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STUDY OF MORPHO-MOLECULAR VARIABILITY AND PATH ANALYSIS IN WHEAT (*Triticum aestivum* L.)

ABSTRACT

The experiment was conducted at Hajee Mohammad Danesh Science and Technology University, Dinajpur during the Rabi season 2022-2023 in RCBD design with three replications. The experimental materials were 11 wheat genotypes viz. 10 HSTU developed advance line and one check variety BARI Gom 32. Significant variations were observed in nine traits in the existing generation. The mean squares against all genotypes were significant for all the characters studied. The mean performance of all traits, the grand mean, and the range value indicated a wide range of variation among the studied genotypes for the quantitative traits. Mean values of days to 50% heading varied from 51.67 to 69.33 days. Days to 50% maturity was ranged from 102.33 to 121.33 days. The grain weight per spike (g) ranged from 1.32 to 1.88 g. The mean value of average plant height varied from 92.35 to 116.33 cm, the average spike length was 8.58 to 10.73 cm, and the average grain per spike was 30.93 to 45.20. The number of spike per 1 square meter ranged from 351.67 to 505.67 g. The minimum value of 1000 grain weight was 31.99 g and the maximum value was 47.23 g. The high-yielding line was HSTUW 1 (2812.73) whereas the low-yielding line was HSTUW 2 (2087.22). Positive significant correlation with 1000 grain weight (0.8292) at the genotypic and phenotypic levels 1000 grain weight (0.5199) but at the phenotypic level moderate positive significant association with average plant height (0.3459), and a moderate negative significant association with average grain per spike (-0.4269) to yield per plot. Path coefficient analysis indicated that the highest direct effect was observed in grain weight per spike (3.573), average spike length also exhibited a maximum positive direct effect on yield per plot (1.198) at the genotypic level but at the phenotypic level in 1000 grain weight exhibited the highest positive direct effect on yield per plot (1.108) and a strong positive significant association with yield per plot (0.520). Average grain per spike also exhibited a maximum positive direct effect on yield per plot (0.673). Average grain per spike contributed indirectly through 1000 grain weight to yield per plant. Selection through 1000 grain weight and average grain per spike may effectively increase yield per plot. Higher genotypic and phenotypic coefficient of variations were observed in grain weight per spike, number of spike, 1000 grain weight, average grain per spike, and yield per plot. High heritability was observed in days to maturity (95.85%), average plant height (93.13%), days to heading (90.78%), and moderate heritability was shown in average grain per spike (73.87%), 1000 grain weight (72.54%), number of spike per 1 square meter (72.17%), grain weight per spike (66.47%), and yield per plot (63.73%). High genetic advance as percentage of mean was observed for the number of spike per 1 square meter (21.77%), grain weight per spike (21.38%), and 1000 grain weight (20.44%). Four SSR markers were employed in 11 wheat genotypes for molecular characterization. All SSRs were polymorphic across the 11 genotypes. Thirty-one alleles were detected with an average of 7.75 alleles per marker. The most polymorphic microsatellite markers were Gwm495, Barc20, TaBarc101, and Xwmc112 each with 6 to 9 alleles. The highest Polymorphic Information Content (PIC) value 0.87 was estimated in Gwm495. In population genetic structure analysis, population I consisted of 27.27% of total genotypes i.e. 3 genotypes were pure, where not found any admixture. Population II comprised 72.73% of total genotypes i.e. 8 genotypes; 7 genotypes were found pure and 1 genotype was found heterogeneous. Cluster analysis using the UPGMA method delineated the 11 genotypes into two clusters. HSTUW 2 and HSTUW 3 are genetically more similar while HSTUW 7 and HSTUW 8, HSTUW 10, and HSTUW 1 show a minimum of showed more divergent. Finally, the significant variability present of HSTU-developed existing lines, 1000 grain weight, and Average grain per spike are two very good traits, based on which will help us to select the breed later.

Keywords: Wheat advance lines, mean performance, correlation, path analysis, variability, SSR marker

CONTENTS

CHAPTER	TITLE	PAGE NO.
	ACKNOWLEDGEMENTS	i
	ABSTRACT	ii
	CONTENTS	iii-vi
	LIST OF TABLES	vii-viii
	LIST OF FIGURES	ix-x
	LIST OF APPENDICES	xi
	LIST OF ACRONYMS AND ABBREVIATIONS	xii-xiii
CHAPTER I	INTRODUCTION	1-5
CHAPTER II	REVIEW OF LITERATURE	6-24
2.1	Germplasms found in the regions of the world	6
2.2	Environmental effects of wheat production	7
2.3	Methods used in the breeding program	8
2.4	Yield and yield contributing traits of wheat cultivars	10
2.5	Importance of genetic diversity analysis of wheat	11
2.6	Dependability on heritability for successful breeding	14
2.7	The Yield performance analysis of wheat	17
2.8	The variability and path analysis of wheat	19
2.9	Molecular marker-assisted wheat breeding	21
2.10	Importance and uses of SSR markers in wheat	23
CHAPTER III	MATERIALS AND METHODS	25-48
3.1	Experimental site and period	25
3.2	Climate	25
3.3	Soil	25
3.4	Soil sample test	25
3.5	Experimental Design and Layout	26
3.6	Experimental materials	27
3.7	Seed rate	27
3.8	Layout of the Experiment	28
3.9	Experimental duration	28
3.10	Preparation of the Main Field	28
3.11	Sowing of seeds	29

CONTENTS (Contd.)

CHAPTER	TITLE	PAGE NO.
3.12	Application of Manure and Fertilizers	29
3.13	Seed treatments	30
3.14	Planting of Seeds in the Field	30
3.15	Intercultural operation	30
3.15.1	Weeding	30
3.15.2	Irrigation	31
3.16	Harvesting, threshing, and cleaning	31
3.17	Measurement of morphological traits	31
3.17.1	Days to 50% Heading	32
3.17.2	Plant height (cm)	32
3.17.3	Days to 50% Maturity	32
3.17.4	Number of spikes per 1 square meter	32
3.17.5	Spike length (cm)	32
3.17.6	The average number of grains per spike	32
3.17.7	Average grain weight per spike	32
3.17.8	1000 grain weight (g)	33
3.17.9	Yield per plot (g)	33
3.18	Study of molecular diversity utilizing Microsatellite/SSR markers	34
3.18.1	Microsatellite/Simple Sequences Repeat (SSR) Markers	34
3.18.2	Data collection for molecular characterizations	35
3.18.3	Sampling and lyophilization of leaves	35
3.18.4	Genomic DNA extraction	35
3.18.4.1	Grinding of leaves	35
3.18.4.2	DNA extraction using the modified CTAB method	35
3.18.4.3	DNA quantification	40
3.18.4.4	DNA dilution	40
3.18.4.5	PCR amplification	40
3.18.4.6	Electrophoresis separation and silver nitrate staining	42
3.18.4.7	Molecular Statistical Analysis	43

CONTENTS (Contd.)

CHAPTER	TITLE	PAGE NO.
3.19	Statistical analyses	43
3.19.1	Equations of analysis	43
3.19.2	Analysis of variance	44
3.19.3	Estimation of genotypic and phenotypic variances	45
3.19.4	Genotypic and Phenotypic Coefficient of Variation	45
3.19.5	Estimation of heritability	46
3.19.6	Estimation of genetic advance (GA)	46
3.19.7	Genetic advance over mean (GAM)	47
3.19.8	Estimation of genotypic and phenotypic correlation coefficients	47
3.19.9	Estimation of path coefficient	48
CHAPTER IV	RESULTS AND DISCUSSION	49-87
4.1	Analysis of variance for different quantitative characters	49
4.2	Mean performances of different yield and yield contributing traits in wheat genotypes	50
4.2.1	Days to heading	53
4.2.2	Days to Maturity	53
4.2.3	Grain weight per spike	53
4.2.4	Average Plant height	55
4.2.5	Average spike length	55
4.2.6	Average grain per spike	55
4.2.7	No. of spike	57
4.2.8	1000 grain weight	57
4.2.9	Yield per plot	57
4.3	Estimation of correlation coefficient	62
4.3.1	Genotypic Correlation coefficients among traits of wheat genotypes	64
4.3.2	Phenotypic Correlation coefficients among traits of wheat genotypes	65

CONTENTS (Contd.)

CHAPTER	TITLE	PAGE NO.
4.4	Direct (Diagonal) and Indirect Effect of Genotypic Path Coefficients Analysis among nine Traits of Wheat genotypes	71
4.5	Direct (Diagonal) and Indirect Effect of phenotypic Path Coefficients Analysis among Nine traits of wheat Genotypes	72
4.6	Genetic parameters on the selected characters in Wheat genotypes	73
4.7	Molecular diversity utilizing Microsatellite/SSR markers SSR marker-based DNA fingerprinting analysis	77
4.7.1	Assessment of Polymorphism from SSR Profiles	80
4.7.2	Population structure of wheat varieties	82
4.7.3	Genetic diversity among the varieties	84
CHAPTER V	SUMMARY AND CONCLUSION	88-91
	REFERENCES	92-107
	APPENDICES	108-114

LIST OF TABLES

TABLE NO.	TITLE	PAGE NO.
1.	Plant genetic materials with their name used in this experiment	27
2.	Doses and methods of application of fertilizers in a wheat field	29
3.	Microsatellite/Simple Sequences Repeat (SSR) Markers	34
4.	Chemicals for DNA extraction	37
5.	Chemicals for CTAB buffer Preparation	37
6.	Chemical Reagents used for PCR, based on SSR markers of wheat genotypes	41-42
7.	Chemicals used for preparation Polyacrylamide gel (8%)-1000 ml	42
8.	The structure of ANOVA	44
9.	Analysis of variance (Mean squares) derived from RCBD one-factor model on morphological characters in Wheat genotypes	51
10.	Mean performance of morphological character of wheat genotypes	52
11.	Mean performance of morphological character of wheat genotypes (Contd.)	54
12.	Mean performance of morphological character of wheat genotypes (Contd.)	56
13.	Genotypic Correlation coefficients among traits of wheat genotypes	67
14.	Phenotypic Correlation coefficients among traits of wheat genotypes	68
15.	Direct (Diagonal) and indirect effect of Genotypic path coefficients analysis among eleven traits of wheat genotypes	69
16.	Direct (Diagonal) and indirect effect of Phenotypic path coefficients analysis among eleven traits of wheat genotypes	70

LIST OF TABLES (Contd.)

TABLE NO.	TITLE	PAGE NO.
17.	Genetic parameters on the characters of Wheat genotypes	75
18.	Number of alleles, allele range, and PIC values of 4 polymorphic markers	81
19.	Cluster groups there containing 11 wheat genotypes name	86

LIST OF FIGURES

FIGURE NO.	TITLE	PAGE NO.
1	Field experimental layout of an experiment of wheat for the Rabi season 2022-2023	26
2	The experimental layout of wheat genotypes after the germination period	28
3	The wedding operation is conducted in the experimental field	30
4	Morphological maturation in the experimental field	31
5	Crushed the leaves with a pestle and motor	35
6	DNA extraction procedure using modified CTAB method	36
7	Showing the protocol for DNA extraction (Modified CTAB method)	39
8	DNA Quantification using a NanoDrop TM 1000 Spectrophotometer	40
9	Mean performance of Days to heading and Days to maturity of wheat genotypes	58
10	Mean performance of Average plant height of wheat genotypes	58
11	Mean performance of Average spike length of wheat genotypes	59
12	Mean performance of Grain weight per spike of wheat genotypes	59
13	Mean performance of average grain per spike of wheat genotypes	60
14	Mean performance of the number of spikes of wheat genotype	60
15	Mean performance of 1000 grain weight of wheat genotypes	61
16	Mean performance of yield performance of wheat genotypes	61
17	Correlation coefficient among morphological characters of wheat genotypes	63
18	The DNA profile of wheat genotypes using TaBarc101	78

LIST OF FIGURES (Contd.)

FIGURE NO.	TITLE	PAGE NO.
19	The DNA profile of wheat genotypes using Xwmc112	78
20	The DNA profile of wheat genotypes using Barc20	79
21	The DNA profile of wheat genotypes using Gwm495	79
22	The best number of groups among locations estimated by Evanno test methods	83
23	Model-based population structure plot for each isolate with K=2, using Structure with SSR markers data. Color codes are as follows: Population I red, Population II green (A). The code of each genotype (B) corresponds to the description in Table 1(1st table of all genotypes with sources)	83
24	UPGMA tree displays the distribution of the wheat genotypes in two groups and presents the genetic similarities and dissimilarities within and between the groups. Names of the genotypes are given on the termini of branches	85
25	Heatmap cluster analysis based on genotypical traits	87

LIST OF APPENDICES

APPENDIX NO.	TITLE	PAGE NO.
I	Location of the experimental site (map of Dinajpur Sadar Upazila showing the research plot)	107
II	The soil nutrient composition of Genetics and Plant breeding Research field of HSTU, Dinajpur	108
III	Graphical representation of temperature during the wheat growing season at the experimental site	109
IV	Graphical representation of the average related humidity and rainfall during the wheat growing season at the experimental site	109
V	Weather data for the growing season of wheat during the period from December,2022 to April, 2023	110
VI	Field observation at the germination stage to harvesting stage for the growing season of wheat, 2022-2023	111-113
VII	Some photographs of Molecular observation	114-115

LIST OF ACRONYMS AND ABBREVIATIONS

%	Percent
°C	Degree Celsius
AEZ	Agro Ecological Zone
ANOVA	Analysis of Variance
BARI	Bangladesh Agricultural Research Institute
Bp	Base pair
cm	Centimeter
CT	Canopy temperature
CV	Coefficient of Variation
D ²	Genetic Divergence
DAP	Days after planting
DFP	Days to 50% flowering
FAO	Food and Agriculture Organization
AGPS	Average grain per spike
g	Gram
GA	Genetic Advance
GA%	Genetic Advance as percent
GAM	Genetic Advance as percent of means.
GCV	Genotypic Coefficient of variation
GPP	Total grain per spike
h ² b	Heritability in broad sense
HSTU	Hajee Mohammad Danesh Science and Technology University
HSD	Honestly Significant Difference
Kg	Kilogram
m	Meter
mm	Millimeter
MOP	Muriate of Potash
Ms	Mean Sum of Square
MSE	Mean Square of Error
σ^2g	Genotypic Variance
σ^2p	Phenotypic Variance
PAGE	Polyacrylamide Gel Electrophoresis Analysis

PCR	Polymerase Chain Reaction
PCV	Phenotypic Coefficient of Variation
PH	Plant height
PIC	Polymorphism Information Content
SL	Spike length
r	Correlation coefficient
R ²	Residual Effect
RCBD	Randomized complete block design
r _g	Genotypic correlation
r _p	Phenotypic correlation
SE	Standard Error
SRDI	Soil Resource Development Institute
SSR	Simple Sequence Repeat
TW	1000 grain weight
TM	Temperature
TSP	Triple Super Phosphate
UPGMA	Unweight Pair Group Method Using Arithmetic Mean
USDA	United States Department of Agriculture
Viz	Namely
YPP	Yield per plant