CAUSE AND EFFECT RELATIONSHIP OF MORPHOLOGICAL ATTRIBUTES WITH YIELD IN A- GENOME WHEAT

Zareen Sarfraz^{1*}, Mohammad Maroof Shah¹, Muhammad Shahid Iqbal², Mian Faisal Nazir², Syeda Akash Fatima³

¹Department of Biotechnology, COMSATS University Islamabad, Abbottabad Campus, Abbottabad, Pakistan

²Ayub Agricultural Research Institute, Faisalabad, Pakistan, ³Department of Plant Breeding and Genetics, MNS University of Agriculture, Multan, Pakistan. *Corresponding: zskpbg@hotmail.com

Article Received 15-04-2020, Revised 28-04-2020, Accepted 8-05-2020

Abstract

Wheat considered to be the most important among all cereal crops, is grown across various agroecological zones around the globe. It is the main staple food playing a prominent role in the economy of the country as well as in the cropping system. The present study was conducted to estimate genotypic correlations among morphological traits and yield using 50 accessions of diploid wheat including 2 parents and 48 RILs at F7:8 stage to determine direct as well as indirect effects. The results presented here showed that generally the coefficients of genotypical correlation (rg) depicted higher values in comparison to the coefficients of phenotypic correlation (rp). Among the morphological traits contributing to the grain yield, genotypic as well as phenotypic coefficients of correlation have been evaluated. All the traits displayed positive correlation with each other except emergence percentage (EP) that depicted negative interaction with booting time (BT), flowering time (FT) and heading time (HT) phenotypically. Highest estimates of direct effect i.e., 2.1217 on grain yield have been counted for booting time however, maximum indirect effect counted on grain yield was for heading time via booting time. Therefore, booting time can be successfully employed as an effective trait in the breeding programs focused on increasing wheat yield.

Keywords: Wheat, Correlation, Path analysis, Direct and indirect effect, Yield.

Introduction

Wheat (*Triticum aestivum* L.) considered to be the most important cereal crop worldwide, is cultivated in diverse agro-ecological zones across the globe. It is chief staple food occupying a prominent role in the country's economy as well as cropping system. Extensive breeding efforts in wheat improvement domain have been carried out so far with astonishing outcomes trying to feed the day by day increasing world population (Khan et al., 2015). However, to cope with drastically changing climatic conditions and increasing world population plant breeders are required to work even harder for more breakthrough in wheat improvement programs. Its importance is a

broad spectrum not only including its nutritional importance but, its essentiality accounts for food security, poverty alleviation as well as improvement in the livelihoods. The FAO predicted that by 2050, the world will need an additional 198 million tonnes of wheat to meet future demands for which wheat production needs to increase by 77% in developing economies (Sharma et al. 2015). Hence in order to achieve this goal, wheat productivity must be continually increased every year (Nazir et al., 2019) so horizonal approach is the only option to accomplish this. It could be either through an increase in area under cultivation or by using vertical approach, including extensive varietal improvement / exploitation of heterosis by

hybrids development. The former approach is considered as the most practical and the strongest option to opt in order to take a quantum jump for the enhancement of productivity across varying agro-ecological conditions. Manifestation in yields of the crop is observed as widely fluctuated resulting from its environmental interactions. Wheat grain yield is generally considered as polygenic trait which is assumed to be inherited quantitatively and in fact is a product of many factors which are contributing to yield directly as well as indirectly (Khan et al., 2013; Naeem et al., 2016). In any crop improvement program, diverse varieties with better yield potential as well as adaptability across wide range of environments are considered important for the productivity enhancement (Mahmood et al., 2013; Rauf et al., 2013; Naeem et al., 2015; Zafar et al. 2020). *Triticum aestivum* $(2n=6x=42)$ which is actually an allohexaploid assumed to be produced through two different events of natural hybridization. The initial hybridization between *Triticum urartu* $(2n=2x=14)$ which is considered as the 'A' genome donor, whereas *Triticum speltoides* $(2n=2x=14)$ considered to be the 'B' genome donor had occurred; gave rise to the Tetraploid wheat $(2n=4x=28)$ as a new species i.e., *Triticum turgidum* (Sarfraz et al., 2016a; Rajput, 2018) or may be Hardum wheat (Durum wheat). *Triticum monococcum* ($2n = 2x = 14$), which is usually referred to be uncorned wheat, was a former diploid plant that had been domesticated in the Fertile Crescent around ten thousand years ago (Sarfraz et al., 2016b; Heun et al., 1997). In Neolithic period this species dominated the human farming practices. However, approaching to Bronze Age the area under its cultivation decreased due to the domestication of hexaploid as well as tetraploid wheat land races (Zohary and Hopf, 1993; Sarfraz et al., 2016a). Even during the recent times several Mediterranean countries used to cultivate *T*. *monococcum* at low scale across some mountainous areas. This species is assumed to retain its genetic diversity

Sarfraz et al., J. appl. Res in Plant Sci. Vol. 1(1), 13-19 [www.joarps.org.](http://www.joarps.org/)

due to its going through very limited improvement and breeding activities (Mahmood et al., 2013; Kilian et al., 2007). Unique quality characteristics of Enkorn wheat made it preferable by quality conscious people for many health benefits (Sarfraz et al., 2014a, b; 2014; Løje et al., 2003). Two different species have been recognized within *T*. *monococcum*, including wild *T*. *monococcum* ssp. *boeoticum* Boiss. (*T*.*m*. *boeoticum*) along with its domesticated counterpart, *T*. *monococcum* ssp. *monococcum* (*T*.*m*. *monococcum*). Moreover, some intermediate undomesticated genotypes derived through hybridization among some wild and cultivated genotypes have also been listed in this taxon *T*. *monococcum* ssp. *aegilopoides* (*T*.*m*. *aegilopoides*) (Sarfraz et al., 20014a; Salamini et al., 2002). Yield, a complex trait possesses polygenic nature thus requires extensive exploration of contributing genetic components. Usually, association between different traits is worked out to get the knowledge about correlation among them but very often the estimates of correlation coefficients alone are assumed to be misleading for the reason that it cancels the shared component characters. This issue necessitates the research to be conducted for correlation coupled with path-coefficient-analysis as an efficient tool in order to examine yield contributing traits (Khan et al., 2013; Rahman et al., 2013). Correlation and path coefficient analyses are characterized by estimating magnitude of correlation within different related traits and its piercing into direct and indirect effects (Hassan et al., 2013) for determination of their effectiveness towards yield (Iqbal et al., 2013; Naeem et al., 2016). The path coefficient analysis is imperative tool to split correlation coefficients into both indirect as well direct effects of underlying factors on complex traits. To improve multifaceted traits (and so, yield), adequate information regarding variability of contributing components can prove to be strongly supportive (Rabani et al., 2015). Hence, determination and assortment of such yield

[www.joarps.org.](http://www.joarps.org/)

contributing components is a pre-requisite which would be definitely followed by calculation of their direct as well as indirect effects (Kumar et al., 2013). Both the techniques of correlation and path coefficient analyses portray a clear picture of mutual relationships of yield contributing components and influences on yield (Ahmad et al., 2003; Rajput et al., 2015; Ibrar et al., 2016). With the above reference, the present study was conducted to estimate genotypic correlations among yield contributing components along with determination of their corresponding direct as well as indirect effect on yield which will ultimately helpful in any breeding program for the achievement of sustainable wheat productivity.

Materials and Methods

Current study involved plant materials consisting of 50 accessions of diploid wheat $(2n=2x=14)$, out of which 2 accessions were parents whereas 48 were RILs at F7:8 generation. The experiment has been executed during winter 2011-2012 at field area of Biotechnology department, COMSATS University Islamabad, Abbottabad Campus.

The current experiment has been executed using a triplicated randomized complete block design. Land preparation was carried out using standard practices and recommendations with east west ridges having 30 cm from each other. Sowing was carried out in the spring season of the year. Dibbling method of sowing was used with 3-4 seeds per dibble. After germination thinning was carried out to maintain only single seedling in each dibble. Standard cultural, agronomic and plant protection practices were carried out through the season following reconditions for fertilizer use for wheat crop in the area for optimum crop growth and development. Counting of Emergence percentage (EP) was carried out followed by emergence by considering 3 seeds in each dibble as maximum slandered. Other data was collected from 10 guarded plants selected randomly for all traits under study including, heading time (HT) taken as days after sowing, Flag leaf sheath length (FLS), Flag leaf diameter (FLD), Flag

15

leaf length (FLL), flowering time (FT), booting time (BT). All these selected plants have been harvested, threshed and processed individually in order to get grain yield (GY) for each plant in grams.

Collected data was subjected to correlation analysis to get genotypic as well as phenotypic correlation coefficients by using equation given by Searle (1971). Genotypic correlation was further split out to get both direct as well as indirect effects following calculation method "path analysis" (Dewey and Lu, 1959), where dependent variable was yield, while all other traits under study were considered as predictor or independent variables. The collected data was further subjected to stepwise regression analysis in order to test the significance of the predictor variables to affect yield.

Results and Discussion

Among the morphological traits, contributing to the grain yield, both negative and positive genotypic as well as phenotypic correlations were observed (Table 1). Emergence percentage (EP) was found to be showing negative interaction with booting time (BT), heading time (HT) and flowering time (FT) phenotypically whereas its positive interaction was found with these traits at genotypic level. Emergence percentage depicted positive interaction with flag leaf length (FLL), flag leaf sheath length (FLS), flag leaf diameter (FLD) and grain yield. Booting time showed significantly high positive correlation with flowering time (Ayer et al., 2017), heading time and grain yield (Rahman et al., 2014) alongside a positive trend in correlation with flag leaf area attributes including diameter, leaf length and sheath length; depicting that increase in one trait will improve and increase the other trait automatically. Yoshida (1972), reported that in case of cereals, the longer leaves cause drooping and less sunlight penetration whereas short leaves are erected causing more photosynthesis occurrence. Davood et al. (2009) also reported increasing grain yield association with wider and vertical leaf blade for provision of more photosynthates production to the grain filling and consequently more grain yield. Heading and flowering time depicted positive correlation with each other and with yield reported previously in Khokhar et al. (2010), Rahman et al. (2014) and Ojha et al. (2018) findings. Both these traits also exhibited significant positive correlations with all the leaf area features including length, diameter and sheath length. Ojha et al. (2018) also discovered positive correlation between flag leaf length and heading time. It has been observed that significant positive correlation was present among flag leaf area features i.e., length, diameter and sheath length. Also, a positive significant correlation was observed between flag leaf area features and grain yield (Ayer et al., 2017; Ojha et al., 2018). These findings of flag leaf area described the relationship of vegetative parts (photosynthate

Sarfraz et al., J. appl. Res in Plant Sci. Vol. 1(1), 13-19 [www.joarps.org.](http://www.joarps.org/)

factories) of plant with yield based on the leaf length and width for more absorption of sunlight to regulate photosynthesis and starch formation and storage. Our results are also in congruence with this fact i.e., the more the area of flag leaf the more will be the grain yield.

Path analysis

This technique was first used for plant selection. The path coefficient (partial regression coefficient) analysis implies simply a measure of both direct as well as indirect effects of one variable via another on the end product by splitting of correlation coefficient. Current investigation comprised of studying the effects of seven independent variables i.e., EP, HT, BT, FT, FLD, FLS, FLL on the obvious dependent variable GY (Table 2).

Table 1: Correlation matrix for genotypic (upper) and phenotypic (lower) correlations for morphological traits and yield

VARIABLES	CORRELATION	BT	HT	FT	FLL	FLS	FLD	GY
EP	r_g	$0.2138*$	$0.2145*$	0.0303	$0.4636**$	0.4251 **	0.1617	$0.4510**$
	$r_{\rm p}$	-0.038	-0.0906	-0.1716	0.0797	0.0729	0.0833	0.1216
BT	r_g		$0.2035*$	$0.9669**$	0.1127	0.1764	$0.2349*$	$0.4068**$
	r_{p}		$0.8659**$	$0.7275**$	0.0672	0.1200	0.0873	$0.2402*$
HT	$\rm r_g$			$0.9479**$	0.148	$0.2037*$	$0.2359*$	$0.4362**$
	$r_{\rm n}$			$0.8236**$	0.1173	0.1421	0.1123	$0.3137**$
FT	$\rm r_g$				0.1277	0.1291	$0.2008*$	$0.3802**$
	r_{p}				0.134	0.1006	0.1335	$0.2313*$
FLL	r_g					$0.4565**$	$0.6539**$	$0.3132**$
	$r_{\rm p}$					0.4006 **	$0.5138**$	0.1907
FLS	r_g						0.8001 **	$0.2659**$
	$r_{\rm p}$						$0.4628**$	0.1168
FLD	r_g							$0.432**$
	$r_{\rm p}$							0.1708

EP: emergence percentage, HT: Heading, BT: booting time, FT: flowering time, FLL: Flag leaf length, FLS: Flag leaf sheath length, FLD: Flag leaf diameter, GY: grain yield per plant.

Emergence percentage (EP) revealed a positive direct effect (0.0767) towards grain yield at genotypic level (Rani et al., 2018) whereas a positive indirect effect towards GY via BT, FLL, FLS and FLD while negative indirect effect via HT and FT. It justifies existence of appropriate associations among GY and these studied attributes, therefore direct selection via mentioned traits would definitely provide sound effects on GY. **Booting time** (BT) exerted

highest positive direct effect (2.1217) towards GY (Rahman et al., 2014; Ayer et al., 2017) revealing that late booting will enhance yield; whereas positive indirect effect through EP, FLL, FLS and FLD however, negative indirect effect though HT and FT on GY. **Heading time** (HT) depicted negative direct effect (-1.3224) towards GY (Rahman et al., 2014; Ojha et al., 2018) whereas positive indirect effect via EP, BT, FLL, FLS and FLD however, negative

[www.joarps.org.](http://www.joarps.org/)

indirect effect was observed via FT towards GY. **Flowering time** (FT) displayed negative direct effect (-0.4693) towards GY whereas positive indirect effect via EP, BT, FLL, FLS and FLD while, negative indirect effect via HT towards GY. Ayer et al. (2017) earlier stated negative direct effect of flowering time towards grain yield. **Flag leaf length** (FLL) exhibited positive direct effect (0.2285) towards GY (Okuyama et al., 2005) while positive indirect effect through EP, BT, FLS and FLD whilst negative indirect effect via HT and FT on GY. Sabit et al. (2017) and Ayer et al. (2017) conveyed positive direct effect of FLL on GY. **Flag leaf sheath length** (FLS) represented positive direct effect (0.0101) on GY (Okuyama et al., 2005; Ayer et al., 2017) and positive indirect effect via EP, BT, FLL and FLD however, negative indirect effect through HT and FT on GY. **Flag leaf diameter** (FLD) revealed positive direct effect (0.0933) on GY genotypically and positive indirect effect via EP, BT, FLL and FLS while negative indirect effect via HT and FT on GY. Positive direct effect of FLD on GY had also been presented earlier by Okuyama et al. (2005) and Ayer et al. (2017).

Table 2: Summary matrix of direct (Bold at diagonal) and indirect effects of morphological attributes related to grain yield.

VARIABLES	EP	BТ	HT	FT	FLL	FLS	FLD	GY
EP	0.0767	0.4536	-0.2837	-0.0142	0.1059	0.0043	0.1084	0.4510
BT	0.0164	2.1217	-1.327	-0.4538	0.0258	0.0018	0.0219	0.4068
HT	0.0164	2.1291	-1.3224	-0.4449	0.0338	0.002	0.022	0.4362
FT	0.0023	2.0515	-1.2535	-0.4693	0.0292	0.0013	0.0187	0.3802
FLL	0.0355	0.2392	-0.1957	-0.0599	0.2285	0.0046	0.061	0.3132
FLS	0.0326	0.3742	-0.2694	-0.0606	0.1043	0.0101	0.0746	0.2659
FLD	0.0891	0.4984	-0.312	-0.0943	0.1495	0.008	0.0933	0.4320

EP: emergence percentage, HT: Heading, BT: booting time, FT: flowering time, FLL: Flag leaf length, FLS: Flag leaf sheath length, FLD: Flag leaf diameter, GY: grain yield per plant.

Based on these findings, we concluded that whatever may be the character chosen for increasing grain yield by selecting ideotypes must possess high emergence percentage, appropriate heading time and more leaf area. These traits displayed positive direct effects and positive significant association with grain yield. The reported results also revealed the significance of including certain characters in the in the improvement of yield. Consequently, the mentioned effective traits are more likely to be used successfully in any breeding program focused at improvement of yield in wheat.

References:

Ahmad, H. M., Khan, B. M., Khan, S., Sadiq, K. N., & Sawan, L. (2003). Path coefficient analysis in bread wheat. Asian J. Plant Sci., 2: 491-194.

- Ayer, D. K., Sharma, A., Ojha, B. R., Paudel, A., & Dhakal, K., (2017). Correlation and path coefficient analysis in advanced wheat genotypes. SAARC J. Agric., 15(1): 1-12.
- Davood, B. T., Ali, G., Hemmal, A. P., & Morteza, N. (2009). Flag Leaf Morphophysiological Response to Different Agronomical Treatment in a Promising Line of Rice (*Oryza sativa* L.). American- Eurasian J. Agric. & Environ. Sci., 5(3): 403-408.
- Dewey, D. R., & Lu, K. N. (1959). A correlation and path coefficient analysis of component of crested wheat grass seed production. Agronomy J., 51: 515-518.
- Hassan, S. F., Iqbal, M. S., Rabbani, G., Shabbir, G., Riaz, M., & Noorka, I. R. (2013). Correlation and path analysis for yield and yield components in sunflower (*Helianthus annus*. L). Afr. J. Biotechnol., 12(16).
- Heun, M., Schäfer-Pregl, R., Klawan, D., Castagna, R., Accerbi, M., Borghi, B., & Salamini, F. (1997). Site of einkorn wheat domestication identified by DNA fingerprinting. Sci., 278: 1312–1314.
- Ibrar, D., Ahmad, R., Mirza, M. Y., Mahmood, T., Khan, M. A., & Iqbal, M. S. (2016). Correlation and Path analysis for yield and yield components in Linseed (*Linum usitatissimum* L.). J. Agric. Res., 54(2): 153-159.
- Iqbal, J., Hussain, F., Ali, M., Iqbal, M. S., & Hussain, K. (2013). Trait association of yield and yield components of linseed (*Linum usitatissimum* L.). Int. J. Modern. Agric., 2(3): 114-117.
- Khan, A., Khaliq, I., Saddam, M. S., H. G. M. D. Ahmed, Zafar, S. A., Aslam, W., & Muhammad, D. (2015). Estimation of genetic mechanism of stomatal traits influencing grain yield in hexaploid wheat (*Triticum aestivum* L.). Int. J. Biosci. 6(6): 72-77.
- Khan, M. I., Shabbir, G., Akram, Z., Shah, M. K. N., Ansar, M., & Cheema, N. M. (2011). Character association studies of seedling traits in different wheat genotypes under moisture stress conditions. SABRAO J. Breed. Genet., 45(3): 458-467.
- Khokhar, I. M., Hussain, M., Anwar, J., Zulkiffal, M., Iqbal, M. M., Khan, B. S., Khan, A. M., Qayyum, A., Sabir, W., & Mehmood, S. (2010). Correlation and path analysis for yield and yield contributing characters in wheat (*Triticum aestivum* L.). Acta Agric. Serb., 15(29): 19-24.
- Kilian, B., Ozkan, H., Walther, A., Kohl, J., Dagan, T., Salamini, F., & Martin, W.

Sarfraz et al., J. appl. Res in Plant Sci. Vol. 1(1), 13-19 [www.joarps.org.](http://www.joarps.org/)

(2007). Molecular diversity at 18 loci in 321 wild and 92 domesticate lines reveal no reduction of nucleotide diversity during *Triticum monococcum* (Einkorn) domestication: implications for the origin of agriculture. Mol. Biol. Evol., 24: 2657–2668.

- Kumar, B., Singh, C. M., & Jaiswal, K. K. (2013). Genetic variability, association and diversity studies in bread wheat. The Bioscan., 8: 143-147.
- Løje, H., Møller, B., Laustsen, A. M., & Hansen, Å. (2003). Chemical composition, functional properties and sensory profiling of einkorn (*Triticum monococcum* L.). J. Cereal Sci., 37: 231– 240.
- Mahmood, A., Mian, M. A., Ihsan, M., Ijaz, M., Rabbani, G., & Iqbal, M. S. (2013). Chakwal-50: A high yielding and disease resistant wheat variety for rainfed region. The J. Anim. Plant Sci., 23(3): 833-839.
- Naeem, M. K., Ahmad, M., Shah, M. K. N., Kamran, M., & Iqbal, M. S. (2016). Character association and path analysis of osmotic adjustment, growth and physiological traits in wheat. The J. Anim. Plant Sci., 26(3): 680-685.
- Naeem, M. K., Ahmed, M., Noreen, S., Shah, M. K. N., & Iqbal, M. S. (2015). Estimation of genetic components for plant growth and physiological traits of wheat (Triticum aestivum L) under normal and stress conditions. SAARC J. Agric., 13(1): 90-98.
- Nazir, M. F., Mahmood, T., Shah, M. K. N., Sarfraz, Z., Ali, W., Metlo, M. A. U., & Iqbal, M. S. (2019). Inheritance studies for morpho-physiological traits in wheat under rainfed condition. Pak. Jr. Biotech., 16(2): 105-113.
- Ojha, R., Sarkar, A., Aryal, A., Rahul, K. C., Tiwari, S., Poudel, M., ... & Shrestha, J. (2018). Correlation and path coefficient analysis of wheat (*Triticum aestivum* L.)

genotypes. Fmg. & Mngmt., 3(2): 136- 141.

- Okuyama, L. A., Federizzi, L. C., & Barbosa Neto, J. F. (2005). Plant traits to complement selection based on yield components in wheat. Cienc. Rural, 35(5): 1010-1018.
- Rabani, G., Tariq, M., Naeem, M. K., & Iqbal, M. S. (2015). Character association and path analysis of yield and yield components in mungbean [*Vigna radiata* (L.) WILCZEK]. J. Agric. Res., (03681157), 53(2).
- Rahman, S. A., Iqbal, M. S., Riaz, M., Mahmood, A., Shahid, M. R., Abbas, G., & Farooq, J. (2013). Cause and effect estimate for yield contributing and morphological traits in upland cotton (*Gossypium hirsutum* L.). J. Agric. Res, 51(4).
- Rahman, M. S., Shoma, M. H. M. I. J., & Ali, L. (2014). Genetic variability correlation and path analysis for some quantitative traits in wheat. Eco-friendly Agril. J., 7(12): 158-162.
- Rajput, R. S. (2018). Correlation, path analysis, heritability and genetic advance for morpho-physiological character on bread wheat (*Triticum aestivum* L.). J Pharmacogn. Phytochem., 7(2): 107-112.
- Rani, K., Singh, V., & Singh, G. (2018). Genetic parameters of variability and path analysis for morpho-physiological and seed vigour character in bread wheat (*Triticum aestivum* L.). J Pharmacogn. Phytochem., 7(3): 1653-1657.
- Rauf, Y., Subhani, A., Iqbal, M. S., Tariq, M., Mahmood, A., & Shah, M. K. N. (2013). Screening of wheat genotypes for drought tolerance based on drought related indices. SABRAO J. Breed. Genet., 45(2).
- Sabit, Z., Yadav, B., & Rai, P. K. (2017). Genetic variability, correlation and path analysis for yield and its components in f5 generation of bread wheat (*Triticum*

aestivum L.). J Pharmacogn. Phytochem., 6(4): 680-687.

- Salamini, F., Özkan, H., Brandolini, A., Schafer-Pregl, R., & Martin, W. (2002). Genetics and geography of wild cereal domestication in the near east. Nat. Rev. Genet., 3: 429– 441.
- Sarfraz, Z., Shah, M. M., & Iqbal, M. S. (2016a). Genetic variability, heritability and genetic advance for agronomic traits among Agenome donor wheat genotypes. J. Agric. Res., 54(1): 15-20.
- Sarfraz, Z., Shah, M. M., & Iqbal, M. S. (2016b). Estimation of components of variation of morphological traits and yield in A-genome wheat populations. SABRAO J. Breed. Genet., 48(2): 105-109.
- Searle, L. (1971). Astrophys. J., 168: 327.
- Sharma. I., Tyagi B.S., Singh, G., Venkatesh. K., & Gupta, O.P. (2015). Enhancing wheat production- a global perspective. Indian. J. Agri. Sci., 85:3–13
- Subhani, G. M., & Chowdhry, M. A. (2000). Correlation and path coefficient analysis in bread wheat under drought stress and normal conditions. Pak. J. of Biol. Sci., 3(1): 72-77.
- Yoshida, S. (1972). Physiological Aspects of Grain Yield. 1st Ann. Rev. Plant Physiol., 23: 437- 64.
- Zafar, S. A., Hameed, A., Khan, A. S., Ashraf, M., Qamar Z., Li X., & Siddique K. H. M. 2020. Agronomic, physiological and molecular characterization of rice mutants revealed key role of ROS and catalase in high temperature stress tolerance. *Funct. Plant Biol*., 47(5) 440-453.
- Zohary, D., & Hopf, M. (1993). Domestication of plants in the Old World: The origin and spread of cultivated plants in West Asia, Europe and the Nile Valley. 2. New York, Oxford University Press.