

**STABILITY ANALYSIS OF GRAIN YIELD AND ITS
COMPONENT TRAITS IN BREAD WHEAT**

[*Triticum aestivum* L.]

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Abstract

“STABILITY ANALYSIS OF GRAIN YIELD AND ITS COMPONENT TRAITS IN BREAD WHEAT [*Triticum aestivum* L.]”

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ABSTRACT

The present investigation entitled “Stability analysis of grain yield and its component traits in bread wheat [*Triticum aestivum* L.]” was carried out to access the stability parameters and to utilize the stable genotype in further wheat improvement programme. The experiment was studied over artificially created four environments (15 Nov, 25 Nov, 05 Dec and 15 Dec) for twenty set of genotypes with three replications in randomized complete block design at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during the *rabi* season 2019-20 for fifteen set of quantitative characters along with validation of known SSR markers linked to heat tolerance in bread wheat.

The analysis revealed significant differences among the genotypes for all the characters studied in all four sowing seasons indicating sufficient variability existing among genotypes. The mean performance evaluated for twenty genotypes across environments indicates the grain yield was seen higher when planted in normal dates of sowing recommended for wheat than late sown conditions where reduction in the grain yield was seen. Variability studies resulting from the pooled environments showed phenotypic co-efficient of variation higher than genotypic co-efficient of variation denoting favourable influence of environment on the characters. There was a closer affinity of GCV and PCV for the characters days to 50% heading, days to maturity, grain filling period and plant height indicating the scope for the selection for these traits and for characters tillers per meter, tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index exhibited larger variation in the values of GCV and PCV showing significant action of environment in the expression of these traits. High heritability with high genetic advance was reported for spike length, number of grains per spike and grain weight per spike indicating effective selection and high heritability with moderate genetic advance were reported for days to 50% heading, grain filling period, plant height, tillers per meter, thousand grain weight and biological yield per plant.

The pooled analysis of variance for stability parameters revealed significant genotypes and environment interaction tested against pooled error for all the characters except number of effective tillers per meter, number of effective tillers per plant, biological yield per meter, biological yield per plant and harvest index showing differential response of genotypes with environment. The genotype VA2019-26 was average stable for grain yield per meter, grain yield per plant and number of effective tillers per meter whereas genotype VA2019-29 was showing average stability for grain yield per meter and harvest index while the genotype VA2019-19 showed average stability for the traits thousand grain weight, biological yield per meter and biological yield per plant indicating adaptation to all the studied environments. The genotype VA2019-29 showed below average stability characteristics for days to maturity and thousand grain weight indicating adaptation to favourable environments and VA2019-30 showed above average stability for grain yield per meter and grain yield per plant showing adaptation to adverse environmental conditions.

Sixteen heat tolerance specific primers were used for validation and diversity analysis out of which fourteen showed amplification and thirteen primers were polymorphic (gwm102, Xgwm484, Xgwm190, Xgwm131, Xwmc48, Xgwm63, barc65, Xgwm11, Xgwm577, Xgwm626, barc186, Xgwm190 and WMS074) amplifying a total of 34 alleles with a range of 2-5 alleles and an average of 2.62 alleles per locus. PIC values ranged from 0.11 (Xgwm11) to 0.68 (Xgwm577) with an average of 0.38. The dendrogram generated through sub-programme cluster tree analysis of the NTSPYC-pc software divided twenty genotypes into two major clusters A and B, formed at the similarity co-efficient of 0.37. These two clusters were further sub divided into sub clusters A1, A2 and B1, B2 respectively. Based on the primers used, genotypes VA2019-17 and VA2019-27 recorded the highest similarity of 1.00. The validated heat tolerance specific primers which showed association for the characters can be used in marker assisted breeding programme for further improvement in bread wheat.

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CERTIFICATE – I

Date: /4/09/2021

This is to certify that the thesis entitled, "**STABILITY ANALYSIS OF GRAIN YIELD AND ITS COMPONENT TRAITS IN BREAD WHEAT [*Triticum aestivum* L.]**" submitted for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **GENETICS AND PLANT BREEDING** is a record of bonafide research work carried out by **ANAND V.** under my guidance and supervision and that no part of this thesis has been submitted for any other degree, diploma, associateship, fellowship or other similar titles. The assistance and help received during the course of investigation have been fully acknowledged.



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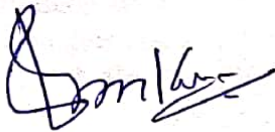
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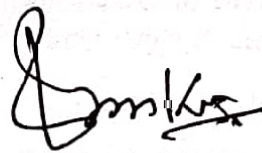
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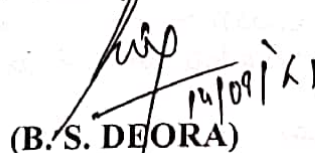
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LIST OF ABBREVIATIONS AND SYMBOLS USED

°C	:	Degree celsius
A ₂₆₀	:	Absorbance at 260 nanometers
A ₂₈₀	:	Absorbance at 280 nanometers
AFLP	:	Amplified Fragment Length Polymorphism
ANOVA	:	Analysis of Variance
b _i	:	Regression co-efficient
bp	:	Base pairs
BYM	:	Biological yield per meter
BYP	:	Biological yield per plant
C D	:	Critical difference
Chl	:	Chlorophyll
CT	:	Canopy temperature
CTD	:	Chlorophyll temperature depression
C V	:	Coefficient of Variation
cm	:	Centimeter
Conti.	:	Continuous
CPCA	:	Chimanbhai Patel College of Agriculture
CTAB	:	Cetyl Trimethyl Ammonium Bromide
CTv	:	Canopy temperature in vegetative stage
df	:	Degree of freedom
DH	:	Days to 50% heading
DM	:	Days to maturity
DNA	:	Deoxyribonucleic Acid
dNTPs	:	Deoxyribonucleotide Triphosphates
e.g.	:	Exempli gratia (For example)
EDTA	:	Ethylene Diamine Tetra Acetic Acid
<i>et al.</i>	:	<i>Et alii</i> (and others)
F	:	Forward primer
F _{1s}	:	First filial generation
F ₂	:	Second filial generation
Fig.	:	Figure
g	:	Gram
GCV	:	Genotypic coefficient of variation
GFP	:	Grain filling period
GN	:	Grain number
GWS	:	Grain weight per spike
GYM	:	Grain yield per meter
GYP	:	Grain yield per plant
HCN	:	Hydrocyanic acid content
HI	:	Harvest index
HSI	:	Heat susceptibility index
<i>i.e.</i>	:	Id est (That is)
kg	:	Kilogram
M	:	Molar
Max.	:	Maximum
Mb	:	Mega Base Pairs
MSe	:	Mean sum of the square for error

MSr	:	Mean sum of the square for replication
MSg	:	Mean sum of the square for genotypes
mg	:	Milli Gram
Min.	:	Minimum
ml	:	Millilitre
mm	:	Millimeter
mM	:	Millimolar
MS	:	Mean Square
NDVIg	:	Normalized difference vegetative index in the grain filling stage
NGS	:	Number of grains per spike
No	:	Number
PCR	:	Polymerase Chain Reaction
PCV	:	Phenotypic coefficient of variation
PH	:	Plant height
PIC	:	Polymorphic Information Content
ppm	:	Parts per million
r	:	Replication
R	:	Reverse primer
RAPD	:	Randomly Amplified Polymorphic DNA
RBD	:	Randomized Block Design
RFLP	:	Restriction Fragment Length Polymorphism
RNase	:	Ribonuclease
S²d_i	:	Deviation from regression line
SDS	:	Sodium Dodecyl Sulphate
S.E.	:	Standard Error
S.Ed.	:	Standard error of difference
S.Em.	:	Standard Error of mean
SDAU	:	Sardarkrushinagar Dantiwada Agricultural University
Sl.	:	Serial
SPL	:	Spike length
SSRs	:	Simple Sequence Repeats
TBE	:	Tris-Borate-EDTA-buffer
TE	:	Tris- EDTA
TGW	:	Thousand grain weight
TLRM	:	Number of effective tillers per meter
TLRP	:	Number of effective tillers per plant
Tm	:	Melting temperature
UPGMA	:	Unweighted Pair Group Method with Arithmetic Mean
viz.	:	Videlicet (Namely)
NDVIg	:	Normalized difference vegetative idex in the grain filling stage

SYMBOLS

=	:	is equal to
°	:	Degree
.	:	Full stop
×	:	Multiply
&	:	And
-	:	Minus
()	:	Bracket
√	:	Square root
[]	:	Square bracket
,	:	Comma
%	:	Per cent
>	:	Greater than
<	:	Less than
/	:	Per
Σ	:	N-ray summation
σ	:	Sigma
;	:	Semi colon
:	:	Colon
μ	:	General Mean

Introduction

I. INTRODUCTION

Bread wheat (*Triticum aestivum* L.), one of the crop belonging to *poaceae* family is the most cultivated cereal grain crop around the world and is being cultivated since *pre*-historic times. Wheat is one of the major sources of calories and proteins in many of the developing countries. Wheat is a strong self pollinating plant (autogamous) with cross pollination less than 1%. The species of wheat which is cultivated and its relatives belongs to diploid (genome AA), tetraploid (genome AABB) and hexaploid groups (genome AABBDD), with chromosome number $2n=14$, 28 and 42 respectively.

The global wheat production is 766.4 million tones and at 758 million tones stands its global wheat utilization (FAO 2019). India's wheat production in 2019-2020 was 107.18 million tonnes with national productivity of 3508 kg/ha, the previous year production was 103.60 million tonnes. Wheat is an annual plant, grown in tropical, sub tropical and temperate climates. In India, three species of wheat are being cultivated; *Triticum aestivum*, *Triticum durum*, and *Triticum dicoccum* (Gupta, 2004). Bread wheat accounts for around 95% cultivation, *durum* wheat of around 4% and *dicoccum* wheat around 1% respectively (Gupta, 2004). The major wheat growing states in India are Uttar Pradesh, Punjab, Haryana, Gujarat, Rajasthan, Madhya Pradesh and Bihar. Wheat is consumed in the form of bread, chapattis, biscuits and several other products.

Naturally wheat grows up to a height of three feet and which normally completes life cycle around 130-140 days. Inflorescence of wheat is made of spikelets enclosed by outer lemma and inner palea, spike takes several days to complete flowering and opening of the flower takes place from middle of the spikelets and proceeds either way. Complete opening of flower requires around 20 minutes and anther dehiscence takes 2-3 minutes. Wheat is grown in wide range of diverse agro-climatic conditions with respect to rainfall, crop duration, soil temperature and other climatic factors which causes variation in yield and quality of the traits, so it is necessary to develop and identify the phenotypically stable genotype which could perform consistently over all kind of varied and fluctuated environments. Besides it is

also important to identify suitable genotypes for favorable and unfavorable environments for sustainable wheat production.

Selection of genotypes which are found to be genetically variable in the existing genetic stock is very important process in systematic plant breeding programme as it helps in individual selection, which will be mated to each other to generate further genetic variability. Thus, effectiveness of selection will be very much dependent on nature, extent and magnitude of genetic variability which is present in the material and the extent to which it is heritable. Hence heritability along with genetic advance are important selection parameters. Heritability specifies proportion of total variability due to genetic causes and it is a good index of transmission of characters from parents to their offspring (Falconer 1981). Genetic advance is the measure of genetic gain under selection and can be defined as difference of mean genotypic value of the selected lines to the mean genotypic value of the parental population.

The variability present in any breeding programme can be assessed by simple measures of variability. The genotypic, phenotypic and environmental co-efficients of variation are helpful in understanding the existing variability in the populations and along with this for transmissibility of characters, heritability and genetic advance provides the good estimates. Hence this investigation attempts to assess the variability of important grain yield and yield contributing traits through genotypic coefficient of variation, phenotypic co-efficient of variation, heritability and genetic advance as percentage of mean.

The genotype will be considered more stable and adaptive one, if it shows high mean yield and low degree of fluctuation in yield contributing characters when grown in diverse environmental conditions. Wheat is grown across all over the world having varied agro climatic conditions causing variation in yield and yield related traits. Hence selection and identification of phenotypically stable genotypes performing consistently in varied environmental conditions is very much essential for sustained wheat production.

The breeders and growers are primarily concerned with yield and stability of the cultivar. The expression of grain yield and its components are the function of genotype, environment and genotype and environment ($G \times E$) interaction. The

breeder's task is to screen out the varieties planted at different intervals to enable selection of those genotypes. The potential genotype may fail to express as an optimum phenotype in different environmental conditions due to high G x E interaction prevailing in its environment which decreases the correlation between genotype and phenotype.

The concept of stability has been defined in several ways and different biometrical methods have been developed to access stability and among those most prominent one is Eberhart and Russell, 1966 model. The stability is defined by high mean yield and regression coefficient ($b_i=1.0$) and deviations from regression as less as possible ($S^2d_i=0$). The main objective of any breeding programme is to develop high yielding varieties with stable performance across all environments as wheat is grown in diverse set of environments all over India.

The long chain success obtained through green revolution is having a break from the past few years; this is attributed to many factors among which global warming accounting for high terminal heat stress appears to be the most prominent. The significance of high temperature stress in limiting the productivity of wheat in India was first indicated by Howard (1924), he stated that "Wheat growing in India is a gamble in temperature". This statement is valid even today (Sharma *et al.* 2002). An increase in temperature of one degree during the crop season is estimated to about 8-10% yield reduction in wheat (Joshi, 2007). Wardlaw (1994) has also reported that mean temperature greater than 15-18 degree Celsius after anthesis as resulted in decrease in grain weight after maturity.

Many areas around north are exposed to heat stress is due to delayed planting caused mostly by long duration paddy varieties in rice-wheat cropping areas (Joshi *et al.* 2007a). The north-western plains are highly productive but are very much prone to stresses of high temperature caused by dry winds from the Thar Desert. On to this contrasting side, the north-eastern plains are too exposed to high temperature coupled with high humidity (Joshi *et al.* 2007c). The significance of this high temperature impact is also felt in eastern gangetic plains by witnessing short winters and development of high temperature much higher than the normal. Thus there is a need in developing wheat genotypes that are tolerant to terminal heat stress or the genotypes

which mature early by escaping this stressed environment without any reduction in yield.

In order to exploit selection, desirable variability among genotypes and the breeding lines which are less influenced by environment are more important. Hence the tool which is environmentally neutral like DNA markers inclusion in the present study gains significance. The use of simple sequence repeats (SSRs) which have high level of polymorphism, co-dominant nature and has equal distribution throughout the wheat genome can be used to characterize the genetic diversity. A robust marker-trait association is one of the main requisite for Marker Assisted Selection (MAS) (Kato *et al.* 2000). The markers which are already reported to have marker trait associations with the genes governing for heat tolerance are validated in the present study.

In view of all the above points, the present investigation on bread wheat genotypes was conducted with the following major research objectives:

1. To determine *per se* performance of genotypes for yield and component traits.
2. To assess variability components for grain yield and other component traits.
3. To estimate the stability parameters ($\bar{X}$, b_i , S^2d_i) for traits under study.
4. Validation of known SSR primers linked with heat tolerance.

Review of Literature

II. REVIEW OF LITERATURE

The genetic variability and to extent to which the traits are heritable along with performance of genotypes across varied environmental conditions would be an effective selection tool for selection of genotypes. The effect of global warming tends to affect the global production of cultivation of wheat. The environmentally neutral molecular tools like DNA markers will provide an effective selection tool for selection of cultivars for heat tolerance.

Hence here the available literature regarding the work on variability, stability analysis and molecular assisted selection has been reviewed and presented.

2.1 Variability, heritability and genetic advance

Johnson *et al.* (1966) on evaluating F₁ lines, back crosses and segregating generations of crosses derived from two winter wheat varieties, showed good heritability percentages for plant height, spike length, kernel weight and maturity.

Zečević (2008) on studying genetic and phenotypic variability of plant height and spike length reported significant difference of these two characters among years and among cultivars.

Eid, M.H. (2009) evaluated estimates of heritability and genetic advance for yield traits in which higher heritability with higher genetic advance were showed by spike length and 1000 grain weight compared to characters like plant height and number of grains per spike which showed low heritability accompanied by low genetic advance.

Kotal *et al.* (2010) on studying with 14 genotypes using randomized block design found highly significant difference and adequate genetic variability for all the ten characters studied among which number of effective tillers per plant and grain yield per plant were having high GCV, high heritability and high genetic advance which would be effective for selection.

Shankarrao *et al.* (2010) evaluated 38 genotypes of bread wheat in randomized block design and found high heritability and high genetic advance for characters like

grain weight per spike, thousand grain weight, number of grains per spike indicating these characters were controlled by additive manner and selection of these characters would be effective, they also noted the magnitude of phenotypic co-efficient of variation was higher than that of genotypic co-efficient of variation.

Zecevic *et al.* (2010) on studying variability and heritability components found significant difference for number of grains per spike and grain weight per spike among years and varieties.

Yadav *et al.* (2011) on studying ten characters of bread wheat concluded number of tillers per plant, biological yield per plant, grain yield per plant had high heritability with high genetic advance.

Bhushan *et al.* (2013) on working with 40 wheat genotypes found higher magnitude of GCV and PCV for traits like grain yield, number of productive tillers per plant, biological yield and for plant height. High heritability along with high genetic advance by *percent* means was recorded higher for plant height, biological yield, grain yield and harvest index indicating predominance of additive gene action in their inheritance.

Baloch *et al.* (2013) found significant difference among genotypes for all the characters studied by using mean square analysis from ANOVA and broad sense heritability estimates was found to be higher for the traits studied like plant height, number of tillers per plant, spike length, grain per spike, grain yield per plant and harvest index.

Sabaghnia *et al.* (2014) investigated 56 bread wheat genotypes for eighteen traits and found significant difference for all the characters studied indicating considerable amount of variation for each trait among genotypes.

Naik *et al.* (2015) studied 78 bread wheat genotypes in which variation was seen in all 8 characters except plant height and the trait grain yield per plot reported to have high heritability and genetic co-efficient of variation with high genetic advance.

Arya *et al.* (2017) on working with 49 wheat genotypes concluded significant difference for all the characters under study and found high PCV, GCV, high heritability along with high genetic advance for grain yield per plant.

Neeru *et al.* (2017) on examining 60 wheat genotypes found significant genotypic difference for all the traits grown in both timely sown and late sown environments. The characters grain yield per meter, effective tillers per meter and grain filling duration showed high heritability coupled with high genetic advance.

Bankapur *et al.* (2018) in their study reported higher estimates of GCV and PCV for the traits 1000 grain weight, grains per spike, spike length and yield per plot. Similarly high heritability accompanied by high genetic advance by percent means were also observed for these characters.

Bhanu *et al.* (2018) found the traits days to heading, days to anthesis, days to maturity and 1000 kernel weight exhibiting high heritability accompanied with high genetic advance by percent means for 20 wheat genotypes grown in the *rabi* season of 2011-12 and 2012-13.

Bharadwaj (2018) evaluated 16 genotypes of wheat and found significant difference for the characters studied by using ANOVA. The GCV and PCV estimates was found to be higher for the characters studied like days to 50% flowering, days to maturity, plant height, number of tillers per plant, spike length, 1000 grain weight, number of grains per spike, biological yield, harvest index and grain yield per plot and high heritability along with high genetic advance by percent means was observed for spike length, number of productive tillers per plant.

Rani *et al.* (2018) reported high heritability with high genetic advance for characters like number of tillers per plant, 100 grain weight, grain weight per ear indicating presence of additive gene effects which were effective for selection.

Rajshree and Singh S. K. (2018) on studying variability for 33 genotypes indicated high to moderate phenotypic and genotypic co-efficient of variation along with high heritability and genetic advance of characters like plant height, number of tillers per plant, spike length, number of grains per spike, grain yield per plot and for harvest index.

Thapa *et al.* (2019) studied 190 diversity wheat genotypes by using simple augmented block design for evaluation of genetic variability, heritability and genetic advance. Their results revealed highly significant treatment mean sum of squares in both normal and heat stress environments. GCV and PCV were highest for characters

like grain weight per spike, biological yield per plant, grain yield per plant and number of tillers per plant. Similarly characters like 1000 grain weight, biological yield per plant, grain number per spike and grain yield per plant, grain weight per spike and number of tillers per plant showed higher heritability estimates.

Ullah *et al.* (2018) evaluated 63 wheat genotypes along with one check cultivar reported to have significant difference for most of the characters studied and for the character grain yield they found high GCV and PCV. Broad sense heritability was found to be higher in the trait days to 50% heading. The highest genetic advance was found in grain yield followed by plant height, days to 59% flowering, 100 grain weight and spike length.

Hazra *et al.* (2019) on experimenting 24 wheat genotypes found little difference in respect to GCV and PCV for all the characters studied suggesting little environmental influence on the expression of these characters in wheat and the characters like plant height, spike length, grains per spike, total biomass and harvest index was found to be governed by additive gene action indicating effective selection of these characters for varietal improvement.

Mishra *et al.* (2019) reported equal magnitude of GCV and PCV for days to heading, days to maturity and 1000 grain weight but the traits plant height and grain yield exhibited higher PCV over GCV indicating effect of environment on these characters. Higher heritability was seen in traits days to heading, plant height and 1000 grain weight and in addition grain yield along with the above characters showed high heritability with high genetic advance.

2.2 Stability parameters

Finlay and Wilkinson (1963) considered regression co-efficient and variety mean yield over all environments as two important indices in stability analysis. High mean yield and low mean yield along with regression co-efficient approximating 1.0 indicates general stability and poor adaptability of genotypes over environments respectively. Similarly regression values above 1.0 describe sensitivity of genotypes to environmental change and regression values below 1.0 measures greater resistance of genotypes to environmental change.

Eberhart and Russell (1966) proposed the criteria for stability would be minimum deviation from regression line, regression co-efficient of unity and a high mean yield performance of the cultivars.

Baker R J (1969) on working among yields of six cultivars of red spring wheat varieties in nine different locations for five years proposed the stability of cultivar is inversely proportional to the sum of squares of $G \times E$ interaction attributed to that cultivar.

Bhullar *et al.* (1983) on studying stability analysis performed in diallel crosses of durum wheat for yield and other traits showed linear and non-linear components of $G \times E$ interaction was significant but non-linear component was of higher magnitude for traits like grain yield and spikes per plant and for the traits like spikelets per spike, grains per spike, spike length and grain weight only the linear component of variation of $G \times E$ interaction was significant indicating linear association of genotypes over varying environments.

Lin *et al.* (1986) proposed a particular cultivar may be considered stable i) if its environmental variance is small ii) if its response to environment is parallel to mean response of all the genotypes under trial and iii) if the residual mean square from the regression model on the environmental index is small

Aseefa *et al.* (1995) evaluated eight bread wheat lines along with one check found significant effect of genotypes, environments, and their interaction using combined analysis of variance for grain yield. The highest yielding line was HAR 1685 with grain yield of 4762 kg/ha, while the lowest was HAR 1331 with the mean grain yield of 3249 kg/ha. The regression co-efficients of grain yield calculated against environment index ranged from 0.406 to 1.451. HAR 1696 and Enkoy were considered most stable genotypes with regression co-efficient close to unity and minimum deviation from regression.

Ahmad *et al.* (1996) concluded linear and non-linear component of $G \times E$ interaction was significant showing genetic differences of 6 genotypes studied under 5 different locations for linear and non-linear components over varying environments for four durum wheat, one bread wheat and one triticale genotype. From their study D-88678 and Wadanak-85 were considered to be most stable and adaptable genotypes

with high yielding performance, unit regression and non-significant non-linear deviation from regression

Ashraf *et al.* (2001) reported highly significant difference among genotypes and environments for the character grain yield using pooled analysis of variance and mean square of both linear and non-linear components of G X E interaction were found highly significant indicating presence of both predictable and unpredictable components of G X E interaction in wheat. Considering the stability parameters, genotypes 89R 35 and 90R 36 showed regression close to unity (1.03) and low deviation from regression.

Amin *et al.* (2005) in their study on ten genotypes of wheat, used deviation from regression and average grain yield for the identification of superior genotypes in nine varied environmental conditions. Their study also found the interaction between genotypes and environment were found significant. Among simultaneous consideration of three stability parameters, genotypes Saleem-2000, CT-99022, CT-99155, SAW-98063 and Bakhtawar-92 showed highest yield over mean yield with regression coefficients of 1.620, 1.593, 0.760, 0.937 and 1.626 respectively and non-significant difference from regression.

Anwar *et al.* (2007) on studying ten wheat varieties in six different sowing dates showed highly significant differences among environment, genotypes, environment (linear) for all the traits studied except grain yield. Wheat varieties Inqilab-91, AS-2002 and V-97112 showed above average yield over trail with regression value of 1.08, 0.95 and 0.97 respectively with non-significant deviation from regression.

Rane *et al.* (2007) studied on 25 advanced breeding lines and released cultivars of wheat in 18 different environments. The genotype x environment interaction biplots for the grain yield showed the Raj 3765 and Raj 4027 was stable across all environments.

Shah (2009) on performing experiments in wheat genotypes for nine locations over three years found variety-location, variety-year and variety-location-year were highly significant for all the characters studied. The stability parameters, regression co-

efficient, deviation from regression mean square depicted a range of stability for all the characters.

Haydar *et al.* (2018) conducted the experiment at three locations using 4 varieties of wheat to estimate the stability parameters of grain yield. Among those four varieties Sourav was considered as most stable for grain yield with average mean performance, $b_i=1$, $S^2d_i=0$ showing stability for wide range of environments.

Anwar *et al.* (2011) experimented on 20 advanced lines including two checks of wheat at 18 different locations in two dates of sowing. The study found that check variety Seher-2006 produced maximum yield under both sowing conditions suggesting its stability across different environments. However the check was followed by the advanced lines Shafaq-2006, V-05066 and V-04022 under delayed sowing and V-04022 and V-05066 in normal sowing. The pooled analysis of variance too showed significant difference of genotypes and environment for grain yield.

Dimitrijevic *et al.* (2011) found significant influence of cultivars, years and their interaction on expression of traits studied for stability of yield components in wheat genotypes and by using ANOVA they found partitioning of total sum of squares to environmental main effect and genotypic main effect was highly significant. Likewise partitioning of environmental sum of squares showing years, location and their interaction were found highly significant source of variation. The traits plant height, harvest index and grain yield per plant showed greater source of variation for the two localities studied, than years.

Koumber *et al.* (2011) showed that the variances due to genotypes (G), environments (E), $E + (G \times E)$, $G \times E$, E (linear), $G \times E$ (linear) and pooled deviation were highly significant ($P < 0.01$) on performing the experiment on 40 wheat genotypes under three locations in Gemmieza, Nubaria and Mallawy of Egypt. From the study genotypes Sakha 93 and promising lines 23, 31 and 32 were considered stable with high grain yield, low deviation from regression and regression co-efficient value close to unity.

Ameen (2012) conducted his experiment in four environments i.e, in two sowing dates with two years in the *rabi* season of 2010-2011 accessing 17 wheat genotypes found combined analysis of variance showing significant difference between

genotypes and for the characters grain yield, 1000 grain weight, number of kernel per spike and spike length. The G X E were highly significant. From the study genotypes No.1, 2, 3 and 7 showed high grain yield and regression co-efficient non-significant from unity.

Mohammadi *et al.* (2012) worked on fourteen bread wheat genotypes for yield stability and performance across four environments using stability statistics. Combined analysis of variance for grain yield showed there is a significant difference among the genotypes and environment and differential performance of genotypes across environments due to significant G x E interactions. Based on deviation from regression mean square, genotypes G2, G12 and G15 were considered most stable genotypes. The results also showed the slope of linear regression by both conventional and independent models would be a very useful tool in selection of genotypes for high yield and stability.

Motamedi *et al.* (2012) worked in finding the stable bread wheat genotype and to access the G x E interaction as their objective by using regression coefficient, mean squares of deviation from regression. The regression co-efficient (b_i) values of the genotype studied ranged from 0.22 to 1.81 and deviation from regression was in the range of 0 to 2.26. The lines 15, 5, 6 and 19 were considered promising, because their yields were above the average, in all three environmental conditions.

Hassan *et al.* (2013) on evaluation of durum wheat genotypes in different environments found the combined analysis of variance for genotype, environment and G x E interaction were highly significant for all the characters studied. The genotypes exhibiting regression co-efficient (b_i less than 1) for number of grains per spike, grain weight per spike and grain yield per plot were considered specially adopted to unfavourable environmental conditions. Similarly the genotypes which exhibited b_i values more than unity for the characters plant height, number of grains per spike, grain weight per spike and grain yield per plot could be adapted to optimum environment. The regression co-efficients value for the genotypes No. 1, 2, 5, 8, 9, 14 and 15 for grain yield per plant were less than 1, indicating its adaptation to unfavourable environmental conditions.

Gulzar *et al.* (2015) worked on 22 wheat genotypes obtained through CIMMYT, Mexico showing genotypes differed significantly for all traits indicating diversity among genotypes and there was also significant difference among environment except grains per spike. The genotypes CMT 198, CMT 125, CMT 1142, CMT 1148 and CMT 1187 showed average responsive for grain yield per plot and were stable with mean grain yield of 1306.5g per plot. The genotypes CMT 1162, CMT 198, CMT 1006, CMT 125, CMT 1193 showed average stability across all the environments for studied yield and yield related traits.

Verman *et al.* (2015) on studying sixteen bread wheat genotypes and two durum wheat varieties found significant mean square for genotypes and genotype x environment for all the characters studied except harvest index. Regression factor was non-significant for traits days to flowering, ear length and grains per ear and the linear components of G x E interactions were significant for all the characters studied except days to heading, 1000 grain weight, harvest index and grains per ear under different sowing times. The genotype GW 273 showed high mean performance, stable and average responsive for grain yield, plant height, biological yield and ear length by estimation of regression co-efficient and non-significant deviation from regression, whereas LOK1 and HI 8627 were found responsive in late sown and stable for tillers per plant, seed per ear, harvest index, biological yield and grain yield.

Uddin *et al.* (2017) on studying wheat genotypes, worked on stability of performance for yield and other yield attributes found significant environment and genotype x environment components of variation of stability indicating prediction of genotypes on the environment appeared practical for the characters studied. Considering three stable parameters, genotypes G11, G22 and G37 were found stable, with reasonable good yield among all genotypes.

Singh *et al.* (2018) studied for 28 diverse wheat genotypes at three locations. Pooled analysis of variance showed a highly significant variance due to environment for characters studied like grain yield, 1000-grain weight indicating differential response of genotypes. The genotype BWL 3584 could be used as a potential donor in hybridization programme for grain yield due to its stable performance across environments under unfavorable conditions.

Krupal *et al.* (2018) on studying eleven varieties of wheat, concluded MACS-6222, PBN-3958 and GW-480 genotypes were stable under all environments by exhibiting higher mean, bi value nearer to unity, non-significant deviation from regression line for grain yield. The component G x E interaction being highly significant indicates the interaction of genotypes was considerable in different environments.

Siddhi *et al.* (2018) studied 45 genotypes of bread wheat in three different sowing environments found mean square due to genotypes and environments were significant for all the characters except days to heading, number of effective tillers per plant, number of grains per main spike, biological yield and harvest index indicating significant variations among genotypes and environments. They also noted that mean sum of square due to environments had significant difference for all the characters studied when tested against pooled error suggesting difference between environments were considerable for all traits studied and environments created by different sowing dates were justified and had linear effects. From the study, parents NW5013 and QLD 46 were found stable for grain yield with 15.94g and 15.78g per plant respectively along with other yield related components.

Thakur *et al.* (2019) on studying ten wheat genotypes, revealed the genotype HUW 234 was stable compared to other genotypes under study due to its at par grain yield with population mean, near unity regression co-efficient and near zero deviation from regression co-efficient. The significant variations due to genotypes showed there was a presence of variability among all genotypes for the characters studied and significant GxE interaction revealed there was a considerable interaction of genotypes to environmental conditions in different environments. The genotype HUW 234 showed at par value with the population mean, unit regression co-efficient and non-significant deviation from regression for grain yield per plant, depicting this genotype found stable across all environments studied.

Sharma *et al.* (2019) assessed the stability of wheat genotypes for grain yield and other associated characters and found the hybrids HI 1544 × HD 2987, PBW 175 × HD 2987, PBW 175 × Lok 1, Raj 4037 × HD 2987, HD 2932 × Raj 4079 were stable

showing high mean values, favorable regression co-efficient and deviation from regression.

Pujer *et al.* (2020) on studying GxE interaction effects and stability in wheat for grain yield concluded genotypes namely NIAW 34, HW 1098 and BMZ 15-16-2 would be suitable for all three different dates of sowing. Their results showed the significant difference of all the genotypes for their characters studied. There was a sufficient variability among genotypes due to their significance of mean squares of genotypes against pooled error and pooled deviation for various characters except thousand grain weight.

2.3 Molecular studies

Yang *et al.* (2002) on analysis of F₂ population derived from the cross of Ventnor (heat-tolerant) and Karl 92 (heat susceptible) in wheat found two SSR markers Xgwm11 and Xgwm293 which were linked to grain filling duration. The Xgwm11-linked QTL had additive gene action and contributed 11% to the total phenotypic variation in F₂ population while Xgwm293-linked QTL had both additive and dominance action and contributed around 12% to total variation in grain filling duration.

Cuthbert *et al.* (2008) evaluated F₁ derived from double haploid population of 402 lines developed from the cross of two spring varieties Superb (high yielding) and BW278 (low yielding) for identification of QTL associated with yield and its component traits. By composite interval mapping they found 53 QTLs on 12 chromosomes for 9 traits which were studied. Among this, five grain yield QTL was detected on 1A, 2D, 3B and 5A revealing the importance of this chromosomal segments for its use in marker assisted selection for the improvement of yield and its components.

Mohammadi *et al.* (2008) evaluated 144 recombinant inbred lines derived from the cross of Kauz and MTRWA116 in wheat using 166 SSR and 3 AFLP markers to construct a linkage map containing 18 linkage groups and by use of composite interval mapping three QTLs on the chromosomes 1B, 5B and 7B were identified. The QTL located on 1B is linked to gwm190 explains 44.3% phenotypic variance. The QTL located on 5B explains 27.3% phenotypic variance and another QTL located on 7B

chromosome was linked to gwm63b had positive additive effects. These three QTLs altogether contributes 16.7% of phenotypic variance of stress susceptibility index.

Pinto *et al.* (2010) phenotyped 167 recombinant inbred lines (RILs) of spring wheat varieties along with their parents used for crossing to identify genomic regions which are associated with stress-adaptive traits and found a total of 104 QTL among 115 traits in 3 environments over 2 years. The common QTL for drought and heat stress were found on 1B-a, 2B-b, 3B-b, 4A-a, 4B-b and 7A-a highlighting their generic importance for further molecular studies.

Barakat *et al.* (2011) studied parents Debra (heat tolerant) and Yecoro Rojo (heat susceptible), their derived F₁ and F₂ population in wheat. On analysis of this F₂ population for QTL they found three SSR markers Xgwm132, Xgwm577 and Xgwm617 which were linked to grain filling rate. The co-efficient of determination (R^2) values were 0.07, 0.25 and 0.03 suggesting that they accounted for 7%, 25% and 3% phenotypic variance of heat tolerance respectively.

Bennet *et al.* (2012) studied double haploid population derived from RAC875 and Kukri in wheat to find the genetic loci for grain yield, yield components and morpho-physiological traits for heat and drought conditions and found 2 of the detected QTL was located on chromosome 3B which had a large effect on grain yield which can be used for further molecular studies.

Paliwal *et al.* (2012) evaluated 148 recombinant inbred lines (RILs) developed by crossing heat tolerant NW1014 and heat susceptible HUW468 in wheat. By using composite interval mapping they found significant genomic regions on 2B, 7B and 7D chromosomes which were associated with heat tolerance. This found 3 major QTLs can be used for marker assisted selection to develop heat stress tolerant varieties in wheat.

Drikvand *et al.* (2013) conducted a study on 92 bread wheat varieties for genetic diversity and to evaluate polymorphism information content (PIC) of wheat SSR primers. By the use of 40 whole genome SSR markers, they found amplification for eighty alleles with 2 alleles per locus. The PIC values ranged from 0.12 for the primer Xbarc148 to 0.80 for the primer Xbarc54, with an average of 0.59 per primer, indicating the markers were highly informative. The cluster analysis carried out by

UPGMA method resulted in formation of six clusters, indicating the studied cultivars were diverse and could be exploited for further breeding programmes.

Mason *et al.* (2013) used 118 recombinant inbred lines (RILs) developed from the cross of Halberd (stress tolerant) and Karl92 (heat stress sensitive) in wheat to identify QTL associated with yield and its components. By using composite interval mapping they detected 25 stable QTLs over 15 traits studied, the amount of phenotypic variation ranged from 3.5 to 27.1% for the individual QTL. They found two QTL for the character grain yield and canopy temperature depression co-localised on chromosomes 3BL and 5DL.

Gupta *et al.* (2015) evaluated F₂, parents PBW373 and WH1081 along with the check varieties of wheat genotypes using 200 SSRs. Among them 22 SSRs produced polymorphic bands of size range between 100-300 bp with an average allele size of 1.45. By using single marker analysis, 19 markers were identified indicating putative QTLs for yield, its components and heat stress related physiological traits and by using composite interval mapping 16 linkage groups were mapped, the number of markers on these 16 linkage groups varied from 1-4. 13 QTLs on A genome, 5 QTLs on B genome, 9 QTLs on D genome were identified.

Mwale *et al.* (2016) studied genetic diversity for 60 bread wheat genotypes using 60 microsatellite SSR markers, over which 48 markers showed polymorphism amplifying over 276 alleles with an average of 5.7 alleles per locus. Cluster analysis resulted in the formation of 4 clusters with 3, 7, 9 and 41 cultivars, with the genetic distance between the clusters in the range of 0.56 to 0.87, with the maximum diversity between the genetic distance of 0.65 and 0.75.

Sharma *et al.* (2016) investigated recombinant inbred line (RIL) population developed from K7903 (heat tolerant and RAJ 4014 (heat susceptible) of spring wheat genotypes to identify QTL for heat tolerance in both timely and late sown conditions. For identification of QTL, heat susceptibility index of grain filling duration, other yield components and traits under late sown condition were used as phenotypic data. The stable QTLs associated with these traits were located on chromosomes 1B, 2B, 3B, 5A and 6B. The range of LOD value was from 2.9 to 5.0 and the corresponding phenotypic variation ranged from 12-22%.

Bhusal *et al.* (2017) evaluated 251 recombinant inbred lines (RILs) derived from the cross HD2808 (heat tolerant) and HUW510 (heat susceptible) of wheat genotypes in both timely sown and late sown conditions for two consecutive crop seasons. Composite interval mapping identified 24 QTLs which were mapped on linkage groups 2A, 2B and 6D. The LOD score of this identified QTLs varied from 3.03 to 21.01, explaining 11.2 and 30.6% phenotypic variance respectively.

Kumar *et al.* (2018) assessed 16 genotypes of wheat with 14 SSR markers for molecular diversity for terminal heat stress tolerance linked to trait of interest. The amplified alleles were ranged from 185-230bp. The primers Xgwm484 and Xcfd43 generated maximum number of polymorphic bands with 4 amplicons followed by primer Xgwm268 with 3 amplicons. The dendrogram classified this studied 16 genotypes into two clusters A and B, where the cluster A and B is further subdivided into 3 clusters of six and ten genotypes respectively. The genotypes namely DBW90, WH1021, HD3059, JOB666, UP2843 AND WH1124 were reported to be suitable for late sown conditions.

Vasantrao *et al.* (2019) screened 19 wheat genotypes for their tolerance to heat stress using 17 wheat microsatellite markers. These markers detected 89 alleles with an average of 4.6 alleles per locus. Polymorphism information content (PIC) ranged from 0.16 for the primer Xgwm516 to 0.83 for the primer Dupw117 with an average of 0.60. The trait thousand grain weight was found to be associated with the markers barc4, barc170, barc311, psp3058, gwm458 and the number of grains per plant was strongly associated with the marker barc311.

Material and Methods

III. MATERIAL AND METHODS

The present investigation of research work was carried out at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during the *rabi* season 2019-20 under four different sowing dates (i.e., 15th November, 25th November, 5th December, 15th December) are described below.

3.1 Experimental material

The experimental material comprised of 20 diverse wheat genotypes which was received from Wheat Research Station, Sardarkrushinagar Dantiwada Agricultural University, Vijapur. The genotypes taken for study are represented in Table 3.1.

Table: 3.1: List of bread wheat genotypes

Sl. No.	GENOTYPES*	PEDIGREE
1	VA2019-16	SUP 152*2 / TECUE#1 // SUP 152 / BAJ#1
2	VA2019-17	WH 1013 / RAJ 4155 // GW 397
3	VA2019-18	LBPY 2006-4 / SYN 02-39 // RAJ 4010
4	VA2019-19	NIAW 835 // CPAN 1931 / WH 147/3/ GW 173
5	VA2019-20	PHS 0827 / GW173
6	VA2019-21	RAJ 4132 / VW 514
7	VA2019-22	GW 173 / GW 397
8	VA2019-23	W.EC.65 / 3 / HDR 70 / CIANO 79 // GW 244
9	VA2019-24	J 430 / V-3 // CDWR 1577 / 3 / HD 2956
10	VA2019-25	MP 4010 / WH 1013
11	VA2019-26	HD 2956 // GW 323 / LBP 98-307
12	VA2019-27	RAJ 4010 / MP 4010
13	VA2019-28	LBPY 2004-3 / KRL99 // DL 1012
14	VA2019-29	LBPY 2006-4 / SYN 02/ 39 // RAJ 4010
15	VA2019-30	NIAW 835 // CPAN 1931 / WH 147 / 3 / GW173 // GW496
16	VA2019-31	GW322/ HI 1544
17	VA2019-32	SUP 152 / BAJ#1 // KFA / 2*KACHU
18	VA2019-33	KSW / SAUAL // SAUAL / 3 / 2 / *BORL 14
19	NI-5439	REMP80-3*NP 710
20	DBW-93	WHEAR-TUKURU // WHEAR

* Source: Genotypes received from Wheat Research Station, SDAU, Vijapur

3.2 Experimental methods

3.2.1 Experimental details

The twenty genotypes were grown in Randomized Block Design (RBD) with 3 replications during *rabi* season 2019-2020 in four different date of sowings with the plot area of 576 m² with the row spacing of 22.5cm between two rows.

3.2.2 Layout description

The size of each individual plot for the research experiment taken was 1m x 2m, incorporating four individual rows for each genotype for each replication.

3.2.3 Fertilizer application

The recommended dose of 120 kg N: 60 kg P₂O₅: 40 kg K₂O per hectare was applied. Initial half dose of nitrogen and full dose of phosphorous and potash were applied at the time of sowing, remaining dose of nitrogen were applied as a top dressing after 21 days after sowing. Irrigation was carried out at regular intervals and weeding operations were performed twice during the crop growth stage.

3.2.4 Harvesting

The crop was harvested at physiological maturity.

3.3 Characters studied

The observations were recorded from five randomly selected plants and averaged out for each genotype in each replication.

3.3.1 Days to 50% heading

The number of days from sowing to 50 *per cent* of shoots having their entire spike out of flag leaves were recorded on plot basis.

3.3.2 Days to maturity

The number of days from sowing to the stage upon 75% plants turning pale yellow due to senescence were recorded on plot basis.

3.3.3 Grain filling period

The difference in the number of days from maturity to that of flowering on plot basis was calculated and recorded.

3.3.4 Plant height (cm)

The height of randomly selected each of five plants was measured from the base of the plant to the tip of the main shoot of the spike (excluding awns) at the time of maturity and averaged out.

3.3.5 Number of effective tillers per meter

Total number of ear bearing effective tillers of two middle rows was recorded at maturity and averaged out for one meter area.

3.3.6 Spike length (cm)

The spike length of randomly selected five spikes from randomly selected five plants was measured from base of the spike to the tip of the spike at the time of maturity excluding awns.

3.3.7 Number of grains per spike

A random sample of five spikes was taken from randomly selected five plants and threshed together and grains were counted and averaged for one spike for each genotype for each replication.

3.3.8 Grain weight per spike (g)

A random sample of five spikes were taken from randomly selected five plants, threshed, cleaned and weighed and the grain weight was averaged for a single spike in each genotype for each replication.

3.3.9 Grain yield (g)

The plants of two middle rows of every genotype were threshed, cleaned and the grain yield was recorded in each genotype for each replication and averaged out for one meter length.

3.3.10 Thousand grain weight (g)

The randomly selected thousand kernels from the harvested bulk of randomly selected five plants were taken and their weight was recorded.

3.3.11 Biological yield (g)

The biological yield was taken after the plants were harvested from the middle two rows in each genotype for each replication and averaged out for one meter length.

3.3.12 Harvest index (%)

Harvest index was calculated in percentage as:

$$HI = \frac{\text{Grain Yield (g)}}{\text{Biological Yield (g)}} \times 100$$

3.4 Statistical analysis

The mean values of the observed plants of each entry for different characters were subjected for data analysis.

3.4.1 Analysis of variance (ANOVA)

The analysis of variance for the Randomized Block Design (RBD) was carried out for every character under each environment on the basis of following model (Panse and Sukhatmc, 1967). This statistical procedure splits up the total variation into three components viz. replication, treatment, error. The form of analysis of variance is represented in Table 3.2.

The ANOVA under fixed effective model is as under

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

where,

Y_{ij} = observations for the i th treatment for the j th replication

μ = General Mean

g_i = Effect of i^{th} genotype,

r_j = Effect of j^{th} replication and

e_i = Random error associated with i^{th} treatment and j^{th} replication

Table 3.2 Analysis of variance for experimental design

Sources of variation	Degrees of freedom	Sum of squares	Mean sq	Expected mean sq	F calculated
Replications	(r-1)	RSS	M_r	$\sigma_e^2 + g \sigma_r^2$	M_G/M_e
Genotypes	(g-1)	GSS	M_g	$\sigma_e^2 + r \sigma_g^2$	
Error	(r-1)(g-1)	ESS	M_e	σ_e^2	
Total	(rg-1)	TSS			

where,

r = Number of replications,

g = Number of genotypes,

$\sigma_e^2, \sigma_r^2, \sigma_g^2$ = Variance due to error, replications and genotypes, respectively,

M_r , M_g , M_e = Mean squares for replication, genotypes and error, respectively.

The significance of M_r and M_g were tested against M_e by F test at 5 *per cent* level of significance. If the variance was found to be greater than tabulated F value at 5% level of significance, the difference between genotypes for the characters studied was significant and if found lower, then it was considered non-significant.

The standard error of mean was calculated as follows:

$$S.E.m. = \sqrt{M_e/r}$$

where,

S.E.m. = Standard error of mean

M_e = Error Mean Sum of Squares

r = Number of replications.

The Critical difference to compare the mean values of each genotype was calculated by using the formula:

$$C.D. = S.E.m \times \sqrt{2} \times t_{0.05 \text{ at } e_{df}}$$

where,

C D = Critical Difference,

S.E.m. = Standard Error of Mean,

t = Table value of t at 5% level of significance at error degree of freedom.

The co-efficient of variation (C.V %) is calculated using the following formula:

$$C.V.\% = \frac{\sqrt{M_e}}{\bar{X}} \times 100$$

where,

C V% = Coefficient of variation

M_e = Error mean sum of square

$\bar{X}$ = General mean

3.4.2 Variability parameters

a) Mean

The mean value of each character was calculated by dividing the totals by the corresponding number of observations

$$\text{Mean} = \frac{\sum x_{ij}}{N}$$

where,

$\sum x_{ij}$ = Sum of all the observations recorded for each character of each genotype in each replication

N = Number of observations

b) Range

The difference between the highest and lowest mean value for each character is taken as range.

$$\text{Range} = X_n - X_t$$

Where,

X_n = The highest mean value of each character

X_t = The lowest mean value of each character

c) Components of variance

i) Genotypic variance (σ^2_g)

The variance due to genotypes present in the population is defined as genotypic variance.

The formula used for calculation is

$$\sigma^2_g = \frac{M_g - M_e}{r}$$

where,

M_g, M_e = Mean squares of genotypes and error respectively

r = Number of replications

ii) Environmental variance or Error Variance (σ^2_e)

The variance due to environmental deviation is environmental variance,

$$\sigma^2_e = M_e$$

where,

M_e = Error mean sum of square

iii) Phenotypic variance (σ^2_p)

The total variance present in the population for that particular character is defined as phenotypic variance

The formula used for calculation is

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

where,

σ_p^2 , σ_g^2 , σ_e^2 = Variances due to phenotype, genotype and error respectively.

3.4.3 Co-efficient of variation

The three types of coefficient of variations were estimated viz. phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV) in this present investigation. The formulae used to calculate PCV, GCV and ECV were given by Burton and De vane (1953):

a) Genotypic co-efficient of variation (GCV):

$$\text{GCV \%} = \frac{\sigma_g}{\bar{X}} \times 100$$

b) Phenotypic co-efficient of variation (PCV):

$$\text{PCV \%} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Population mean

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

Burton and Devane (1953) classified GCV and PCV as low (0 – 10 %), moderate (10 – 20 %) and high (20 % and above).

3.4.4 Heritability (h^2_b)

Ratio of genotypic to the phenotypic variance which is expressed in percentage is defined as broad sense heritability and is given by the formula

$$h^2 \text{ (broad sense)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Heritability is classified as low, moderate, high as given by Johnson *et al.* (1955)

Low : 0-30%

Medium : 30-60%

High : >60%

3.4.5 Genetic Advance

The improvement in mean genotypic value of selected plants over parental population is defined as genetic advance

It is given by the formula

$$GA = K. \sigma_p. h^2$$

where,

GA = Genetic advance

k = Selection differential at 5% intensity level i.e. 2.06 (constant)

h^2_b = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.4.6 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean was worked out as suggested by Johnson *et al.* (1955).

$$GAM (\%) = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Expected genetic advance

$\bar{X}$ = Mean of the character

Johnson *et al.* (1955) categorized genetic advance as per cent of mean as follows:

Low : 0 – 10 %

Medium : 10 – 20 %

High : 20 % and above.

3.5 Stability analysis

In this present study Eberhart and Russell model (1966) was used. The structure of pooled analysis for stability is presented in Table 3.3 They suggested three parameters i.e. mean, regression, and deviation from regression to characterize the stability of cultivars. These parameters are as under:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where,

- Y_{ij} = Mean performance of i^{th} genotype in j^{th} environment
 g = Number of genotype
 e = Number of environments
 μ_i = Mean performance of i^{th} genotype over all environments
 b_i = Regression coefficient of i^{th} genotype on environment index
 I_j = Deviation of mean of all the varieties at a given location mean from overall mean defined as environmental index.

It was obtained by the difference of mean of j^{th} environment to the grand mean and expressed as

$$I_j = [(\sum Y_{ij}/g) - (\sum \sum y_{ij}/ge)] \text{ and } \sum I_j = 0$$

δ_{ij} = deviation from regression of the i^{th} genotype at the j^{th} environment

Table 3.3 Analysis of variance structure for stability analysis by Eberhart and Russel (1966)

Source	df	SS	MSS	F
Total	$(ge-1)$	$\sum_i \sum_j \sum_i Y_{ij}^2 - CF = TSS$		
Genotype(g)	$(g-1)$	$1/e \sum_i Y_i^2 - CF = GSS$	MS_1	MS_1/MS_6
Environments (e)	$(e-1)$	$1/g \sum_j Y_j^2 - CF = ESS$	MS_2	MS_2/MS_6
G x E	$(g-1)(e-1)$	$TSS - (GSS+ESS)$	MS_3	MS_3/MS_7
E + (G x E)	$g(e-1)$	$\sum_i \sum_j \sum_i Y_{ij}^2 - 1/n \sum_i Y_i^2$		
E (linear)	1	$1/g(\sum_j Y_j I_j)^2 / (\sum_j I_j^2)$	MS_4	MS_6
G x E (linear)	$(g-1)$	$\sum_i [(\sum_j Y_{ij} I_j)^2 / (\sum_j I_j^2)] - E$ (linear) SS	MS_5	MS_6
Pooled deviation	$g(e-2)$	$\sum_i \sum_j \delta_{ij}^2 = \sum_i [\sum_j$	MS_6	MS_6/MS_7
Genotype 1	$(e-2)$	$\sum_j Y_{ij}^2 - (Y_1^2/n) - (\sum_j y_{ij} I_j)^2 /$ $\sum I_j^2 = \sum_i \sum \delta_{ij}^2$		
Genotype g	$(e-2)$	$\sum_j Y_{gj}^2 - (Y_g^2/n) - (\sum_j y_{gj} I_j)^2 /$ $\sum I_j^2 = \sum_i \sum d_{gi}^2$		
Pooled Error	$ge(r-1)$	$\sum_j S_{ej}^2 / r$	MS_7	

where,

- S_{ej}^2 = Estimate of error mean square at each environment
 g = Number of genotype
 e = Number of environments

r = Number of replication

3.5.1 Stability parameters and their test of significance

a) The regression of performance of environmental means over all the genotypes is the first stability parameter regression co-efficient (b_i) and is given by formula

$$b_i = \Sigma Y_{ij} I_j / \Sigma I_j^2$$

where,

$\Sigma Y_{ij} I_j$ = Sum of products

ΣI_j^2 = Sum of squares

It was tested for its deviation from unity by the following formula

$$t = (1 - b_i) / SE(b_i)$$

This calculated 't' value was compared with the table t value at n-1 degree of freedom

where,

n = Number of genotypes.

$SE(b_i) = \sqrt{MSS \text{ due to pooled deviations} / \Sigma I_j^2}$

b) The second stability parameter mean square deviation (S^2d_i), was estimated with the following formula

$$S^2d_i = \Sigma \delta_{ij}^2 / n - 2 - S^2e/r$$

Where,

$\Sigma \delta_{ij}^2 = \Sigma Y_{ij}^2 - (\Sigma Y_{ij})^2 / \Sigma I_j^2$

S^2e = estimate of pooled error

The average of error mean sum of square over all environments was taken as estimate of pooled error (S^2e/r). Its significance for each genotype was tested by

$$F = S^2d_i / \text{mean square due to pooled error}$$

The calculated F value will be tested against tabulated F value at 1 degree of freedom (for genotype) and degree of freedom for pooled error.

A variety with higher mean ($\bar{X}$), unit regression co-efficient ($b=1$) and the deviation not significantly different from 0 (S^2d_i) was considered to be stable one.

3.6 Molecular analysis

3.6.1 DNA Isolation

The isolation of genomic DNA of wheat genotypes was carried out as per cTAB method of Doyle and Doyle (1987).

3.6.2 Chemicals and Reagents for DNA Isolation

S.No	Chemicals	S.No	Chemicals
1.	DNA extraction buffer	6.	TE buffer
2.	B-Mercaptoethanol	7.	Distilled water
3.	Chloroform : Isoamyl alcohol solution (24:1)	8.	RNase A
4.	Phenol : Chloroform : Isoamyl alcohol (25:24:1)	9.	Liquid nitrogen
5.	Pre-chilled Isopropanol	10.	Ethanol

Various stock solutions and buffers were prepared and used during isolation of genomic DNA and during gel electrophoresis. Their composition and procedure for their preparation is mentioned in the Table 3.4 and Table 3.5

Table 3.4 Preparation of stock solutions for extraction of DNA and gel electrophoresis

Sl. No.	Solution	Method of preparation
1	1M Tris HCl (pH 8.0), 100 ml	12.11 g Tris base is dissolved in 50 ml distilled water. The pH was then adjusted to 8.0 by addition of concentrated HCl and the final volume is made to 100 ml, then the solution is dispensed into reagent bottle and sterilized by autoclaving.
2	0.5 M EDTA (pH 8.0) 100 ml	14.61g of EDTA was dissolved in 50 ml distilled water. The pH was adjusted to 8.0 by addition of NaOH pellets and final volume is made to 100 ml, then the solution is dispensed into reagent bottle and sterilized by autoclaving.
3	5 M NaCl, 100 ml	29.22 g NaCl was dissolved in 50 ml distilled water and thoroughly mixed. After the salt gets completely dissolved, final volume was adjusted to 100 ml, then the solution is dispensed into reagent bottle and sterilized by autoclaving.
4	70% ethanol, 100 ml	70ml of ethanol was taken and 30 ml of distilled water was added, and mixed well, then dispensed into reagent bottle and stored at 4°C.
5	Chloroform: Isoamyl alcohol (24:1), 500 ml	480 ml of chloroform and 20 ml of isoamyl alcohol was mixed well and stored in a reagent bottle and at room temperature.
6	Ethidium Bromide (10mg/ml)	10 mg of Ethidium Bromide was added to 1.0 ml of distilled water and kept on magnetic stirrer to ensure complete dissolution of dye and stored in an amber coloured eppendorf tube.
7	Gel loading dye (6X)	0.25% of bromophenol blue, 0.25% of xylene cyanol FF and 30% of glycerol was mixed and the distilled water was added to it.

Table: 3.5 Buffers preparation

Sl.No.	Buffer	Method of preparation
1	cTAB Extraction Buffer (4%), 10 ml	0.4g of cTAB, 1.0 ml of 1M Tris HCl (pH 8.0), 2.8 ml of 5M NaCl and 1.0 ml of 0.5M EDTA (pH 8.0), 0.1g of PVP and 5.2 ml of hot distilled water was taken in a flask and mixed well for complete dissolution of cTAB and PVP.
2	1X TE Buffer	1 ml of 1M Tris HCl (pH 8.0), 200µl of 0.5M EDTA (pH 8.0) were taken and distilled water was added to make the final volume to 100 ml, mixed thoroughly and solution was autoclaved and stored at room temperature.
3	5X TBE Buffer (pH 8.0), 1 litre	54g of Tris base, 27.5g of boric acid and 20 ml of 0.5M EDTA (pH 8.0) was dissolved in 400 ml of distilled water and final volume was made to 1 litre after adjusting the pH to 8.0. Later the solution is dispensed into reagent bottle.

3.6.3 Isolation of genomic DNA

1. The fresh leaves were taken from 20-25 days old seedlings and were made to grind to a fine powder using liquid nitrogen in a pestle and mortar and were filled into 2 ml centrifuge tube.
2. 1 ml of cTAB extraction buffer and 10µl β-mercaptoethanol was added into the tubes and kept in a water bath for 45 minutes to 1 hour, where tubes are given a jerk for every 10-15 minutes interval.
3. After incubation the tubes were centrifuged at 12000 rpm for 12 minutes at 24°C.
4. The supernatant was carefully transferred to a fresh tube and equal volume of chloroform: isoamyl alcohol (24:1) was added and again centrifuged for 12 minutes at 12000 rpm.
5. The supernatant was transferred to a fresh tube and given a RNase A treatment and kept in water bath at 37°C for 45 minutes.
6. Equal volume of chloroform: isoamyl alcohol (24:1) was added after the RNase A treatment and centrifuged at 12000rpm for 12 minutes.
7. The supernatant was taken and equal volume of chloroform: isoamyl alcohol (24:1) was added and again centrifuged at 12000 rpm for 12 minutes.

8. After centrifugation the supernatant was transferred to 1.5ml centrifuge tube and 0.6 volume of chilled isopropanol was added and stored overnight at -20°C for better precipitation of DNA.
9. Next day morning, the fine pellets of DNA will be obtained after it has been given a centrifugation at 4°C for 10 minutes at 10000rpm.
10. The pellets obtained was washed with 70% ethanol, twice and kept in the oven for the evaporation of ethanol.
11. Later, the pellets were made to dissolve in 100 µl of 1X TE buffer by tapping on the tubes and stored at -20°C.

3.6.4 Quantification of genomic DNA

The quantification of nucleic acid was performed using UV spectrophotometer. The principle here is nucleic acid absorb ultraviolet light in a specific pattern. The more light the sample absorbed the more will be the concentration of DNA. The sample was loaded into the cuvette well, and the sample was exposed to UV at 260nm wavelength and 280nm wavelength. The quantity of DNA was estimated using Beer-Lambert law of 1.0 O.D. as 260nm equivalent to 50ng DNA per ml by the following formula:

$$\text{DNA (ng/}\mu\text{l)} = \text{O.D. A}_{260} \times \text{Dilution factor} \times 50$$

3.6.5 Quality estimation of genomic DNA

Usually while extraction of DNA, the contamination with molecules like proteins, organic compounds and RNA will occur. The quality of DNA was verified by both UV spectrophotometer and 0.8% agarose gel run. The good quality DNA will have the O.D. in the range of 1.8-2.0. The O.D. below 1.8 or 1.7 indicates protein contamination and O.D. above 2.0 will be indicating contamination of RNA. The 0.8% agarose gel run will show bands with less shearing indicates good quality and amount of DNA.

3.6.6 PCR (Polymerase Chain Reaction) based amplification by SSR primers

Sixteen SSR primers were used for the validation of heat tolerance mentioned in the Table 3.6. PCR reactions were performed in the reaction volume of 15 µl containing 1.5µl of Taq bufferB (10X) with MgCl₂, 0.5 µl dNTP mix (10 mM), 1.0 µl

of each primer (5 p mol), 0.1 µl of Taq DNA polymerase and 1.0 µl of genomic template DNA(50ng/ml), with the cycle for each step mentioned in the Table 3.7

Table 3.6 List of SSR primers used in the present study

Sl. No.	Primer name		Sequence	Ba ses	Tm value (°C)	% GC
1	gwm102	F	TCTCCCATCCAACGCCTC	18	58.24	61.11
		R	TGTTGGTGGCTTGACTATTG	20	55.25	45.00
2	Xgwm484	F	ACATCGCTCTTCACAAACCC	20	57.30	50.00
		R	AGTTCCGGTCATGGCTAGG	19	58.82	57.89
3	Xgwm190	F	GTGCTTGCTGAGCTATGAGTC	21	59.32	52.38
		R	GTGCCACGTGGTACCTTTG	19	58.82	57.89
4	Xgwm131	F	AATCCCCACCGATTCTTCTC	20	57.30	50.00
		R	AGTTCGTGGGTCTCTGATGG	20	59.35	55.00
5	Xwmc48	F	GAGGGTTCTGAAAGTTTTACC	21	55.92	42.86
		R	ACGTGCTAGGGAGGTATCTTGC	22	62.12	54.55
6	Xgwm63	F	TCGACCTGATCGCCCCTA	18	58.24	61.11
		R	CGCCCTGGGTGATGAATAGT	20	59.35	55.00
7	barc65	F	CCCATGGCCAAGTATAATAT	20	53.20	40.00
		R	GCGAAAAGTCCATAGTCCATAGTCTC	26	63.22	46.15
8	Xgwm11	F	GGATAGTCAGACAATTCTTGTG	22	56.53	40.91
		R	GTGAATTGTGTCTTGTATGCTTCC	24	59.30	41.67
9	Xgwm577	F	ATGGCATAATTTGGTGAAATTG	22	52.80	31.82
		R	TGTTTCAAGCCCAACTTCTATT	22	54.66	36.36
10	Xgwm626	F	GATCTAAAATGTTATTTTCTCTC	23	51.74	26.09
		R	TGACTATCAGCTAAACGTGT	20	53.20	40.00
11	barc186	F	GGAGTGTCGAGATGATGTGGAAAC	24	62.72	50.00
		R	CGCAGACGTCAGCAGCTCGAGAGG	24	69.55	66.67
12	Xgwm60	F	TGTCCTACACGGACCACGT	19	58.82	57.89
		R	GCATTGACAGATGCACACG	19	56.67	52.63
13	Xgwm190	F	GTGCTTGCTGAGCTATGAGTC	21	59.82	52.38
		R	GTGCCACGTGGTACCTTTG	19	58.82	57.89
14	Xgwm293	F	TACTGGTTCACATTGGTGCG	20	57.30	50.00
		R	TCGCCATCACTCGTTCAAG	19	56.67	52.63
15	Xgwm133	F	ATCTAAACAAGACGGCGGTG	20	57.30	50.00
		R	ATCTGTGACAACCGGTGAGA	20	57.30	50.00
16	WMS0745	F	TATGAATTCAGGTAATATTCA	21	48.11	23.81
		R	GTCATGTGATGTTTTTTTCA	20	49.10	30.00

Table 3.7 PCR cycle for SSR primers

Sl.No.	Step	Temperature (°C)	Duration	No. of cycles
1	Initial Denaturation	94	5:00 min	1
2	Denaturation	94	1:00 min	35
3	Annealing	Depending on T _m value	1:00 min	
4	Extension	72	2:00 min	
5	Final Extension	72	10:00 min	1

3.6.7 Agarose gel electrophoresis and resolution of amplified products

The PCR amplified products were resolved in 3% agarose gel. Agarose was prepared by melting with 0.5X TBE buffer with 10µl ethidium bromide and casted on to the gel plate, inserted with appropriate combs. After solidification of agarose the combs were removed and casting tray was placed into the electrophoresis gel unit submerged in 0.5X TBE buffer. The amplified products (15 µl) was mixed with 2 µl of 6X gel loading dye and loaded on to the wells. The 100 bp standard DNA marker was also loaded to measure the size of DNA bands and the constant voltage of 80 was given to the electrophoresis unit for about 3 hours and after the ladder as been separated the gel was carefully taken out of gel casting tray and photographed using gel documentation system (Alpha Innotech Corporation, U.S.A.).

3.6.8 Scoring and Analysis

The scoring was done based on the presence (taken as 1) or absence (taken as 0). Faint and unclear bands were not considered. Based on the relative migration of amplified bands the size was determined by comparing it with standard 100 bp DNA ladder.

The binary matrix data was used and genetic distance similarity was calculated using Simqual software subprogram of NTSYSpc and dendrogram was constructed for twenty genotypes using UPGMA (Un-weighted Pair Group Method with Arithmetic Mean) method by SAHN clustering function of NTSYSpc (version 2.20).

3.6.9 Determination of molecular weight

The software program Alpha Ease FC version 4.0.0 developed by Alpha Innotech Corporation, U.S.A. was used for calculating the Molecular Weight of bands separated on the gel.

3.6.10 Determination of polymorphism information content and heterozygosity

The polymorphism information content (PIC) values provides information about amount of variability for a primer among the genotypes and Heterozygosity (H) is a parameter indicating the average frequency of heterozygous individual's occurrence. PIC and H were determined using Gene-Calc software (Binkowski and Miks, 2018).

Results and Discussion

IV. RESULTS AND DISCUSSION

The results of the present investigation entitled “**Stability analysis of grain yield and its component traits in bread wheat [*Triticum aestivum* L.]**” are presented below.

4.1 Analysis of variance for experimental designs

4.2 Mean performance

4.3 Genetic variability, Heritability and Genetic advance

4.4 Stability analysis

4.5 Molecular studies

4.1 Analysis of variance for experimental designs

The analysis of variance for 15 characters studied under four different sowing seasons is presented in Table 4.1(a) (b) (c) (d). The analysis revealed significant differences among the genotypes for all the characters studied in all four sowing seasons indicating sufficient variability existing among genotypes sufficing the present investigation. Similar results were been reported by Sabaghnia *et al.* (2013), Arya *et al.* (2017) and Bharadwaj (2018)

Table 4.1(a): Analysis of variance under Environment I (15 November)

Source of variation df	Replications 2	Treatments 19	Error 38	C D (5%)	C V (%)
Days to 50% heading	0.35	47.46**	0.80	1.49	1.56
Days to maturity	3.72	7.24**	1.44	2.13	1.20
Grain filling period	4.02	39.24**	1.63	2.21	2.70
Plant height (cm)	15.08	245.67**	5.96	4.00	2.75
Number of effective tillers per meter	25.05	130.79**	45.52	10.86	5.97
Number of effective tillers per plant	0.01	0.05**	0.01	0.18	5.92
Spike length (cm)	0.02	5.09**	0.10	0.53	3.57
Number of grains per spike	16.75	156.79**	5.71	3.92	4.89
Grain weight per spike (g)	0.01	0.50**	0.02	0.24	6.11
Grain yield per meter (g)	1742.00	5335.45**	610.11	40.42	5.89
Grain yield per plant (g)	0.08	1.48**	0.17	0.68	5.93
Thousand grain weight (g)	20.93	75.54**	6.94	4.32	5.05
Biological yield per meter (g)	6759.50	26297.63**	6778.59	135.18	7.56
Biological yield per plant (g)	1.90	6.69**	1.70	2.14	7.05
Harvest index (%)	7.40	48.33**	9.56	5.07	8.02

**Significant at 1% probability level

Table 4.1(b): Analysis of variance under Environment II (25 November)

Source of variation df	Replications 2	Treatments 19	Error 38	C.D (5%)	C.V (%)
Days to 50% heading	0.65	52.47**	0.93	1.44	1.51
Days to maturity	3.60	19.00**	1.45	2.06	1.19
Grain filling period	4.85	54.70**	1.85	2.14	2.77
Plant height (cm)	7.31	198.05**	6.12	4.06	2.81
Number of effective tillers per meter	21.37	143.53**	55.91	12.30	6.96
Number of effective tillers per plant	0.01	0.05**	0.02	0.21	7.02
Spike length (cm)	0.30	3.02**	0.13	0.59	3.96
Number of grains per spike	16.23	166.19**	5.29	3.77	4.97
Grain weight per spike (g)	0.06	0.36**	0.02	0.25	6.84
Grain yield per meter (g)	1425.35	7268.51**	737.315	44.44	6.81
Grain yield per plant (g)	0.13	2.01**	0.19	0.72	6.47
Thousand grain weight (g)	10.72	69.97**	7.32	4.44	5.50
Biological yield per meter (g)	7759.54	38977.80**	5678.84	123.64	6.81
Biological yield per plant (g)	2.12	12.40**	1.44	1.97	6.42
Harvest index (%)	9.19	34.81**	6.53	4.19	7.11

**Significant at 1% probability level

Table 4.1(c): Analysis of variance under Environment III (05 December)

Source of variation d. f	Replications 2	Treatments 19	Error 38	C.D (5%)	C.V (%)
Days to 50% heading	2.52	63.68**	0.96	2.18	2.35
Days to maturity	3.88	9.34**	1.55	2.06	1.23
Grain filling period	5.41	42.54**	1.81	2.23	2.99
Plant height (cm)	18.46	180.60**	5.96	4.01	2.66
Number of effective tillers per meter	28.47	145.13**	51.48	11.73	6.95
Number of effective tillers per plant	0.01	0.04**	0.01	0.19	6.63
Spike length (cm)	0.36	3.12**	0.12	0.56	3.45
Number of grains per spike	11.10	141.80**	4.78	3.59	5.07
Grain weight per spike (g)	0.06	0.20**	0.02	0.25	7.93
Grain yield per meter (g)	1488.95	3932.58**	610.91	40.67	7.47
Grain yield per plant (g)	0.28	1.06**	0.20	0.73	7.73
Thousand grain weight (g)	6.17	73.20**	5.65	3.90	5.29
Biological yield per meter (g)	7268.45	24954.49**	4598.32	111.28	6.46
Biological yield per plant (g)	1.44	5.99**	1.53	2.03	7.10
Harvest index (%)	8.19	22.30**	5.73	3.93	7.56

**Significant at 1% probability level

Table 4.1(d): Analysis of variance under Environment IV (15 December)

Source of variation d. f	Replications 2	Treatments 19	Error 38	C.D (5%)	C.V (%)
Days to 50% heading	0.15	58.96**	0.90	1.49	1.70
Days to maturity	3.55	14.86**	1.26	1.79	1.13
Grain filling period	4.05	28.12**	1.89	2.22	3.11
Plant height (cm)	2.30	98.14**	6.21	4.09	2.92
Number of effective tillers per meter	30.12	240.33**	38.37	10.20	6.41
Number of effective tillers per plant	0.01	0.07**	0.01	0.16	5.85
Spike length (cm)	0.05	3.35**	0.12	0.56	3.54
Number of grains per spike	14.09	119.61**	4.51	3.49	5.16
Grain weight per spike (g)	0.01	0.23**	0.02	0.24	8.35
Grain yield per meter (g)	1260.55	2490.72**	536.29	38.06	7.89
Grain yield per plant (g)	0.27	0.63**	0.14	0.62	7.54
Thousand grain weight (g)	16.32	62.08**	5.30	3.78	5.45
Biological yield per meter (g)	8209.50	17571.73**	5451.00	121.12	7.48
Biological yield per plant (g)	1.19	4.64**	1.75	2.17	8.07
Harvest index (%)	13.03	22.16**	6.63	4.23	8.67

**Significant at 1% probability level

4.2 Mean performance

The prevailing environment at the stage of plant growth has a significant effect on the development of plant affecting the mean and range of grain yield and its various quantitative characters. Here the mean performance of 20 genotypes under four sowing seasons for 15 characters is presented in the Table 4.2

4.2.1 Days to 50% heading

Days to heading ranged from 48.67 (VA2019-29) to 63.33 (DBW 93) with the mean value of 58.30 under E1 condition, it ranged from 50.33 (VA2019-29) to 66.67 (VA2019-32) with the mean value of 58.35 days under E2 condition, 49.67 (VA2019-29) to 64.33 (DBW 93) was the range of performance under E3 condition with the mean of 56.67 days, whereas in E4 condition the genotype VA2019-20 took a minimum of 46.00 days to heading and genotype DBW93 showed a maximum of 61.67 days to heading with the mean of 53.38 days.

4.2.2 Days to maturity

The mean of 108.22 days were recorded with the range of 106.00 (VA2019-25) to 112.00 (NI5439) under E1 condition, in E2 days to maturity ranged from 100.00 (VA2019-31) to 110.00 (VA2019-17) with the mean of 105.55 days, maturity time

ranged from 98.67 (VA2019-20) to 105.33 (VA2019-32) with the mean of 102.12 days under E3 condition, whereas in E4 environment the mean of 96.83 days were recorded with the range of 92.00 (VA2019-20) to 101.00 (DBW93)

4.2.3 Grain filling period

The grain filling period ranged from 45.00 (DBW 93) to 59.00 (VA2019-29), 39.00 (VA2019-32) to 54.00 (VA2019-22, VA2019-23, VA2019-29), 40.00 (VA2019-17, DBW 93) to 52.00 (VA2019-22) and 37.00 (VA2019-32) to 48.00 (VA2019-29) in E1, E2, E3, E4 environments, respectively with the mean values averaging 49.88, 47.22, 45.50, 43.55 in E1, E2, E3, E4 environmental conditions, respectively.

4.2.4 Plant height (cm)

The genotype NI 5439 recorded the highest plant height of 111.47cm, 111.68cm, 112.36cm and 100.63cm in all four environments E1, E2, E3 and E4, respectively, whereas the lowest plant height of 78.17 (VA2019-22) in E1, 77.65 (VA2019-27) in E2, 82.79 (VA2019-18) in E3 and 76.74 cm (VA2019-25) in E4 environments were recorded, with the mean values depicting 88.61cm, 88.01cm, 91.81cm and 85.34 cm in E1, E2, E3 and E4 environments, respectively.

4.2.5 Number of effective tillers per meter

The effective tillers per meter in wheat ranged from 96.00 (VA2019-23) to 121.33 (VA2019-19) in E1, 86.33 (VA2019-23) to 116.00 (NI5439) in E2, 88.67 (VA2019-32) to 115.33 (VA2019-22) in E3, 81.00 (VA2019-23) to 112.67 (VA2019-22) in E4 with mean values of 110.82, 107.68, 102.82, 96.97 in E1, E2, E3, E4, environments respectively.

4.2.6 Number of effective tillers per plant

The mean of 1.89, 1.85, 1.74, and 1.63 were recorded for number of effective tillers per plant in E1, E2, E3, E4 environments, respectively, whereas the tillers per plant values ranged from 1.70 (VA2019-17, VA2019-23) to 2.10 (VA2019-19, NI 5439) in E1, 1.50 (VA2019-23) to 2.00 (VA2019-26) in E2, 1.50 (VA2019-32) to 1.96 (VA2019-22) in E3, and the highest range of 1.30 (VA2019-23) to 1.80 (VA2019-20, VA2019-29) in E4 environments.

Table 4.2 Mean performance and average of twenty genotypes for fifteen characters under four sowing seasons.

Genotypes	Days to 50% heading				Days to maturity				Grain filling period			
	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
VA2019-16	58.67	57.33	56.67	52.33	107.33	103.00	101.00	98.33	48.67	46.00	44.33	46.00
VA2019-17	62.33	61.00	63.33	55.33	110.67	110.00	103.33	96.33	48.33	49.00	40.00	41.00
VA2019-18	61.67	61.33	58.33	56.67	109.67	103.00	101.33	97.33	47.33	42.00	43.00	40.67
VA2019-19	58.33	60.33	58.33	51.00	106.33	105.67	104.00	95.00	48.33	45.00	45.67	44.33
VA2019-20	55.00	54.00	50.33	46.00	106.33	100.67	98.67	92.00	51.33	46.67	48.33	45.67
VA2019-21	55.33	54.33	51.67	50.00	107.67	106.00	103.33	97.00	52.33	52.00	51.67	46.67
VA2019-22	51.67	53.67	50.33	46.67	106.67	107.67	102.00	94.00	55.67	54.00	52.00	47.67
VA2019-23	57.00	55.33	54.33	53.00	109.00	109.00	99.67	98.00	52.00	54.00	45.67	45.00
VA2019-24	56.00	55.67	56.00	50.00	110.00	104.67	102.33	95.33	53.67	48.67	46.33	45.33
VA2019-25	58.67	59.67	59.33	55.00	106.00	105.00	102.33	95.33	47.00	45.00	43.00	40.33
VA2019-26	59.00	58.33	55.00	53.00	107.67	107.00	103.33	98.67	49.00	48.67	48.00	45.67
VA2019-27	60.67	60.00	58.67	56.00	107.67	106.00	101.67	98.33	47.00	46.00	43.00	42.33
VA2019-28	54.67	54.00	52.33	51.67	108.67	105.33	101.33	97.00	54.33	51.00	48.67	46.33
VA2019-29	48.67	50.33	49.67	46.33	108.00	104.67	100.00	94.00	59.00	54.00	50.67	48.00
VA2019-30	57.33	57.33	53.33	52.67	106.33	105.33	102.00	98.33	49.00	48.00	49.00	45.67
VA2019-31	59.67	57.33	55.33	53.00	107.67	100.00	99.67	95.00	47.33	43.00	44.33	42.00
VA2019-32	63.33	66.67	63.33	60.33	109.00	105.67	105.33	97.33	45.67	39.00	41.67	37.00
VA2019-33	62.67	62.67	60.67	57.67	109.33	107.33	104.00	98.33	46.67	44.67	43.67	41.00
NI5439	62.00	63.33	62.00	59.33	112.00	108.00	102.67	100.00	50.00	44.67	41.00	40.33
DBW93	63.33	64.33	64.33	61.67	108.33	107.00	104.33	101.00	45.00	43.00	40.00	40.00
MEAN	58.30	58.35	56.67	53.38	108.22	105.55	102.12	96.83	49.88	47.22	45.50	43.55
MIN	48.67	50.33	49.67	46.00	106.00	100.00	98.67	92.00	45.00	39.00	40.00	37.00
MAX	63.33	66.67	64.33	61.67	112.00	110.00	105.33	101.00	59.00	54.00	52.00	48.00

Table 4.2 (Continued...)

Genotypes	Plant height (cm)				Number of effective tillers per meter				Number of effective tillers per plant			
	E1	E1	E1	E1	E1	E2	E3	E4	E1	E2	E3	E4
VA2019-16	94.64	92.56	96.88	86.51	117.33	110.33	108.00	102.00	1.93	1.93	1.80	1.63
VA2019-17	87.30	88.20	88.74	84.05	105.00	108.67	102.67	99.33	1.70	1.90	1.77	1.67
VA2019-18	83.17	81.70	82.79	77.85	109.33	108.00	100.00	101.00	1.83	1.93	1.70	1.70
VA2019-19	82.03	84.68	86.18	80.95	121.33	115.33	103.33	90.00	2.10	1.93	1.73	1.53
VA2019-20	80.69	85.70	85.18	81.75	110.33	104.00	103.33	105.67	1.83	1.93	1.73	1.80
VA2019-21	84.97	86.77	93.19	86.82	107.00	100.33	105.00	100.67	1.83	1.70	1.80	1.70
VA2019-22	78.17	80.12	85.08	78.74	120.67	114.33	115.33	112.67	2.06	1.93	1.96	1.77
VA2019-23	87.05	84.88	88.77	89.78	96.00	86.33	91.67	81.00	1.70	1.50	1.57	1.30
VA2019-24	86.43	89.12	94.40	88.29	113.00	108.33	102.67	101.33	2.00	1.86	1.74	1.77
VA2019-25	81.75	79.33	86.64	76.74	109.67	110.33	104.33	91.67	1.87	1.90	1.70	1.50
VA2019-26	86.73	93.16	89.77	91.33	114.33	114.33	111.67	100.33	1.93	2.00	1.86	1.67
VA2019-27	82.29	77.65	85.08	81.68	108.33	107.00	97.00	93.67	1.83	1.86	1.63	1.60
VA2019-28	82.62	82.19	88.23	80.14	112.33	106.33	97.00	85.33	1.90	1.83	1.63	1.43
VA2019-29	78.95	79.16	83.73	82.84	111.00	113.33	105.67	104.33	1.90	1.90	1.80	1.80
VA2019-30	90.55	87.36	87.81	84.94	112.67	111.33	106.00	105.00	1.93	1.90	1.80	1.77
VA2019-31	90.19	88.75	98.27	84.47	117.33	109.33	106.00	102.67	2.07	1.83	1.80	1.73
VA2019-32	98.29	91.95	100.67	88.16	102.33	98.33	88.67	82.33	1.77	1.63	1.50	1.40
VA2019-33	98.55	94.56	101.60	91.51	104.33	103.67	91.33	81.33	1.77	1.70	1.57	1.37
NI5439	111.47	111.68	112.36	100.63	119.67	116.00	112.33	103.00	2.10	1.93	1.90	1.77
DBW93	106.27	100.72	100.77	89.69	104.33	108.00	104.33	96.00	1.80	1.86	1.80	1.67
MEAN	88.61	88.01	91.81	85.34	110.82	107.68	102.82	96.97	1.89	1.85	1.74	1.63
MIN	78.17	77.65	82.79	76.74	96.00	86.33	88.67	81.00	1.70	1.50	1.50	1.30
MAX	111.47	111.68	112.36	100.63	121.33	116.00	115.33	112.67	2.10	2.00	1.96	1.80

Table 4.2 (Continued...)

Genotypes	Spike length (cm)				Number of grains per spike				Grain weight per spike (g)			
	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
VA2019-16	10.13	9.26	9.79	9.77	50.07	50.93	45.10	42.20	2.75	2.47	1.91	1.67
VA2019-17	8.88	9.03	9.68	9.74	48.40	47.20	46.53	44.47	2.56	2.36	2.47	2.18
VA2019-18	8.58	9.29	9.40	8.76	40.33	41.40	37.20	36.60	2.02	2.04	1.62	1.53
VA2019-19	10.28	10.92	11.36	10.74	42.93	40.93	37.27	37.87	2.40	2.21	1.75	1.76
VA2019-20	7.69	8.18	9.08	8.84	31.27	31.27	30.60	29.47	1.71	1.69	1.66	1.49
VA2019-21	7.79	8.60	9.46	9.30	45.33	37.20	37.46	35.33	1.90	2.01	1.89	1.57
VA2019-22	8.19	8.09	10.06	8.53	47.13	40.20	39.60	38.27	2.01	1.97	1.55	1.26
VA2019-23	9.86	9.02	10.29	9.81	50.33	51.27	47.94	45.07	3.23	2.77	1.97	1.92
VA2019-24	9.52	10.20	11.52	10.84	57.67	41.47	37.00	37.07	2.01	1.94	1.97	1.70
VA2019-25	8.86	8.38	9.74	9.56	46.40	43.73	43.40	41.40	2.39	1.98	1.88	1.79
VA2019-26	7.54	8.29	8.89	8.64	49.73	51.00	48.73	46.67	2.28	2.06	1.80	1.81
VA2019-27	7.38	8.32	9.07	9.07	50.27	47.13	44.93	42.74	2.30	2.43	1.94	1.72
VA2019-28	8.88	9.11	9.73	9.79	47.07	43.47	35.40	33.53	2.52	1.92	2.10	1.48
VA2019-29	7.23	7.84	8.80	8.47	39.00	36.20	37.53	36.07	2.38	2.08	1.96	1.76
VA2019-30	9.09	10.09	10.80	9.49	52.13	51.00	44.60	40.60	2.24	2.13	1.99	1.68
VA2019-31	7.75	7.64	8.22	7.94	50.60	53.80	44.06	42.87	2.65	2.36	2.11	1.71
VA2019-32	10.82	9.82	10.56	10.70	55.80	50.20	46.80	44.87	2.74	2.43	1.98	2.06
VA2019-33	11.23	10.24	11.83	12.14	63.40	63.00	60.93	59.87	3.29	3.10	2.67	2.53
NI5439	8.95	8.89	9.45	9.28	50.87	52.67	44.53	44.13	2.59	2.65	1.85	1.58
DBW93	11.54	11.11	11.57	11.27	58.47	51.87	52.60	44.33	2.75	1.88	1.84	1.62
MEAN	9.01	9.12	9.97	9.63	48.86	46.30	43.11	41.17	2.44	2.22	1.95	1.74
MIN	7.23	7.64	8.22	7.94	31.27	31.27	30.60	29.47	1.71	1.69	1.55	1.26
MAX	11.54	11.11	11.83	12.14	63.40	63.00	60.93	59.87	3.29	3.10	2.67	2.53

Table 4.2 (Continued...)

Genotypes	Grain yield per meter (g)				Grain yield per plant (g)				Thousand grain weight (g)			
	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
VA2019-16	452.00	403.33	367.33	279.00	7.70	6.90	6.43	4.60	55.36	48.47	42.38	39.69
VA2019-17	357.67	361.67	337.33	318.33	6.10	6.20	5.77	5.43	53.08	50.34	53.47	48.90
VA2019-18	377.00	395.00	271.67	262.33	6.40	6.63	4.73	4.50	50.43	49.79	43.44	41.86
VA2019-19	381.00	376.33	377.67	340.00	6.57	6.33	6.50	5.77	55.91	54.00	46.95	46.11
VA2019-20	381.33	395.33	292.67	276.33	6.37	6.77	5.17	4.73	53.22	54.19	54.61	50.82
VA2019-21	349.00	350.67	320.67	289.00	5.83	6.03	5.40	4.90	58.57	54.10	50.50	46.31
VA2019-22	392.00	380.67	326.67	325.33	6.63	6.37	5.60	5.53	49.59	48.61	39.28	33.12
VA2019-23	396.33	406.33	286.00	267.00	6.63	7.00	4.93	4.60	64.15	54.08	41.66	42.61
VA2019-24	404.33	401.00	338.67	304.33	6.70	6.83	5.87	5.13	48.31	47.37	47.55	43.13
VA2019-25	433.33	453.33	325.33	259.00	7.20	7.83	5.60	4.47	51.59	45.29	43.45	43.51
VA2019-26	457.00	460.33	390.67	336.33	7.67	7.87	6.77	5.70	45.73	40.52	36.87	36.92
VA2019-27	389.00	354.67	310.33	285.33	6.50	6.14	5.36	5.07	48.25	51.85	43.18	40.28
VA2019-28	439.00	360.67	281.67	267.33	7.30	6.12	5.07	4.77	52.06	52.90	44.31	42.34
VA2019-29	434.67	444.33	342.00	320.33	7.40	7.73	5.90	5.43	60.97	57.44	52.30	48.78
VA2019-30	426.67	419.00	365.33	341.33	7.17	7.16	6.27	5.80	43.18	41.62	45.01	41.83
VA2019-31	454.00	396.67	367.33	292.33	7.66	6.86	6.18	4.96	52.45	44.97	48.05	41.17
VA2019-32	480.00	315.00	297.67	263.33	8.10	5.47	5.12	4.53	49.44	48.70	42.35	42.83
VA2019-33	473.67	471.67	371.33	301.67	8.00	8.00	6.33	5.10	51.67	49.21	43.83	42.20
NI5439	494.67	492.00	366.33	297.33	8.23	8.27	6.37	5.07	51.31	50.23	42.21	35.70
DBW93	386.00	310.67	297.67	250.33	6.50	5.47	5.27	4.38	47.79	39.94	37.62	36.58
MEAN	417.93	397.43	331.72	293.81	7.03	6.80	5.73	5.02	52.15	49.18	44.95	42.23
MIN	349.00	310.67	271.67	250.33	5.83	5.47	4.73	4.38	43.18	39.94	36.87	33.12
MAX	494.67	492.00	390.67	341.33	8.23	8.27	6.77	5.80	64.15	57.44	54.61	50.82

Table 4.2 (Continued...)

Genotypes	Biological yield per meter (g)				Biological yield per plant (g)				Harvest index (%)			
	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
VA2019-16	1179.67	1043.00	1134.67	880.67	19.92	17.79	18.32	14.38	39.30	38.47	32.35	31.85
VA2019-17	1114.00	1162.00	1108.67	1088.33	18.55	20.05	18.46	17.85	32.00	31.01	30.43	29.17
VA2019-18	1124.67	1180.33	1104.33	1045.33	18.92	19.99	17.85	17.32	33.48	33.49	24.87	25.11
VA2019-19	1108.00	1194.33	1136.33	1042.67	18.72	20.06	18.46	17.31	34.38	31.52	33.19	32.51
VA2019-20	944.67	988.67	970.33	933.00	16.46	16.66	15.92	15.52	40.40	39.88	30.20	29.54
VA2019-21	983.33	940.00	966.33	924.33	16.59	15.79	16.85	15.25	35.58	37.32	33.11	31.04
VA2019-22	1110.67	1114.00	1010.67	1058.67	18.79	18.92	17.65	17.58	35.26	34.31	32.69	30.78
VA2019-23	1063.67	1046.67	1045.00	1025.67	18.32	17.59	18.05	16.98	37.23	38.21	27.37	25.95
VA2019-24	1114.67	1054.33	1078.33	1097.67	19.32	17.92	17.92	17.92	36.31	38.18	31.29	27.72
VA2019-25	1136.33	1200.67	1049.00	896.67	18.86	19.99	17.52	15.18	38.17	37.73	31.17	28.84
VA2019-26	1001.67	1172.67	1143.00	995.67	17.05	19.72	18.39	16.58	45.54	39.32	34.17	33.70
VA2019-27	969.67	978.33	981.00	927.00	16.65	16.12	15.66	15.51	40.06	36.21	31.60	31.05
VA2019-28	1028.00	960.33	923.67	933.33	17.52	16.19	15.92	15.45	42.76	37.50	30.26	28.53
VA2019-29	1007.33	1114.67	962.67	921.67	17.12	18.52	15.92	15.32	43.15	39.81	35.46	34.64
VA2019-30	1109.00	1236.00	1154.00	1077.00	18.79	21.39	19.39	17.38	38.40	33.87	31.66	31.84
VA2019-31	1040.33	1007.33	970.00	980.00	17.56	16.73	15.79	16.32	43.56	39.42	37.75	29.86
VA2019-32	1124.33	996.67	892.33	871.33	18.92	16.73	15.12	14.32	42.81	31.55	33.32	28.03
VA2019-33	1092.33	1274.33	1164.67	944.00	18.79	21.32	19.39	16.12	43.31	36.92	31.80	31.88
NI5439	1370.33	1352.33	1209.33	1109.33	23.05	23.19	19.85	18.58	36.11	36.38	30.50	26.76
DBW93	1157.00	1116.33	989.67	988.33	19.52	18.92	16.26	17.32	33.28	27.87	29.97	25.18
MEAN	1088.98	1106.65	1049.70	987.03	18.47	18.68	17.43	16.41	38.55	35.95	31.66	29.70
MIN	944.67	940.00	892.33	871.33	16.46	15.79	15.12	14.32	32.00	27.87	24.87	25.11
MAX	1370.33	1352.33	1209.33	1109.33	23.05	23.19	19.85	18.58	45.54	39.88	37.75	34.64

4.2.7 Spike length (cm)

The wheat varieties studied showed the spike length in the range of 7.23 (VA2019-29) to 11.54 cm (DBW 93) in E1, 7.64 (VA2019-31) to 11.11 cm (DBW 93) in E2, 8.22 (VA2019-31) to 11.83 cm (VA2019-33) in E3 and the highest range of 7.94 (VA2019-31) to 12.14 cm (VA2019-33) was seen in E4 environment. The mean of spike length in E1, E2, E3 and E4 were 9.01, 9.12, 8.22 and 7.94 cm respectively.

4.2.8 Number of grains per spike

The genotype VA2019-20 exhibited the lowest number of grains per spike of 31.27, 31.27, 30.60 and 29.47 and genotype VA2019-33 showed the highest number of grains per spike of 63.40, 63.00, 60.93, and 59.87 in all four environments, respectively whereas the mean were of 48.86, 46.30, 43.11 and 41.17 in E1, E2, E3 and E4 environments, respectively.

4.2.9 Grain weight per spike (g)

The mean grain weight per spike of 2.44g, 2.22g, 1.95g and 1.74g were recorded in E1, E2, E3 and E4 environments, respectively. The genotype VA2019-20 exhibited the lowest grain weight per spike of 1.71 and 1.69g in E1 and E2 environments, respectively and genotype VA2019-22 showed lowest grain weight per spike of 1.55 and 1.26g in E3 and E4 environments, respectively, whereas the genotype VA2019-33 exhibited the highest grain weight per spike of 3.29g, 3.10g, 2.67g and 2.53g in all four environments studied respectively.

4.2.10 Grain yield per meter (g)

The grain yield per meter were recorded the highest for genotype NI5439 in E1 and E2 environments as 494.67 and 492.00g respectively, in E3 390.67g (VA2019-26) and in E4 341.33g (VA2019-30) were recorded. Likewise the genotype DBW 93 exhibited the lowest grain yield per meter of 310.67 and 250.33g in E2 and E4 environments, respectively whereas in E1 349.00g (VA2019-21) and 271.67g (VA2019-18) in E3 were recorded the lowest. The mean grain yields were 417.93g, 397.43g, 331.72g and 293.81g in E1, E2, E3 and E4 environments respectively.

4.2.11 Grain yield per plant (g)

The range of grain yield per plant recorded from 5.83g (VA2019-21) to 8.23g (NI5439), 5.47g (VA2019-32) to 8.27g (NI 5439), 4.73g (VA2019-18) to 6.77g

(VA2019-26) and 4.38g (DBW 93) to 5.80g (VA2019-30) in E1, E2, E3 and E4 environments, respectively whereas the mean grain yield per plant recorded was 7.03g, 6.80g, 5.73g and 5.02g in E1, E2, E3 and E4 environments respectively.

4.2.12 Thousand grain weight (g)

The mean values of 1000-grain weight recorded were 52.15g, 49.18g, 44.95g and 42.23g in E1, E2, E3 and E4 environments, respectively whereas the range of thousand grain weight exhibited under each environments were 43.18g (VA2019-30) to 64.15g (VA2019-23), 39.94g (DBW 93) to 57.44g (VA2019-29), 36.87g (VA2019-26) to 54.61g (VA2019-20) and 33.12g (VA2019-22) to 50.82g (VA2019-20) respectively.

4.2.13 Biological yield per meter (g)

The genotype NI 5439 recorded the highest biological yield per meter of 1370.33g, 1352.33g, 1209.33g and 1109.33g in all four environments likewise the lowest biological yield per meter observed was 944.67g (VA2019-20) in E1, 940.00g (VA2019-21) in E2 and the genotype VA2019-32 recorded the lowest both in E3 and E4 environments with 892.33 and 871.33g respectively. The mean values in each environment recorded were 1088.98g, 1106.65g, 1094.70g and 987.03g respectively.

4.2.14 Biological yield per plant (g)

The genotype NI 5439 exhibited the highest biological yield per plant of 23.05g, 23.19g, 19.85g and 18.58g in all four environments and lowest biological yield per plant recorded was 16.46g (VA2019-20) in E1, 15.79g (VA2019-21) in E2 and the genotype VA2019-32 showed the lowest value of 15.12 and 14.32g in both E3 and E4 environments. The mean values in each environment recorded for biological yield per plant was 18.47g, 18.68g, 17.43g and 16.41g respectively.

4.2.15 Harvest index (%)

The calculated values of harvest index for all the genotypes ranged from 32.00 (VA2019-17) to 45.54 (VA2019-26), 27.87 (DBW 93) to 39.88 (VA2019-20), 24.87 (VA2019-18) to 37.75 (VA2019-31) and 25.11 (VA2019-18) to 34.64 (VA2019-29) in E1, E2, E3 and E4 environments, respectively whereas the means recorded were 38.55, 35.95, 31.66, and 29.70 in each environment respectively.

4.3 Genetic variability, Heritability and Genetic advance

In this present investigation, variability parameters like phenotypic co-efficient of variation, genotypic co-efficient of variation, broad sense heritability and genetic advance as percent of mean for 20 genotypes for yield and its component traits under four different sowing dates were pooled and data is presented in Table 4.3. This attempt will help to adapt suitable breeding strategies for the improvement in bread wheat and will help in determining suitable method of selection for the improvement of particular population for a specific trait.

Table 4.3. Estimation of coefficient of variations, broad sense heritability (h^2), genetic advance as per cent of mean in fifteen quantitative traits of twenty genotypes in wheat evaluated across four environments.

Sl.No.	Characters	GCV (%)	PCV (%)	h^2 (%)	GAM (%)
1	Days to 50% heading	7.27	7.60	91.40	14.31
2	Days to maturity	1.28	1.98	41.52	1.70
3	Grain filling period	7.05	7.94	78.88	12.90
4	Plant height (cm)	8.12	8.77	85.66	15.48
5	Number of effective tillers per meter	5.98	7.11	70.69	10.35
6	Number of effective tillers per plant	5.76	7.33	61.71	9.32
7	Spike length (cm)	10.84	11.69	86.09	20.73
8	Number of grains per spike	14.35	15.56	85.11	27.28
9	Grain weight per spike (g)	12.90	15.72	67.37	21.82
10	Grain yield per meter (g)	7.13	11.05	41.60	9.47
11	Grain yield per plant (g)	6.79	10.68	40.43	8.90
12	Thousand grain weight (g)	7.99	10.26	60.56	12.80
13	Biological yield per meter (g)	6.85	8.96	58.48	10.79
14	Biological yield per plant (g)	6.93	8.86	61.20	11.17
15	Harvest index (%)	6.65	9.60	48.02	9.50

4.3.1 Genotypic and Phenotypic co-efficients of variation

In the present study, PCV were comparatively higher than GCV suggesting significant influence of environment on the phenotypic expression of these traits. Similar findings were reported by Kotal *et al.* (2010), Thapa *et al.* (2018). However closer affinity between PCV and GCV indicates limited influence of environment on the expression of these traits. The GCV and PCV showed low to moderate variability among all the characters studied across environments. The characters days to 50%

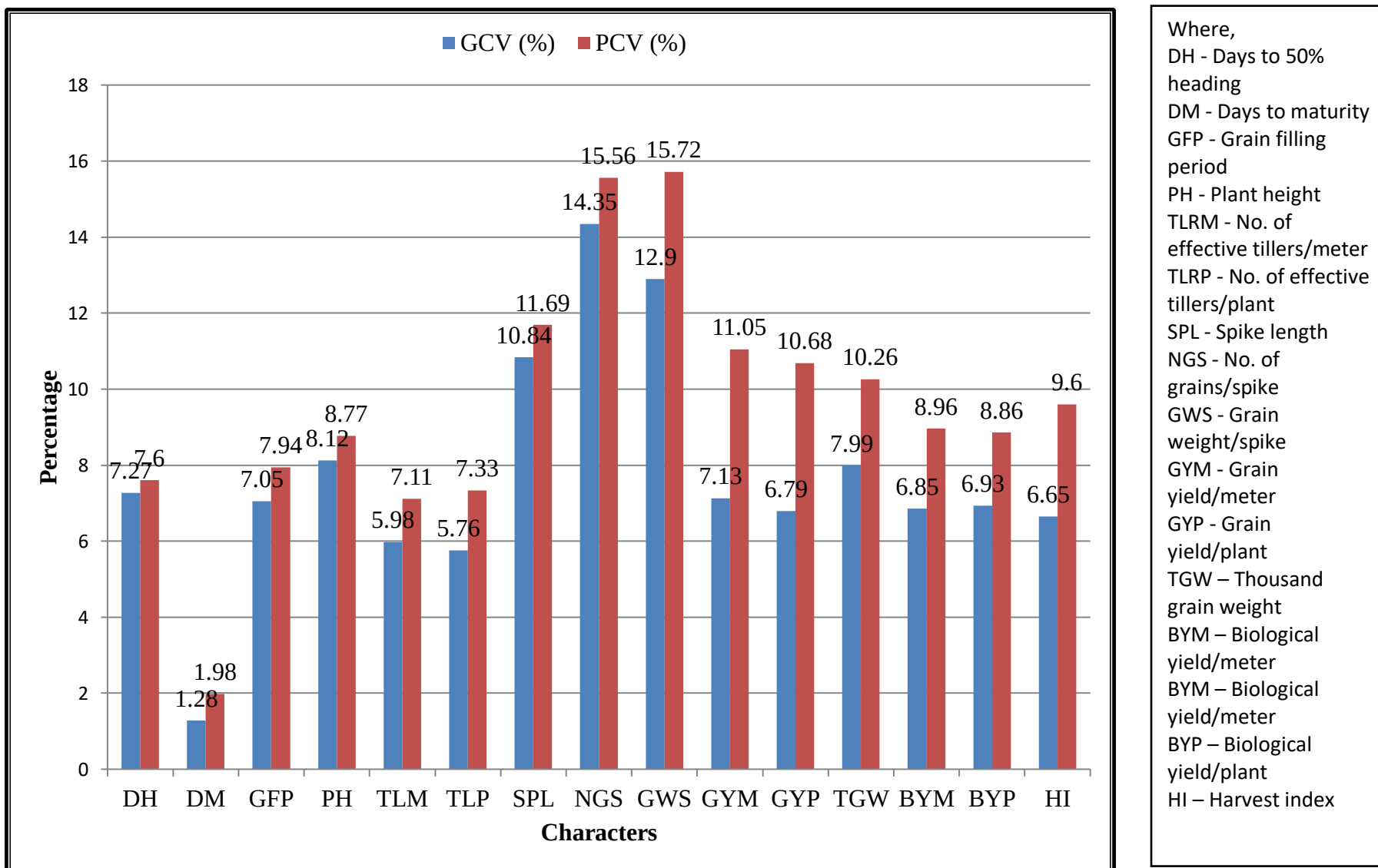


Fig. 4.1 Pooled estimation of genotypic and phenotypic coefficients of variation for different characters in bread wheat.

heading (7.27 and 7.60%), days to maturity (1.28 and 1.98%), grain filling period (7.05 and 7.94%), plant height (8.12 and 8.77%), number of effective tillers per meter (5.98 and 7.11%), number of effective tillers per plant (5.76 and 7.33%), biological yield per meter (6.85 and 8.96%), biological yield per plant (6.93 and 8.86%) and harvest index (6.65 and 9.60%) showed low estimates of GCV and PCV, respectively indicating low variability for these traits. Similar results were been reported by Bhushan *et al.* (2013) for the characters days to heading, days to maturity, grain filling period and harvest index, Hazra *et al.* (2019) for days to heading, days to maturity, plant height, biological yield per meter. The traits spike length (10.84 and 11.69%), number of grains per spike (14.35 and 15.56%) and grain weight per spike (12.90 and 15.72%) showed moderate estimates of GCV and PCV, respectively indicating average chances for selection for these characters. Similar findings were reported by Arya *et al.* (2017) for spike length. The characters grain yield per meter (7.13 and 11.05%), grain yield per plant (6.79 and 10.68%) and thousand grain weight (7.99 and 10.26%) showed low GCV and moderate PCV, respectively. Similar results were reported by Mishra *et al.* (2019) for grain yield which showed moderate values of PCV and for thousand grain weight showing low GCV.

The characters tillers per meter, tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index exhibited larger variation in the values of GCV and PCV showing significant action of environment in the expression of these traits. Similar findings were reported by Kotal *et al.* (2010) for the characters tillers per plant, grain yield per plant, thousand grain weight and harvest index while for the characters days to 50% heading, days to maturity, grain filling period and plant height GCV and PCV were in close affinity indicating the scope for the selection for these traits. These results were in line with Hazra *et al.* (2019) and Rani *et al.* (2018).

4.3.2 Heritability and Genetic advance as percent of mean (GAM)

In the present study, broad sense heritability estimates ranged from 40.43% (grain yield per plant) to 91.40% (days to 50% heading) [Table 4.3]. High heritability estimates were observed for days to 50% heading (91.40%), grain filling period

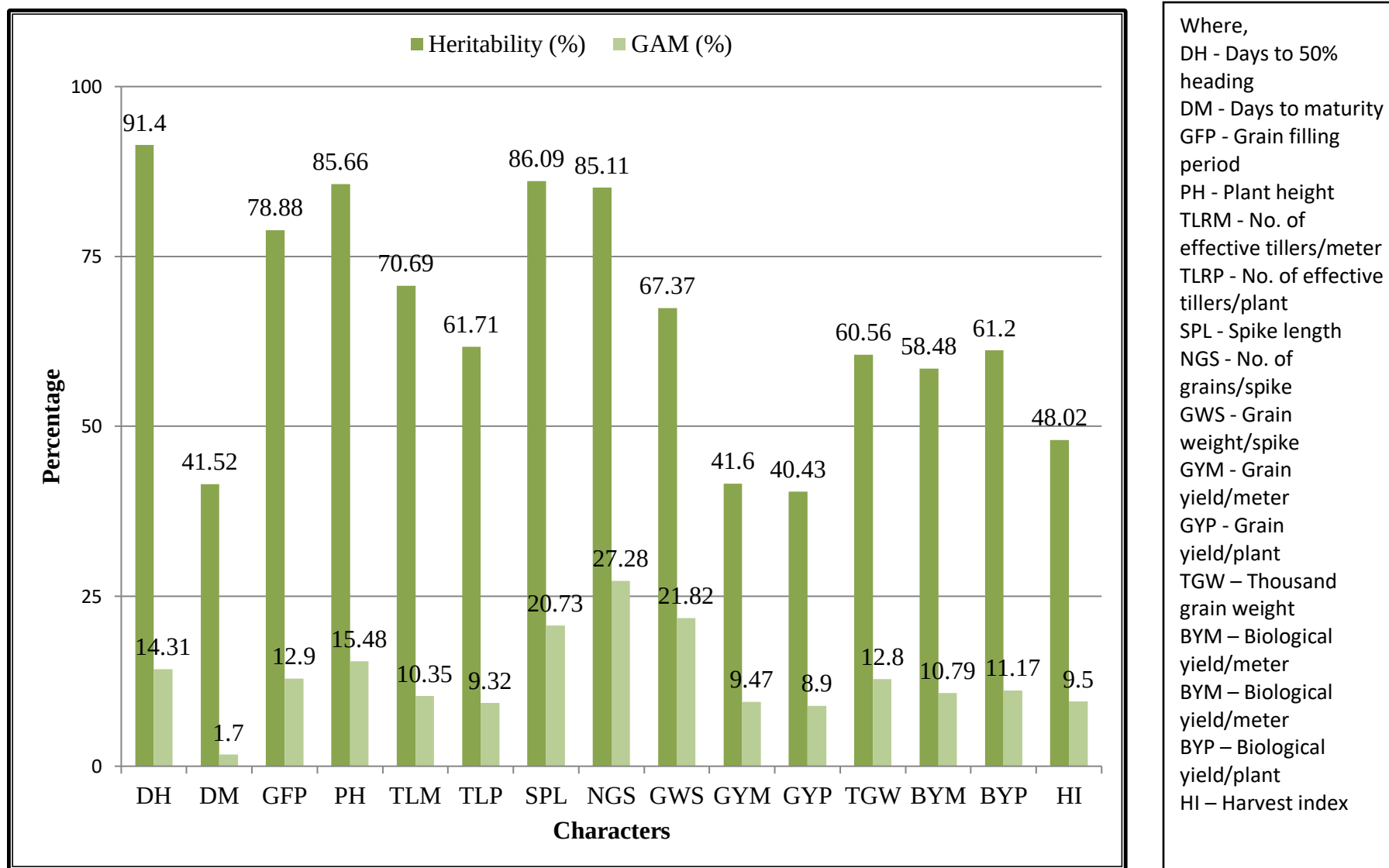


Fig. 4.2 Pooled estimates of heritability (%) and genetic advance as per cent of mean for different characters in bread wheat.

(78.88%), plant height (85.66%), number of effective tillers per meter (70.69%), number of effective tillers per plant (61.71%), spike length (86.09%), number of grains per spike (85.11%), grain weight per spike (67.37%), thousand grain weight (60.56%) and biological yield per plant (61.20%) indicated variation for these characters were solely due to genetic control, less influenced by environment and selection would be effective. Similar results were obtained by Bankapur *et al.* (2018) for the characters days to heading, plant height, spike length, thousand grain weight and Rajshree *et al.* (2018) for tillers per plant and number of grains per spike. Moderate estimates of heritability were observed for days to maturity (41.52%), grain yield per meter (41.60%), grain yield per plant (40.43%), biological yield per meter (58.48%) and harvest index (48.02%) indicates variation seen were partly due to genetic control and more influence of environment. These results were in line with Mishra *et al.* (2019) for grain yield and days to maturity.

The GAM values ranged from 1.70% (days to maturity) to 27.28% (number of grains per spike) [Table 4.3]. For the characters like spike length (20.73%), number of grains per spike (27.28%) and grain weight per spike (21.82%) GAM was recorded high. Rani *et al.* (2018) also reported high genetic advance as percent of mean for number of grains per spike and grain weight per spike. The characters days to 50% heading (14.31%), grain filling period (12.90%), plant height (15.48%), number of effective tillers per meter (10.35%), thousand grain weight (12.80%), biological yield per meter (10.79%) and biological yield per plant (11.71%) the GAM were moderate. Mishra *et al.* (2019) and Yadav *et al.* (2011) too reported moderate GAM for thousand grain weight and Rani *et al.* (2018) for biological yield per plant. Low estimates of GAM were recorded for days to maturity (1.70%), number of effective tillers per plant (9.32%), grain yield per meter (9.47%), grain yield per plant (8.90%) and harvest index (9.50%). Mishra *et al.* (2019) and Yadav *et al.* (2011) also reported low genetic advance as percent mean for days to maturity and harvest index respectively.

The estimates of heritability and genetic advance alone will not yield good estimates for selection, hence for selection to be effective, heritability and genetic advance as percent of mean should be considered together (Johnson *et al.* 1955). High heritability with high genetic advance were reported for spike length, number of grains

per spike and grain weight per spike exhibited predominance of additive gene action with less environmental influence and effective selection. Similar findings were reported by Rajshree *et al.* (2018) for spike length and number of grains per spike, whereas high heritability with moderate genetic advance were reported for days to 50% heading, grain filling period, plant height, tillers per meter, thousand grain weight and biological yield per plant indicating predominance of both additive and non-additive gene action hence mass selection can be used for the improvement of these traits. Similar results were obtained by Naik *et al.* (2015) for days to heading and thousand grain weight and Hazra *et al.* (2019) for plant height and biological yield per plant, while high heritability with low genetic advance for tillers per plant was observed which indicated predominance of non additive gene action and selection will not be effective but heterosis breeding can be adopted. Moderate heritability with moderate genetic advance was observed for biological yield per meter showed less scope for direct selection but delayed selection might be effective and moderate heritability with low genetic advance for days to maturity, grain yield per meter, grain yield per plant and harvest index indicates high macro environmental influence in the expression of these traits.

4.4 Analysis of variance for stability

The analysis of variance for yield and its component traits studied across different environments are presented in Table 4.4. The 20 genotypes studied for the over four environments were pooled and tested against pooled error showed significant difference among genotypes at 1% probability level indicated highly significant variation for all the characters studied. The environments in which observations were recorded were tested against pooled error exhibited highly significant variation for all the characters found the significance in changing environment. The genotypes and environment interaction tested against pooled error were significant at 5% probability level for all the characters except number of effective tillers per meter, number of effective tillers per plant, biological yield per meter, biological yield per plant and harvest index showing differential response of genotypes with environment.

Since most of the characters showed significance for GxE interaction the data were subjected to stability analysis. The E+(GxE) component showed significance at

1% probability level for all the characters except number of effective tillers per meter, number of effective tillers per plant, biological yield per meter, biological yield per plant and harvest index, which showed no significance at both 5% and 1% probability level suggesting the interaction between the genotypes on different conditions of sowing were considerable for majority of the traits. In order to find the linear and non linear components of variation the $E+(G \times E)$ component is partitioned into $E(\text{linear})$, $G \times E$ (linear) and pooled deviations. The component E (linear) showed significance at 1% probability for all the characters found that the environments in which wheat were cultivated were random and different and were expressing their influence in the expression of these traits whereas the component $G \times E$ (linear) showed significance only for the characters number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant and thousand grain weight at 1% probability and for the characters days to 50% heading and grain filling period at 5% probability indicating the prediction of differential response of genotypes with in different environments. The component pooled deviation tested against pooled error showed significance only for the character days to maturity at 5% probability, found some portions of $G \times E$ interactions were unpredictable. Similar findings were reported by Koumber *et al.* (2011), Hassan *et al.* (2013) and Sidhi *et al.* (2018).

Stability analysis

All the 15 characters studied were analyzed for stability parameters viz., mean performance ($\bar{X}_i$), regression co-efficient (b_i), deviation from regression line (S^2d_i) and are presented in Table 4.5.

4.5.1 Days to 50% heading

The mean values from the Table 4.5 showed the genotype VA2019-29 (48.75) requires the minimum number of days for 50% heading while the genotype DBW 93 (63.42) requires the maximum number of days to 50% heading, whereas the population mean was 56.68 days. Out of 20 genotypes studied all the genotypes showed non-significant S^2d_i values indicating all were stable except VA2019-17 among which 11 genotypes showed lesser mean value compared to population mean which is desired for days to 50% heading. The genotypes VA2019-21 and VA2019-30 (Genotype mean <

Table 4.4 Pooled analysis of variance over environments for different characters in bread wheat.

Sl. No.	Source of variation df	Genotypes 19	Environments 3	GxE 57	E+(GxE) 60	E(linear) 1	GxE(linear) 19	Pooled deviation 40	Pooled error 152
1	Days to 50% heading	69.44**	108.57**	1.59*	6.94**	325.71**	1.83*	1.40	1.05
2	Days to maturity	9.39**	482.48**	2.46*	26.46**	1447.45**	2.43	2.35*	1.51
3	Grain filling period	45.97**	144.38**	2.88*	9.96**	433.15**	3.14*	2.62	1.80
4	Plant height	214.89**	140.75**	8.64*	15.25**	422.25**	9.95	7.59	6.06
5	Number of effective tillers per meter	172.39**	730.73**	16.17	51.90	2192.18**	33.10	7.34	47.41
6	Number of effective tillers per plant	0.05**	0.28**	0.01	0.02*	0.85**	0.01	0.00	0.01
7	Spike length	4.35**	4.02**	0.17*	0.36**	12.05**	0.18	0.15	0.12
8	Number of grains per spike	173.07**	231.55**	7.25*	18.46**	694.64**	11.99**	4.63	5.07
9	Grain weight per spike	0.32**	1.88**	0.04*	0.13**	5.63**	0.06**	0.02	0.02
10	Grain yield/meter	3563.68**	66248.27**	926.04*	4192.15**	198744.80**	1501.55**	606.37	622.93
11	Grain yield/plant	0.95**	17.63**	0.26*	1.13**	52.89**	0.40**	0.18	0.18
12	Thousand grain weight	65.92**	387.75**	9.23*	28.15**	1163.26**	17.64**	4.77	6.30
13	Biological yield per meter	24730.95**	56220.80**	3727.47	6352.13	168662.41**	4837.90	3013.57	5625.75
14	Biological yield per plant	7.02**	21.87**	0.96	2.01	65.61**	1.16	0.82	1.60
15	Harvest index	25.96**	323.37**	5.53	21.42**	970.11**	8.22	3.97	7.11

* Significant at 5 per cent probability level, when tested against pooled error ** Significant at 1 per cent probability level, when tested against pooled error.

Population mean, b_i closer to unity and $S^2d_i=0$) showed average stability while no genotypes exhibited significance at $b_i=1$, hence none of the genotypes among 20 genotypes can be recommended for unfavourable and favourable environmental conditions for the character days to 50% heading

The genotypes VA2019-21 and VA2019-30 can be adapted to all the environments. Similar results were reported by Gulzar *et al.* (2015) and Sidhi *et al.* (2018).

4.5.2 Days to maturity

The mean values for days to maturity varied from 99.42 (VA2019-20) to 105.67 (NI 5439) with the population mean of 103.18. Out of 20 genotypes, 17 genotypes showed non-significant S^2d_i values indicating all these genotypes were stable except VA2019-19, VA2019-23 and VA2019-31 of which 9 genotypes had lesser mean values compared to population mean which is desired for days to maturity. The genotypes VA2019-18, VA2019-25 and VA2019-28 (Genotype mean < Population mean, b_i closer to unity and $S^2d_i=0$) showed average stability with earliness towards days to maturity. The genotypes VA2019-29 (Genotype mean < Population mean, $b_i > 1$ and $S^2d_i=0$) showed below average stability with high responsiveness to environmental changes, whereas VA2019-30 (Genotype mean < Population mean, $b_i < 1$ and $S^2d_i=0$) will be considered as above average stable and can be recommended for unfavourable environment, while the genotype DBW 93 (Genotype mean > Population mean, $b_i < 1$ and $S^2d_i=0$ non significant) also can be considered above average stable with lateness for maturity.

The genotypes VA2019-18, VA2019-25 and VA2019-28 were adapted to all the environments while VA2019-29 can be adapted to favourable environmental conditions and VA2019-30 can be adapted to unfavourable environmental conditions by showing earliness for days to maturity. Similar results were obtained by Gulzar *et al.* (2015) and Pujer *et al.* (2020).

4.5.3 Grain filling period

The mean values of grain filling period ranged from 40.83 (VA2019-32) to 52.92 (VA2019-29) with the population mean of 46.54. Out of 20 genotypes all showed non-significant S^2d_i values except VA2019-17, VA2019-23 and VA2019-32 of

which 9 genotypes had their genotype mean lesser than population mean for grain filling period. The genotypes VA2019-18 and VA2019-25 (Genotype mean < Population mean, b_i closer to unity and $S^2d_i=0$) showed average stability taking minimum number of days for grain filling than population mean, whereas the genotypes VA2019-28 and VA2019-29 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$ non significant) exhibited below average stability by taking more number of days for grain filling than population mean.

The genotypes VA2019-18 and VA2019-25 were adapted to all the environments by having below average mean representation, unit regression coefficient and zero deviation from regression and hence considered stable across the environments, recommended for grain filling period. Similar findings were reported by Sidhi *et al.* (2018).

4.5.4 Plant height (cm)

The population mean for plant height was 88.44cm with the genotype VA2019-22 (80.53cm) exhibiting the lowest plant height, while, NI 5439 (109.03cm) showed the highest plant height. The deviation from regression line was non-significant for all the genotypes except DBW 93, of which 12 genotypes had lower plant height than population mean. The genotypes VA2019-21 and VA2019-22 (Genotype mean < Population mean, b_i closer to unity and $S^2d_i=0$) were considered average stable with lower mean value whereas the genotype VA2019-31 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$) showed below average stable with higher mean value and can be considered for favorable environment conditions.

The dwarfness of wheat is preferred over tall genotypes, here VA2019-21 and VA2019-22 showed below average mean values showing stable expression over variable environments. These results were in line with Gulzar *et al.* (2015) reporting average stability for this character.

4.5.5 Number of effective tillers per meter

There was a population mean of 104.57, the genotype VA2019-23 (88.75) had lower number of tillers per meter, while the VA2019-22 (115.75) recorded the highest number of tillers per meter over the studied genotypes. All the genotypes exhibited

Table 4.5: Stability parameters for days to 50% heading, days to maturity, grain filling period and plant height.

	Genotypes	Days to 50 % heading			Days to maturity			Grain filling period			Plant height (cm)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	VA2019-16	56.25	1.14	0.26	102.42	0.74	1.28	46.25	0.49	1.60	92.64	1.59	1.01
2	VA2019-17	60.50	1.28	5.53**	105.08	1.34	1.77	44.58	1.43	10.91**	87.07	0.69	-0.39
3	VA2019-18	59.50	0.98	0.58	102.83	0.99	3.98	43.25	0.96	1.91	81.38	0.75	0.91
4	VA2019-19	57.00	1.69	1.78	102.75	1.01	4.36*	45.83	0.58	0.43	83.46	0.76	0.41
5	VA2019-20	51.33	1.72	0.60	99.42	1.18	1.29	48.00	0.78	2.05	83.33	0.46	5.01
6	VA2019-21	52.83	0.98	0.82	103.50	0.94	0.18	50.67	0.80	3.19	87.94	1.00	6.90
7	VA2019-22	50.58	1.22	0.63	102.58	1.21	4.63	52.33	1.23	0.99	80.53	0.98	2.71
8	VA2019-23	54.92	0.64	0.59	103.92	1.10	7.97**	49.17	1.33	10.69**	87.62	-0.08	4.84
9	VA2019-24	54.42	1.18	1.38	103.08	1.22	0.79	48.50	1.34	0.56	89.56	0.94	6.13
10	VA2019-25	58.17	0.84	0.80	102.17	0.96	1.13	43.83	1.05	-0.34	81.12	1.56	-1.20
11	VA2019-26	56.33	1.15	0.95	104.17	0.83	0.13	47.83	0.50	0.11	90.25	-0.32	8.02
12	VA2019-27	58.83	0.88	-0.21	103.42	0.85	0.07	44.58	0.80	0.11	81.67	0.63	7.88
13	VA2019-28	53.17	0.54	0.23	103.08	1.02	-0.09	50.08	1.27##	-0.59	83.30	1.27	-0.95
14	VA2019-29	48.75	0.64	0.89	101.67	1.24#	-0.42	52.92	1.76#	-0.43	81.17	0.19	6.78
15	VA2019-30	55.17	0.95	1.87	103.00	0.73#	-0.23	47.92	0.43	1.12	87.66	0.45	3.76
16	VA2019-31	56.33	1.11	1.73	100.58	0.98	6.24*	44.17	0.74	1.47	90.42	2.16#	-1.16
17	VA2019-32	63.42	0.95	2.35	104.33	0.97	2.40	40.83	1.18	5.43*	94.77	1.99	5.42
18	VA2019-33	60.92	1.01	-0.31	104.75	0.98	-0.34	44.00	0.86	-0.33	96.55	1.60	0.39
19	NI5439	61.67	0.68	0.15	105.67	1.06	2.32	44.00	1.60	1.21	109.03	1.73	13.79
20	DBW93	63.42	0.44	0.45	105.17	0.66##	-0.45	42.00	0.87	0.27	99.36	1.67	41.15**
Population mean		56.68			103.18			46.54			88.94		

*, ** Significant at 5 per cent and 1 per cent levels, respectively.

#, ## Significant at 5 per cent and 1 per cent levels, respectively, when $H_0: b=1$

Table 4.5 (Cont..) : Stability parameters for number of effective tillers per meter, number of effective tillers per plant and spike length.

	Genotypes	No. of effective tillers per meter			No. of effective tillers per plant			Spike length (cm)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	VA2019-16	109.42	1.01	-11.94	1.82	1.18	-0.003	9.74	0.04	0.15
2	VA2019-17	103.92	0.53	-8.32	1.76	0.39	0.009	9.33	0.92	0.00
3	VA2019-18	104.58	0.69	-7.83	1.79	0.76	0.003	9.01	0.42	0.15
4	VA2019-19	107.50	2.29##	-15.41	1.82	2.04#	-0.003	10.83	0.77	0.08
5	VA2019-20	105.83	0.26	-4.45	1.82	0.38	0.003	8.45	1.37	0.00
6	VA2019-21	103.25	0.28	-4.01	1.76	0.29	0.001	8.79	1.56	0.10
7	VA2019-22	115.75	0.46	-9.50	1.93	0.91	0.001	8.72	1.83	0.21
8	VA2019-23	88.75	0.84	9.43	1.52	1.21	0.007	9.74	0.80	0.19
9	VA2019-24	106.33	0.84	-11.24	1.84	0.83	0.002	10.52	1.86	0.02
10	VA2019-25	104.00	1.35	-3.92	1.74	1.50	-0.002	9.14	1.27	0.07
11	VA2019-26	110.17	1.01	-5.32	1.87	1.12	0.000	8.34	1.18	0.06
12	VA2019-27	101.50	1.16+	-10.41	1.73	1.05	-0.001	8.46	1.57	0.18
13	VA2019-28	100.25	1.95##	-15.77	1.70	1.78##	-0.004	9.38	0.94	0.00
14	VA2019-29	108.58	0.61	-8.99	1.85	0.45	-0.004	8.09	1.48	0.02
15	VA2019-30	108.75	0.60	-13.76	1.85	0.65	-0.004	9.87	1.13	0.41*
16	VA2019-31	108.83	0.97	-8.28	1.86	1.04	0.005	7.89	0.54	-0.03
17	VA2019-32	92.92	1.49	-13.87	1.57	1.32	-0.002	10.48	0.25	0.24
18	VA2019-33	95.17	1.78	-9.22	1.60	1.48#	-0.004	11.36	1.35	0.46*
19	NI5439	112.75	1.17	-13.95	1.92	1.07	-0.001	9.14	0.58#	-0.03
20	DBW93	103.17	0.68	-2.60	1.78	0.58	-0.001	11.37	0.16	0.03
Population mean		104.57			1.78			9.43		

*, ** Significant at 5 per cent and 1 per cent levels, respectively.

#, ## Significant at 5 per cent and 1 per cent levels, respectively, when $H_0: b=1$

Table 4.5 (Cont..) : Stability parameters for number of grains per spike, grain weight per spike, grain yield/meter and grain yield/plant.

	Genotypes	No. of grains per spike			Grain weight per spike (g)			Grain yield per meter (g)			Grain yield per plant (g)		
		Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
1	VA2019-16	47.08	1.12	2.22	2.20	1.62#	-0.004	375.42	1.22	439.07	6.41	1.32	0.24
2	VA2019-17	46.65	0.46#	-1.33	2.39	0.42	0.008	343.75	0.34+##	-168.15	5.88	0.36##	-0.05
3	VA2019-18	38.88	0.60	0.33	1.80	0.82	0.005	326.50	1.14	565.23	5.57	1.13	0.10
4	VA2019-19	39.75	0.74	-0.59	2.03	1.03	0.005	368.75	0.27#	-2.56	6.29	0.29	0.03
5	VA2019-20	30.65	0.22##	-1.49	1.64	0.28#	-0.004	336.42	1.01	245.62	5.76	0.98	0.06
6	VA2019-21	38.83	1.12	5.98	1.84	0.47	0.016	327.33	0.49#	-129.30	5.54	0.51#	-0.03
7	VA2019-22	41.30	1.03	3.40	1.70	1.14	0.004	356.17	0.59	-87.55	6.03	0.56	-0.03
8	VA2019-23	48.65	0.72	0.85	2.47	2.03	0.028	338.92	1.22	325.06	5.79	1.22	0.13
9	VA2019-24	43.30	2.56	28.83**	1.90	0.36	0.002	362.08	0.84	-156.90	6.13	0.83	-0.03
10	VA2019-25	43.73	0.57	-1.04	2.01	0.79	0.009	367.75	1.55	485.06	6.28	1.57	0.19
11	VA2019-26	49.03	0.43	0.15	1.99	0.71	0.000	411.08	1.01	1.50	7.00	1.02	0.02
12	VA2019-27	46.27	0.94	-1.50	2.10	0.96	0.023	334.83	0.79	-118.79	5.77	0.70	-0.04
13	VA2019-28	39.87	1.88#	-0.36	2.00	1.20	0.069*	337.17	1.31	766.99	5.81	1.14	0.22
14	VA2019-29	37.20	0.27	-0.13	2.05	0.83	-0.003	385.33	1.07	154.05	6.62	1.15	0.07
15	VA2019-30	47.08	1.56	0.72	2.01	0.76	-0.001	388.08	0.72#	-191.72	6.60	0.72#	-0.05
16	VA2019-31	47.83	1.28	10.80	2.21	1.28	-0.003	377.58	1.11	410.90	6.42	1.18	0.05
17	VA2019-32	49.42	1.38	-0.43	2.30	1.07	0.017	339.00	1.35	4639.61**	5.80	1.33	1.32**
18	VA2019-33	61.80	0.48#	-1.50	2.90	1.16	-0.004	404.58	1.44	38.63	6.86	1.49	-0.02
19	NI5439	48.05	1.11	5.45	2.17	1.65	0.039	412.58	1.68	53.75	6.98	1.65#	-0.01
20	DBW93	51.82	1.52	8.44	2.02	1.43	0.080*	311.17	0.88	704.09	5.40	0.84	0.15
Population mean		44.86			2.09			360.23			6.15		

*, ** Significant at 5 per cent and 1 per cent levels, respectively.

#, ## Significant at 5 per cent and 1 per cent levels, respectively, when H₀: b=1

Table 4.5 (Cont.): Stability parameters for thousand grain weight, biological yield/plant, biological yield/meter and harvest index.

	Genotypes	1000 grain weight (g)			Biological yield per meter (g)			Biological yield per plant (g)			Harvest index (%)		
		Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
1	VA2019-16	46.48	1.56	-0.22	1059.50	1.78	10976.70	17.60	1.81	2.24	35.49	0.95	-1.08
2	VA2019-17	51.45	0.24	3.45	1118.25	0.50	-1461.38	18.73	0.72	-0.07	30.65	0.28##	-2.22
3	VA2019-18	46.38	0.96	-0.39	1113.67	1.01	-1509.56	18.52	1.06	-0.27	29.24	1.15	1.88
4	VA2019-19	50.74	1.09	-0.29	1120.33	1.02	-299.42	18.64	0.98	-0.20	32.90	0.10#	-0.47
5	VA2019-20	53.21	0.18	1.24	959.17	0.33	-1378.93	16.14	0.49##	-0.53	35.00	1.42	1.72
6	VA2019-21	52.37	1.18	-1.54	953.50	0.26	-1126.48	16.12	0.29	0.13	34.26	0.59	0.65
7	VA2019-22	42.65	1.74	2.97	1073.50	0.56	411.65	18.24	0.64	-0.43	33.26	0.48#	-2.11
8	VA2019-23	50.63	2.30	13.73	1045.25	0.24#	-1757.57	17.74	0.36	-0.24	32.19	1.50	4.91
9	VA2019-24	46.59	0.43	0.72	1086.25	-0.17	-984.51	18.27	0.31	0.04	33.38	1.07	3.83
10	VA2019-25	45.96	0.76	3.19	1070.67	2.48##	-1763.81	17.89	1.95	-0.36	33.98	1.14	-0.67
11	VA2019-26	40.01	0.89	1.07	1078.25	0.89	7646.20	17.94	0.82	1.36	38.18	1.33	0.68
12	VA2019-27	45.89	0.99	9.48	964.00	0.40	-1596.08	15.99	0.41	-0.41	34.73	1.04	-1.49
13	VA2019-28	47.90	1.14	3.29	961.33	0.51	343.72	16.27	0.62	0.02	34.76	1.63#	-1.58
14	VA2019-29	54.87	1.23##	-2.09	1001.58	1.38	404.53	16.72	1.25	-0.09	38.27	0.98	-1.91
15	VA2019-30	42.91	-0.01	1.56	1144.00	0.96	1408.41	19.24	1.25	1.03	33.94	0.71	0.07
16	VA2019-31	46.66	0.85	11.09	999.42	0.39	-1021.75	16.60	0.44	-0.02	37.65	1.31	5.26
17	VA2019-32	45.83	0.80	0.65	971.17	1.63	7100.39	16.27	1.62	1.34	33.93	1.29	17.07
18	VA2019-33	46.73	1.00	-1.68	1118.83	2.23	6008.24	18.90	1.75	1.36	35.98	1.29	1.64
19	NI5439	44.86	1.62	2.57	1260.33	2.26	-349.86	21.17	2.17	-0.23	32.44	1.10	0.79
20	DBW93	40.48	1.05	4.52	1062.83	1.35	1715.95	18.00	1.04	1.02	29.07	0.65	4.96
Population mean		47.13			1058.09			17.75			33.97		

*, ** Significant at 5 per cent and 1 per cent levels, respectively.

#, ## Significant at 5 per cent and 1 per cent levels, respectively, when H₀: b=1

non-significant deviations from regression line, of which 11 genotypes exhibited more number of effective tillers per meter than population mean. The genotypes VA2019-16, VA2019-26 and VA2019-31 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) exhibited average stability with maximum amount of tillers than population mean value. The genotype VA2019-19 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$) showed stability for favourable environments with more number of tillers than population mean values, while VA2019-28 (Genotype mean < Population mean, $b_i > 1$ and $S^2d_i=0$ non significant) also showed adaptation to favourable environments but with lesser number of tillers per meter than population mean.

The genotypes VA2019-16, VA2019-26 and VA2019-31 showed adaptability to varying environments for number of effective tillers per meter. The genotype VA2019-19 showed high response to environmental changes. Similar results were obtained by Pujer *et al.* (2020).

4.5.6 Number of effective tillers per plant

Among 20 genotypes, VA2019-23 (1.52) showed minimum number of effective tillers per plant whereas VA2019-22 (1.93) exhibited maximum tillers per plant with the overall population mean of 1.78. The deviation from regression line was non-significant for all the genotypes. The genotype VA2019-31 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) was average stable adapted to all the environments with maximum number of tillers per plant than population mean. The genotype VA2019-19 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$ non significant) showed stability for favorable environments while VA2019-28 and VA2019-33 (Genotype mean < Population mean, $b_i > 1$ and $S^2d_i=0$ non significant) showed below average stable performance for tillers per plant with lower mean value.

The genotype VA2019-31 showed average responsiveness over all environments and VA2019-19 exhibited responsiveness to favourable environment for more number of tillers per plant. Similar findings were reported by Krupal *et al.* (2018) and Gulzar *et al.* (2015).

4.5.7 Spike length (cm)

The mean values for spike length varied from 7.89 (VA2019-31) to 11.37 cm (DBW 93) exhibiting lower and higher spike length, respectively, with the population

mean of 9.43 cm. All the genotypes studied showed non-significant deviation from regression line except VA2019-30 and VA2019-33, of which 8 genotypes showed maximum value of spike lengths than population mean. The genotype NI 5439 (Genotype mean < Population mean, $b_i < 1$ and $S^2d_i = 0$) with lower spike length than population mean was considered above average stable and hence can be adapted to favourable environments.

The genotype with higher mean value, regression coefficient of unity and minimum deviation from regression will show good stability over varying environmental conditions as reported by Eberhart and Russel (1966). Here the genotype NI5439 showed adaptability to unfavourable environmental conditions with lower mean performance than population mean. Sidhi *et al.* (2018) and Gulzar *et al.* (2015) also reported the similar findings.

4.5.8 Number of grains per spike (g)

The genotype VA2019-20 (30.65g) showed lowest number of grains per spike while the genotype VA2019-33 (61.80g) exhibited maximum number of grains per spike. The overall population mean was 44.86g. All the genotypes showed non-significant deviation from regression line except VA2019-24, of which 11 genotypes recorded more number of grains per spike than population mean. The genotypes VA2019-17 and VA2019-33 (Genotype mean > Population mean, $b_i < 1$ and $S^2d_i = 0$) with higher mean values showed above average stability and can be adapted to unfavorable environment, while the genotype VA2019-28 (Genotype mean < Population mean, $b_i > 1$ and $S^2d_i = 0$ non significant) was below average stable with lower mean value than population mean.

The genotypes VA2019-17 and VA2019-33 showed adaptation to adverse environmental conditions with above average mean performance. Similar findings were reported by Hassan *et al.* (2013) and Pujer *et al.* (2020).

4.5.9 Grain weight per spike (g)

The genotype VA2019-20 (1.64g) showed lowest grain weight per spike, whereas VA2019-33 (2.90g) recorded highest grain weight per spike with the population mean of 2.09g for 20 genotypes. All the genotypes were non-significantly deviating from regression line except VA2019-28 and DBW 93. The genotypes

VA2019-27 and VA2019-32 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) recorded average stability with higher mean value than population mean. The genotype VA2019-16 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$ non significant) showed below average stability with more number of grains per spike than population mean.

The genotypes VA2019-27 and VA2019-32 were found fit for varying environmental conditions and genotype VA2019-16 for favorable environmental conditions with above average mean performance as indicated by stability parameters. Similar findings were reported by Hassan *et al.* (2013) and Sidhi *et al.* (2018).

4.5.10 Grain yield per meter (g)

The genotype DBW 93 (311.17g) recorded the lowest amount of grain yield per meter, whereas the genotype NI5439 (412.58g) showed the highest grain yield per meter with the overall population mean of 360.22g. The deviation from regression showed non-significance for all the genotypes except VA2019-32. The genotypes VA2019-26 and VA2019-29 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) were considered average stable and is adaptable to all environments with their higher mean yield than population mean. The genotype VA2019-30 (Genotype mean > Population mean, $b_i < 1$ and $S^2d_i=0$) was above average stable with higher mean value, whereas VA2019-17 and VA2019-21 (Genotype mean < Population mean, $b_i < 1$ and $S^2d_i=0$ non significant) were also above average stable with lower mean value than population mean.

The genotypes VA2019-26 and VA2019-29 showed average stability over varying environment conditions with higher grain yield while genotype VA2019-30 showed above average stability by adapting to favorable environmental conditions with higher grain yield. These results were in line with Gulzar *et al.* (2015), Pujer *et al.* (2020) and Singh *et al.* (2018).

4.5.11 Grain yield per plant (g)

The genotype DBW 93 (5.40g) recorded lowest grain yield per plant and the genotype VA2019-26 (7.00g) showed the highest grain yield per plant among 20 genotypes with the overall population mean of 6.15g. All the genotypes studied were showing non-significance for deviation from regression except VA2019-32. The

genotype VA2019-26 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) showed average stability and can be adapted to all the environments with its higher mean value. The genotypes VA2019-17 and VA2019-21 (Genotype mean < Population mean, $b_i < 1$ and $S^2d_i=0$) were considered above average stable but with lower mean value, whereas VA2019-30 (Genotype mean > Population mean, $b_i < 1$ and $S^2d_i=0$) was also above average stable with higher mean value than population mean. The genotype NI5439 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$) was below average stable but with higher mean value than population mean.

The genotypes VA2019-26 showed stable expression over varying environmental conditions while VA2019-30 showed adaptability to unfavourable environment conditions with higher grain yield per plant and NI5439 for favourable environmental conditions. These results were in accordance with that of Sharma *et al.* (2019) and Verman *et al.* (2015).

4.5.12 Thousand grain weight (g)

The overall population mean recorded was 47.13g with the genotype VA2019-26 (40.01g) showing the lowest thousand grain weight, whereas VA2019-29 (54.87g) recording the highest thousand grain weight. All the genotypes were non-significantly deviating from regression line. The genotype VA2019-19 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) were average stable with higher mean value, while one genotype VA2019-29 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i=0$) showed below average stability with higher mean value than population mean and can be adapted to favorable environment.

The genotypes VA2019-19 were considered average stable over variable environments with above average mean and VA2019-29 was showing higher responsiveness to environmental changes with below average stability with more thousand grain weight than population mean value. Similar results were obtained by Haydar *et al.* (2010) and Singh *et al.* (2018).

4.5.13 Biological yield per meter (g)

The genotype VA2019-21 (953.50g) showed lesser biological yield per meter while the genotype NI 5439 (1260.33g) recorded the highest biological yield per meter among 20 genotypes with the overall population mean of 1058.09g. All the genotypes

showed non-significant deviation from regression line. The genotypes VA2019-18, VA2019-19 and VA2019-30 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) showed average stability with higher mean value than population mean, while VA2019-25 (Genotype mean > Population mean, $b_i=1$ significant and $b_i>1$ and $S^2d_i=0$ non significant) showed below average stability with higher mean value and can be adapted to favorable environment.

The higher biomass than average mean were recorded by VA2019-18, VA2019-19 and VA2019-30 with average stability and good adaptation over varying environment conditions while VA2019-25 also showed higher biomass than population mean but adapted to favorable environment conditions with sensitiveness to environmental change. Similar results were reported by Pujer *et al.* (2020) and Sidhi *et al.* (2018).

4.5.14 Biological yield per plant (g)

The overall population mean of 17.75g was recorded for 20 genotypes with VA2019-27 (15.99g) showing minimum biological yield per plant, while NI 5439 (21.17g) recording higher biological yield per plant. All the genotypes were non significantly deviating from regression line among which VA2019-18, VA2019-19 and DBW93 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) were average stable with higher mean value than population mean while VA2019-20 (Genotype mean < Population mean, $b_i<1$ and $S^2d_i=0$) was showing above average stability with lower mean value than population mean and can be adapted to unfavorable environment.

The genotypes VA2019-18, VA2019-19 and DBW93 with higher mean performance showed average stability and good adaptation to variable environments. Similar findings were obtained by Sidhi *et al.* (2018).

4.5.15 Harvest index

The genotype DBW 93 (29.07) recorded lower harvest index while VA2019-29 (38.27) showed higher harvest index among 20 genotypes with the overall population mean of 33.97. All the 20 genotypes were non significantly deviating from regression among which VA2019-16, VA2019-27 and VA2019-29 (Genotype mean > Population mean, b_i closer to unity and $S^2d_i=0$) showed average stability with higher harvest index

than population mean whereas VA2019-17 and VA2019-22 (Genotype mean < Population mean, $b_i < 1$ and $S^2d_i = 0$) recorded above average stability with lower mean value and VA2019-28 (Genotype mean > Population mean, $b_i > 1$ and $S^2d_i = 0$ non significant) showed above average stability with higher harvest index than population mean and can be adapted to favorable environment.

The genotypes VA2019-16, VA2019-27 and VA2019-29 with higher harvest index value than population mean were considered adaptable to variable environments with average stability and VA2019-28 with above average mean was showing adaptation to favorable environments with more responsiveness to environmental changes. Similar results were reported by Krupal *et al.* (2018), Verman *et al.* (2015) and Gulzar *et al.* (2015).

The genotypes which were studied under the present investigation didn't show stability for all the characters but some of the genotypes showed stability characteristics for more than two or three characters. The genotype VA2019-26 was average stable for grain yield per meter, grain yield per plant and number of effective tillers per meter. The genotype VA2019-29 was showing average stability for grain yield per meter and harvest index. The genotype VA2019-19 showed average stability for the traits thousand grain weight, biological yield per meter and biological yield per plant, whereas the genotype VA2019-27 for the traits grain weight per spike and harvest index showed average stability and VA2019-30 for days to 50% heading and biological yield per meter indicated average stability. The genotypes exhibiting average stability can be adapted across all studied environments. The genotype VA2019-29 showed below average stability characteristics for days to maturity and thousand grain weight, indicating adaptation to favorable environments for these traits and VA2019-30 showed above average stability for grain yield per meter and grain yield per plant showing adaptation to adverse environmental conditions.

4.6 Molecular studies

4.6.1 SSR marker analysis

A total of sixteen heat tolerant specific SSR primers were used for the study of twenty genotypes, of which thirteen primers showed amplification, among thirteen primers twelve were polymorphic amplifying a total of 34 alleles with an average of

2.62 alleles per locus, the primer Xgwm293 was monomorphic. The total number of amplified bands ranged from two to five. The maximum number of amplified product was recorded for primer Xgwm577 (5), followed by primers Xgwm131 (4), the primers Xgwm484, Xgwm63, Xgwm626 amplified 3 alleles and the primers gwm102, Xgwm190, Xwmc48, barc65, Xgwm11, barc180, Xgwm190, WMS0745 amplified two alleles. The PIC values for the thirteen polymorphic primers ranged from 0.11 (Xgwm11) to 0.68 (Xgwm577) with an average of 0.38. The PIC values provide information about amount of variability for a primer among the genotypes studied. The PIC value was more for Xgwm577 (0.68) followed by Xgwm626 (0.54), Xgwm131 (0.49) and Xgwm484 (0.46) whereas lowest PIC were recorded for Xgwm11 (0.11) followed by Xwmc48 (0.25) and barc180 (0.27). The primers Xgwm577, Xgwm626 and Xgwm131 were showing PIC equal or more than 0.5. Hence these primers can be used further for molecular diversity analysis in wheat. Similar findings were obtained by Drikvand *et al.* (2013) and Mwale *et al.* (2016). The heterozygosity ranged from 0.00 (gwm102, Xgwm484, Xgwm190, Xgwm11, barc180, Xgwm190, WMS0745) to 1.00 (Xgwm626) with an average of 0.19. The results obtained for these thirteen polymorphic primers are presented in the Table 4.6.

Table 4.6: List of SSR primers reported polymorphic for twenty wheat genotypes.

Sl.No.	Primer	Molecular band size (bp)	No. of alleles amplified	PIC	Heterozygosity
1	gwm102	145-161	2	0.38	0.00
2	Xgwm484	144-183	3	0.46	0.00
3	Xgwm190	188-218	2	0.37	0.00
4	Xgwm131	112-177	4	0.49	0.89
5	Xwmc48	124-144	2	0.25	0.05
6	Xgwm63	251-306	3	0.32	0.11
7	barc65	94-110	2	0.37	0.35
8	Xgwm11	197-219	2	0.11	0.00
9	Xgwm577	133-183	5	0.68	0.05
10	Xgwm626	104-143	3	0.54	1.00
11	barc186	204-205	2	0.27	0.00
12	Xgwm190	199-220	2	0.36	0.00
13	WMS0745	112-125	2	0.35	0.00
	Mean		2.62	0.38	0.19

The similarity matrices were developed using SIMQUAL sub-programme of NTSPYC-pc software for twenty genotypes by data generated from thirteen polymorphic SSR primers. The allelic diversity were used to produce dendrogram by the sub-programme cluster tree analysis of the same NTSPYC-pc software which revealed the genetic relationship among the genotypes studied, represented in the figure 4.1. Based on the dendrogram, two clusters were formed for twenty genotypes *i.e.*, cluster A and cluster B which is formed at the similarity co-efficient of 0.37. Cluster A is subdivided into two sub clusters A₁ and A₂. Sub cluster A₁ includes five genotypes *viz.*, VA2019-16, VA2019-32, VA2019-28, VA2019-21 and VA2019-30 whereas sub cluster A₂ consists of nine genotypes *viz.*, VA2019-17, Va2019-27, VA2019-25, VA2019-18, VA2019-29, VA2019-19, VA2019-20, VA2019-31 and DBW 93. Similarly Cluster B is subdivided into two sub clusters *i.e.*, B₁ and B₂. Sub cluster B₁ consists of three genotypes VA2019-22, VA2019-23 and VA2019-33, likewise sub cluster B₂ consists of three genotypes VA2019-24, VA2019-26 and NI 5439. Drikvand *et al.* (2013) and Mwale *et al.* (2016) also reported the similar findings. Based on the primers used, genotypes VA2019-17 and VA2019-27 recorded highest similarity of 1.00.

4.6.2 Marker validation for heat tolerance

The validation of markers linked to specific traits will help in determining the effectiveness of markers in different genetic backgrounds across environments, which will be further useful in molecular assisted breeding programmes. There are various number of QTL's for heat tolerance specific characters like grain yield, grain number, grain filling duration, thousand grain weight which were reported by many workers in bread wheat which are available in public domain. Among those, sixteen heat tolerance specific markers were selected and been validated under heat stress conditions for twenty genotypes. Among sixteen primers, fourteen primers showed amplification, from which thirteen of them were polymorphic and other one primer was monomorphic which was not considered in studies. These thirteen primers amplified a total of 34 alleles with an average of 2.62 alleles per locus.

Table 4.7: Validation of heat tolerance markers in twenty wheat genotypes.

Sl. No	Primer	Molecular band size (bp)	Alleles (no.)	Traits	References
1	gwm102	145-161	2	Grain yield	Pinto <i>et al</i> 2010
2	Xgwm484	144-183	3	Grain filling duration	Mohammadi <i>et al</i> 2008a
3	Xgwm190	188-218	2	Grain yield	Mohammadi <i>et al</i> 2008b
4	Xgwm131	112-177	4	CTv, NDVIg	Pinto <i>et al</i> 2010
5	Xwmc48	124-144	2	GN, MAT, Grain yield	McIntyre <i>et al</i> 2010
6	Xgwm63	251-306	3	Grain yield	Mohammadi <i>et al</i> 2008a
7	barc65	94-110	2	CT, GN, grain yield, Total chl, Ht	Pinto <i>et al</i> 2010
8	Xgwm11	197-219	2	Grain filling duration	Yang <i>et al</i> 2002, Mohammadi <i>et al</i> 2008
9	Xgwm577	133-183	5	Thousand grain weight, yield, CTD, HSI (yield)	Paliwal <i>et al</i> 2012
10	Xgwm626	104-143	3	HSI(TGW)	Tiwari <i>et al</i> 2013
11	barc186	204-205	2	Anthesis	Pinto <i>et al</i> 2010
12	Xgwm190	199-220	2	Kernel hardness	Mohammadi <i>et al</i> 2008
13	WMS0745	112-125	2	-	Paliwal <i>et al</i> 2012

Validation experiment was conducted to confirm the reproductive ability of these selected markers for the heat tolerance specific traits like grain yield, grain number, thousand grain weight, anthesis and grain filling duration studied among twenty genotypes which is represented in the Table 4.7. Among the thirteen polymorphic markers, the below mentioned markers showed association for heat tolerance specific traits studied under the present study, in different genetic backgrounds. The marker gwm102, Xgwm190 and Xgwm63 showed association with the character grain yield under heat stress with an allele polymorphism range from 2 to 3. The markers Xgwm484, Xgwm11 and Xgwm293 showed association for the character grain filling duration under heat stress with an allele polymorphism range from 2 to 3. The markers Xwmc48 and barc65 showed association with the character grain number and grain yield under heat stress with an allele polymorphism of 2. The marker Xgwm577 with an allele polymorphism 5, showed association with the character thousand grain weight and grain yield under heat stress. The marker barc186 showed association with the character anthesis under heat stress with an allele polymorphism of 2. Similar findings were reported by Bhushal *et al.* (2017), Paliwal *et al.* (2012), Mohammadi *et al.* (2008) and Yang *et al.* (2002) for heat tolerance under late sown conditions.

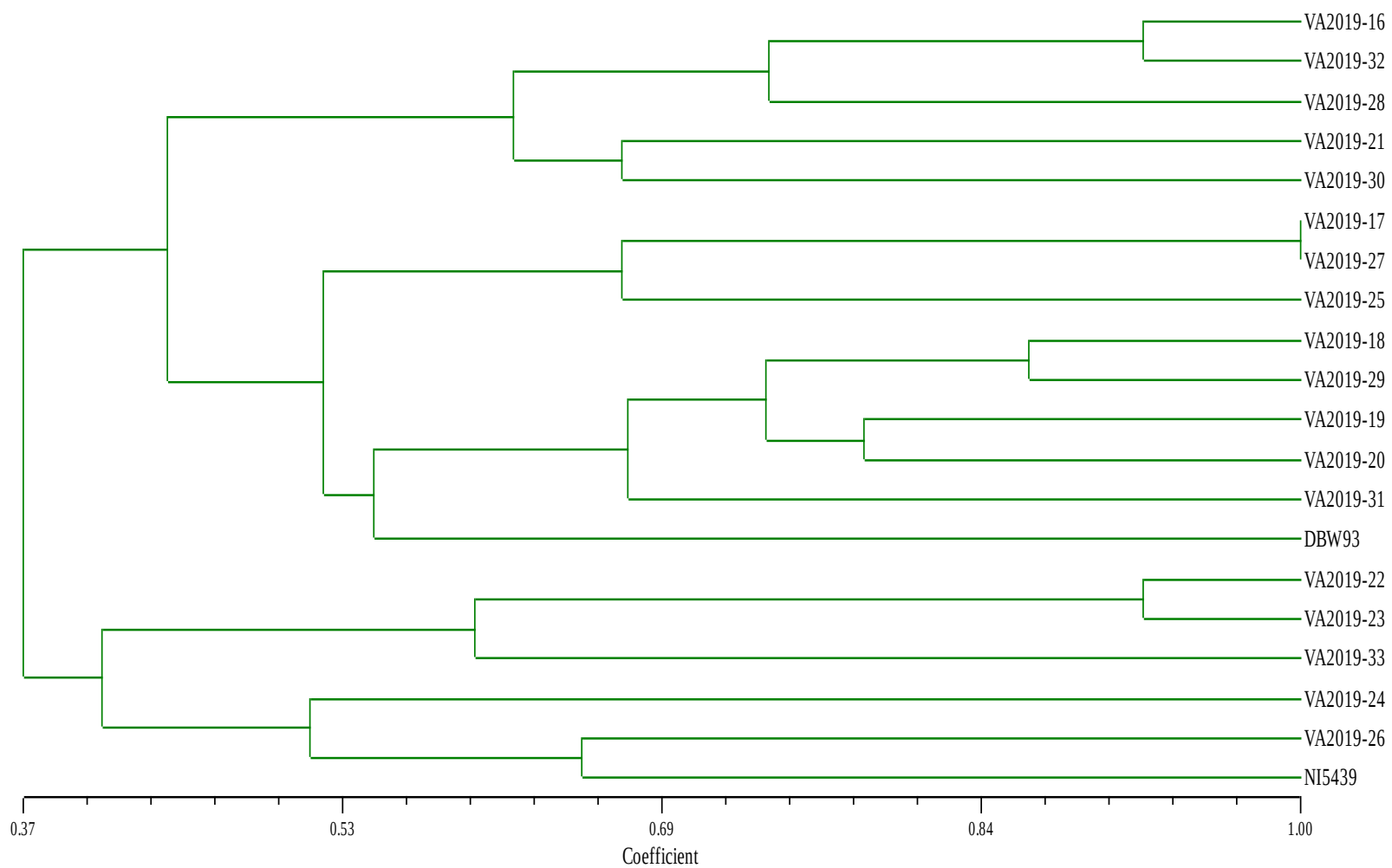


Fig. 4.3 Dendrogram showing clustering of 20 wheat genotypes constructed using UPGMA based on Jaccard's similarity co-efficient obtained from SSR based PCR analysis

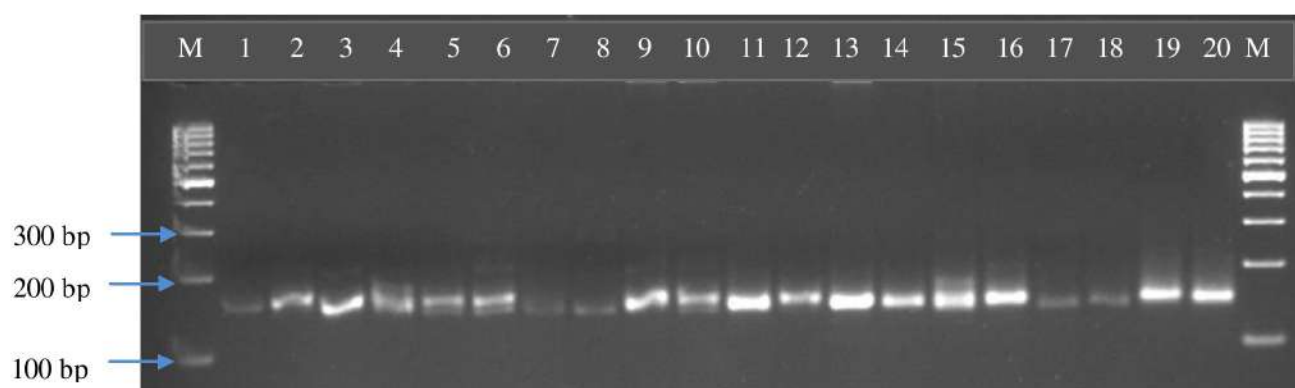


Plate 1.SSR amplification profile in wheat by primer gwm102

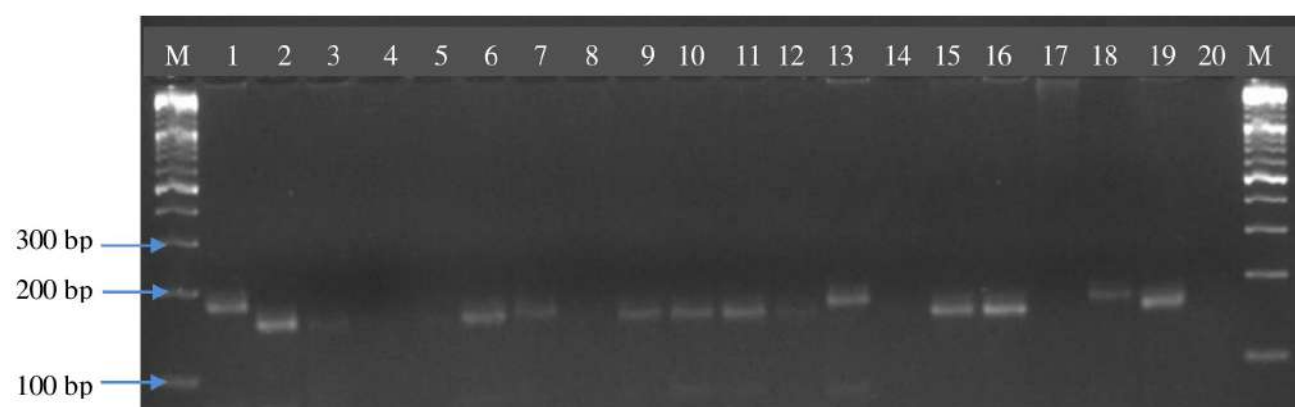


Plate 2.SSR amplification profile in wheat by primer Xgwm484

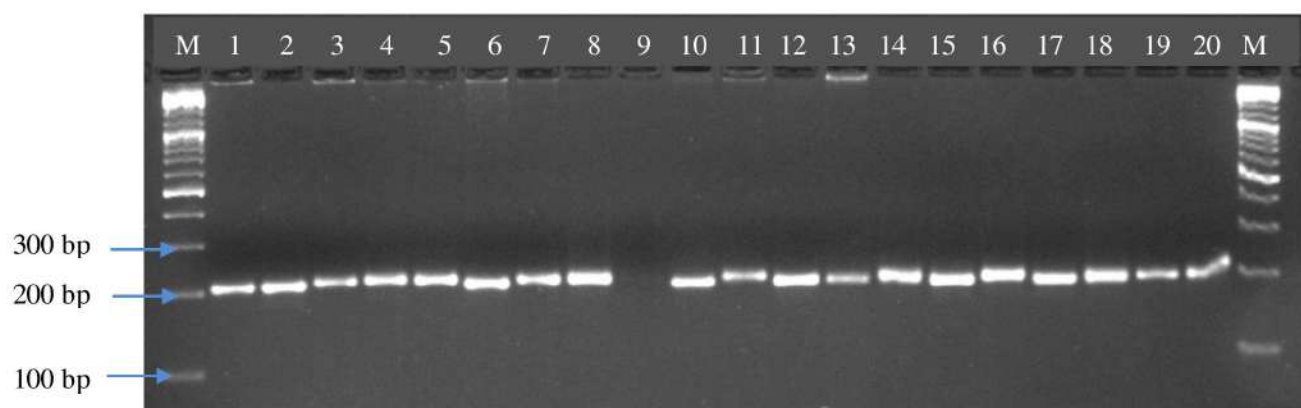


Plate 3.SSR amplification profile in wheat by primer Xgwm190

Where,

M-Ladder	6.VA2019-21	12.VA2019-27	18.VA2019-33
1.VA2019-16	7.VA2019-22	13.VA2019-28	19.NI5439
2. VA2019-17	8.VA2019-23	14.VA2019-29	20.DBW93
3. VA2019-18	9.VA2019-24	15.VA2019-30	
4. VA2019-19	10.VA2019-25	16.VA2019-31	
5.VA2019-20	11.VA2019-26	17.VA2019-32	

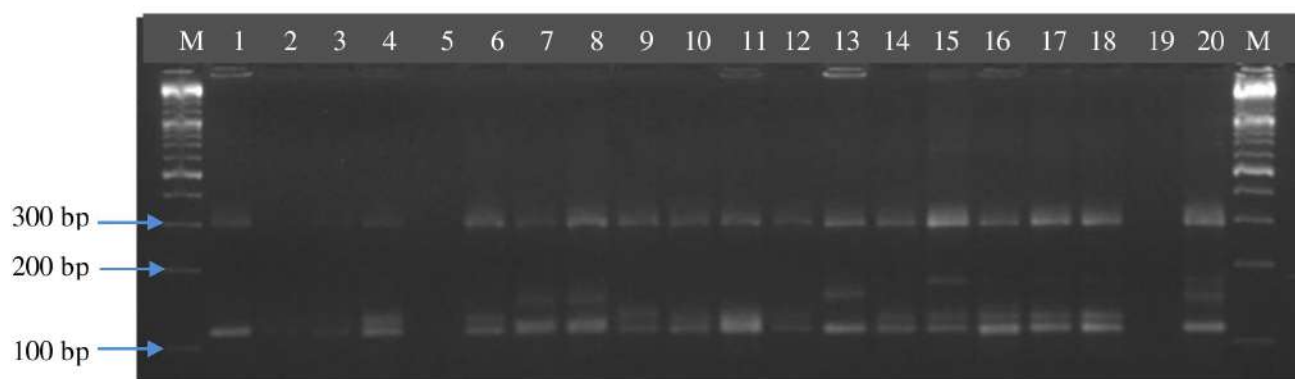


Plate 4.SSR amplification profile in wheat by primer Xgwm131

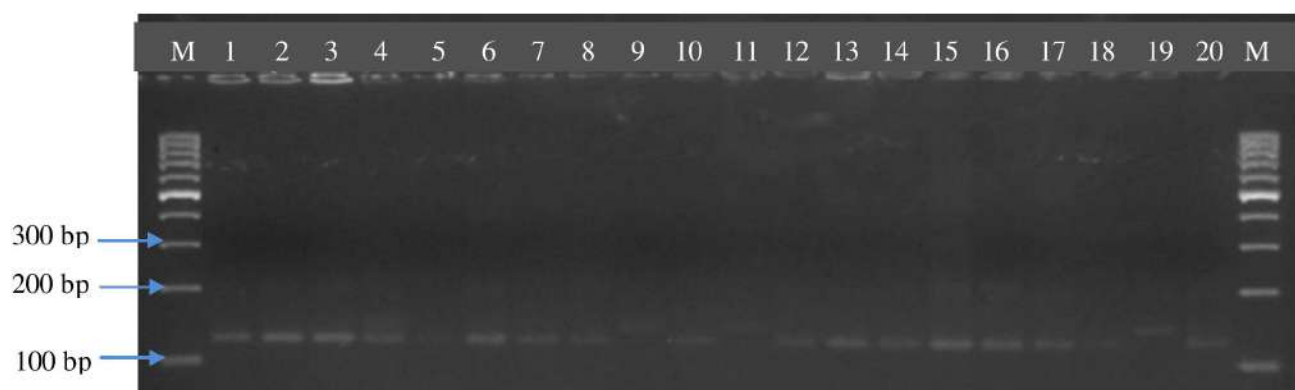


Plate 5.SSR amplification profile in wheat by primer Xwmc48

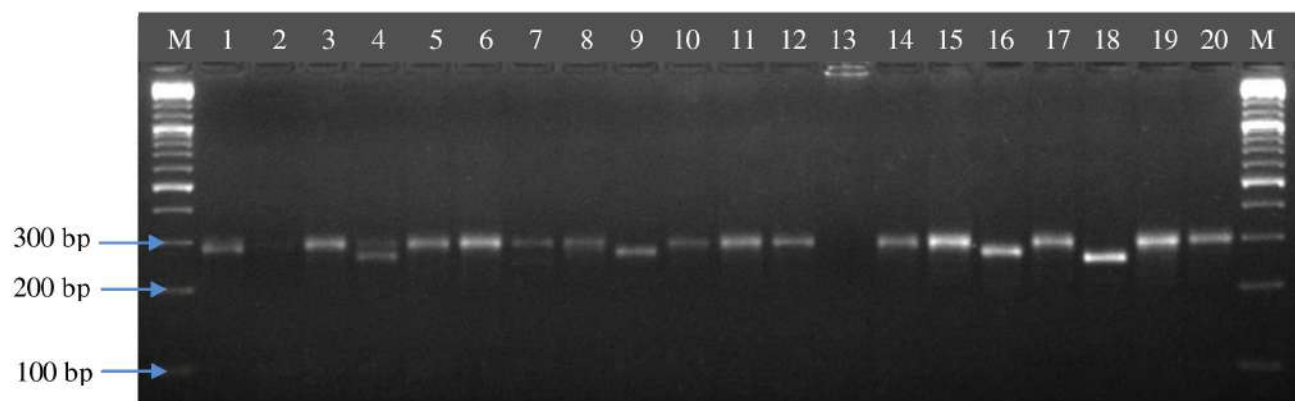


Plate 6.SSR amplification profile in wheat by primer Xgwm63

Where,

M-Ladder	6.VA2019-21	12.VA2019-27	18.VA2019-33
1.VA2019-16	7.VA2019-22	13.VA2019-28	19.NI5439
2.VA2019-17	8.VA2019-23	14.VA2019-29	20.DBW93
3.VA2019-18	9.VA2019-24	15.VA2019-30	
4.VA2019-19	10.VA2019-25	16.VA2019-31	
5.VA2019-20	11.VA2019-26	17.VA2019-32	

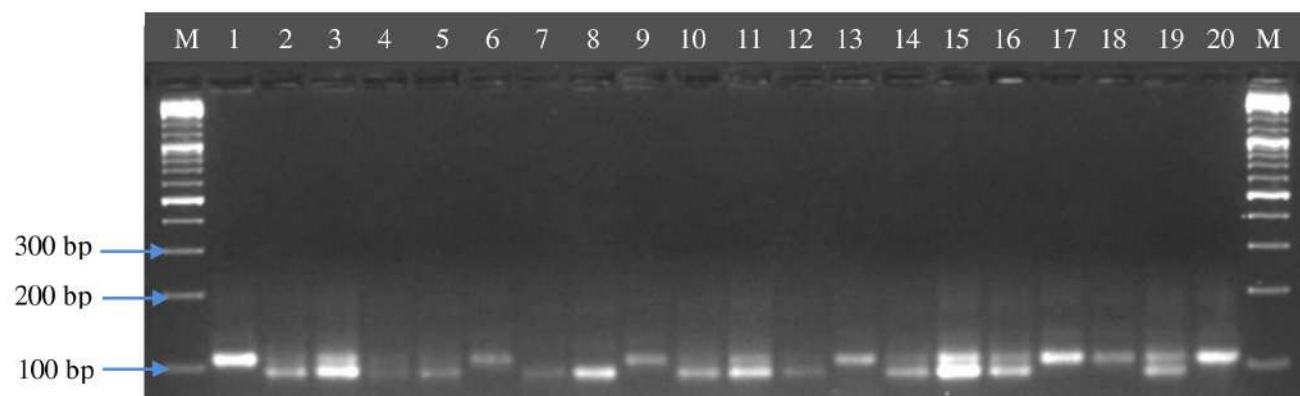


Plate 7.SSR amplification profile in wheat by primer barc65

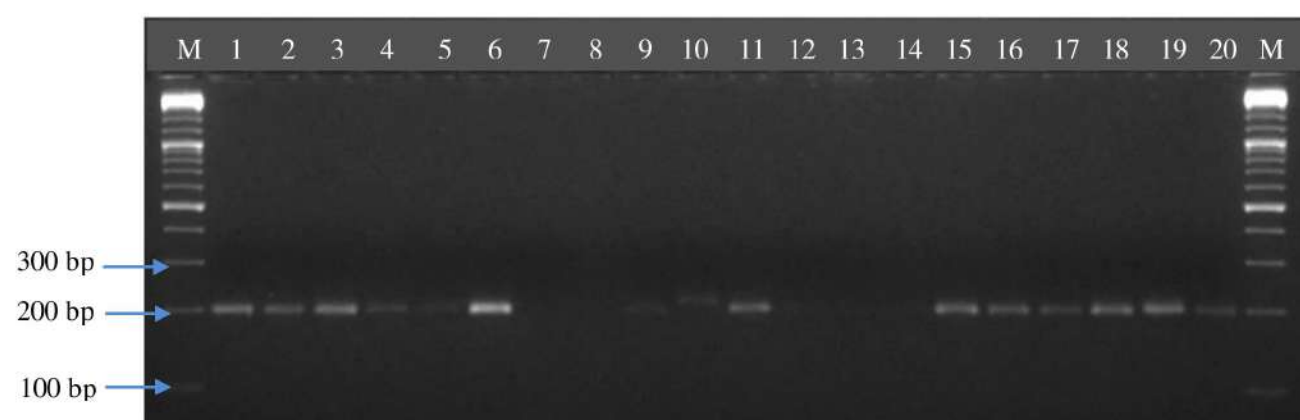


Plate 8.SSR amplification profile in wheat by primer Xgwm11

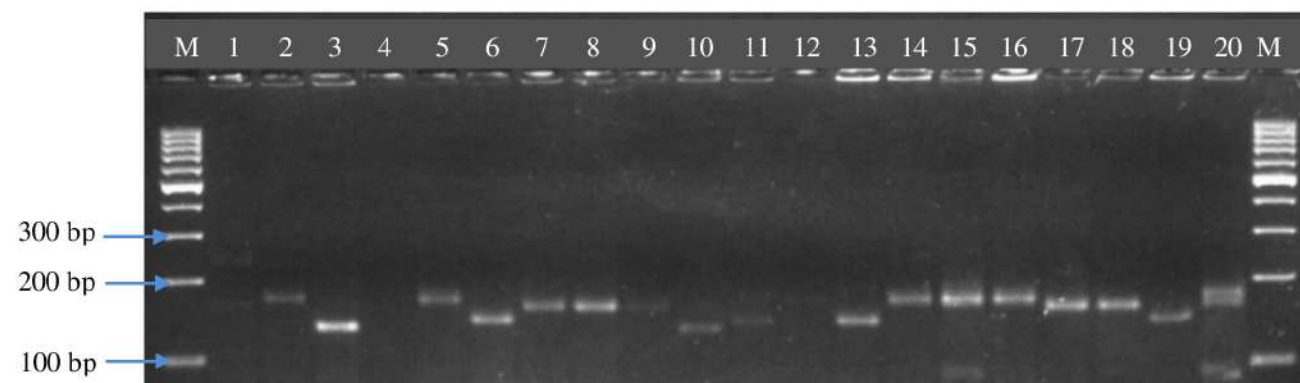


Plate 9.SSR amplification profile in wheat by primer Xgwm577

Where,

M-Ladder	6.VA2019-21	12.VA2019-27	18.VA2019-33
1.VA2019-16	7.VA2019-22	13.VA2019-28	19.NI5439
2. VA2019-17	8.VA2019-23	14.VA2019-29	20.DBW93
3. VA2019-18	9.VA2019-24	15.VA2019-30	
4. VA2019-19	10.VA2019-25	16.VA2019-31	
5.VA2019-20	11.VA2019-26	17.VA2019-32	

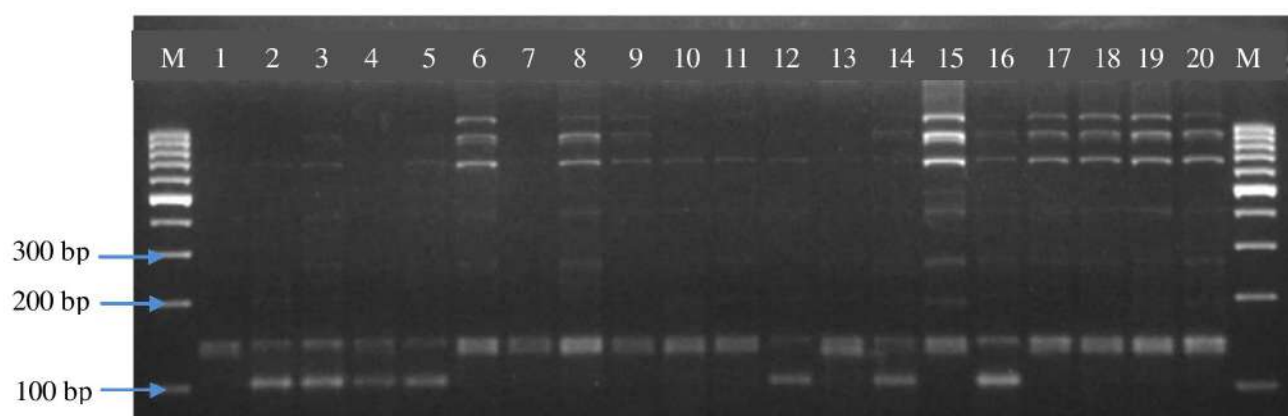


Plate 10.SSR amplification profile in wheat by primer Xgwm626

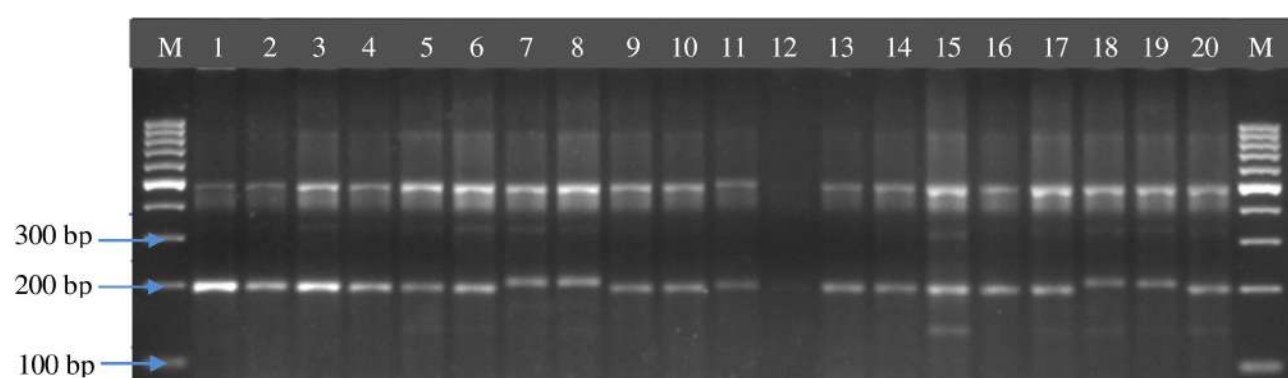


Plate 11.SSR amplification profile in wheat by primer barc186

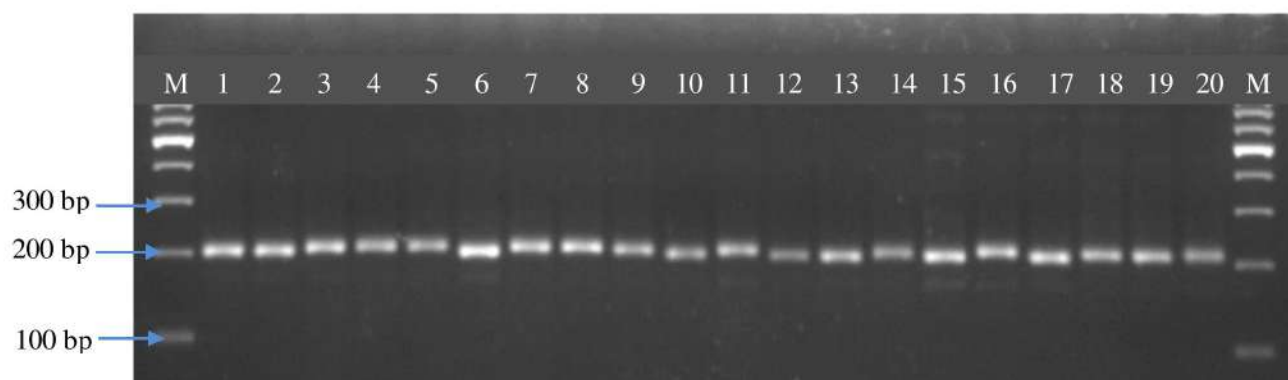


Plate 12.SSR amplification profile in wheat by primer Xgwm190

Where,

M-Ladder

1.VA2019-16

2. VA2019-17

3. VA2019-18

4. VA2019-19

5.VA2019-20

6.VA2019-21

7.VA2019-22

8.VA2019-23

9.VA2019-24

10.VA2019-25

11.VA2019-26

12.VA2019-27

13.VA2019-28

14.VA2019-29

15.VA2019-30

16.VA2019-31

17.VA2019-32

18.VA2019-33

19.NI5439

20.DBW93

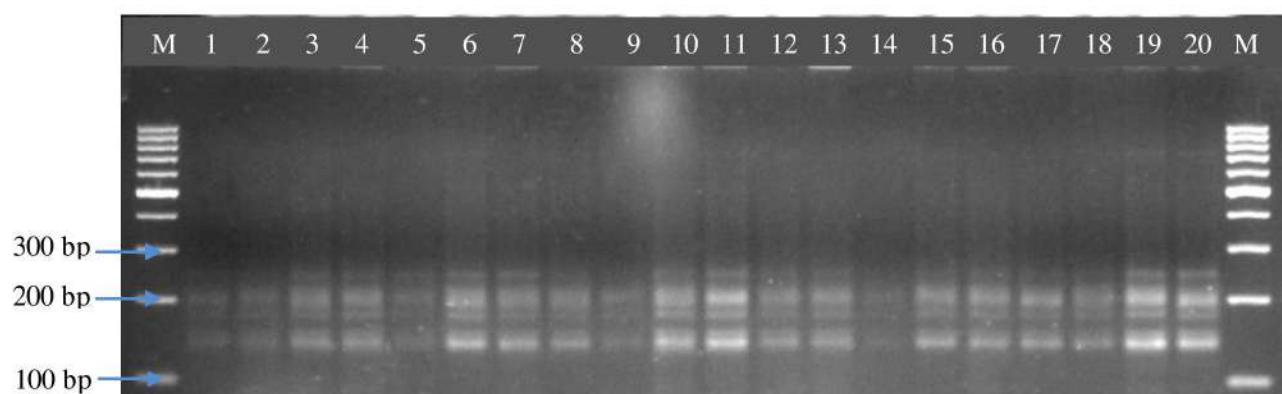


Plate 13.SSR amplification profile in wheat by primer Xgwm293

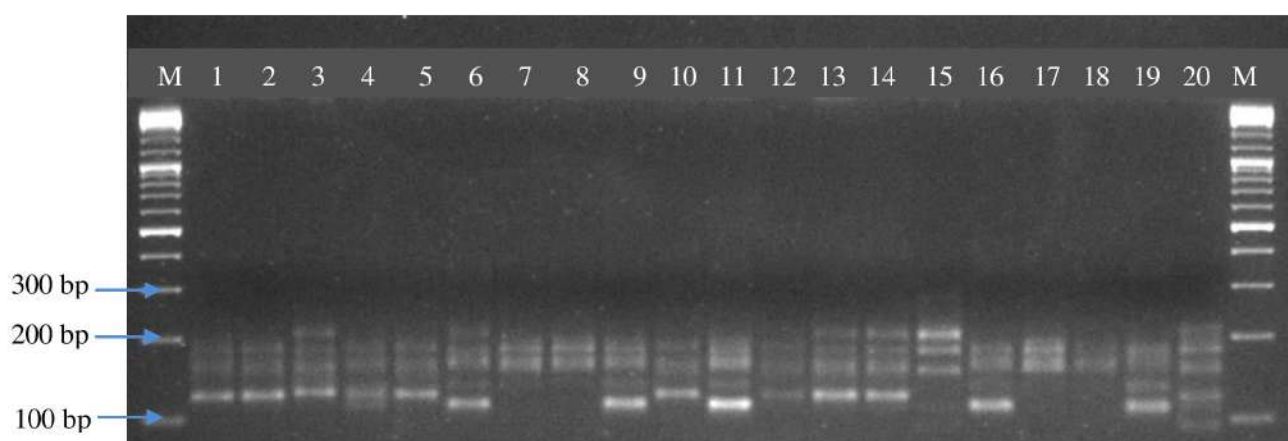


Plate 14.SSR amplification profile in wheat by primer WMS0745

Where,

M-Ladder	6.VA2019-21	12.VA2019-27	18.VA2019-33
1.VA2019-16	7.VA2019-22	13.VA2019-28	19.NI5439
2. VA2019-17	8.VA2019-23	14.VA2019-29	20.DBW93
3. VA2019-18	9.VA2019-24	15.VA2019-30	
4. VA2019-19	10.VA2019-25	16.VA2019-31	
5.VA2019-20	11.VA2019-26	17.VA2019-32	

Summary and Conclusions

V. SUMMARY AND CONCLUSIONS

A set of twenty genotypes were evaluated for stability across environments and to access the genetic variability along with validation of known molecular markers linked to heat tolerance in bread wheat. The field level experiment was conducted by randomized block design (RBD) with three replications at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during the *rabi* season 2019-20 under four different sowing dates (i.e., 15th November, 25th November, 5th December, 15th December). Twenty genotypes were evaluated for fifteen quantitative characters viz. days to 50% heading, days to maturity, grain filling period, plant height, number of effective tillers per meter, number of effective tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index while molecular analysis was performed at Department of Genetics and Plant Breeding, C. P. College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The salient findings of this study is presented below

1. The analysis revealed significant differences among the genotypes for all the characters studied in all four sowing seasons indicating sufficient variability existing among genotypes.
2. The mean performance of twenty genotypes across environments indicates the grain yield was seen higher when planted in normal dates of sowing recommended for wheat. Under late sown conditions there is a reduction in the grain yield.
3. The estimation of genetic parameters revealed closer affinity of GCV and PCV for the characters days to 50% heading, days to maturity, grain filling period and plant height indicating the scope for the selection for these traits.
4. The characters tillers per meter, tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and

harvest index exhibited larger variation in the values of GCV and PCV showing significant action of environment in the expression of these traits.

5. High heritability with high genetic advance was reported for spike length, number of grains per spike and grain weight per spike indicating predominance of additive gene action with effective selection. Whereas, high heritability with moderate genetic advance were reported for days to 50% heading, grain filling period, plant height, tillers per meter, thousand grain weight and biological yield per plant.
6. The genotypes and environment interaction tested against pooled error were significant at 5% probability level for all the characters except number of effective tillers per meter, number of effective tillers per plant, biological yield per meter, biological yield per plant and harvest index showing differential response of genotypes with environment.
7. The genotype VA2019-26 was average stable for grain yield per meter, grain yield per plant and number of effective tillers per meter whereas genotype VA2019-29 was showing average stability for grain yield per meter and harvest index while the genotype VA2019-19 showed average stability for the traits thousand grain weight, biological yield per meter and biological yield per plant indicating adaptation to all the studied environments
8. The genotype VA2019-29 showed below average stability characteristics for days to maturity and thousand grain weight, indicating adaptation to favorable environments and VA2019-30 showed above average stability for grain yield per meter and grain yield per plant showing adaptation to adverse environmental conditions.
9. A total of sixteen heat tolerance specific primers were used for validation and diversity analysis out of which fourteen showed amplification and thirteen primers were polymorphic amplifying a total of 34 alleles with a range of 2-5 alleles and an average of 2.62 alleles per locus. PIC values ranged from 0.11 (Xgwm11) to 0.68 (Xgwm577) with an average of 0.38. The heterozygosity ranged from 0.00 (gwm102, Xgwm484, Xgwm190, Xgwm11, barc180, Xgwm190, WMS0745) to 1.00 (Xgwm626) with an average of 0.19.

10. The dendrogram generated through sub-programme cluster tree analysis of the NTSPYC-pc software divided twenty genotypes into two major clusters A and B. Cluster A is subdivided into two sub clusters A₁ and A₂. Sub cluster A₁ includes five genotypes whereas sub cluster A₂ consists of nine genotypes. Similarly Cluster B is subdivided into two sub clusters i.e., B₁ and B₂. Sub cluster B₁ consists of three genotypes, likewise sub cluster B₂ also included three genotypes.
11. The markers gwm102, Xgwm190 and Xgwm63 showed association with the character grain yield, markers Xgwm484, Xgwm11 and Xgwm293 showed association for the character grain filling duration, markers Xwmc48 and barc65 showed association with the character grain number and grain yield, marker Xgwm577 showed association with the character thousand grain weight and grain yield, marker barc186 showed association with the trait anthesis, under heat stress. These markers can be further used in marker assisted breeding.

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Appendices

Appendix-A

Weekly meteorological data recorded during the crop season (*Rabi* 2019-2020)

Season and Year	Month	Standard weeks	Temperature (°C)		Relative Humidity (%)		Bright Sunshine (hrs/day)	Rainfall (mm)
			Max.	Min.	Morn.	Even.		
Rabi 2019- 2020	October	40	32.7	23.3	76	63	5.6	80
		41	35.4	21.0	68	54	9.2	0
		42	36.5	21.5	72	55	9.0	0
		43	34.6	17.5	53	56	8.2	0
	November	44	34.7	18.3	60	67	5.3	14
		45	32.4	20.7	64	67	4.6	0
		46	31.4	18.4	61	64	7.7	5
		47	31.8	15.3	53	58	7.8	0
	December	48	29.9	17.4	56	54	7.7	0
		49	28.6	13.3	55	51	7.7	0
		50	27.1	9.5	49	42	8.4	4
		51	25.7	10.7	53	40	9.1	0
		52	25.8	6.9	48	26	8.6	0
	January	1	24.3	9.3	55	40	8.4	0.0
		2	24.0	8.0	52	38	6.9	0.0
		3	23.6	7.3	46	29	9.3	0.0
		4	27.8	10.4	47	28	9.8	0.0
	February	5	25.8	6.4	46	25	9.9	0.0
		6	27.6	8.4	52	28	10.2	0.0
		7	32.5	11.5	58	22	10.2	0.0
		8	35.3	12.1	62	20	9.9	0.0
		9	34.5	13.2	67	24	9.9	0.0
	March	10	32.1	13.0	68	42	9.7	0.0
		11	32.5	12.7	62	34	9.8	0.0
		12	35.5	16.9	66	36	6.8	0.0
		13	36.0	16.3	68	34	6.3	3.0
	April	14	42.1	20.0	63	22	9.5	0.0
		15	43.0	21.3	65	25	9.1	0.0
16		41.0	20.9	66	33	10.1	0.0	
17		41.4	23.8	73	38	10.6	0.0	
Source:	Agricultural Meteorology Department,Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar.							

CERTIFICATE

This is to certify that, I have no objection for supplying to any scientist only one copy or any part of thesis at a time through reprographic process, if necessary for rendering reference service in a library or documentation centre.

Place: Sardarkrushinagar
Date: 14, SEPTEMBER, 2021


(ANAND V.)