 and Bima-4, used specific markers. Forty samples of individual plants from each maize hybrid variety were tested. From five markers tested, three markers namely phi96100, phi328175 and phi072 produced polymorphic bands and capable to distinguish parental line of two maize hybrids. Microsatellite marker phi96100 was specifically used for testing hybrid purity of cv. Bima-4 and phi072 for cv. Bima-3. While phi 328175 was the specific marker for both maize hybrids. The genetic purity test of cv. Bima-3 and Bima-4 indicated that both varieties had purity levels of 97.5% and 80%, respectively. This study showed that SSR markers were more reliable for assessing hybrid purity as compared to morphological marker. The results of study are expected to be useful in the verification of purity of maize hybrid seeds accurately.

3. Material and Method:

(Including location, place of work and facility available)

The experimental material of present study comprised of 28 hybrids developed from half diallel mating design (8 X 8). The crosses were made during *rabi* season 2017-18 by half diallel mating design which will be evaluated during *rabi* season 2018-19 along with parents at field of Lovely Professional University, Phagwara, India.

3.1 Experimental detail

1st season (crossing)

Crop	:	Wheat
Mating design	:	Half Diallel Design
Genotype	:	Different varieties of wheat
Parent	:	8
Experimental year	:	2017-18 (crossing), 2018-19 (evaluation)
Row to Row distance	:	20 cm
Season	:	*Rabi*

2nd season (evaluation)

Number of genotype	:	36 (hybrid 28, parent 8)
Design	:	RBD (Randomize Block Design)
Replication	:	3

3.2 Genotype Detail

Sr. No.	Genotype	:	Pedigree/ Source
1.	MP-1203	:	FASN/2*TEPOCA/3/CHEN/TR.TA/TRANSVAAL-AFRICA[4281]
2.	LOK-1	:	S-308/S-331[793][1378][2848]; SONALIKA/CHOTI-LERMA[1324]
3.	HD-2932	:	HD-2252/UP-262[4281]; KAUZ/STAR//HD-2643[4314]
4.	MP-3173	:	JNKVV, Sagar
5.	HI-1544	:	HINDI-62/BOBWHITE/CPAN-2099[4138][4277]
6.	HI-8498	:	RAJ-6070/RAJ-911[4281][4318]
7.	MP-4010	:	TEETER(SIB)/(SIB)JUNCO[4191][4277]
8.	GW-273	:	CPAN-2084/VW-205[3320]

3.3 Statistical Analysis:

1. Analysis of variance (Panse and Sukhatme, 1952)
2. Estimation of heterosis (Fonseca and Patterson 1968)
3. Combining ability analysis (Griffing's method)
4. Analysis of gene action (Hill 1982, Lynch 1991)

3.4 Collaboration with other Departments:

➢ Indian Institute of Wheat and Barley Research, Karnal, Haryana (IARI Regional Research Station)

3.5 Observations:

A	Quantitative traits	B	Physiological Traits
1	Days to 50% heading	14	Canopy temperature
2	Days to maturity	15	Chlorophyll content
3	Plant height (cm)	C	**Quality Traits**
4	Number of productive tillers plant^{-1}	16	Sedimentation value (mm)
5	Number of spikelets ear^{-1}	17	Hectolitre (g/litre)
6	Ear length (cm)	18	Protein content (%)
7	Ear weight (g)	19	Wet gluten content (%)
8	Number of ears plant^{-1}	**20**	Starch (%)
9	Number of grains ear^{-1}		
10	1000-grain weight (g)		
11	Biological yield plant^{-1} (g)		
12	Grain yield plant^{-1} (g)		
13	Harvest index (%)		

4. References

Ahmad, I.; Mahmood, N. and Khan, N. (2016). Genetics analysis for five important morphological attributes in wheat. The Journal of Animal & Plant Sciences, 26(3): 725-730.

Ahmed, M.S.; Khaliq, I.; Farooq, J.; Awan, S.I.; Ahmed, N. and Awan, F.S. (2011). Assessment of the combining ability and authentification of F1 Hybrids using SSR markers in wheat (triticumaestivum L.). Frontiers of agriculture in China, 5(2): 135-140.

Akbar, M.; Anwar, J.; Hussain, M and Khan, S. (2009). Line X Tester analysis in bread wheat (Triticumaestivum L.). Journal agric. res., 47(1): 411.

Ali, F.; Ali, A.; Ali, S.; Mahar, A.; Ali, A. and Ali, F. (2015). Heterosis and Combing Ability in *F*1 Population of Hexaploid Wheat (*TriticumAestivum*L.). American Journal of Plant Sciences, 6: 1011-1026

Avinashe, H.A. (2015). Authentification of F1 Wheat crosses and genetic analyses for yield and quality attributes under different environments. Krishikosh.

Fakhar, U.; Fida, M. and Sheraz, A. (2015). Genetic divergence in wheat Recombinant inbred lines for yield and yield components.Academia Journal of Agricultural Research 3(10): 303-307.

Farzi A. and ShekariMosta'liBigloo B. (2010). Evaluation of genetic diversity of wheat lines by related traits to drought tolerance. The 11th Iranian Congress of Agronomy Science and Plant Breeding pp: 155-157.

Fonseca, S. and Patterson, F. L. (1968). Hybrid vigour in a seven parent diallel crosses in common wheat (*T. aestivum* L.). *Crop Sci.*, 8 : 85-88.

Habtamu. S.; Murugan, A. and Kannan, S. (2012). Combining Ability Analysis for Bread Wheat (TriticumAestivum L.), East African Journal of Sciences Volume 3 (1):87-94.

Ibrahim, E.M.A. (2016). Gene Action for Yield and Yield Component Traits in Bread Wheat (*Triticumaestivum*l.) Under late Sown Conditions. *J.Agric.Chem.andBiotechn., Mansoura Univ.Vol. 7(7)*: 219 – 225

Jadoon, S.; Mohammad, F.; Ullah, H. and Khalil, I. (2012). Gene action for pre and post-Harvest traits in F2 wheat populations.A qatar foundation academic journal.

Jain, S.K.; and Sastry, EVD. (2012). Heterosis and combining ability for grain yield and its

contributing traits in bread wheat (Triticumaestivum L.). Journal of Agriculture and Allied Sciences, 1(1).

Joshi, A. K.; Mishra, B.; Chatrath, R.; Ferrara, G. O. and Singh, R. P. (2007). Wheat improvement in India: present status, emerging challenges and future prospects. *Euphytica.*157: 431- 446.

Kandil, A.A.; Sharief, A.E. and Gomaa, H. (2016). Estimates of gene action for yield and its components in bread wheat (Triticumaestivum L.). International Journal of Agronomy and Agricultural Research, 3(1): 34-40.

Kandil, A.A.; Sharief, A.E. and Gomaa, H. (2016). Estimation of general and specific combining ability in bread wheat (Triticumaestivum L.). International Journal of Agronomy and Agricultural Research, 8(2): 37-44.

Khodadadi, E.; Sabzi, M.; and Khodadadi, E. (2012). Combining ability analysis of bread quality in wheat. Annals of Biological Research, 3 (5):2464-2468

Kumar, A.; Mishra, H. and Singh, V. (2011). Heterosis and combining ability analysis in Bread Wheat (TriticumaestivumL.), Journal of Plant Breeding and Crop Science Vol. 3(10):209-217.

Kumar, A.; Vyas, R. P. and Singh, V. (2011). Heterosis and combining ability analysis in bread wheat (Triticumaestivum L.). Journal of plant breeding and crop science, 3(10): 209-217.

Kumar, P.; Singh, G.; Singh, Y.P.; Abhisek, D. and Singh, S. (2015). Study of combining ability in half diallel crosses of spring wheat(Triticumaestivum L.). International journal of research advance, 3(9): 1363-1370.

Panse, V. G. and Sukhatme, P. V. (1952). Statistical methods for agricultural workers, ICAR, New Delhi.

Sharma, J.; Sharma, S.; Singhania, M. and Sain, A. (2004). Combining ability in the F_1 and F_2 generations of diallelcross in hexaploid wheat (Triticumaestivum L. em. Thell). Hereditas 141: 115_/121.

Singh, V.; Krishna, R.; Singh, S. and Vikram, P. (2012). Combining ability and heterosis analysis for yield traits in bread wheat (*Triticumaestivum*). *Indian Journal of Agricultural Sciences* 82 (11): 916–21.

Tsegaye, D.; Tadese, D.; Yigzan, D. and Getnet, S. (2012). Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum* Desf.). *Agricultural research and reviews* **1**4: 107-112.

Yagdi, K. (2009). Path coefficient analysis of some yield components in durum wheat (*Triticumdurum* Desf.) *Pak. J. Bot.* 41(2):745-751.