Multivariate Analysis for Evaluation of Mutant Bread Wheat Lines Using Metric Traits

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Abstract

An assessment of genetic variation within diverse germplasm is needed to allow more efficient genetic improvement. The study assessed genetic divergence in wheat (Triticum aestivum L.). Principal component analysis was applied to explore major modes of joint variability in yield and yield contributing traits. A multivariate approach was used to investigate the correlations between yield and yield contributing traits. The experiment was planted M_4 mutant lines from Marvi, and Sassui varieties were sown along with two check varieties viz. NIA-Amber and NIA-Saarangat Nuclear Institute of Agriculture, Tandojam during the rabi season 2014-15. following randomized complete block design with three replications. This study has shown considerable genetic variation among the genotypes considered, which may help further selection and breeding. Parents may be selected from clusters with significant genetic distances for crossing to obtain genetic recombination and transgressive segregation in the subsequent generations. However, further study across locations and years needs to be done to corroborate the results obtained in the present investigation.

Introduction

Wheat (*Triticum aestivum* L.) belongs to the family *Poaceae*; it is the most important staple crop (Ortiz et al., 2008). Wheat (*Triticum spp* L.) is a crop having more than 22 sub-species around the globe. It originated from the Levant region of the Near East but is now cultivated worldwide. Common wheat (*Triticum aestivum* L.), also known as bread wheat, is an allohexaploid (an allopolyploid with six sets of chromosomes, two sets from each of three different species). The World production of wheat was 651 million tons, making it the third most-produced cereal after maize (844 million tons) and rice (672 million tons) (Öfversten et al., 2002). In addition to agronomic adaptability, wheat offers ease of grain storage and converting grain into flour to make edible, palatable, interesting, and satisfying foods. Wheat is the most important source of carbohydrates in most countries (PirzadoSutahar et al., 2021; Shewry, 2009). Wheat wild progenitors are potent resistance and genetic diversity sources due to their worldwide distribution. For millions of years, natural selection and the process of evolution evolved genes for resistance, especially the Aegilops tauschii (DD), the D-genome progenitor of bread wheat. Synthetic hexaploidy wheat (AABBDD) was produced by hybridizing various Ae. tauschii (DD) accessions with elite durum wheat (*Triticum turgidum*: AABB) cultivars (Gill et al., 2004; Khan et al., 2012; G Muhammad et al., 2022). Seed yield in bread wheat is complex because it is expressed with many component traits and environmental interactions. The important aspiration of plant breeders is to know the extent of the relationship between various traits. Thus, measuring the mutual relationship between various plant characters is necessary to determine the component traits on which selection can be based for genetic improvement in yield and other important traits. Thus, it helps to base selection procedures required to balance two contrary but desirable characters affecting the primary character (Khushnood et al., 2014; Raj Kumar et al., 2021; Memon et al., 2014). Correlation studies also help to improve different characters simultaneously. Correlation studies determine how far two variables are associated with each other. The correlation reduces the chance of uncertainty happening; thus, the predictions based on correlation analysis are likely to be much closer to reality (Naeem et al., 2016). The use of physical mutagens, like X-rays, gamma rays and neutrons, and chemical mutagens for inducing variation is well established. Mutation breeding is relatively a quicker method for improving crops (Nazarenko, 2016; Oladosu et al., 2016). Hundreds of valuable mutants have been induced for various plant characters in various crops, including wheat, through treatment with physical and chemical mutagens(Abaza et al., 2020; Arain et al., 2022;

Nazarenko, 2016; Oladosu et al., 2016). Therefore, present studies are planned to evaluate the advanced mutant genotypes for yield and yield associated traits in bread wheat (*Triticum aestvum* L.) Evaluating and identifying fine lines from introduced plant materials in wheat development programs is the first and leading step in a crop improvement program. Promising genotypes with high yielding, good adaptation, and agronomically desirable characteristics could reliably be exploited for commercial cultivation. evertheless, an efficient and immense hybridization program would be a feasible approach, and for the success of such hybridization programs, the evaluation of the essential traits and pattern of genetic variability of the existing germplasm keeps a promise(Ravindra Kumar et al., 2013; PirzadoJatoi et al., 2021; Rasmusson et al., 1984; Suprasanna et al., 2015). Induced mutation has become an enormous tool in plant breeding to improve genotypes in particular traits. Many improved varieties of many crop species have been released, revealing the economic value of the technology (Mahmood et al., 2013; G Muhammad, Khan, S., Khan, M. A., Anjum, J., Alizai, N. A., Anjum, K., & Ziad, T. , 2022; Suprasanna et al., 2015). To genetically dissect a biological system further, new mutations were created by scientists by treating an organism with mutagenic agents (X-rays, gamma rays and neutrons, and chemical mutagens). These mutations are called induced mutations. These induced mutations assist in flourishing many enormous traits such as early maturity, increased tolerance, or resistance to biotic and abiotic stresses. Induced mutations improve rice, barley, cotton, peanuts, and beans(Liu et al., 2018; Steffen et al., 2019; Suprasanna et al., 2015).

Material and Methods
Plant material:

The experiment was carried out on the Evolution of Mutant Lines Bread wheat using Multivariate Techniques Based on Agronomic and Quantity Traits (*Triticum aestivum* L.) genotypes. In this regard, M_4 mutant lines from Marvi and Sassui varieties were sown along with two parental lines and check varieties viz. NIA-Amber and Saarang on 14-11-2014.for producing the mutant genotypes, a single dose of 300 Gy was applied. The experiment was conducted in a randomized complete block design (RCBD) with three replications at the Nuclear Institute of Agriculture (NIA), Tandojam, during the Rabi season 2014-15. Each genotype was sown by the single seed dibbler method in 6 rows 2 m long, keeping 30 cm between rows. Ten plants from each genotype per replication were randomly selected and tagged to study the yield components of the mutant lines as compared with check varieties

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Measurement of studies traits: For studies parameters measurement, ten representatives of spoiled and healthy plants were randomly selected from each genotype and then marked with labels for identification. The genotypes were estimated for the plant. Days to 75% heading, Days to 75% maturity, Plant height (cm), Spike length (cm), Tillers plant^{-1}, Main spike weight (g), Grains spike^{-1}, Grain weight spike^{-1}(g), Spikelets spike^{-1}, Grain yield plant^{-1}, Harvest Index, (%), Seed index (1000-grains weight) (g), Biological yield plot^{-1} (kg), Grain yield plot-1 (kg),

Analysis of Data: The results of average data were subjected to basic statistics (descriptive), correlation investigation, cluster analysis, and other most important factors estimated through the use of statistical procedures as previously described by different scientists (Gabriel, 1971; Gomez et al., 1984; Sharma, 1998; Singh et al., 1968; R Steel, 1997; RGD Steel et al., 1960).

Results and Discussion

To evaluate the performance of mutants of bread wheat (*Triticum aestivum* L.) in M_4 generation, the present research work was carried out during the crop year 2014-15 at the experimental field at NIA, Tandojam. The breeding materials for this experiment has consisted of six genotypes, i-e. Two mutants (M_4 generation), two varieties (Marvi and Sassui) as parents, and two varieties as a check (NIA-Amber and Sarang). For induction of the mutation, a single dose of 300 GY was applied to the seed material of the mother varieties. The observations were recorded on days to heading, days to maturity, plant height (cm), tillers plant^{-1}, spike length (cm), spikelet spike^{-1}, grains spike^{-1}, biological yield plot^{-1} (kg), harvest index (%), grain weight spike^{-1}(g), grain yield plot^{-1} (kg), spike weight plant^{-1} and seed index or 1000-grains weight (g). The recorded data was used to determine the mutants' performance and other genotypes/varieties.

was observed in the GWS, SS, MSW, and SL. The basic summary statistics of various traits studied have shown considerable variability among six genotypes between Marvi Mutant, Marvi Parent, Sassui Mutant, Sassui Parent and two checks Nia Amber, and Saarang wheat genotypes (Table 1). The most significant variation observed was for BYP, GY/Plot, DM, and DH; comparatively, low variation.

Correlation analysis:

Moreover, the correlation between these parameters was also calculated. The current research demonstrated a significant (P<0.05) positive correlation among various traits, such DH made a significantly positive correlation with DM the character MSW demonstrated a significantly positive correlation with GPS. Also, GWS and SI The trait GPS indicated a positive and significant correlation with GWS. A scree plot was drawn from the eigenvalues associated with a component or factor in descending order, the number of the components in a Scree plot is usually the number of changes in the data. The diversity index (Ortiz-Burgos, 2016) was estimated to measure phenotypic diversity for each trait figure 1 Scree plot exhibited variance percentage Associated with each principal component attained by drawing a graph between eigenvalue and PC numbers.PC1 showed 45.3239% variability, followed by PC2 with 26.9045% having eigenvalues of 6.3454 and 3.7666, respectively figure 1. results like above were reported by (Mangi et al., 2021; ZS Sarfraz, Mohammad Maroof.; et al., 2021).

Variables Axes F1 and F2: The variable values resulting from F1 and F2 variables axes demonstrate variation among the clusters. This is represented in (figure 2).in this figure, the F1 and F2 variables axes demonstrate high significance between agronomic traits, but no high difference was found in Quantity related traits. There are highly significant differences are to be found in the agronomic traits between all traits, whereas no high significance is found in quantity traits, as shown in figure 2.

Observation Axes F1 and F2 values: as shown above in figure 3, an observation axes F1 and F2 values demonstrate that there is a significant difference between Marvi M, Marvi P, Sassui M, Sassui P and two checks Nia Amber, and Saarang (figure 3).observation plot is divided into three groups group one is Marvi M, Marvi p, is group two Sassui M, Sassui P and check Nia Amber is found group three only check Saarang between mutant lines, parent lines and check lines each other significant.

Principal component analysis

Principal component analysis (PCA) indicates the genetic variation of the variety. It measures the important character that has a more significant impact on the total variable, and each coefficient of proper vectors indicates the degree of contribution of the very original variable with which each principal component is associated (Price et al., 2006). A principal component analysis was conducted to determine the independent impact of all the characters under study. The five principal components (PCs) extracted had eigenvalue > 1 and contributed 100% of the variation among the wheat varieties (**Table 1). Pic-1**

The first principal component accounted for more than 45.3239% of the total variation. MSW (0.9762), GWS (0.9621), TP (0.8306), GPS, (0.7564) DH (0.7189), SI (0.6068), DM (0.5589), SL (0.4478) for first PC. The eight mentioned variables are strongly correlated with the first principal component. It will increase with the upgradation in scores of these variables, which suggests that these eight criteria vary altogether. MSW came to be a strong correlation with this principal component; indeed, it could be stated that this PC is predominantly a measure of MSW. These findings align with those (Abro et al., 2022; Khodadadi et al., 2011; Qaseem et al., 2017; Z Sarfraz et al., 2020). The second principal component accounted for 26.9045% of the total variation characters highly, and a positive correlation was GY/Plot (0.9843), GYP (0.5741) BYP (0.4524), HI (0.4358), and PH (0.3688). The third principal component accounted for 15.6819% of the total variation. This component consists of SS (0.9712). Thus, the third component registered a positive contribution of the variable; it was determined to set the cut-off limit for the coefficients of the proper vectors (Raji, 2002). According to this criterion, coefficients greater than 0.3 (regardless of the positive or negative direction) have a large enough effect to be considered important.

In contrast, traits with a coefficient less than 0.3 were considered not to have important effects on the overall variation observed in the present study. **Biplot:** The principal component of wheat genotypes revealed that closely located genotypes on the graph are perceived as alike when rated on given attributes (figure 4). In the biplot, the results showed that most wheat genotypes in the present investigation were situated close to each other on the graph, indicating the narrow genetic background of wheat genotypes; this might be because of extensive breeding for a limited number of traits.

Cluster analysis:

To calculate the appropriate genotypes variability existing among all studies clusters. A ward's dendrogram was constructed in figure 5 (Jaradat, 1991; Jarwar et al., 2019). The tree diagram showed wide variation among clusters based on cluster and tree diagram analysis of the cultivars included. They represented three different clusters along a dendrogram where the x-axis represents variables while the Y-axis represents the placement of different genotypes across the dendrogram. This method provided a clearer genotypic distribution among and within traits representing them as different groups. These results clearly indicate a substantial variability across the genotypes under study.

Similar results have been witnessed through studies reported by different scientists (Hailu et al., 2006; Jaradat, 1991; Khodadadi et al., 2011; Moghaddam et al., 2000).

Table 1. Summary Statistics of investigated metric traits related to the mutant bread wheat lines evaluated.

Variable	Minimum	Maximum	Mean	Std. deviation
Heading	70.6667	90.3333	82.6667	8.4275
Maurity	123.3333	142.6667	132.7222	9.8396
Plant HEIGHT	84.1000	92.8000	87.6111	3.1494
Spike length	11.3333	13.6833	12.8333	1.0748
Tiller/per plant	6.5333	11.6667	8.5833	2.0200
spike weight	3.1440	4.7570	4.0354	0.5609
No o f Grains/sp	59.6000	73.7333	64.8611	5.5022
G W/S	2.3933	3.5833	3.0044	0.4226
Spikelet/s	19.4667	21.0333	20.2944	0.5674
G. yield/plant	15.2000	21.8200	17.5333	2.6069
Harvest Index	30.2067	35.5033	32.9817	2.1708
1000-grain wt	37.6600	47.1400	44.5489	3.4406
B.Y/Plot	2466.6667	2766.6667	2600.0000	133.3333
G.y/plot	783.3333	983.3333	858.3333	66.4580

Table 2. Pearson's Correlation coefficient matrix demonstrates the amount and direction of correlation between each pair of traits investigated from mutant bread wheat lines.

Variables	Heading	Maturity	Plant HEIGHT	Spike length	Tiller/p	Spike weight	no of G/sp	G W/S2	Siplet/s	G.yild /plant	Harvest Index	1000- grain wt	B.Y /Plot	G.y /plot
Heading	**1**	**0.9334**	0.3501	-0.2220	0.6296	-0.8033	**-0.8654**	**-0.8590**	0.2681	0.2398	-0.2699	-0.5521	-0.2512	-0.3710
Maturity	**0.9334**	**1**	0.0113	-0.0288	0.5060	-0.7389	**-0.8120**	**-0.8141**	0.1991	0.0157	-0.2722	-0.5064	-0.5285	-0.5854
Plant HEIGHT	0.3501	0.0113	**1**	-0.6131	0.4811	-0.4040	-0.4545	-0.3759	0.2530	0.7092	0.1622	-0.1837	0.4758	0.5410
Spike length	-0.2220	-0.0288	-0.6131	**1**	**-0.8270**	0.6859	0.3294	0.5773	0.4901	-0.4828	-0.3789	0.7371	-0.2846	-0.5087
Tiller/p	0.6296	0.5060	0.4811	**-0.8270**	**1**	**-0.9015**	-0.6230	**-0.8367**	-0.2048	0.5719	0.3321	**-0.8185**	0.0462	0.2727
Main spike weight	-0.8033	-0.7389	-0.4040	0.6859	**-0.9015**	**1**	**0.8384**	**0.9878**	0.1898	-0.3205	-0.1010	**0.8357**	0.2721	0.0950
no of G/sp	**-0.8654**	**-0.8120**	-0.4545	0.3294	-0.6230	**0.8384**	**1**	**0.9035**	-0.2830	-0.3653	-0.0699	0.4237	0.4731	0.2104
G W/S	**-0.8590**	**-0.8141**	-0.3759	0.5773	**-0.8367**	**0.9878**	**0.9035**	**1**	0.0900	-0.2815	-0.0470	0.7666	0.3695	0.1954
Spikelet/s	0.2681	0.1991	0.2530	0.4901	-0.2048	0.1898	-0.2830	0.0900	**1**	0.4589	0.0679	0.6135	-0.0206	0.0751
G. yield/plant	0.2398	0.0157	0.7092	-0.4828	0.5719	-0.3205	-0.3653	-0.2815	0.4589	**1**	0.6650	-0.0210	0.3471	0.7770
Harvest Index	-0.2699	-0.2722	0.1622	-0.3789	0.3321	-0.1010	-0.0699	-0.0470	0.0679	0.6650	**1**	0.1055	-0.0709	0.7301
1000-grain wt	-0.5521	-0.5064	-0.1837	0.7371	**-0.8185**	**0.8357**	0.4237	0.7666	0.6135	-0.0210	0.1055	**1**	0.0157	0.1265
B.Y/Plot	-0.2512	-0.5285	0.4758	-0.2846	0.0462	0.2721	0.4731	0.3695	-0.0206	0.3471	-0.0709	0.0157	**1**	0.6144
G.y/plot	-0.3710	-0.5854	0.5410	-0.5087	0.2727	0.0950	0.2104	0.1954	0.0751	0.7770	0.7301	0.1265	0.6144	**1**

Values in bold are different from 0 with a significance level α=0.05

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Table 3. The multivariate analysis of mutant bread wheat lines revealed squared cosines of the variables (traits) and eigenvalues.

Traits	F_1	F_2	F_3	F_4	F_5
Heading	0.7189	0.1186	0.0829	0.0652	0.0145
Maturity	0.5589	0.3451	0.0574	0.0003	0.0383
Plant HEIGHT	0.2466	0.3688	0.0653	0.1825	0.1368
Spike length	0.4478	0.3222	0.2085	0.0000	0.0215
Tiller/p	0.8306	0.0882	0.0306	0.0041	0.0465
spike weight	0.9762	0.0038	0.0146	0.0046	0.0008
no of G/sp	0.7564	0.0402	0.1430	0.0076	0.0528
G W/S	0.9621	0.0280	0.0002	0.0053	0.0045
Siplet/s	0.0035	0.0006	0.9712	0.0148	0.0099
G.yild/plant	0.1837	0.5741	0.2147	0.0033	0.0242
Harvest Index	0.0126	0.4358	0.0204	0.5281	0.0031
1000-grain wt	0.6068	0.0044	0.3603	0.0095	0.0189
B.Y/Plot	0.0402	0.4524	0.0234	0.4402	0.0438
G.y/plot	0.0011	0.9843	0.0031	0.0088	0.0028
Eigenvalue	6.3454	3.7666	2.1955	1.2743	0.4182
Variability (%)	45.3239	26.9045	15.6819	9.1023	2.9874
Cumulative %	45.3239	72.2284	87.9103	97.0126	100.0000

Values in bold correspond for each variable to the factor for which the squared cosine is the largest
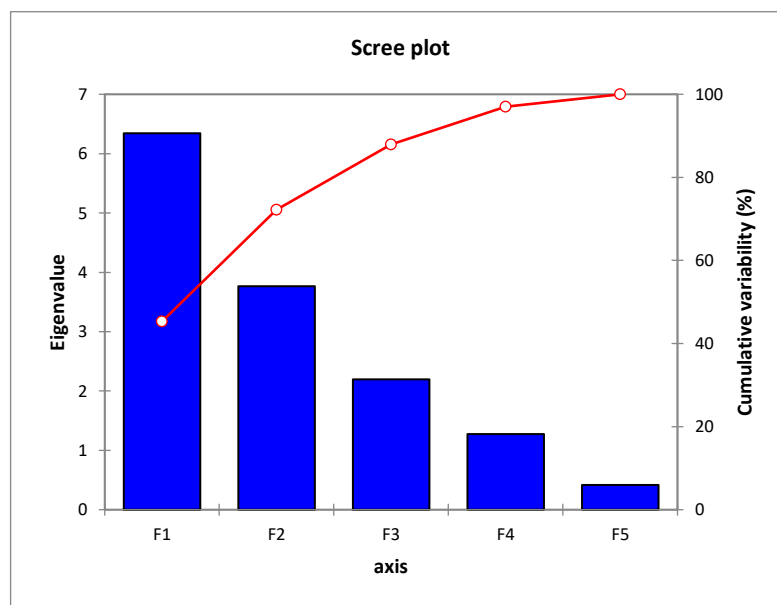

Figure 1. Scree plot representing eigen values with reference to number of PCs for metric traits of mutant wheat accessions
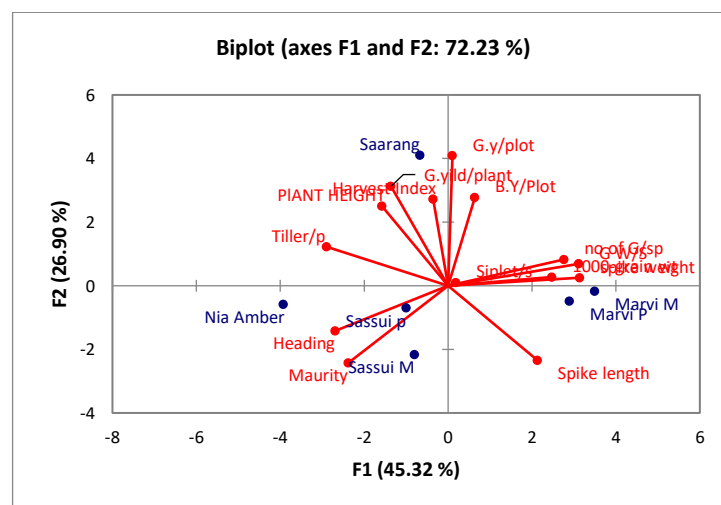

Figure 2. Biplot among PC-1, PC-2 displays contribution of different metric traits in the variability of mutant wheat accessions.
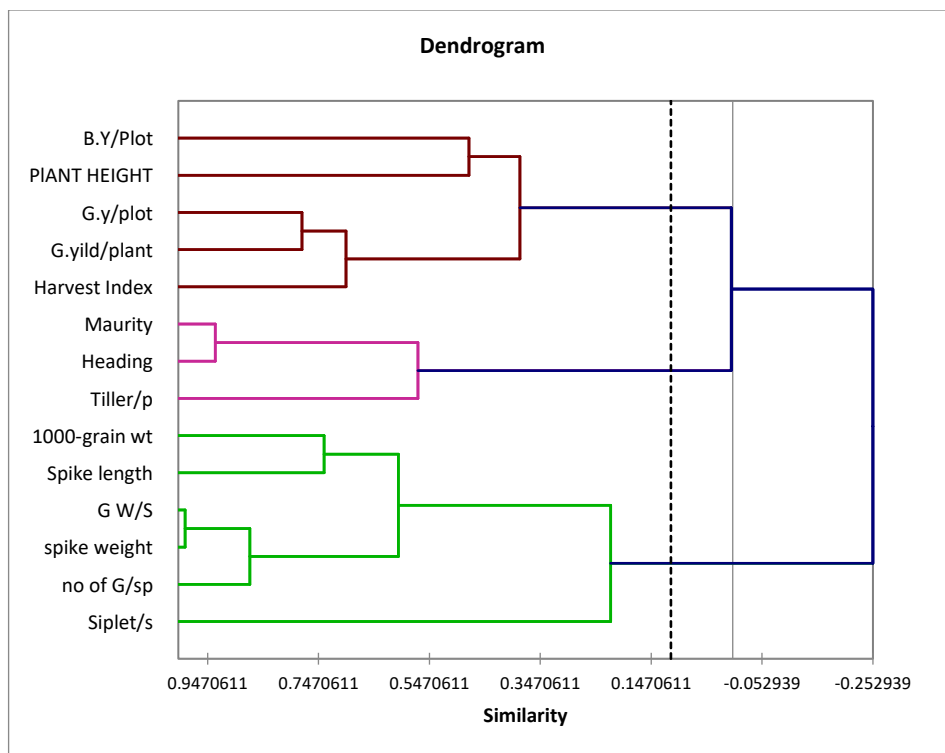
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Figure 3. Hierarchical Clustering of mutant wheat accessions for metric traits Genotypes

Conclusion: Results obtained from the current study are evident about the considerable genetic variation different mutant wheat genotypes under study. Parents selected through multivariate methods with significant genetic distances for crossing to obtain genetic recombination and transgressive segregation in the subsequent generations. Multivariate methods can help in breeding program through continuing selection process for wheat crop improvement and creation of mutant wheat genotypes with desirable characters. However, further study across locations and years needs to be done to corroborate the results obtained in the present investigation.

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