Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

By
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CERTIFICATE – I

This is to certify that this thesis entitled, **Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]** submitted for the degree of Master of Science in the subject of Genetics and Plant Breeding to the Chaudhary Charan Singh Haryana Agricultural University, Hisar, is a bonafide research work carried out by **Mr**. **Mohit Dhukia**, Admn. No. **2018A54M** under my supervision and that no part of the thesis has been submitted by him for any other degree.

All the assistance and help received during the course of investigation have been duly acknowledged.

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CERTIFICATE - II

This is to certify that this thesis entitled, **Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]** submitted by **Mohit Dhukia**, Admn. No. **2018A54M** to the Chaudhary Charan Singh Haryana Agricultural University, Hisar in partial fulfillment of the requirements for the degree of Master of Science in the subject of Genetics and Plant Breeding, has been approved by the Student's Advisory Committee after an oral examination on the same.

MAJOR ADVISOR **EXTERNAL EXAMINER**

HEAD OF DEPARTMENT

DEAN, POST-GRADUATE STUDIES

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Date:

Place: Hisar **Mohit Dhukia**

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LIST OF ABBREVIATION

%	:	Per cent
ANOVA	:	Analysis of Variance
Approx.	:	Approximately
cm	:	Centi meter (s)
C.V.	:	Coefficient of variation
DFY	:	Dry fodder yield per plant
et al.	:	*Et alia* = and others
etc.	:	and other things" or "and so on
g	:	Gram
GCV	:	Genotypic coefficient of variation
ha	:	Hectare
i.e.	:	*id.est* (that is)
Max	:	Maximum
Min	:	Minimum
No.	:	Number
PCV	:	Phenotypic coefficient of variation
per se	:	by or in itself
S. No.	:	Serial number
SCA	:	Specific combining ability
viz.	:	Namely

Non-renewable natural resources such as plant germplasm are very crucial for the sustenance of human life on this planet. Germplasm screening for desirable genes in different crop species is a regular task by plant breeders as they exploit the crop diversity as an immediate resource to use in developing new varieties and for reconstructing the existing genotypes in accordance with the necessities of time and space. Exploration of genetic relationships in crop species is the most key component of crop improvement programs as it serves to deliver information about genetic diversity available, which can be useful for various breeding applications.

Pearl millet [*Pennisetum glaucum* (L.) R. Br.], is an annual diploid (2n=2x=14) plant of the family *Poaceae* and is commonly known as Bajra, Cumbu, Cat tail millet and Bulrush millet in different fragments of the world. It is a C_4 monocot species and highly cross pollinated. Genome size is comparatively small with a DNA content of 1C=2.36 pg (Martel *et al*., 1997). It serves as an important forage and food crop in the drier semi-arid and arid regions of Asia and Africa. It stands at sixth most important position among cereals of the world after maize (*Zea mays* L.), rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), sorghum [*Sorghum bicolor* (L.) Moench] and barley (*Hordeum vulgare* L.).

Efficient utilization of soil moisture and higher level of heat tolerance than sorghum and maize makes it the most suitable and efficient crop for arid and semiarid conditions of our country. Rajasthan, Uttar Pradesh, Gujarat, Haryana, Maharashtra, Madhya Pradesh, Karnataka, Tamil Nadu, Andhra Pradesh, and Jammu & Kashmir are the major pearl millet cultivating states of India. Low cost of cultivation and low risk option marks this crop as necessity for farmers (Harinarayana, 1987). During the year 2018-19 in India, pearl millet was grown in an area of 6.8 million ha with production and productivity of 8.5 million tons and 1236 kg/ha, respectively. During the year 2018-19 in Haryana, area covered by crop was 0.42 million ha with production and productivity of 0.88 million tons and 2068 kg/ha, respectively (Anonymous, 2018-19).

Human diet must include optimum protein content with balanced amino acids, carbohydrate and other essential micronutrients which are present at higher levels in its grains, and its nutritive value is considered to be comparable to other cereal crops .Starch, fat, protein, calcium, iron and zinc are the key contents of this crop and it also serves as the staple food for poor families of Asian and African region. Vital role as a source of fodder in many regions of the world is played by pearl millet. India has the leading area under pearl millet cultivation with highest production as well among all the countries of Asian continent. Areas with low and erratic rainfall (200-600 mm), high temperature, high salinity or low pH and

impoverished infertile soils are usually covered with this crop. It is a hardy crop tolerant to harsh growing conditions and hence it can be easily propagated in the areas where other cereal crops, such as wheat, maize or rice would not endure. Occurrence of essential nutrients in enormous amount have made its production popular to larger extent such as, high protein and oil content, gluten free nature and richness in vitamin B (especially niacin, B6 and folic acid), calcium, potassium, magnesium *etc*. Pearl millet is furnished with huge amount of variability for micronutrients especially for grain Fe and Zn content (Anuradha *et al*., 2017).

Cytoplasmic male sterile line Tift 23A was first developed by Burton (1958). A new field for hybrid seed production in pearl millet was opened by this breakthrough. In 1965, first pearl millet hybrid HB-1 was released and afterward high number of promising hybrids have been developed and released for general cultivation by both public and private organizations in India. One must have adequate information about genetic distance and prepotency of parents in hybrid combinations before development of effective heterosis breeding programme in pearl millet. A study on genetic diversity among parental lines is essential in choosing appropriate parents because selection made exclusively on phenotypic performance may not lead to expected success in hybrid breeding programme.

Enormous phenotypic variability for traits such as flowering time, panicle length, grain and stover characteristics, tolerance to diseases, pests, and drought, as well as for the nutritional value is exhibited by cultivated pearl millet (Bhattacharjee *et al.,* 2007). Therefore, the first step in any crop improvement programme is the genetic variability estimation and identification of superior genotypes for further improvement.

The potential genetic gain through selection is chiefly affected by the genetic diversity in the germplasm. Classification of germplasm into heterotic groups with the help of information about genetic diversity is predominantly important to hybrid breeding programme. The genetic mechanisms to describe heterosis are not fully understood yet, even though it is well accepted that crosses between unrelated genetically distant parents, shows greater hybrid vigour than crosses between closely related parents of similar heterotic pool (Stuber, 1994 and Hallauer, 1999).

Meaningful facts and information about genetic variability among various inbred lines or genotypes are being usually estimated exclusively on the basis of morphological characters, but as these characters are affected by environmental factors, so their reliability can be improved using various other markers. Expression of various biochemical markers are least affected by environmental conditions. Therefore, they can be employed to improve the selection of superior genotypes among diverse germplasm. Now-a-days the utilization of various biochemical markers has been employed to assess the differences among the pearl millet genotypes because they directly evaluate the biochemical differences between germplasm lines. It is generally agreed that the maximum heterosis and the maximum chance

of isolating transgressive segregants are present due to crossing of the most genetically diverse parents. The present study was carried out to study the genetic variability present among A/B lines, R lines and hybrids of pearl millet developed at CCS Haryana Agricultural University, Hisar, Haryana.

In general, incidence of various diseases and pests affects the growth and productivity of pearl millet crop. Incidence of blast disease caused by *Pyricularia grisea* Sacc. (Teleomorph: *Magnaporthe grisea),* has increased at a considerable rate in the recent past, especially on the commercial hybrids in various states of India, which was once considered a minor disease of pearl millet (Thakur *et al*., 2009). The fungus becomes much more severe during humid weather conditions and can infect at all growth stages from seedling to adult plant, thereby reducing grain yield (Lukose *et al*., 2011). Even though the pathogen is highly variable in its nature, it is also highly specialized in its host range. As a result, *M. grisea* strains from rice or any other crops do not infect pearl millet and vice versa (Mehta *et al*., 1952). Therefore, to increase production and productivity of pearl millet, development of new variety/hybrid for blast resistance is of great significance.

The most feasible and economical means of managing this disease is to use the host plant resistance. For exploitation of various different sources in breeding programme, efforts should be made to identify large number of effective and stable resistant sources. Still, very little information is available on sources of resistance to this disease especially in CCS HAU pearl millet breeding material. Keeping these in view, the present study was carried out with the following major objectives:

1. To study extent of genetic variability for yield traits and blast in pearl millet genotypes
2. To estimate correlation and path coefficients among various traits in pearl millet genotypes

For pearl millet, productivity is the one of the most significant characters for higher production. Yield is a very complex trait which is controlled polygenically. Environmental factors also severely affect the expression of this trait to a greater extent. Numerous biometrical techniques are used on a regular basis by plant breeders to predict the genetic worth of a plant. For developing sound crop enhancement programmes, a profound understanding of the genetic diversity and the nature of association between yield and its components is essential. Even though several reports are available on genetic variability, correlation, heritability and path coefficient between grain yield and its attributing traits, still limited studies are available pertaining to stable germplasm lines which also show high resistance against blast disease as well.

A brief review of available evidence is presented in this section under the following sub heads on above revealed aspects in pearl millet.

1. Genetic variability
2. Correlation and path coefficient analysis
3. Screening studies

2.1 Genetic variability:

A vital role in the improvement of different crops is played by the genetic and phenotypic variability. Variability can be used efficiently to improve genotypes suitable for diverse climatic conditions, as it offers a great scope for natural and artificial selection among the germplasm available already with us. Thus, chances of improvement are relatively higher in the base material representing more genetic variability. Increasing the yield is the main objective in any crop enhancement programme, which depends majorly on the magnitude of genetic variability already present in the crop. To understand the genetic nature of yield and its different contributing components, estimation of genetic variability and its partitioning into various components is a prerequisite. The quantitative traits are majorly influenced by environment and governed by a large number of genes (Polygenes). It is essential to know the proportion of observed phenotypic variability that is heritable because the phenotype observed is not transmitted entirely to the next generation.

Govindaraj *et al*. (2011a) surveyed the local accessions of pearl millet in India. For all the characters examined namely; number of days to 50 percent flowering, plant height, panicle length, number of tillers, panicle girth, 1000 grain weight, days to maturity and grain yield/plant the phenotypic co-efficient of variation (PCV) was found higher than genotypic co-efficient of variation (GCV). Except for seed weight trait which had moderate heritability,

high heritability was witnessed for all the traits examined. For the character namely; number of productive tillers, high value of heritability and genetic advance were recorded.

Ghazymona *et al.* (2012) evaluated 13 selected genotypes and check cultivar of pearl millet to estimate heritability, genetic variability, and genetic advance for yield and its contributing components. For all the examined traits among all the genotypes, analysis of variance (ANOVA) manifested high significant difference. The genotypic coefficient of variation (GCV) was found relatively lower than the phenotypic coefficient of variation (PCV). It was cleared on the basis of results that significant positive correlation was present among most of examined characters and variations were present for various characters among all evaluated genotypes.

Subi and Idris (2013) evaluated 15 pearl millet genotypes for numerous growth and grain yield contributing characters to assess the magnitude of genetic variability, genetic advance and heritability in broad sense. On the basis of results of genetic advance and high estimates of heritability for the character *viz*., number of days to 50 % flowering and days to maturity, it was concluded that both these characters were under direct control of additive genes.

Vagadiya *et al*. (2013) studied heritability, genetic variability and genetic advance for grain yield and its nine other contributing factors among 64 genotypes including 48 F_1s along with 12 pollinators and four male sterile lines of pearl millet at Jamnagar, Gujarat. For the characters *viz*., grain yield/plant, ear head weight and fodder yield/plant, the variability analysis discovered high magnitude of phenotypic coefficient of variation, genotypic coefficient of variation, phenotypic range, heritability and genetic advance.

Singh *et al*. (2014) evaluated 55 pearl millet genotypes for estimation of variability among them. For several traits *viz*., dry fodder yield/plant, plant height, biological yield/plant and days to maturity broad range of variation was witnessed. Phenotypic variance value and genotypic variance value were closer for most of the characters studied, indicating little environment effect on the characters expression. For characters *viz*., panicle length, panicle girth, plant height, dry fodder yield/plant, biological yield/plant and test weight, the heritability coupled with genetic advance as percent over mean observed was high.

Kumar *et al*. (2014a) evaluated 97 genotypes of pearl millet for numerous traits namely; panicle diameter and panicle length, grain yield and plant height and estimated high heritability, genetic advance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). Estimated phenotypic and genotypic coefficients of variation were very high for grain yield character. For effective tillers trait, estimates of heritability ranged from 18.15 percent, while it exhibited 88.75 percent for grain yield. Traits *viz*., panicle length, panicle diameter, number of days to 50 per cent flowering, plant height and grain yield

shown high genetic advance as per cent of mean coupled with high heritability, indicating the importance of these traits in crop improvement and selection.

Kumar *et al*. (2014b) estimated genotypic and phenotypic coefficients of variation among 26 genotypes of pearl millet and were noted highest in dry fodder yield followed by grain yield, 1000-seed weight and productive tillers per plant. Range of estimated heritability in broad sense varied from 26% for plant population trait to 99% for 1000-seed weight trait, while grain yield character exhibited 75% heritability. Estimates of heritability coupled with genetic advance as per cent of mean for various traits *viz*., grain yield, 1000-seed weight, dry fodder yield, productive tillers per plant, ear length and plant height were from moderate to high.

Sabiel *et al*. (2014) recorded heritability (above 95 %) and high genotypic coefficient of variation for grain yield (kg/ha) followed by straw yield (kg/ha) among evaluated 12 genotypes of bajra in a semi-arid zone of El Fasher Research Station, Sudan under the rain-fed conditions. Both low genetic advance and heritability were expressed by the number of heads per plant character in both seasons. All the traits studied except number of heads per plant expressed highly significant differences among all the genotypes evaluated.

Bind *et al.* (2015) revealed wide spectrum of variation among evaluated 36 genotypes of fodder pearl millet [*Pennisetum glaucum* (L.) R. Br.] for several traits studied. Large difference between PCV and GCV was estimated for green fodder yield per plant trait among all the 11 characters studied, while the difference was less among characters *viz*., dry matter yield per plant, grain yield per plant and panicle length. They observed high genetic advance as per cent of mean coupled with high heritability among characters *viz*., dry matter yield per plant, grain yield per plant and panicle length and thus made conclusion about their control under additive gene effects.

Yadav *et al.* (2016) evaluated a set of 40 inbred lines to examine phenotypic and genotypic coefficient of variation based on 28 morphological traits (8 quantitative and 20 qualitative) and concluded that except for the panicle diameter which exhibited substantial amount of variation in the selected lines, mean squares of all the characters studied to be significant. High magnitude of heritability, PCV, GCV, and genetic advance as per cent of mean was exhibited by various characters *viz*., productive tillers, grain yield per plant and dry fodder yield per plant. The magnitude of phenotypic correlation coefficients was found lower than their corresponding correlation coefficients at genotypic level, which revealed strong inherent association of dry fodder yield per plant (g), plant height, 1000 grain weight, panicle length and productive tillers. Panicle length (cm), Dry fodder yield per plant (g), productive tillers and 1000 grain weight (g) had high direct effect towards grain yield per plant as per path coefficient analysis.

Kaushik *et al.* (2018) examined nine quantitative traits among a set of 48 maintainer lines to study presence of variation. Presence of sufficient variation in the lines was indicated by significant mean sum of squares. The PCV was slightly higher than GCV which directed the presence of slight influence on the expression of characters by environment. High heritability with high genetic advance as per cent of mean was exhibited by several traits *viz*., plant height (cm), 1000 grain weight (g), number of productive tillers per plant and grain yield per plant (g), indicating the prevalence of additive gene action. Thereby, selection based on these traits will be more effective.

Rasitha *et al.* (2019) studied genetic parameters and association studies for 11 quantitative characters among a set of 42 maintainers and 17 restorer lines. The influence of environment on the expression of traits was very low because the values of GCV were lower than PCV but in a narrow range only. For numerous characters namely; leaf blade length, leaf sheath length, spike length *etc*., the estimates of genetic advance as a percentage of mean coupled with heritability were observed very high indicating that these characters are directly controlled by additive gene action.

2.2 Correlation and path coefficient analysis:

Sankar *et al*. (2013) studied 13 quantitative characters for the investigation of genetic advance, phenotypic & genotypic variance, heritability, path analysis and correlation coefficients for yield and its contributing traits in pearl millet genotypes. For various characters *viz.*, spike girth (cm), 1000 seed weight (g), leaf blade width (cm) and grain yield per plant (g) highly significant and positive correlation was recorded, whereas significant negative correlation was estimated for characters namely; number of days to 50% flowering and days to maturity.

Kumar *et al*. (2014b) studied correlation among 26 genotypes of pearl millet, which revealed that several traits exhibited high and significant positive correlation with grain yield *viz*., plant height (cm), number of productive tillers per plant, dry fodder yield (g) and ear length (cm).

Kumar *et al.* (2015) evaluated 21 diverse populations of pearl millet to study trait association under rainfed conditions using several quantitative traits namely; plant height, days to 50 per cent flowering, dry fodder yield, number of effective tillers per plant, panicle length, panicle diameter and grain yield. Estimated genotypic correlations were found greater than the phenotypic correlations for almost all the characters according to the information revealed by correlation studies. Grain yield showed either negative (number of days to flowering) or positive (dry fodder yield & plant height) but highly significant association with all the traits studied.

Animasaun *et al.* (2017) in order to screen genotypes of superior traits based on morpho-agronomic characters, surveyed the genetic diversity among accessions of pearl

millet grown in both Nigeria & India, which could be promoted in future crop improvement programmes. Evaluations for both morphological and agronomic characters were performed among 24 accessions of Bajra. Among numerous traits *viz*., plant height, leaf length, leaf width and number of leaves, a highly significant positive correlation was suggested.

Kumawat *et al.* (2019) generated 50 single cross hybrids of pearl millet by crossing ten genetically diverse restorers with five male sterile lines and examined them to study character association and variability parameters. High correlation and variability were exhibited by several traits *viz*., number of effective tillers per plant, grain yield per plant, ear head diameter, ear head length and plant height. Hence, for developing improved cultivars of pearl millet in future breeding programmes these characters were found out to be of prime importance for selection of genotypes.

Summary on correlations between quantitative traits reported by selected works is presented in Table 2.1

Table 2.1: Summary on correlations between quantitative traits reported by selected works

Correlation between	Type	Reference(s)
Days to 50 per cent flowering & productive tillers per plant	Positive	Govindraj *et al.* (2009); Kumar *et al.* (2014a)
Days to 50 per cent flowering & plant height (cm)	Negative	Govindraj *et al.* (2009); Kumar *et al.* (2014b)
Days to 50 per cent flowering & 1000 grain weight (g)	Negative	Govindraj *et al.* (2009); Kumar *et al.* (2014b)
Days to 50 per cent flowering & ear length (cm)	Positive	Kumar *et al.* (2014a & 2014 b)
Days to 50 per cent flowering & ear girth (cm)	Positive	Kumar *et al.* (2014b)
Days to 50 per cent flowering & dry fodder yield (kg/plot)	Positive	Kumar *et al.* (2014b)
Days to 50 per cent flowering & grain yield (kg/plot)	Negative	Gupta & Dhillon (1974); Rao (1981)
Leaf width (mm) & grain yield (pounds)	Positive	Burton (1951); Pokhriyal *et al.* (1967)
Tiller number per plant & plant height (cm)	Positive	Kumar *et al.* (2014a); Abuali *et al.* (2012)
Number of productive tillers & panicle girth (cm)	Positive	Govindraj *et al.* (2009)
Productive tillers per plant & grain yield (g)	Positive	Gupta & Nanda (1971); Gupta & Sidhu (1972); Phul *et al.* (1974); Rao (1981); Bhamre & Harinarayana (1992); Abuali *et al* (2012); Singh *et al.* (1995)
Productive tillers per plant & panicle length (cm)	Positive	Govindraj *et al.* (2009)
Number of productive tillers & grain yield per plant (g)	Positive	Govindraj *et al.* (2009); Kumar *et al.* (2014b); Kumari & Nagarajan (2008)
Tiller number per plant & spike length (cm)	Positive	Abuali *et al.* (2012)

Correlation between	Type	Reference(s)
Plant height (cm) & dry fodder yield (kg/plot)	Positive	Kumar *et al.* (2014b)
Plant height (cm) & grain yield (kg/plot)	Positive	Gupta & Sidhu (1972); Gupta & Dhillon (1974); Rao (1981); Mukherji *et al.* (1981) Singh *et al.* (1995); Kumari & Nagarajan (2008)
Plant height (cm) & panicle length (cm)	Positive	Kumar *et al.*(2014a); Kumar *et al.* (2014b)
Plant height (cm) & productive tillers per plant	Positive	Abuali *et al.* (2012)
Plant height (cm) & 1000 grain weight (g)	Positive	Kumar *et al.* (2014b)
	Negative	Abuali *et al.* (2012)
Plant height (cm) & number of nodes	Positive	Kumar *et al.* (2014a)
Dry fodder yield (kg/plot) & grain yield (kg/plot)	Positive	Mahadevappa and Ponnaiya (1967); Patil *et al.* (1989)
Dry fodder yield (kg/plot) & grain yield per plant (g)	Positive	Kumar *et al.* (2014b); Bikash *et al.* (2013)
Panicle size (cm) & grain yield (g)	Positive	Bidinger *et al.* (1993); Bhamre and Harinarayana (1992); Kumar *et al.* (2014a); Govindaraj *et al.* (2009); Kumar *et al.* (2014b); Singh *et al.* (1995); Kumari & Nagarajan (2008); Mukherji *et al.* (1981); Bikash *et al.* (2013)
Panicle length (cm) & panicle girth (cm)	Positve	Govindraj *et al.* (2009); Kumar *et al.* (2014a)
Panicle length (cm) & number of nodes	Positive	Kumar *et al.* (2014a)
Panicle length (cm) & dry fodder yield (kg/plot)	Positive	Kumar *et al.* (2014b)
Panicle length (cm) & 1000 grain weight (g)	Positive	Govindraj *et al.* (2009); Kumar *et al.* (2014b)
Panicle girth (cm) & 1000 grain weight (g)	Positive	Kumar *et al.* (2014b)
1000 grain weight (g) & grain yield per plant (g)	Positive	Govindraj *et al.* (2009); Singh *et al.* (1995); Kumari and Nagarajan (2008); Mukherji *et al.* (1981)

2.3 Screening studies:

Thakur *et al.* (2009) screened 211 lines of hybrid parents to recognise resistance to the blast disease, made efforts to develop the greenhouse and field screening techniques and acknowledged 25 (8 B-, 3 R- and 14 R-lines) blast resistant lines (score $\leq$3.0 on 1–9 scale) under the condition of greenhouse screening technique . All the 25 lines which were blast resistant also exhibited downy mildew disease resistance when grown under the field conditions.

Gupta *et al.* (2012) screened two susceptible maintainer lines (ICMB 89111 and ICMB 95444) and two resistant restorer lines (ICMR 07555 and ICMR 06222) selected on

the basis of blast disease reaction to derive information regarding inheritance pattern of blast resistance. Resistance to foliar blast disease was discovered to be controlled by single dominant gene in pearl millet as per the information revealed by this study.

Sharma *et al.* (2013) evaluated 238 accessions from pearl millet mini-core to study pathogenic variations among blast disease pathogen and also identified several resistant sources under greenhouse screening technique conditions. Five different pathotypes of *M. grisea* isolates (Pg45, Pg53, Pg56, Pg118 and Pg119) were identified by this study.

Prakash *et al.* (2016) made attempts to standardize the phenotyping procedure for blast disease in pearl millet and further screened three resistant entries namely; PPMI 660, PPMI 1087 and PPMI 1089 from the evaluated 15 inbred lines of pearl millet. For screening of lines on large-scale against the pathogen, these procedures were found very useful.

Singh *et al.* (2018) generated various populations *viz*., F_1s, F_2s and backcrosses by crossing two susceptible genotypes namely; ICMB 89111 and ICMB 95444 with six genotypes of pearl millet resistant to blast disease *viz.*, ICMB 11003, ICMB 06222, ICMR 06444, ICMR 97222, ICMR 93333 and IP 21187-P1 to study inheritance of blast disease. The screening of various F_1, F_2 and backcross generations was performed in a glasshouse against two isolates of *M. grisea* (Pg 45 & Pg 53) and the study revealed that the disease is governed by a single dominant gene in the resistant genotypes.

Sharma *et al.* (2019) surveyed 305 accessions of a pearl millet wild relative, *Pennisetum violaceum* to identify diverse sources of blast and rust resistance under the conditions of greenhouse. One local isolate of *P. substriata* var. *indica* and five *M. grisea* pathotype-isolates were used to screen these accessions and 17 accessions were screened resistant (score ≤ 3.0) to all the five pathotype-isolates. To introgress various resistance genes from wild lines into the potential parental lines of cultivated hybrids of pearl millet, some of the blast resistant genetic stocks are being currently utilized in breeding program at ICRISAT.

The adopted techniques, materials used and details of experimental site for the proposed investigation entitled "**Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**" are presented here below in detail in this chapter.

3.1 Experimental site and conditions:

The field experiment for the proposed investigation was conducted in research area of Bajra Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. It is present at 29^0-10^0N latitude and 750-46^0E longitude with 215.52 meter elevation above mean sea level and soil characteristic sandy-loam in nature. It is localised in semi-arid sub-tropical region which is present on the outer margins of the south-west (SW) monsoon region and has tropical monsoonal climate with average annual rainfall of around 452 mm.

3.2 Experimental material:

In the present investigation, 100 pearl millet genotypes (comprising of designated A/B lines, R lines and hybrids) were evaluated during *kharif* (Rainy) season 2019.

Table 3.1: Details of designated pearl millet lines evaluated in the present investigation:

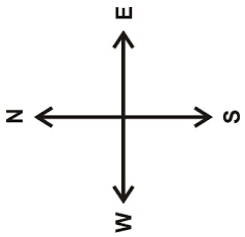
Sr. No.	Genotypes	Sr. No.	Genotypes
1	ICMB 02333	**51**	A5RLT-14/106
2	ICMB 04888	**52**	AC 04/13
3	HMS 13B	**53**	DMBRL-15/102
4	HMS 14B	**54**	EBL-12-237
5	HMS 16B	**55**	EMRLT-14/103
6	HMS 18B	**56**	EMRLT-14/105
7	HMS 26B	**57**	EMRLT-14/107
8	HMS 28B	**58**	EMRLT-14/111
9	HMS 29B	**59**	EMRLT-14/121
10	HMS 30B	**60**	EMRLT-14/123
11	HMS 32B	**61**	EMRLT-14/124
12	HMS 33B	**62**	EMRLT-14/127
13	HMS 34B	**63**	EMRLT-14/229
14	HMS 36B	**64**	EMRLT-14/237
15	HMS 37B	**65**	EMRLT-14/243
16	HMS 38B	**66**	EMRLT-15/109
17	HMS 39B	**67**	EMRLT-15/133
18	HMS 40B	**68**	G73-107
19	HMS 41B	**69**	H13/0001
20	HMS 43B	**70**	H14/003
21	HMS 44B	**71**	H77/29-2
22	HMS 45B	**72**	H77/833-2

Sr. No.	Genotypes	Sr. No.	Genotypes
23	HMS 47B	**73**	H77/833-2-202
24	HMS 48B	**74**	H90/4-5
25	HMS 49B	**75**	HB-15/085
26	HMS 50B	**76**	HBL 11
27	HMS 52B	**77**	HHB 197
28	HMS 53B	**78**	HHB 216
29	HMS 54B	**79**	HHB 223
30	HMS 55B	**80**	HHB 226
31	HMS 56B	**81**	HHB 234
32	HMS 57B	**82**	HHB 272
33	HMS 58B	**83**	HHB 299
34	HMS 59B	**84**	HHB 311
35	HMS 60B	**85**	HHB67 IMP
36	HMS 62B	**86**	HPT-2-12-32
37	HMS 63B	**87**	HTP 03/13
38	HMS 64B	**88**	HTP 94/54
39	HMS 65B	**89**	HTP-10-129
40	HMS 66B	**90**	IH 8
41	HMS 68B	**91**	LTRL 15/123
42	HMS 69B	**92**	PRLT 101
43	HMS 6B	**93**	PRLT-107
44	HMS 70B	**94**	PRLT-121
45	HMS 74B	**95**	PRLT-124
46	HMS 75B	**96**	PRLT-132
47	HMS 7B	**97**	PRLT-134
48	ICMB 843-22	**98**	PT-1-1047
49	ICMB 94555	**99**	SGP-10-107
50	ICMB 97111	**100**	TCP-10-110

3.3 Experimental design and layout plan:

- Plant Material : 100 pearl millet genotypes (comprising of designated A/B lines, R lines and hybrids)
- Experimental design : Randomized Block Design
- Replications : Two
- Number of rows per genotype : One
- Row length : 4 m
- Row to row distance : 0.45 m
- Plant to plant distance : 10-12 cm
- Season : *kharif* (Rainy) 2019
- Location : Research Area of Bajra Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar

Fig. 3.1: Layout of the experiment during *kharif* (Rainy) 2019:



REP 2	NE Filler (Ac 04/13)	PLOT NO 269 → PLOT NO 300	2 NE Filler (Ac 04/13)	NE Filler (Ac 04/13)
		PLOT NO 268 ← PLOT NO 235		
		PLOT NO 201 → PLOT NO 234		
REP 1		PLOT NO 169 → PLOT NO 200	2 NE Filler (Ac 04/13)	
		PLOT NO 168 ← PLOT NO 135		
		PLOT NO 101 → PLOT NO 134		
		FIELD NUMBER 58/3		
→	→	→	→	

3.4 Observation of traits under proposed investigation:

The observations for all the parameters were logged on five randomly selected competitive plants from each row.

3.4.1. Days to 50 per cent flowering

It was noted by counting the number of days from the date of sowing to the date when 50 per cent of the plants in each row came to blossoming in each replication.

3.4.2. Panicle length (cm):

Panicle length (PL) was estimated in centimeter from the tip to base of the panicle of main tiller of plant in five representative plants in each row.

3.4.3. Panicle diameter (cm):

Measure of diameter of panicle was recorded at the point slightly below from center of panicle in centimeter using Vernier caliper instrument.

3.4.4. Productive tillers (number per plant):

Number of productive tillers per plant of five randomly selected competitive plants from each row was noted only from ear head bearing tillers.

3.4.5. Plant height (cm):

Plant height was recorded in centimeter from tip of the panicle to the ground level from five representative plants in each row.

3.4.6. Grain yield/plant (g):

Grains of each plant threshed from panicles of productive tillers were recorded in grams as grain yield per plant.

3.4.7. Dry fodder yield/plant (g):

The plants from each row were first harvested & sun dried and then the weight of plants was recorded in grams.

3.4.8. 1000-seed weight (g):

Well-developed 1000 grains were counted and weight recorded from panicles harvested from productive tillers of five randomly selected plants.

3.4.9. Screening and scoring for the severity of blast reaction:

A total 100 pearl millet genotypes (comprising of designated A/B lines, R lines and hybrids) were screened under natural field condition at Research Area of Bajra Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The severity of blast disease was recorded on the 1-9 progressive scale developed for rice blast at International Rice Research Institute (IRRI) on five representative plants in each row of all the genotype. The disease severity rating scale was modified to classify plants/lines into different classes of blast disease.

Table 3.2: Rating scale (1-9) for foliar blast severity:

Rating Scale	Symptoms and lesions	Disease reaction
1	no lesion to small brown specks of pinhead size	Highly resistant
2	large brown specks	Resistant
3	small, roundish to slightly elongated, necrotic gray spots, about 1-2 mm in diameter with a brown margin	
4	typical blast lesions, elliptical, 1-2 cm long, usually confined to the area between main veins, covering <2% of the leaf area	Moderately resistant
5	typical blast lesions covering <10% of the leaf area	
6	typical blast lesions covering 10-25% of the leaf area	Susceptible
7	typical blast lesions covering 26-50% of the leaf area	
8	typical blast lesions covering 51-75% of the leaf area and many leaves dead	Highly susceptible
9	>75% leaf area covered with lesions and most leaves dead	

3.5 Statistical analysis:

The mean data recorded on the different quantitative characters were subjected to various statistical procedures:

3.5.1 Analysis of variance:

Analysis of variance (ANOVA) for the recorded observations on different traits was carried out. The model adopted for the variance analysis of various traits was:

$$\mathbf{Y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}}$$

Where,

$\mathbf{Y_{ij}}$ = Observation of i^{th} treatment and j^{th} block

$\boldsymbol{\mu}$ = General mean

$\boldsymbol{\alpha_i}$ = i^{th} treatment effect

$\boldsymbol{\beta_j}$ = j^{th} block effect

$\mathbf{e_{ij}}$ = random error associated with the i^{th} treatment and j^{th} block

The assumptions of the model are as follows:

a) All the observations should be independent.

b) The different effects in the model should be additive.

c) Error involved in the population should be distributed normally and independently with mean zero and variance.

Table 3.3: Analysis of variance (ANOVA)

Source of variation (S.V)	**Degree of freedom (d.f)**	**Sum of Square (SS)**	**Mean sum of Square (MS)**	**Expected mean square (EMS)**	**F-calculated**
Replication	(r-1)	SSr	MSr	$\sigma^2e+g\ \sigma^2r$	MSr/ MSe
Genotype	(g-1)	SSg	MSg	$r\sigma^2g + \sigma^2e$	MSg/ MSe
Error	(r-1) (g-1)	SSe	MSe		
Total	gr-1				

Where,

r = Number of replications

g = Number of treatments (genotypes)

MSr = Mean sum of squares due to replications

MSg = Mean sum of squares due to genotypes

MSe = Mean sum of squares due to error

$\boldsymbol{\sigma^2g}$ = Genotypic variance of character Xi

$\boldsymbol{\sigma^2r}$ = Variance due to replications

$\boldsymbol{\sigma^2e}$ = Error variance of character Xi

The genotypic and phenotypic variances were calculated by adopting the following formulae:

Genotypic variance $\boldsymbol{(\sigma^2g)} = \frac{\mathbf{MSg-MSe}}{\mathbf{r}}$

Phenotypic variance $\boldsymbol{(\sigma^2p) = \sigma^2g + \sigma^2e}$

Parameters of ANOVA

i) Mean

Mean was worked out by dividing total sum of all the values by number of corresponding observations.

$$\overline{X} = \frac{1}{n}\sum_{i=1}^{n} X_i$$

Where,

$\bar{X}$ = Simple mean

X_i = Individual value

n = Number of observations

ii) Standard Error of difference SE $_{(d)}$

Standard error of difference for two means was calculated with the help of error mean square from ANOVA table

$$S.E._{(d)} \pm = \sqrt{\frac{2MSe}{r}}$$

Where.

MSe = Error mean square

SE = Standard error

r = number of replications

iii) Critical difference

Critical difference was calculated to compare the means of various genotypes. It was calculated with the help of standard error of difference and t value at error degree of freedom at 1% and 5% level of significance

CD = SE $_{(d)}$ × t (1% & 5%) error degree of freedom

iv) Range

Range for each character was worked out by depicting the lowest and highest values.

v) Coefficient of variation (C.V.)

For comparing the magnitude of variance among different traits the coefficient of variation is suitable as it is a standardized form and it was computed according to Burton and Devane (1953).

Genotypic coefficient of variability **(GCV %)** = $\frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$

Phenotypic coefficient of variation **(PCV %)** = $\frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$

Where,

$\bar{X}$ = General mean of the particular character

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The phenotypic and genotypic coefficients of variation were categorized as proposed by Sivasubramanian and Menon (1973):

0-10%= Low **10-20% = Moderate** **>20% = High**

vi) Heritaility

Calculation of heritability in broad sense was done as the ratio of genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 g$) and was expressed in the form of percentage (Hanson *et al.,* 1956):

$$\text{Heritability } h^2 \text{ (bs)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The calculated heritability was categorized majorly into three groups:

0-30% = Low **30-60% = Moderate** **>60% = High**

vii) Expected genetic advance (GA)

Genetic advance was worked out by adopting the following formula given by Johanson *et al.* (1955):

$$\text{Genetic advance (GA)} = k \times h^2(bs) \times \sigma^2 p$$

Where,

$h^2(bs)$ = Heritability in broad sense

k = Selection differential (= 2.06) at 5% intensity of selection

$\sigma^2 p$ = Phenotypic standard deviation

viii) Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean for each character was worked out by the following formula:

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

Where,

GA = Genetic advance

$\bar{X}$ = General mean

The genetic advance as per cent of mean was categorized below as:

0-10% = Low **10-20% = Moderate** **>20 % = High**

ix) Correlation coefficient analysis

To determine the degree of association of various characters among the yield components and with yield itself also, the correlation coefficients were worked out.

Both phenotypic and genotypic coefficients of correlation between two characters were determined as suggested by Al-Joubri *et al.* (1958).

$$r_g(x,y) = \frac{cov_g(x,y)}{\sqrt{\sigma_g^2(x)+\sigma_g^2(y)}} \qquad r_p(x,y) = \frac{cov_p(x,y)}{\sqrt{\sigma_p^2(x)+\sigma_p^2(y)}}$$

Where,

r_g (xy) and **r_p (xy)** are the genotypic and phenotypic correlation coefficients, respectively.

Cov_g and Cov_p are the genotypic and phenotypic covariance of x and y, respectively.

$\sigma^2 g$ and **$\sigma^2 p$** are the genotypic and phenotypic variance of **x** (independent trait) and **y** (dependent trait) respectively.

The calculated value of **'r'** was compared with table **'r'** value with (**n-2)** degrees of freedom at **5%** and **1%** level of significance, where, n refers to number of pairs of observation.

x) Path coefficient analysis

Path coefficient analysis was carried out using genotypic correlation values of yield components on yield as suggested by Wright (1921) and further illustrated by Dewey and Lu (1959). Standard path coefficients, which are the standardized partial regression coefficients, were calculated. These values were obtained by solving the following set of 'p' simultaneous equation using above package.

$$P_{01} + P_{02}\, r_{12} + \text{----------} + P_{0P}\, r_{1P} = r_{01}$$

$$P_{01} + P_{12}\, r_{02} + \text{----------} + P_{0P}\, r_{2P} = r_{02}$$

$$\downarrow$$

$$P_{01} + r_{1P} + P_{02}\, r_{2P} + \text{----------} + P_{0P} = r_{0P}$$

Where,

P_{01}, P_{02}, ---------- P_{0P} are the direct effects of variables **1,2,--------p** on the dependent variable **0** and r_{12}, r_{13}, ----------r_{1P}--------- $r_{P(P-1)}$ are the possible correlation coefficients between various independent variables and r_{01}, r_{02}, r_{03} ---- r_{0P} are the correlation between dependent and independent variables.

The indirect effects of the i^{th} variable *via* j^{th} variable are attained as $(P_{oj}x\ r_{ij})$. The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below:

$$P^2_{ox} = 1 - [P^2_{01} + 2P_{01}\, P_{02}\, r_{12} + 2P_{01}\, P_{03}\, r_{13} + \text{----------} + P^2_{02} + 2P_{02}\, P_{03}\, r_{13} + \text{--------} + P^2_{0P}]$$

$$\textbf{Residual factor} = \sqrt{(P^2_{ox})}$$

The present research investigation was undertaken to study extent of genetic variability for yield traits and blast among 100 pearl millet genotypes. The genotypes comprised of 50 designated B lines, 41 R lines and nine hybrids. During *kharif* (Rainy) season, 2019, these lines of pearl millet were evaluated in a randomized block design with two replications in a single row of 4 m length for each line at research area of Bajra Section, CCS Haryana Agricultural University, Hisar.

The observations recorded and statistically computed results obtained for various parameters are presented under following heads:

4.1) Parameters of genetic variation

4.2) Correlation coefficient analysis

4.3) Path coefficient analysis

4.4) Screening studies

4.1) PARAMETERS OF GENETIC VARIATION

The presence of adequate genetic variability quantum in the population is the foremost key point in success of any breeding programme. Selection of desired inbred line requires the presence of wide range of variability. In addition to the knowledge of genetic variability quantum, knowing heritability and genetic advance helps the worker to achieve the objective rapidly by selecting the appropriate breeding strategy. Hence, necessary knowledge of available variability in genetic material is required for successful improvement of any crop.

4.1.1 Analysis of variance (ANOVA)

Mean sum of squares were highly significant due to genotypes for all the characters studied which clearly indicated the occurrence of sufficient genetic variability in the genotypes chosen for the investigation. In contrast, the mean squares were non-significant due to replications for all the traits. The fitness of all the characters under study for further statistical analysis was expressed by the significant mean sum of squares and the analysis of variance for all the characters studied is presented in Table 4.1.

4.1.2 Mean, Range, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability and Genetic Advance as per cent of mean

The mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as per cent of mean (GAM) of different genotypes included in the study for various characters have been computed and tabulated in Table 4.4 and brief description for them is given as under:

4.1.2.1 Days to 50% flowering

Mean value of number of days to flowering was 45±1days ranging from 37 to 59 days. Both PCV (9.0%) and GCV (8.8%) estimate were found low. The hybrid (HHB 272) flowered earliest (37 days), while the R line (TCP-10-110) flowered late at 59 days. High heritability (95.9%) with moderate genetic advance as per cent of mean (17.8%) was recorded for this trait (Table 4.4).

4.1.2.2 Plant height (cm)

Plant height for various lines ranged from 85.8 cm to 229.8 cm with a mean value of 154.9±7.7 cm. This observed variation might be due to variability present in the germplasm lines chosen for investigation. HTP 94/54 recorded the maximum height of 229.8 cm and the minimum plant height was recorded by line ICMB 04888 (85.8 cm). Both PCV (22.4%) and GCV (21.3%) estimate were found high for this trait. High heritability (90.1%) with high genetic advance as per cent of mean (41.6%) was observed, clearly enlightening the role of additive gene action for this trait (Table 4.4).

4.1.2.3 Productive tillers per plant (no. /plant)

Productive tillers per plant ranged from 1.3 to 3.7 with general mean value of 2.5±0.4. The line HPT-2-12-32 showed minimum number of productive tillers (1.3) and lines HMS 60B and HBL 11 showed the maximum number of productive tillers (3.7). While the GCV estimate was found moderate (17.7%), the PCV was computed high (28.1%), clearly indicating the high influence of environment on this trait. Moderate heritability (39.8%) with high genetic advance as per cent of mean (23%) was observed for this trait, which indicated unsuitability of exploitation of this trait through simple selection procedures (Table 4.4).

4.1.2.4 Panicle length (cm)

The range estimates for this trait varied from 11.9 cm to 33.2 cm with a mean value of 19.4±0.8. The lines HMS 26B showed the minimum panicle length (11.9 cm) whereas maximum panicle length was recorded by the line HTP 94/54 (33.20 cm). Both GCV (16.8%) and PCV (17.8%) were computed moderate for this trait. High heritability (88.4%) with high genetic advance as per cent of mean (32.5%) was observed for this trait which indicated the presence of additive gene action effects (Table 4.4).

4.1.2.5 Panicle diameter (cm)

Mean value of panicle diameter was computed 2.45±0.1cm ranging from 1.29 cm to 3.84 cm. The HHB 311 recorded maximum panicle girth (3.84 cm) while the line HMS 18B recorded minimum panicle girth (1.29 cm). Both the PCV (22.1%) and GCV (21.1%) were computed high for this trait. High heritability (90.9%) with high genetic advance as per cent of mean (41.4%) was perceived for this trait which shown the importance of additive gene effects regarding the selection of this trait (Table 4.4).

4.1.2.6 1000-seed weight (g)

1000-seed weight for various lines ranged from 2.61 g to 16.02 g with a mean value of 7.28±0.6 g. The minimum value recorded by line HPT-2-12-32 was 2.61 g, while the max weight was recorded by the line HB-15/085 (16.02 g). High GCV and PCV estimates were computed (26.8% & 29% respectively). High heritability (85.6%) as well as high genetic advance as per cent of mean (51%) was exhibited by the trait, which further indicated the significance of additive gene effects in further improvement of this trait (Table 4.4).

4.1.2.7 Grain yield per plant (g)

Significant variation from 1.4 g to 53 g with the mean value of 20.8±2.2 g was exhibited by the trait. The R line HPT-2-12-32 showed the minimum grain yield of 1.4 g while the maximum grain yield per plant of 53 g was recorded by the hybrid HHB 311. Both computed PCV (56.7%) and GCV (54.7%) estimates were high for this trait. High heritability (93.1%) as well as high genetic advance as per cent of mean (108.7%) was exhibited by the trait, which further revealed the preponderance of additive gene action (Table 4.4).

4.1.2.8 Dry Fodder Yield per Plant (g)

The trait exhibited a wide range from 15.4 g to 142 g with the mean value of 48.3±2.8 g. The hybrid (HHB 299) showed maximum dry fodder weight of 142 g, while the designated R line (HPT-2-12-32) recorded the minimum dry fodder weight of 15.4 g. Both computed PCV (51.1%) and GCV (50.4%) estimates were high for this trait. High heritability (97.4%) as well as high genetic advance as per cent of mean (102.5%) was exhibited by the trait, which shows the dominance of additive gene effects in the inheritance of the trait (Table 4.4).

Table 4.1 Analysis of Variance (ANOVA) for morphological characters in pearl millet germplasm lines

	Mean sum of squares				
Source of variation (SV)	**Degree of freedom (df)**	**Days to 50% Flowering**	**Plant Height (cm)**	**Panicle Length (cm)**	**Panicle Diam. (cm)**
Replication	1	0.41	1.07	1.07	0.13
Treatment	99	32.10**	2292.43**	22.57**	0.56**
Error	99	0.67	119.55	1.39	0.02

	Mean sum of squares				
Source of variation (SV)	**Degree of freedom (df)**	**Prod. Tillers (No./Plant)**	**Grain Yield/Plant (g)**	**Dry Fodder Yield/Plant (g)**	**1000-seed weight (g)**
Replication	1	1.69	33.70	34.36	0.31
Treatment	99	0.68**	269.27**	1199.71**	8.24**
Error	99	0.29	9.63	15.99	0.64

* Significant at p= 0.05, ** Significant at p= 0.01

Table 4.2 Mean values for morphological characters in pearl millet germplasm lines

S. No.	Germplasm lines	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diameter (cm)	Productive Tillers (No./Plant)	Grain Yield/Plant (g)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)
1	**ICMB 02333**	41	146.7	13.5	3.20	2.0	30.1	84.6	7.51
2	**ICMB 04888**	45	85.8	14.9	2.80	1.7	13.0	22.5	9.72
3	**HMS 13B**	46	164.4	19.9	2.18	2.7	25.2	58.7	9.01
4	**HMS 14B**	43	112.7	25.1	2.22	3.0	10.8	21.3	5.91
5	**HMS 16B**	46	131.6	17.5	1.74	3.4	6.8	25.8	5.86
6	**HMS 18B**	42	147.8	20.1	1.29	2.3	4.2	16.2	4.32
7	**HMS 26B**	45	121.2	11.9	1.89	2.9	14.9	27.4	6.54
8	**HMS 28B**	44	157.9	17.1	1.93	3.1	12.9	36.4	6.52
9	**HMS 29B**	42	163.0	22.4	1.89	2.7	23.3	49.3	7.48
10	**HMS 30B**	50	145.0	14.4	2.16	2.9	21.3	53.3	5.96
11	**HMS 32B**	50	102.4	16.9	1.92	2.0	9.3	26.3	4.03
12	**HMS 33B**	42	115.9	19.0	1.52	3.3	9.4	22.4	8.61
13	**HMS 34B**	46	110.1	20.5	2.14	3.1	5.1	16.6	3.59
14	**HMS 36B**	40	96.9	15.4	1.93	3.5	6.6	23.6	7.84
15	**HMS 37B**	45	135.7	17.3	1.73	2.4	10.4	29.4	2.94
16	**HMS 38B**	45	123.2	17.4	2.08	2.9	5.6	21.1	5.40
17	**HMS 39B**	40	94.0	17.2	1.92	3.1	8.2	24.7	8.45
18	**HMS 40B**	44	137.6	17.7	2.24	2.2	11.2	25.2	6.22
19	**HMS 41B**	45	115.5	16.6	2.15	2.8	8.9	20.4	6.12
20	**HMS 43B**	42	163.4	19.4	2.50	2.8	17.6	39.6	7.20
21	**HMS 44B**	42	161.6	18.6	2.32	2.6	22.8	42.3	7.79

Continue……..

S. No.	Germplasm lines	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diameter (cm)	Productive Tillers (No./Plant)	Grain Yield/Plant (g)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)
22	**HMS 45B**	43	149.2	16.6	2.49	2.4	12.8	29.3	8.46
23	**HMS 47B**	44	167.7	15.8	3.02	2.2	23.4	56.4	9.22
24	**HMS 48B**	43	157.1	18.8	2.53	1.6	17.8	40.3	9.76
25	**HMS 49B**	45	141.7	18.3	2.44	2.5	24.6	56.6	7.61
26	**HMS 50B**	44	180.3	18.9	2.44	2.9	13.4	24.4	6.58
27	**HMS 52B**	52	139.3	21.4	2.17	3.1	24.5	61.5	8.75
28	**HMS 53B**	46	140.8	20.2	2.61	2.1	11.3	29.8	7.06
29	**HMS 54B**	51	123.4	22.4	1.90	2.6	10.4	24.4	6.78
30	**HMS 55B**	46	91.7	16.0	2.55	2.3	7.0	23.5	3.92
31	**HMS 56B**	53	138.5	25.4	2.18	2.1	13.4	33.4	7.08
32	**HMS 57B**	45	110.8	18.2	1.88	2.5	4.6	16.1	4.74
33	**HMS 58B**	49	116.1	20.6	1.72	2.6	7.2	22.7	4.54
34	**HMS 59B**	45	112.8	18.3	2.41	3.1	15.0	36.5	6.11
35	**HMS 60B**	44	140.0	19.4	2.54	3.8	33.3	79.3	7.75
36	**HMS 62B**	48	103.5	19.1	3.27	1.7	13.6	29.6	9.94
37	**HMS 63B**	45	120.4	21.6	2.22	3.2	17.4	43.4	7.81
38	**HMS 64B**	50	177.9	17.1	2.35	3.1	16.2	38.2	3.53
39	**HMS 65B**	44	131.2	16.3	2.40	3.0	19.6	44.6	5.72
40	**HMS 66B**	46	161.2	21.6	1.79	2.9	15.0	30.5	5.60
41	**HMS 68B**	46	99.2	16.4	2.08	3.4	11.4	26.4	8.01
42	**HMS 69B**	41	121.7	16.8	2.00	2.6	13.0	28.5	7.23

Continue……..

S. No.	Germplasm lines	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diameter (cm)	Productive Tillers (No./Plant)	Grain Yield/Plant (g)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)
43	**HMS 6B**	45	132.2	21.4	2.32	2.3	24.5	63.5	10.53
44	**HMS 70B**	51	125.2	18.2	2.20	2.1	10.6	40.6	6.13
45	**HMS 74B**	50	134.1	25.6	2.68	2.2	23.4	49.4	6.47
46	**HMS 75B**	54	92.5	16.9	3.36	2.2	13.6	33.6	8.01
47	**HMS 7B**	46	135.0	22.6	1.70	2.8	10.2	25.2	4.24
48	**ICMB 843-22**	43	132.4	16.9	2.23	3.0	11.6	29.6	8.02
49	**ICMB 94555**	48	115.9	20.1	2.28	2.1	8.8	30.3	7.30
50	**ICMB 97111**	45	167.2	18.6	2.45	1.7	20.2	44.2	8.01
51	**A5RLT-14/106**	56	195.3	24.2	2.62	1.7	9.4	24.5	7.66
52	**AC 04/13**	42	140.4	19.9	2.11	2.5	12.8	26.3	4.87
53	**DMBRL-15/102**	45	185.8	18.3	2.47	2.0	18.6	48.6	7.14
54	**EBL-12-237**	45	189.5	20.9	2.93	1.8	41.7	78.7	11.33
55	**EMRLT-14/103**	46	182.1	21.3	3.62	1.9	26.6	50.6	9.06
56	**EMRLT-14/105**	46	197.5	25.3	2.07	2.3	26.2	45.2	5.32
57	**EMRLT-14/107**	42	224.2	24.4	2.67	2.0	15.8	31.3	7.53
58	**EMRLT-14/111**	44	215.5	20.5	2.95	1.9	42.0	80.0	7.00
59	**EMRLT-14/121**	45	185.8	20.7	3.08	3.1	44.5	83.5	7.03
60	**EMRLT-14/123**	43	168.7	18.9	2.18	1.9	23.6	49.6	8.04
61	**EMRLT-14/124**	48	178.6	19.4	3.72	1.5	29.2	82.2	8.78
62	**EMRLT-14/127**	43	204.7	24.1	2.62	2.1	39.3	74.3	8.83
63	**EMRLT-14/229**	45	177.9	16.7	2.79	2.2	23.5	58.5	7.61

Continue……..

S. No.	Germplasm lines	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diameter (cm)	Productive Tillers (No./Plant)	Grain Yield/Plant (g)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)
64	**EMRLT-14/237**	42	180.9	21.9	3.49	2.1	43.8	82.3	7.55
65	**EMRLT-14/243**	44	161.6	19.9	2.02	1.8	25.8	57.3	8.54
66	**EMRLT-15/109**	41	151.9	22.3	2.13	2.6	16.0	40.0	6.20
67	**EMRLT-15/133**	43	179.0	20.9	3.01	1.9	30.4	83.4	9.88
68	**G73-107**	50	155.3	19.1	2.12	3.0	29.6	81.6	8.91
69	**H13/0001**	52	137.2	20.8	2.84	2.2	15.2	48.2	5.15
70	**H14/003**	57	143.6	18.4	2.93	1.3	17.3	43.8	10.32
71	**H77/29-2**	43	159.7	17.5	1.84	2.7	19.1	49.1	4.89
72	**H77/833-2**	42	159.7	16.5	1.45	3.1	15.8	49.3	5.00
73	**H77/833-2-202**	42	167.1	17.2	1.51	3.1	16.8	42.3	4.55
74	**H90/4-5**	45	159.0	19.2	2.23	3.6	21.2	53.2	6.98
75	**HB-15/085**	45	167.9	15.0	3.46	1.5	18.2	48.7	16.02
76	**HBL 11**	43	133.9	16.3	1.99	3.7	22.4	39.4	6.17
77	**HHB 197**	40	188.5	20.9	2.73	2.1	27.1	83.1	9.71
78	**HHB 216**	42	207.1	21.2	2.69	2.1	37.5	97.5	7.22
79	**HHB 223**	42	206.7	22.9	2.68	3.0	50.4	113.4	8.02
80	**HHB 226**	40	186.3	19.7	2.54	3.4	51.7	82.2	7.51
81	**HHB 234**	41	213.2	25.1	2.08	2.8	32.2	55.2	6.22
82	**HHB 272**	37	184.1	20.0	2.69	3.0	32.6	68.1	8.51
83	**HHB 299**	42	190.2	23.3	3.41	2.2	49.0	142.0	10.69
84	**HHB 311**	43	202.5	26.8	3.84	1.6	53.0	121.5	8.57

Continue……..

S. No.	Germplasm lines	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diameter (cm)	Productive Tillers (No./Plant)	Grain Yield/Plant (g)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)
85	**HHB67 IMP**	38	190.0	20.8	2.24	3.6	27.8	47.3	7.64
86	**HPT-2-12-32**	44	141.1	16.6	3.04	1.3	1.4	15.4	2.61
87	**HTP 03/13**	46	190.0	18.6	2.47	2.7	41.2	77.2	7.81
88	**HTP 94/54**	49	229.8	33.2	2.40	1.5	22.0	61.5	10.85
89	**HTP-10-129**	43	127.3	13.5	3.19	1.8	17.4	43.4	6.64
90	**IH 8**	44	139.0	16.6	2.50	2.5	26.5	50.5	6.70
91	**LTRL 15/123**	44	194.3	25.1	2.61	2.6	33.6	79.9	6.06
92	**PRLT 101**	54	190.3	16.2	2.51	1.8	21.0	52.5	7.50
93	**PRLT-107**	44	229.4	25.4	2.60	2.7	38.4	71.4	8.93
94	**PRLT-121**	43	181.8	20.7	3.26	2.5	33.4	79.2	9.79
95	**PRLT-124**	49	151.3	18.7	2.63	1.7	14.6	27.1	8.24
96	**PRLT-132**	43	195.8	20.2	2.85	2.3	26.6	50.6	9.27
97	**PRLT-134**	52	161.5	14.2	2.95	2.5	17.9	44.4	8.70
98	**PT-1-1047**	41	160.5	19.0	2.19	2.4	11.2	29.7	5.85
99	**SGP-10-107**	43	153.6	19.0	2.88	2.9	27.8	51.8	7.71
100	**TCP-10-110**	59	183.4	14.6	3.43	2.1	19.6	50.1	5.25
Grand Mean		45	154.9	19.4	2.45	2.5	20.8	48.3	7.28
S.E.		0.578	7.732	0.834	0.115	0.382	2.195	2.828	0.566
C.D.		1.624	21.73	2.344	0.324	1.074	6.17	7.948	1.592
C.V		1.817	7.058	6.074	6.653	21.789	14.898	8.288	10.999

Table 4.3 Summary of mean values for morphological characters in pearl millet germplasm lines

S. No.	Morphological traits		B Lines	R Lines	Hybrids
1	Days to 50% flowering	Mean	45	46	41
		Range	40-54	41-59	37-43
2	Plant Height (cm)	Mean	132	174	197
		Range	86-180	127-230	184-213
3	Panicle Length (cm)	Mean	19	20	22
		Range	12-26	13-33	20-27
4	Panicle Diameter (cm)	Mean	2.24	2.64	2.77
		Range	1.29-3.36	1.45-3.72	2.08-3.84
5	Productive Tillers (No./Plant)	Mean	2.6	2.3	2.6
		Range	1.6-3.8	1.3-3.7	1.6-3.6
6	Grain Yield/Plant (g)	Mean	15	24	40
		Range	4-33	1-45	27-53
7	Dry Fodder Yield/Plant (g)	Mean	36	55	90
		Range	16-85	15-84	47-142
8	1000-seed weight (g)	Mean	6.84	7.62	8.23
		Range	2.94-10.53	2.61-16.02	6.22-10.69

Table 4.4 Estimates for grand mean ±S.E. (m), range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as per cent of mean for morphological characters in pearl millet germplasm lines

S. No.	Morphological traits	Mean ±S.E(m)	Range	GCV (%)	PCV (%)	Heritability (h^2) (%)	Genetic advance as % of mean
1	**Days to 50 % Flowering**	45±1	37-59	8.8	9.0	95.9	17.8
2	**Plant Height (cm)**	154.9±7.7	85.8-229.8	21.3	22.4	90.1	41.6
3	**Panicle Length (cm)**	19.4±0.8	11.85-33.2	16.8	17.8	88.4	32.5
4	**Panicle Diameter (cm)**	2.45±0.1	1.29-3.84	21.1	22.1	90.9	41.4
5	**Productive Tillers (No./Plant)**	2.5±0.4	1.3-3.7	17.7	28.1	39.8	23.0
6	**Grain Yield/Plant (g)**	20.8±2.2	1.4-53	54.7	56.7	93.1	108.7
7	**Dry Fodder Yield/Plant (g)**	48.3±2.8	15.4-142	50.4	51.1	97.4	102.5
8	**1000-seed weight (g)**	7.28±0.6	2.61-16.02	26.8	29.0	85.6	51.0

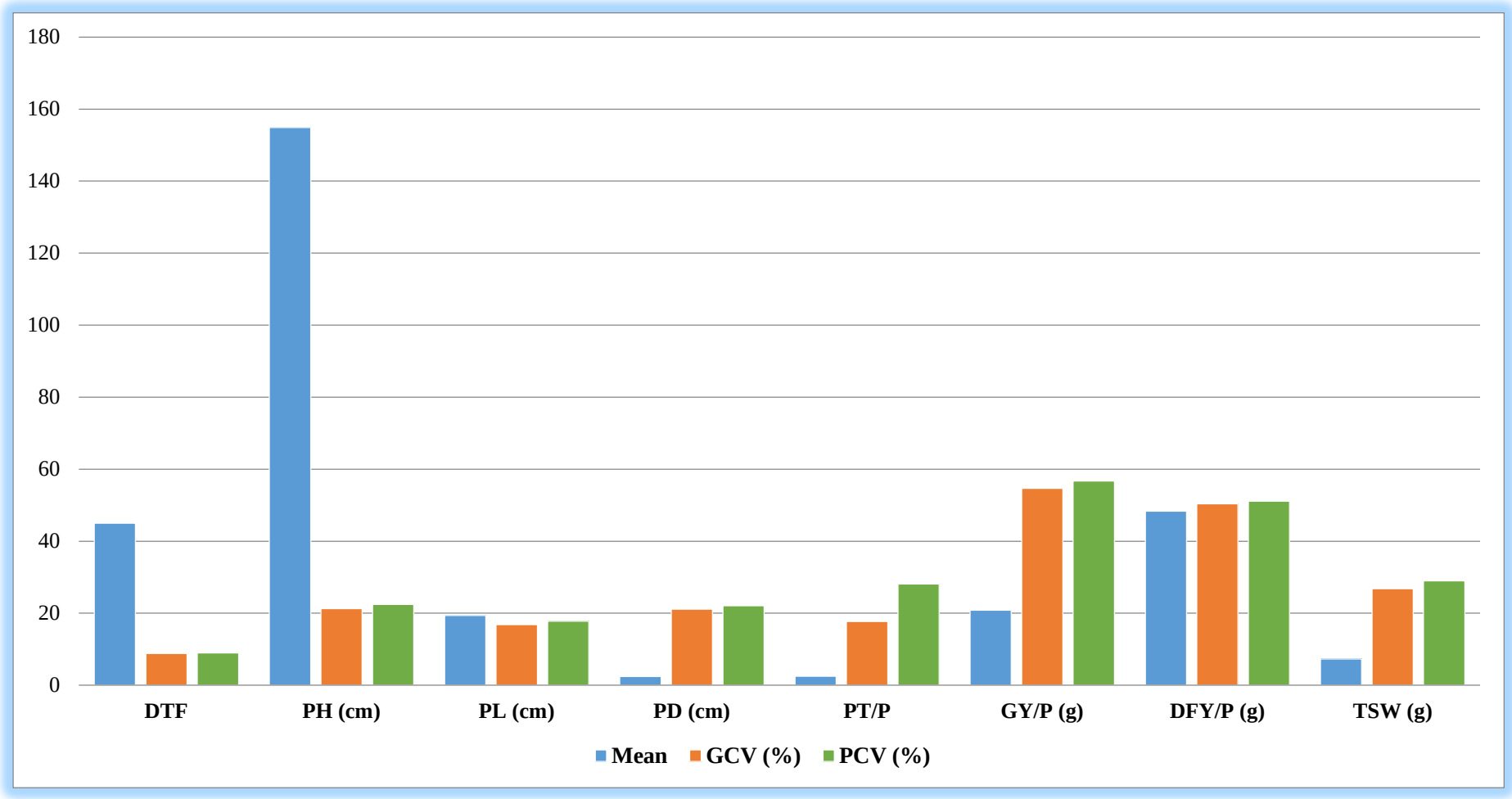


Fig. 4.1 Estimates of Mean, GCV (%) & PCV (%) for morphological characters in pearl millet germplasm lines

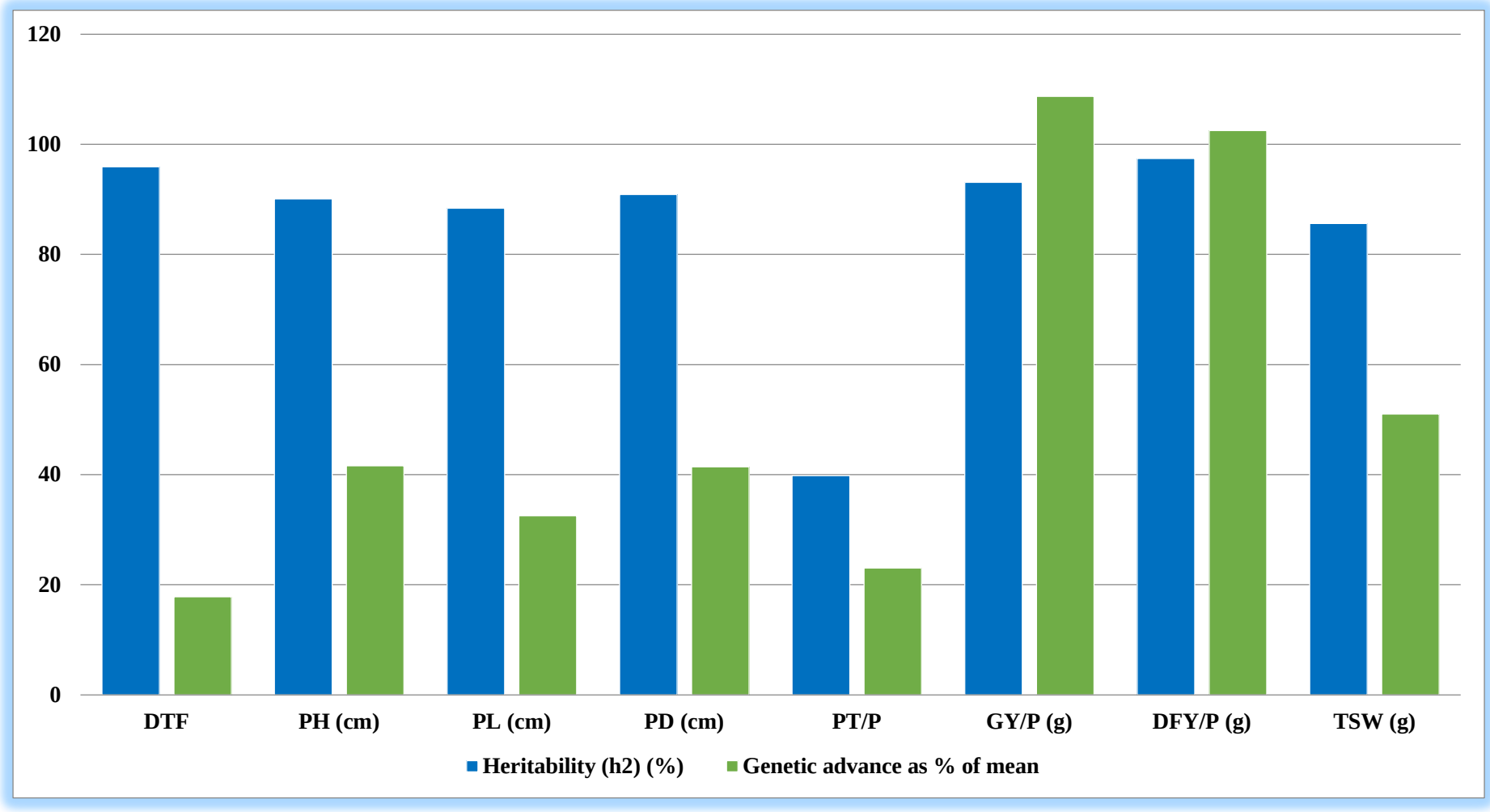


Fig. 4.2 Estimates of Heritability (h)2 (%) and Genetic Advance as percent of mean for morphological characters in pearl millet germplasm lines

Table 4.5 Estimates for Genotypic (above diagonal) and Phenotypic (below diagonal) Correlation Coefficients for morphological and disease traits in pearl millet germplasm lines

Characters	Blast	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diameter (cm)	Productive Tillers (No./Plant)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)	Grain Yield/Plant (g)
Blast	1	-0.01	-0.25**	-0.04	-0.27**	0.05	-0.38**	-0.50**	-0.42**
Days to 50 % Flowering	0.02	1	-0.14	-0.02	0.15*	-0.40**	-0.18*	-0.04	-0.25**
Plant Height (cm)	-0.25**	-0.15*	1	0.52**	0.36**	-0.31**	0.66**	0.29**	0.72**
Panicle Length (cm)	-0.04	-0.02	0.46**	1	0.03	-0.20**	0.33**	0.16*	0.37**
Panicle Diameter (cm)	-0.25**	0.15*	0.31**	0.08	1	-0.73**	0.54**	0.52**	0.52**
Productive Tillers (No./Plant)	0.01	-0.27**	-0.17*	-0.09	-0.43**	1	-0.14	-0.44**	-0.03
Dry Fodder Yield/Plant (g)	-0.36**	-0.17*	0.61**	0.31**	0.52**	-0.10	1	0.45**	0.93**
1000-seed weight (g)	-0.45**	-0.04	0.26**	0.12	0.46**	-0.23**	0.42**	1	0.43**
Grain Yield/Plant (g)	-0.38**	-0.23**	0.65**	0.34**	0.49**	-0.05	0.92**	0.41**	1

* Significant at p = 0.05, ** Significant at p = 0.01

4.2) CORRELATION COEFFICIENT ANALYSIS

Because the selection for any particular character brings about undesirable changes in various other associated traits, so to know the fitness of various characters for indirect selection the study of correlation is primary. As the yield is a very complex quantitative trait which is tremendously influenced by environment, so any direct selection done is incompetent. Consequently, the correlation between the trait (grain yield), its related component traits and among themselves is of worthwhile importance for any selection programmes.

The genotypic and phenotypic correlation coefficients between grain yield and other component characters and among themselves were computed, tabulated and demonstrated in Table 4.5. The magnitudes of correlation coefficients for almost all the traits at genotypic level were higher than their corresponding correlation coefficients at the phenotypic level, which revealed a robust inherent association between different attributes.

4.2.1 Blast

Blast expressed significant negative correlation with plant height (0.25, 0.25), panicle diameter (0.25, 0.27), 1000-seed weight (0.45, 0.50), dry fodder yield per plant (0.36, 0.38) and grain yield per plant (0.38, 0.42). While with panicle length (0.04, 0.04) it exhibited negative and non-significant correlation. With number of productive tillers per plant (0.01, 0.05) it showed positive and non-significant correlation at both phenotypic and genotypic levels, respectively (Table 4.5).

4.2.2 Days to 50% flowering

This trait exhibited significant positive correlation with the panicle diameter (0.15, 0.15) at both phenotypic and genotypic levels respectively. While with plant height (0.15, 0.14), number of productive tillers per plant (0.27, 0.40), dry fodder yield per plant (0.17, 0.18) and grain yield per plant (0.23, 0.25) it was negatively and significantly correlated. However, with panicle length (0.02, 0.02) and 1000-seed weight (0.04, 0.04) it was negatively and non-significantly correlated at both phenotypic and genotypic levels, respectively (Table 4.5).

4.2.3 Plant Height (cm)

Plant height was found to be significantly and positively correlated with panicle length (0.46, 0.52), panicle diameter (0.31, 0.36), 1000-seed weight (0.26, 0.29), dry fodder yield per plant (0.61, 0.66) and grain yield per plant (0.65, 0.72) while it was significantly and negatively correlated with blast (0.25, 0.25), days to 50% flowering (0.15, 0.14) and number of productive tillers per plant (0.17, 0.31) at both phenotypic and genotypic levels, respectively (Table 4.5).

4.2.4 Panicle Length (cm)

Panicle length depicted significant positive correlation with plant height (0.46, 0.52), dry fodder yield per plant (0.31, 0.33) and grain yield per plant (0.34, 0.37). However, with blast (0.04, 0.04) and days to 50% flowering (0.02, 0.02) it exhibited negative and non-significant correlation, while with panicle diameter (0.08, 0.03) it expressed positive and non-significant correlation at both phenotypic and genotypic levels, respectively. With number of productive tillers per plant (0.20) it exhibited negative and significant correlation and it showed positive and significant correlation with 1000-seed weight (0.16) at genotypic level only (Table 4.5).

4.2.5 Panicle Diameter (cm)

Panicle diameter revealed significant positive correlation with days to 50% flowering (0.15, 0.15), plant height (0.31, 0.36), 1000-seed weight (0.46, 0.52), dry fodder yield per plant (0.52, 0.54) and grain yield per plant (0.49, 0.52) but showed negative and significant correlation with blast (0.25, 0.27) and number of productive tillers per plant (0.43, 0.73). It also expressed non-significant positive correlation with panicle length (0.08, 0.03) at both phenotypic and genotypic levels, respectively (Table 4.5).

4.2.6 Productive Tillers (No. /Plant)

The trait expressed negative significant correlation with most of the traits *viz.* days to 50% flowering (0.27, 0.40), plant height (0.17, 0.31), panicle length (0.09, 0.20), panicle diameter (0.43, 0.73) and 1000-seed weight (0.23, 0.44). With dry fodder yield per plant (0.10, 0.14) and grain yield per plant (0.05, 0.03), it exhibited negative and non-significant correlation at both phenotypic and genotypic levels, respectively but with blast (0.01, 0.05), it revealed positive and non-significant correlation (Table 4.5).

4.2.7 1000-seed weight (g)

1000-seed weight was found to be positively and significantly correlated with plant height (0.26, 0.29), panicle diameter (0.46, 0.52), dry fodder yield per plant (0.42, 0.45) and grain yield per plant (0.41, 0.43) at both phenotypic and genotypic levels, respectively but with panicle length (0.16), it was positively and significantly correlated at only genotypic level (Table 4.5). It was found to be non-significantly and negatively correlated with days to 50% flowering (0.04, 0.04) and it also revealed negative significant correlation with blast (0.45, 0.50) and number of productive tillers per plant (0.23, 0.44).

4.2.8 Dry fodder yield per plant (g)

Dry fodder yield per plant exhibited positive and significant correlation with plant height (0.61, 0.66), panicle length (0.31, 0.33), panicle diameter (0.52, 0.54), 1000-seed weight (0.42, 0.45) and grain yield per plant (0.92, 0.93). However, with days to 50% flowering (0.17, 0.18) and blast (0.36, 0.38), it exhibited negative and significant correlation.

With number of productive tillers per plant (0.10, 0.14) it exhibited negative and non-significant correlation at both phenotypic and genotypic levels, respectively (Table 4.5).

4.2.9 Grain yield per plant (g)

Significant positive correlations were observed for grain yield per plant with plant height (0.65, 0.72), panicle diameter (0.49, 0.52), panicle length (0.34, 0.37), 1000-seed weight (0.41, 0.43) and dry fodder yield per plant (0.92, 0.93). However, with days to 50% flowering (0.23, 0.25) and blast (0.38, 0.42) it was negatively and significantly correlated. With number of productive tillers per plant (0.05, 0.03) it was negatively and non-significantly correlated at both phenotypic and genotypic levels, respectively (Table 4.5).

4.3) PATH COEFFICIENT ANALYSIS

The cause and effect relationship is studied using the path coefficient analysis as it delineates the correlation coefficient into indirect and direct effects and delivers the genuine situation of association between traits.

Considering genotypic correlations, the direct and indirect effects of various traits on grain yield per plant were computed and have been tabulated in Table 4.6.

High contribution of independent traits on the dependent trait (grain yield per plant) was indicated by low residual effect (0.0391).

Direct effects-

An inspection of data in Table 4.6 divulged that number of productive tillers per plant (0.715) had the highest direct contribution towards grain yield per plant followed by panicle diameter (0.644), plant height (0.379), dry fodder yield per plant (0.330), panicle length (0.165), 1000-seed weight (0.128) and days to 50% flowering (0.056).

The characters *viz*. panicle diameter (0.518), plant height (0.722) and dry fodder yield per plant (0.934) had high significant correlation coefficients and had high positive direct effects which indicated that the selection should be done in positive direction for these traits.

Indirect effects-

Results of Table 4.6 divulged that days to 50% flowering had poor direct positive effect (0.056) but, negative and significant genotypic correlation coefficient (-0.253) which may be due to indirect contribution to grain yield per plant *via* number of productive tillers per plant (-0.287).

Plant height had relatively high positive direct effect (0.379) and positive significant genotypic correlation coefficient (0.722) which may be due to high indirect contribution to grain yield *via* panicle diameter (0.232) and dry fodder yield per plant (0.216).

Panicle length had poor direct positive effect (0.165) but, positive significant genotypic correlation coefficient (0.369) which may be due to indirect contribution to grain yield per plant *via* plant height (0.197) and dry fodder yield per plant (0.110).

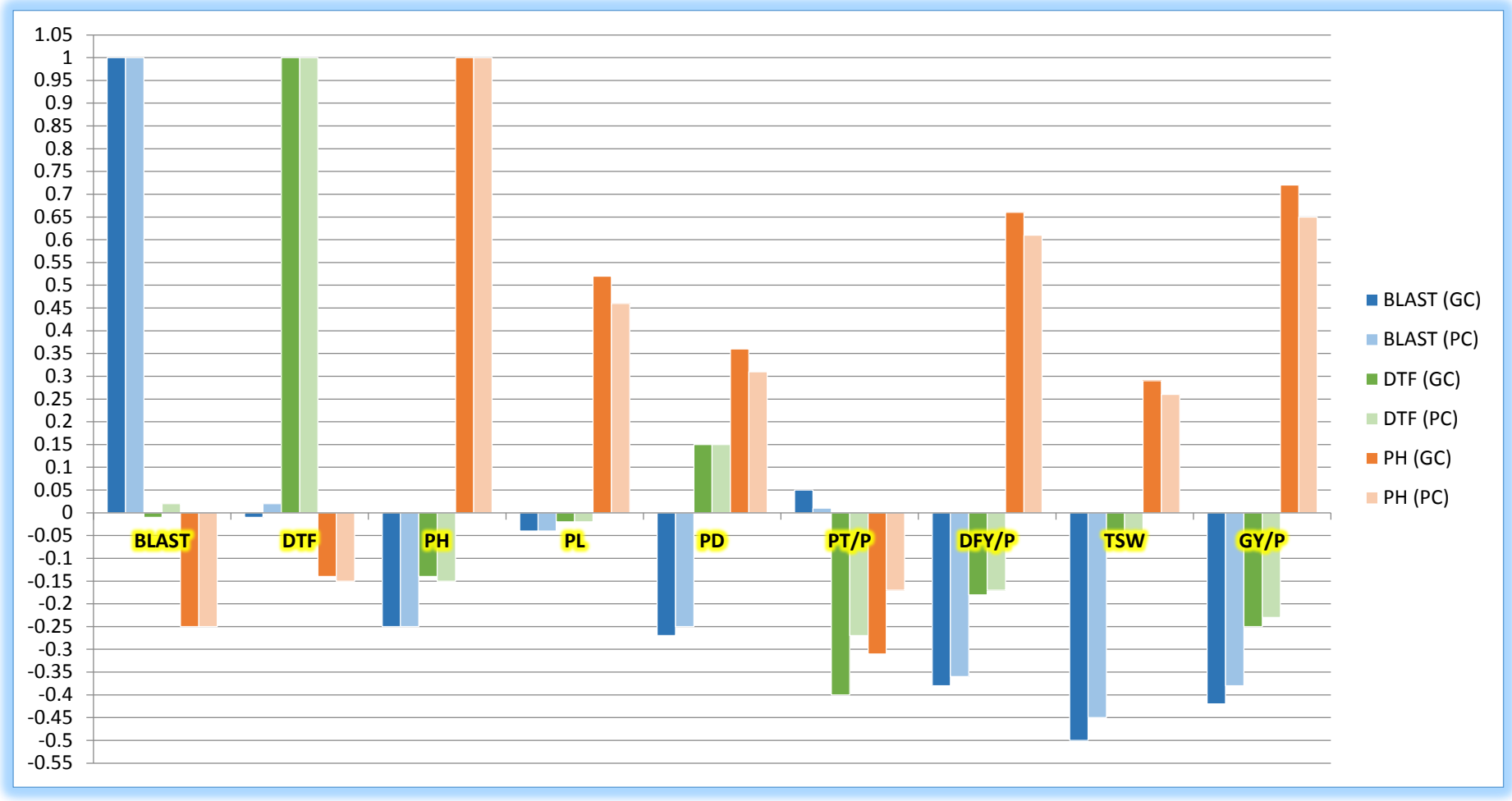


Fig. 4.3 Estimates of Genotypic and Phenotypic correlations for BLAST, Days to 50% Flowering (DTF) and Plant Height (PH) with other morphological characters in pearl millet germplasm lines

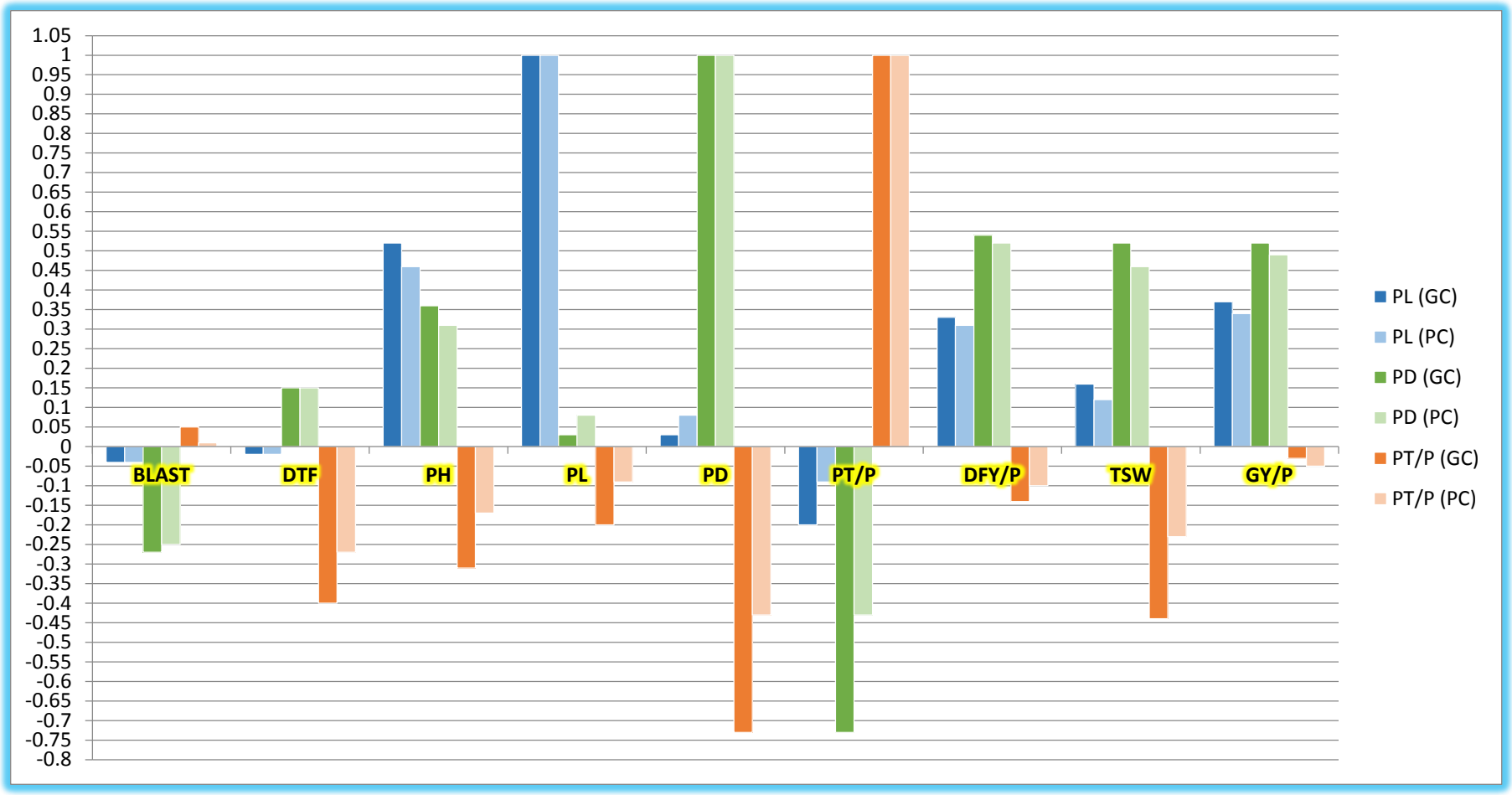


Fig. 4.4 Estimates of Genotypic and Phenotypic correlations for Panicle Length (PL), Panicle Diameter (PD) and Number of Productive Tillers per plant (PT/P) with other morphological characters in pearl millet germplasm lines

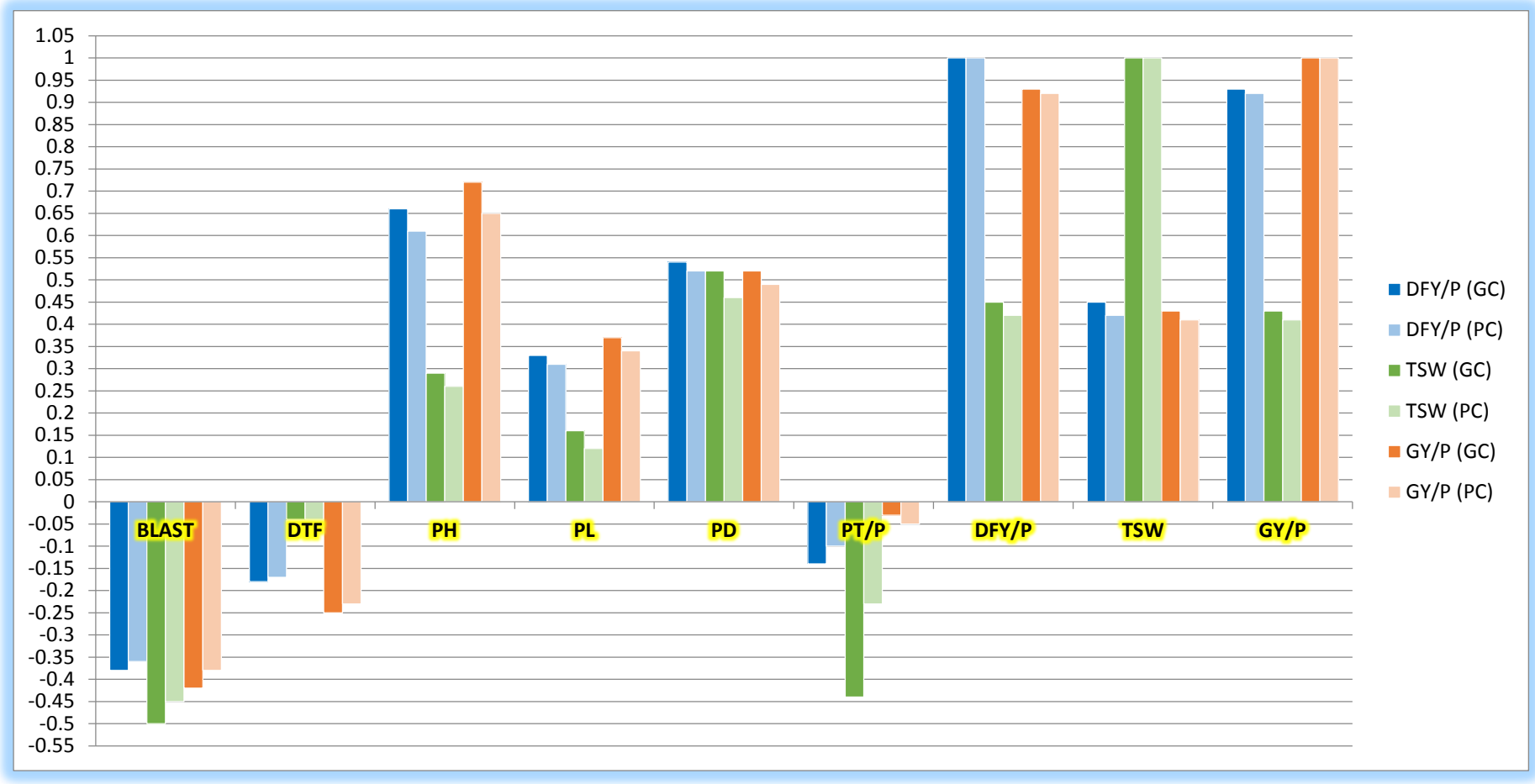


Fig. 4.5 Estimates of Genotypic and Phenotypic correlations for 1000-seed weight (TSW), Dry Fodder Yield per plant (DFY/P) and Grain Yield per plant (GY/P) with other morphological characters in pearl millet germplasm lines

Table 4.6 Estimates of Path coefficient analysis of grain yield per plant with its component characters in pearl millet germplasm lines

Characters	Days to 50 % Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Diam. (cm)	Productive Tillers (No./Plant)	Dry Fodder Yield/Plant (g)	1000-seed weight (g)
Days to 50 % Flowering	**0.056**	-0.051	-0.004	0.098	-0.287	-0.059	-0.006
Plant Height (cm)	-0.008	**0.379**	0.086	0.232	-0.221	0.216	0.037
Panicle Length (cm)	-0.001	0.197	**0.165**	0.017	-0.140	0.110	0.020
Panicle Diam. (cm)	0.008	0.137	0.004	**0.644**	-0.521	0.179	0.067
Productive Tillers (No./Plant)	-0.022	-0.117	-0.032	-0.469	**0.715**	-0.045	-0.056
Dry Fodder Yield/Plant (g)	-0.010	0.249	0.055	0.350	-0.097	**0.330**	0.058
1000-seed weight (g)	-0.002	0.110	0.026	0.335	-0.312	0.150	**0.128**
Genotypic Correlation coefficient	-0.253**	0.722**	0.369**	0.518**	-0.027	0.934**	0.434**

Residual effect- 0.0391

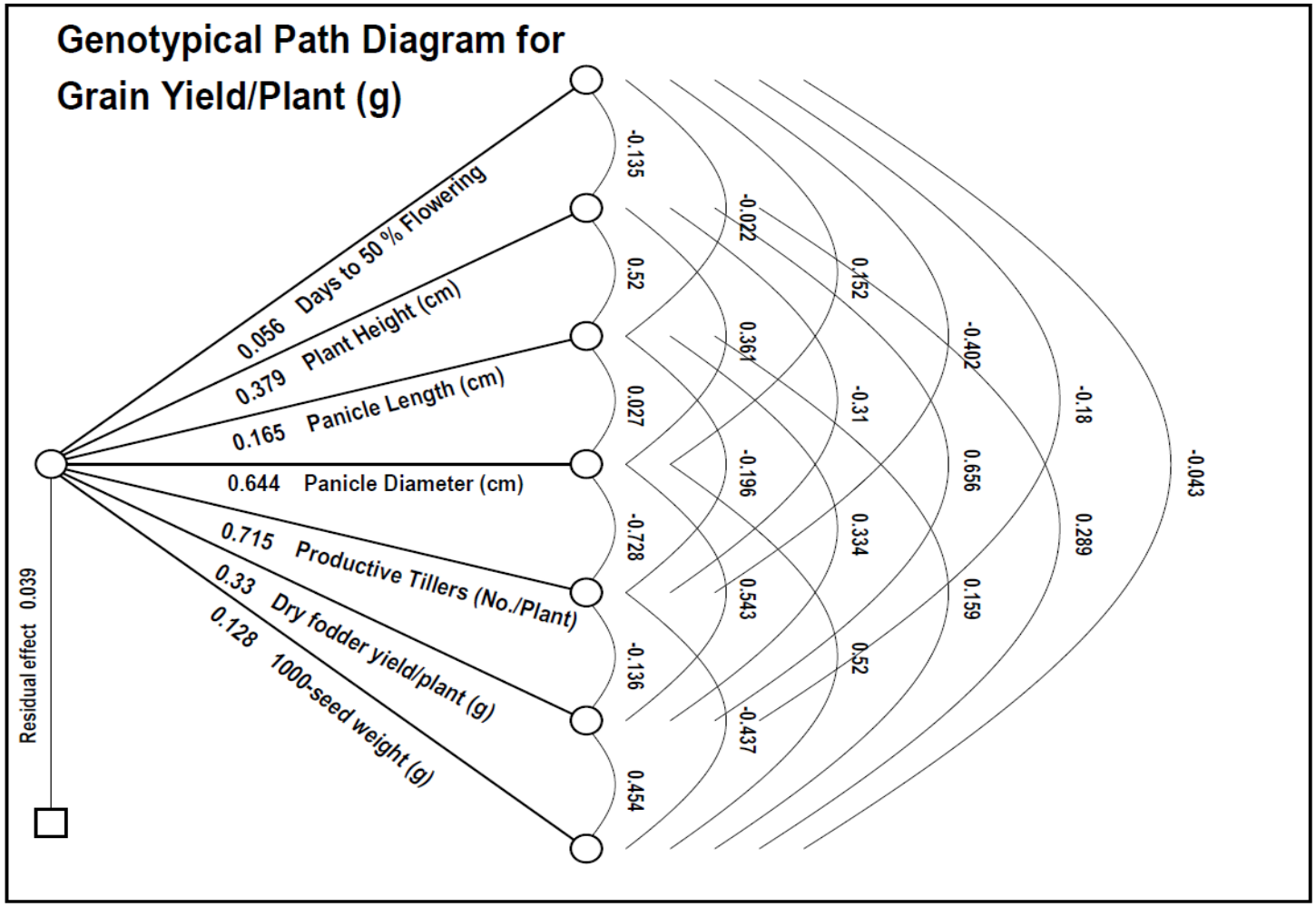


Fig. 4.6 Genotypical Path diagram for the grain yield/ plant (dependent variable) with other contributing characters (independent variables) in pearl millet germplasm lines

Panicle diameter had very high positive direct effect (0.644) and positive significant genotypic correlation coefficient (0.518) which may be due to high indirect contribution to grain yield per plant *via* plant height (0.137) and dry fodder yield per plant (0.179).

Number of Productive tillers per plant had maximum positive direct effect (0.715) among all the traits but it revealed negative and non-significant genotypic correlation coefficient (0.027) which may be due to high indirect contribution to grain yield per plant *via* panicle diameter (-0.469) and plant height (-0.117).

1000-seed weight had positive direct effect (0.128) and positive significant genotypic correlation coefficient (0.434) which may be due to high indirect contribution to grain yield *via* panicle diameter (0.335), dry fodder yield per plant (0.150) and plant height (0.110).

Dry Fodder yield per plant had relatively high direct positive effect (0.330) as well as highest positive significant genotypic correlation coefficient (0.934) among all the traits which may be due to high indirect contribution to grain yield *via* panicle diameter (0.350) and plant height (0.249).

4.4) SCREENING STUDIES

Screening of 100 pearl millet genotypes (designated A/B lines, R lines and hybrids) for blast severity reaction was done under natural epiphytotic conditions at research area of Bajra Section, Department of Genetics and Plant Breeding, CCSHAU, Hisar. Disease severity was recorded at hard dough grain stage and the results have been tabulated (Table 4.7).

The recorded data divulged that, out of 100 genotypes screened, 34 lines were found to be highly resistant. Among 34 pearl millet lines, 12 were designated B lines (ICMB 04888, HMS 26B, HMS 65B, HMS 66B, HMS 59B, HMS 30B, HMS 39B, HMS 6B, HMS 36B, HMS 60B, HMS 68B and HMS 45B), 18 were designated R lines (EMRLT-14/121, EMRLT-14/123, EMRLT-14/103, EMRLT-14/243, HTP 03/13, EBL-12-237, EMRLT-14/107, EMRLT-15/133, H13/0001, H77/29-2, PRLT-132, H14/003, PRLT 101, PRLT-124, IH 8, PT-1-1047, HB-15/085 and PRLT-134) and four were hybrids (HHB 299, HHB 216, HHB 272 and HHB 311).

A total of 23 lines were found resistant and among these lines, nine were designated B lines (HMS 49B, HMS 55B, HMS 33B, HMS 63B, ICMB 97111, HMS 47B, HMS 53B, HMS 28B and HMS 75B), nine were designated R lines (EMRLT-14/111, H90/4-5, G73-107, HBL 11, A5RLT-14/106, AC 04/13, EMRLT-14/127, LTRL 15/123 and PRLT-121) and five were hybrids (HHB 223, HHB 226, HHB67 IMP, HHB 197 and HHB 234).

Among the total lines, 24 lines were found moderately resistant and in this same category, 12 were designated B lines (HMS 69B, HMS 62B, HMS 52B, HMS 54B, HMS 56B, HMS 57B, HMS 74B, HMS 48B, ICMB 94555, HMS 64B, HMS 70B and ICMB 843-22).

Table 4.7 Estimates of blast severity analysis in pearl millet germplasm lines

Scale	Disease Reaction	Number of genotypes	Genotypes (B lines)	Genotypes (R lines)	Genotypes (Hybrids)
1.0	Highly Resistant	12(B lines) 18(R lines) 4(Hybrids) Total = 34	ICMB 04888, HMS 26B, HMS 65B, HMS 66B, HMS 59B, HMS 30B, HMS 39B, HMS 6B, HMS 36B, HMS 60B, HMS 68B, HMS 45B	EMRLT-14/121, EMRLT-14/123, EMRLT-14/103, EMRLT-14/243, HTP 03/13, EBL-12-237, EMRLT-14/107, EMRLT-15/133, H13/0001, H77/29-2, PRLT-132, H14/003, PRLT 101, PRLT-124, IH 8, PT-1-1047, HB-15/085, PRLT-134	HHB 299, HHB 216, HHB 272, HHB 311
2.0-3.0	Resistant	9(B lines) 9(R lines) 5(hybrids) Total = 23	HMS 49B, HMS 55B, HMS 33B, HMS 63B, ICMB 97111, HMS 47B, HMS 53B, HMS 28B, HMS 75B	EMRLT-14/111, H90/4-5, G73-107, HBL 11, A5RLT-14/106, AC 04/13, EMRLT-14/127, LTRL 15/123, PRLT-121	HHB 223, HHB 226, HHB67 IMP, HHB 197, HHB 234
3.1-5.0	Moderately resistant	12(B lines) 12(R lines) Total = 24	HMS 69B, HMS 62B, HMS 52B, HMS 54B, HMS 56B, HMS 57B, HMS 74B, HMS 48B, ICMB 94555, HMS 64B, HMS 70B, ICMB 843-22	EMRLT-14/237, TCP-10-110, HTP 94/54, PRLT-107, DMBRL-15/102, H77/833-2-202, EMRLT-14/229, EMRLT-14/105, EMRLT-14/124, EMRLT-15/109, SGP-10-107, H77/833-2	----------
5.1-7.0	Susceptible	12(B lines) 01(R lines) Total = 13	HMS 44B, HMS 50B, HMS 7B, HMS 58B, HMS 43B, HMS 29B, ICMB 02333, HMS 38B, HMS 13B, HMS 16B, HMS 18B, HMS 14B	HTP-10-129	----------
7.1-9.0	Highly Susceptible	05(B lines) 01(R lines) Total = 06	HMS 40B, HMS 32B, HMS 37B, HMS 34B, HMS 41B	HPT-2-12-32	----------

Among the 24 moderately resistant lines, 12 were designated R lines (EMRLT-14/237, TCP-10-110, HTP 94/54, PRLT-107, DMBRL-15/102, H77/833-2-202, EMRLT-14/229, EMRLT-14/105, EMRLT-14/124, EMRLT-15/109, SGP-10-107 and H77/833-2).

A total of 13 lines were found susceptible and among these lines, 12 were designated B lines (HMS 44B, HMS 50B, HMS 7B, HMS 58B, HMS 43B, HMS 29B, ICMB 02333, HMS 38B, HMS 13B, HMS 16B, HMS 18B and HMS 14B) and one line (HTP-10-129) was designated R line.

Among the total 100 lines, a total of six lines were found highly susceptible and among these lines, five were designated B lines (HMS 40B, HMS 32B, HMS 37B, HMS 34B and HMS 41B) and one line (HPT-2-12-32) was designated R line.

There is a need to develop high yielding varieties to feed large population of India. As the yield is a very complex quantitative trait which is tremendously influenced by environment, so any direct selection done is incompetent. Consequently, the correlation between the trait (grain yield), its related component traits and among themselves is of worthwhile importance for any selection programmes. To investigate these points, germplasm collections are evaluated by different biometrical techniques like ANOVA, coefficient of variation, principal component and clusters analysis which further make clear understanding about population structure. The presence of adequate genetic variability quantum in the population is the foremost key point in success of any breeding programme.

Among all the cereal crops of India, pearl millet is one of the most important and popular coarse grain cereal crops. It is an important food as well as forage crop in arid and semi-arid regions of the world because of its hardy nature. In addition to food and fodder, it is also used as an important animal feed, fuel and also in beverage industries. Once considered among the minor diseases of pearl millet, incidence of blast disease caused by *Pyricularia grisea* Sacc. (Teleomorph: *Magnaporthe grisea*), now has become a very important disease in the recent past, especially on the commercial hybrids of India.

Thus, keeping in view of the above facts, in the present investigation, besides various morphological components of grain yield, blast severity analysis was also recorded. The results are discussed in the light of following objectives:

OBJECTIVES

1. To study extent of genetic variability for yield traits and blast in pearl millet genotypes
2. To estimate correlation and path coefficients among various traits in pearl millet genotypes

In the light of the above consideration, salient features of the results computed are under the following heads:

5.1) Analysis of variance

5.2) Parameters of genetic variation

5.3) Correlation coefficient analysis

5.4) Path coefficient analysis

5.5) Screening studies

5.1) Analysis of variance

The analysis of variance divulged highly significant differences among 100 different pearl millet germplasm lines evaluated for all the eight morphological characters studied indicating the presence of sufficient variability (Table 4.1). Large variation among germplasm lines was found for the traits like days to 50% flowering (37-59 days), plant height (85.8-229.8), number of productive tillers per plant (1.3-3.7), panicle length (11.85-

33.20), panicle diameter (1.29-3.84), 1000-seed weight (2.61-16.02), grain yield per plant (1.4-53) and dry fodder yield per plant (15.4-142) (Table 4.4). The results were almost in collaboration with Singh *et al.* (2015).

Similar studies were also conducted by Shah *et al.* (2012) in which they evaluated 27 accessions of pearl millet and reported considerable variability for various qualitative and quantitative traits *viz.*, days to 50 % flowering, leaf area, flag leaf area, plant height and green fodder yield. Sharma *et al.* (2003) evaluated 115 germplasm of pearl millet and recorded highly significant differences among the accessions for green fodder yield as well as quality traits. Khairwal *et al.* (2007) evaluated a large pearl millet germplasm for grain and fodder yield and their component traits and revealed considerable variation among accessions for all the traits studied. Similar investigation was also conducted by Yadav *et al.* (2016) to study variability in a set of 40 inbred lines of pearl millet *via* 20 qualitative and 8 quantitative and found significant mean sum of squares for all the characters studied except for a single quantitative trait (panicle diameter). These results were in collaboration with an earlier investigation by Satyavathi *et al.* (2009).

5.2) Parameters of genetic variation

For the improvement of any particular trait in a population, firstly the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean are estimated which further determine the appropriate method of selection. The results of present investigation deduced that it is not always necessary for the trait with high heritability to be coupled with high genetic advance.

However, high heritability coupled with high genetic advance as per cent of mean was observed for the traits *viz*., grain yield per plant, dry fodder yield per plant, plant height, panicle length, panicle diameter and 1000-seed weight, clearly indicating the importance of additive gene action and the contribution of these traits to the total variability (Table 4.4). Further, narrow range of difference between PCV and GCV indicated that any selection pressure operated on these characters and days to 50 % flowering may assist us to grasp improvement at early generation of breeding.

Phenotypic coefficient of variation (PCV) was found to be always higher than the corresponding genotypic coefficient of variation (GCV) for all the traits, clearly denoting the influence of environmental factors on trait expression and similar conclusion was made by the investigation of Kalpande *et al.* (2014) and Mohanraj *et al.* (2011).The traits *viz.*, plant height, panicle diameter, grain yield per plant, dry fodder yield per plant and 1000-seed weight recorded both high PCV and GCV values and Vinodhana *et al.* (2013), Talawar *et al.* (2017) and Singh *et al.* (2015) also reported the similar result.

5.3) Correlation coefficient analysis

Because the selection for any particular character brings about undesirable changes in various other associated traits, so to know the fitness of various characters for indirect selection, the study of correlation is primary. As the yield is a very complex quantitative trait which is tremendously influenced by environment, so any direct selection done is incompetent. Consequently, the correlation between the trait (grain yield), its related component traits and among themselves is of worthwhile importance for any selection programmes.

The magnitudes of correlation coefficients for almost all the traits at genotypic level were higher than their corresponding correlation coefficients at the phenotypic level, which revealed a robust inherent association between different attributes.

The results of correlation coefficient analysis presented in the table (Table 4.5) revealed that the traits *viz.*, plant height, panicle diameter, panicle length, 1000-seed weight and dry fodder yield per plant exhibited significant positive correlation with grain yield per plant. Depke *et al*. (2014) and Kumar *et al.* (2015) also reported similar results and found days to 50% flowering negatively and significantly correlated with grain yield per plant and traits *viz*., plant height, panicle diameter and dry fodder yield per plant positively and significantly correlated with grain yield per plant.

Non-significant and negative correlation of number of productive tillers per plant with grain yield per plant in the present investigation is in agreement to the previous work of Basavaraj (2015). Shanthi *et al.* (2014) and Sankar *et al.* (2013) findings were also in close agreement with the present investigation revealing the positive association of plant height with grain yield per plant. Kulkarni *et al.* (2000), Arya *et al.* (2009) and Singh *et al.* (2015) also reported significant positive correlation of 1000 seed weight with grain yield per plant. Harrer & Karad (1998), Kulkarni *et al.* (2000) and Kumar *et al.* (2015) findings were also in close agreement with the present investigation revealing the positive association of dry fodder yield with grain yield per plant. Significant positive association of dry fodder yield with grain yield per plant was found inspiring for the future development of dual purpose hybrids. Panicle length and panicle diameter were also another important yield determinant characters because of their positive and high significant association with grain yield per plant and this result entirely agrees with the research findings of Singh *et al.* (2015) and Ezeaku *et al.* (2015).

The positive correlation of these characters with the grain yield per plant clearly implies that improving one or more of these traits can result in higher grain yield. This study discovered substantial genetic variability for various traits among the designated A/B lines, R lines and hybrids and also the scope for rapid improvement through selection, where the selection procedure may be constructed in such a way that the genetic improvement in one of

these components is not compromised by the downturn effect of the other. Consequently, results of association study divulged that the following traits *viz.*, plant height, panicle diameter, panicle length, 1000-seed weight and dry fodder yield per plant were the important component traits of grain yield per plant and during the course of development of inbred lines and populations, these traits may get perfidious attention of the pearl millet breeders.

5.4 Path coefficient analysis

As we start considering more number of variables in the association studies, the indirect association becomes more and more complex, less manifest and somewhat mystifying. Under such puzzling circumstances, the path coefficient analysis (Wright, 1921; Dewey & Lu, 1959) provides an effective means of separating indirect and direct causes of association and permits scathing examination of the specific forces acting and measures the comparative importance of each and every casual factor. The positive or negative relationship developed by the yield component traits facilitates the selection of component traits of a crop species for the genetic improvement in a desired direction during the breeding programme. An obvious association of a particular character to the grain yield might be appearing due to balancing of their both negative and positive contribution. Consequently, path coefficient analysis can be additional effective method for use in selection programme of a crop species, which is based on component breeding.

Considering grain yield per plant as effect (dependent variable) and other traits as causes (independent variables), computed magnitude of genotypic correlation coefficients were partitioned using path coefficient analysis method to find out the direct and indirect effects (Table 4.6 and Figure 4.6). The computed estimates revealed that number of productive tillers per plant and panicle diameter had high and positive direct effects on grain yield per plant which further supports the finding of Abuali *et al*. (2012) and Talawar *et al*. (2017) for these characters. Consequently, it is suggested that these traits can be considered as main components traits for adequate selection in pearl millet breeding programme for obtaining higher grain yield. Estimates of indirect effects of various independent characters *viz*., plant height, dry fodder yield per plant, panicle length and 1000-seed weight indicated high indirect effects on dependent trait (grain yield per plant). Low value of residual effects (0.039) indicated that the contribution of various independent traits included in this investigation explained about 99.96 % of variation for grain yield per plant. Based on the on-going discussion, the traits *viz*., number of productive tillers per plant, panicle diameter, plant height, dry fodder yield per plant, panicle length and 1000-seed weight may be devoted great attention in breeding of pearl millet.

5.5) Screening studies

The management of this disease through host plant resistance has been the most feasible and economical mean in all the crops. Employment of highly disease resistant

cultivars in farming systems is the simple, highly effective and most economical method in the management of this disease. In addition to these benefits, these highly resistant cultivars also conserve natural resources and reduce the energy, time and cost. Also exploiting resistant cultivars is a very eco-friendly technique as compared to the other methods of management to this disease.

In general, incidence of pest and diseases hamper the growth and productivity of pearl millet crop. Among several diseases, blast has now become a disease of considerable importance in past few years especially in the commercial hybrids of India. The fungus rigorously infect at all growth stages from seedling to adult plant and affects both grain yield and dry fodder value and thereby limiting the total yield. The fungus is highly variable but also highly specialized in its host range. In India, it is caused by *Pyricularia grisea* Sacc. (Teleomorph: *Magnaporthe grisea*). Consequently, development of hybrid with blast resistance assumes great significance to increase production and productivity of the crop. In the previous years, little work has been done on this part and therefore the present investigation was carried out to screen 100 pearl millet genotypes for blast severity reaction.

A total of 100 pearl millet genotypes (designated A/B lines, R lines and hybrids) were screened for blast resistance under natural epiphytotic condition at research area of Bajra Section, Department of Genetics and Plant Breeding, CCSHAU, Hisar. Disease severity was recorded at hard dough grain stage on 1-9 progressive scale developed for rice blast at International Rice Research Institute (IRRI).

Table 5.1 Estimates of blast variability among hybrids & their parents

S. No.	Genotypes (Hybrids)	Rating Scale	Parents (A line)	Rating Scale	Parents (R line)	Rating Scale
1	HHB 67 Imp.	2.8	ICMA 843-22	4.3	H 77/833-2-202	3.9
2	HHB 197	3.0	ICMA 97111	2.2	HBL 11	2.3
3	HHB 216	1.4	HMS 37A	7.8	HTP 03/13	1.4
4	HHB 223	2.1	ICMA 94555	4.0	HBL 11	2.3
5	HHB 226	2.8	ICMA 843-22	4.3	HBL 11	2.3
6	HHB 272	1.5	HMS 47A	2.3	AC 04/13	2.4
7	HHB 299	1.2	ICMA 04888	1.4	H 13/0001	1.5
8	HHB 311	1.9	ICMA 02333	6.0	H 14/003	1.6
9	HHB 234	2.8	HMS 7A	5.1	H 77/833-2-202	3.9

A perusal of Table 5.1 reveals that disease reaction has shown dominance in F_1 hybrids and male parent seems to have a major contribution in resistant towards the blast infection.

The study revealed 34 genotypes to be highly resistant *viz.*, ICMB 04888, HMS 26B,

HMS 65B, HMS 66B, HMS 59B, HMS 30B, HMS 39B, HMS 6B, HMS 36B, HMS 60B, HMS 68B, HMS 45B, EMRLT-14/121, EMRLT-14/123, EMRLT-14/103, EMRLT-14/243, HTP 03/13, EBL-12-237, EMRLT-14/107, EMRLT-15/133, H13/0001, H77/29-2, PRLT-132, H14/003, PRLT 101, PRLT-124, IH 8, PT-1-1047, HB-15/085, PRLT-134, HHB 299, HHB 216, HHB 272 and HHB 311 (Table 4.7), 23 genotypes to be resistant and 24 genotypes to be moderately resistant. However, 13 genotypes found susceptible and the remaining six genotypes were found to be highly susceptible.

Various attempts have been made in India in the past by several workers to identify the potential sources of resistance to pearl millet blast pathogen. Goud *et al*. (2016) screened 123 designated B-lines of pearl millet including a resistant (ICMR 06444) and a susceptible (ICMB 95444) check against five pathotypes of blast disease and found that nine lines exhibited complete resistance to all the five pathotypes. Similar observations were also reported earlier by Sharma *et al*. (2013).

Similar study was also conducted by Thakur *et al*. (2009), who screened 211 advanced breeding lines (126 designated B-lines, 20 designated R-lines and 65 potential R-lines) of pearl millet against blast resistance. The screening was first conducted in nursery and later the selected lines were screened in the greenhouse to confirm their field resistance against the disease. This study revealed that All the designated B-lines (except ICMB 03444), three designated R-lines and 14 potential R-lines were resistant to blast (<3.0 score) confirming their field resistance to blast pathogen.

In a similar investigation, among evaluated 15 inbred lines of pearl millet, three entries were found highly resistant *viz*., PPMI 1087, PPMI 1089 and PPMI 660 and two entries (PPMI 1084 and J 108) were identified as resistant (Prakash *et al*., 2016).

The present study entitled, "**Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**" comprised of 100 pearl millet genotypes (50 designated A/B lines, 41 R lines and nine hybrids) developed by Chaudhary Charan Singh Haryana Agricultural University over the years with the objective to study extent of genetic variability for yield traits and blast and to estimate correlation and path coefficients among various traits in pearl millet genotypes.

The experiment was laid out in two replications in randomized block design at experimental field of Bajra section, CCS HAU, Hisar. One row of 4 m length was sown and plant to plant and row to row spacing was 10-12 cm and 45 cm, respectively. Mean data recorded on five representative plants for eight morphological traits and also for blast severity estimation was subjected to statistical computation.

The salient features of the findings of this investigation have been summarized below:

1. Mean sum of squares were highly significant due to genotypes for all the characters studied which clearly indicated the occurrence of sufficient genetic variability in the genotypes chosen for the investigation for future improvement.
2. The traits *viz*., panicle diameter, plant height, 1000-seed weight, dry fodder yield per plant and grain yield per plant exhibited high estimates of GCV, PCV, heritability and genetic advance as per cent of mean, indicating the scope of adequate selection in germplasm lines of pearl millet for these traits.
3. The magnitudes of correlation coefficients for almost all the traits at genotypic level were higher than their corresponding correlation coefficients at the phenotypic level, which revealed a robust inherent association of traits *viz*., plant height, panicle diameter, panicle length, 1000-seed weight and dry fodder yield per plant with grain yield per plant.
4. Blast expressed significant negative correlation with most of the recorded traits *viz*., plant height, panicle diameter, 1000-seed weight, dry fodder yield/plant and grain yield/plant.
5. According to the estimates of path coefficients analysis, high direct contribution towards the grain yield per plant was revealed by the traits *viz*., number of productive tillers per plant and panicle diameter whereas the traits *viz*., plant height, dry fodder yield per plant, panicle length and 1000-seed weight indicated high contribution of indirect effects towards grain yield. Consequently, it would be worthwhile to devote greater attention towards these traits in breeding of pearl millet for getting higher yield.

6. This study revealed presence of sufficient variability among B lines, R lines and hybrids for blast disease reaction and a total of 57 genotypes were found resistant towards the disease.
7. Germplasm lines *viz*., ICMB 04888, HMS 26B, HMS 65B, HMS 66B, HMS 59B, HMS 30B, HMS 39B, HMS 6B, HMS 36B, HMS 60B, HMS 68B and HMS 45B among B lines, EMRLT-14/121, EMRLT-14/123, EMRLT-14/103, EMRLT-14/243, HTP 03/13, EBL-12-237, EMRLT-14/107, EMRLT-15/133, H13/0001, H77/29-2, PRLT-132, H14/003, PRLT 101, PRLT-124, IH 8, PT-1-1047, HB-15/085 and PRLT-134 among R lines and HHB 299, HHB 216, HHB 272 and HHB 311 among the hybrids revealed highly resistant reaction to blast disease and hence, can be used for further disease resistance breeding programmes.
8. Disease reaction has shown dominance in F1 hybrids and male parent seems to have a major contribution in resistant towards the blast infection.
9. Lines *viz*., HMS 6B, HMS 30B, HMS 60B, HMS 49B and HMS 47B among the B lines and HTP 03/13, EBL-12-237, EMRLT-14/121, EMRLT-15/133, EMRLT-14/111 and EMRLT-14/127 among the R lines revealed both highly resistant reaction towards the blast pathogen as well as high *per se* performances, hence can be can be used as parents to develop superior hybrids in future pearl millet breeding programmes.

A wide range of variation for the traits among the pearl millet germplasm lines was illustrated by the present investigation which clearly indicates about the opportunities of the high genetic gain through adequate selection or hybridization. Correlation coefficient analysis revealed the positive correlation of grain yield with several important morphological traits.

The positive correlation of these characters with the grain yield per plant clearly implies that improving one or more of these traits can result in higher grain yield. Direct selection for number of productive tillers per plant and panicle diameter suggested rapid improvement in grain yield in germplasm lines of pearl millet. However, grain yield being severely affected by the incidence of pest and diseases, it is pertinent to have more detailed analysis on the blast severity reaction involving the present germplasm lines. The present study also demonstrates the presence of sufficient variability among B lines, R lines and hybrids for blast disease reaction and a total of 57 genotypes were found resistant towards the disease which can be can be used for future disease resistance breeding programmes. This investigation revealed that the germplasm lines developed at CCS HAU over years have sufficient variability for various morphological traits.

■■■

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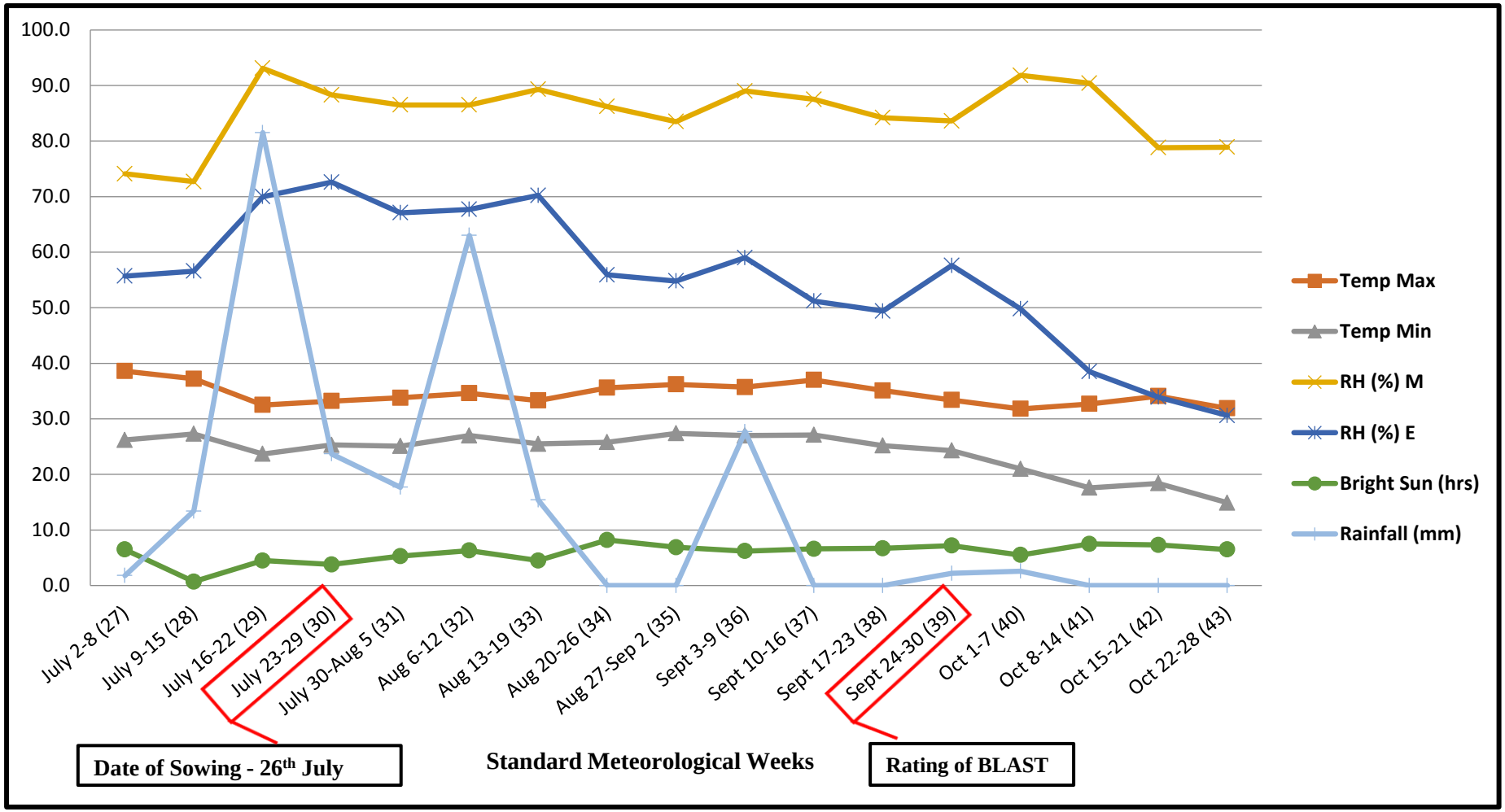
Appendix I. Average weekly weather data of Hisar center during *kharif* 2019

WEEK		Temperature (^{o}C)		Relative Humidity (%)		Bright Sun (hrs)	Rainfall (mm)
No.	Dates	Max	Min	M	E		
27	July 2-8 (27)	38.6	26.2	74.1	55.7	6.5	1.8
28	July 9-15 (28)	37.2	27.3	72.7	56.6	0.7	13.4
29	July 16-22 (29)	32.5	23.7	93.1	70.0	4.5	81.5
30	July 23-29 (30)	33.2	25.3	88	73	3.8	23.7
31	July 30-Aug 5 (31)	33.8	25.1	87	67	5.3	17.7
32	Aug 6-12 (32)	34.6	27.0	87	68	6.3	63
33	Aug 13-19 (33)	33.3	25.5	89	70	4.5	15.4
34	Aug 20-26 (34)	35.6	25.8	86	56	8.2	0
35	Aug 27-Sep 2 (35)	36.2	27.4	84	55	6.9	0
36	Sept 3-9 (36)	35.7	27.0	89	59	6.2	27.7
37	Sept 10-16 (37)	37.0	27.1	88	51	6.6	0
38	Sept 17-23 (38)	35.1	25.2	84	49	6.7	0
39	Sept 24-30 (39)	33.4	24.3	84	58	7.2	2.2
40	Oct 1-7 (40)	31.8	21.0	92	50	5.5	2.6
41	Oct 8-14 (41)	32.7	17.6	90	39	7.5	0
42	Oct 15-21 (42)	34.1	18.4	79	34	7.3	0
43	Oct 22-28 (43)	31.9	14.9	78.9	30.6	6.5	0

Continue……

Appendix I. (Contd…)



Appendix II. Estimates of blast severity analysis among pearl millet germplasm lines

S. No.	Germplasm lines	Rating	S. No.	Germplasm lines	Rating	S. No.	Germplasm lines	Rating	S. No.	Germplasm lines	Rating
1	ICMB 02333	**6**	28	HMS 53B	**2.4**	55	EMRLT-14/103	**1.4**	82	HHB 272	**1.5**
2	ICMB 04888	**1.4**	29	HMS 54B	**3.7**	56	EMRLT-14/105	**4.3**	83	HHB 299	**1.2**
3	HMS 13B	**6.6**	30	HMS 55B	**2**	57	EMRLT-14/107	**1.5**	84	HHB 311	**1.9**
4	HMS 14B	**7**	31	HMS 56B	**3.7**	58	EMRLT-14/111	**2.2**	85	HHB67 IMP	**2.8**
5	HMS 16B	**6.7**	32	HMS 57B	**3.8**	59	EMRLT-14/121	**1.3**	86	HPT-2-12-32	**8.6**
6	HMS 18B	**6.7**	33	HMS 58B	**5.3**	60	EMRLT-14/123	**1.3**	87	HTP 03/13	**1.4**
7	HMS 26B	**1.4**	34	HMS 59B	**1.5**	61	EMRLT-14/124	**4.6**	88	HTP 94/54	**3.3**
8	HMS 28B	**2.5**	35	HMS 60B	**1.8**	62	EMRLT-14/127	**2.5**	89	HTP-10-129	**5.9**
9	HMS 29B	**5.7**	36	HMS 62B	**3.5**	63	EMRLT-14/229	**4.1**	90	IH 8	**1.8**
10	HMS 30B	**1.6**	37	HMS 63B	**2.2**	64	EMRLT-14/237	**3.1**	91	LTRL 15/123	**2.5**
11	HMS 32B	**7.7**	38	HMS 64B	**4.2**	65	EMRLT-14/243	**1.4**	92	PRLT 101	**1.7**
12	HMS 33B	**2.1**	39	HMS 65B	**1.4**	66	EMRLT-15/109	**4.9**	93	PRLT-107	**3.3**
13	HMS 34B	**8.1**	40	HMS 66B	**1.4**	67	EMRLT-15/133	**1.5**	94	PRLT-121	**2.6**
14	HMS 36B	**1.8**	41	HMS 68B	**1.8**	68	G73-107	**2.3**	95	PRLT-124	**1.8**
15	HMS 37B	**7.8**	42	HMS 69B	**3.2**	69	H13/0001	**1.5**	96	PRLT-132	**1.5**
16	HMS 38B	**6.4**	43	HMS 6B	**1.7**	70	H14/003	**1.6**	97	PRLT-134	**1.6**
17	HMS 39B	**1.7**	44	HMS 70B	**4.2**	71	H77/29-2	**1.5**	98	PT-1-1047	**1.8**
18	HMS 40B	**7.3**	45	HMS 74B	**3.8**	72	H77/833-2	**5**	99	SGP-10-107	**4.9**
19	HMS 41B	**8.2**	46	HMS 75B	**3**	73	H77/833-2-202	**3.9**	100	TCP-10-110	**3.2**
20	HMS 43B	**5.4**	47	HMS 7B	**5.1**	74	H90/4-5	**2.2**			
21	HMS 44B	**5.1**	48	ICMB 843-22	**4.3**	75	HB-15/085	**1.6**			
22	HMS 45B	**1.9**	49	ICMB 94555	**4**	76	HBL 11	**2.3**			
23	HMS 47B	**2.3**	50	ICMB 97111	**2.2**	77	HHB 197	**3**			
24	HMS 48B	**3.8**	51	A5RLT-14/106	**2.4**	78	HHB 216	**1.4**			
25	HMS 49B	**2**	52	AC 04/13	**2.4**	79	HHB 223	**2.1**			
26	HMS 50B	**5.1**	53	DMBRL-15/102	**3.5**	80	HHB 226	**2.8**			
27	HMS 52B	**3.7**	54	EBL-12-237	**1.5**	81	HHB 234	**3**			

ABSTRACT

Title of Thesis	:	Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]
Name of the Degree Holder	:	**Mohit Dhukia**
Admission Number	:	2018A54M
Title of the Degree	:	**Master of Science**
Degree Awarding University	:	CCS Haryana Agricultural University Hisar-125 004 (Haryana), India
Major Advisor	:	**Dr. Dev Vart**
Year of Award of Degree	:	2020
Major Subject	:	Genetics and Plant Breeding
Total Number of Pages in Thesis	:	52 + v + c
Number of Words in Abstract	:	212

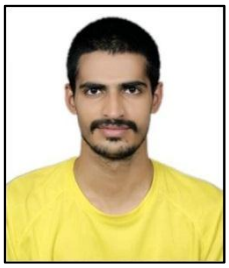
Key words: Genetic variability, GCA, SCA, Correlation, Blast

The present study entitled, "Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]" comprised of 100 pearl millet genotypes (50 designated A/B lines, 41 R lines and nine hybrids) and was laid out in two replications in randomized block design at experimental field of Bajra section, CCS HAU, Hisar during *kharif* (Rainy) 2019. Mean sum of squares were found to be highly significant due to genotypes for all the characters studied. The traits *viz*., panicle diameter, plant height, 1000-seed weight, dry fodder yield per plant and grain yield per plant exhibited high estimates of GCV, PCV, heritability and genetic advance as per cent of mean. Significant positive correlations were observed for grain yield per plant with plant height, panicle diameter, panicle length, 1000-seed weight and dry fodder yield per plant while with days to 50% flowering and blast it was negatively and significantly correlated. According to path coefficients analysis, high direct contribution towards the grain yield per plant was revealed by the traits *viz*., number of productive tillers per plant and panicle diameter. As per the blast screening studies, a total of 57 genotypes were found resistant towards the disease and male parent seems to have a major contribution in resistant towards the blast infection.

MAJOR ADVISOR **STUDENT**

HEAD OF THE DEPARTMENT

CURRICULUM VITAE



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10+2	CBSE	2012	71.6	Physics, Chemistry, Biology, English, Computer Science
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k) Training/ Experience attained: One week training on Freshwater Aquaculture at Central Institute of Fisheries Education (ICAR-CIFE), Kolkata and seven days training on Spices at ICAR-Indian Institute of Spices Research, Kozhikode, Kerala.

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3) Got excellence certificate in State Level Computer Jagrukta Abhiyan

4) Participated in 44th Haryana State Level Swimming Competition

I, hereby declare that all the information given in the curriculum vitae are true to the best of my knowledge.

(Mohit Dhukia)

UNDERTAKING OF COPY RIGHT

I, **Mohit Dhukia**, **Admission No. 2018A54M** undertake that I give copy right to the CCS Haryana Agricultural University, Hisar of my thesis entitled, **Genetic variability studies and screening for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**. I also undertake that patent, if any, arising out of the research work conducted during the programme shall be filed by me only with due permission of the competent authority of CCS HAU, Hisar.

SIGNATURE OF STUDENT