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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

CONTENTS (Contd.)

CONTENTS (Contd.)

CONTENTS (Contd.)

LIST OF TABLES

LIST OF TABLES (Contd.)

LIST OF FIGURES

LIST OF FIGURES (Contd.)

LIST OF APPENDICES

LIST OF ACRONYMS AND ABBREVIATIONS

%	Percent
^{0}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
DFF	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^2b	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