

**Character association, path analysis and genetic
diversity in finger millet (*Eleusine coracana* (L.)
Gaertn) genotypes**

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BHUBANESWAR-751003, ODISHA
2021**

**Mishra P, M. Sc. (Ag.) Thesis (2021), Character association, path analysis and genetic
diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes**

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Gaertn) genotypes**

A

***Thesis submitted to the
Odisha University of Agriculture and Technology
in Partial fulfilment of the Requirements for the degree of
Master of Science in Agriculture
(Plant Breeding and Genetics)***

By

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Date: 13th Sept, 2021

CERTIFICATE I

This is to certify that the thesis entitled “**Character association, path analysis and genetic diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes**” submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science in Agriculture (Plant Breeding and Genetics)** to the **Odisha University of Agriculture and Technology, Bhubaneswar** is a faithful record of bonafide and original research work carried out by **Pratikshya Mishra, Adm. No. 191222106** under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma.

It is further certified that the assistance and help received by her from various sources during the course of investigation has been duly acknowledged.

Tapash Kumar Mishra.

CHAIRMAN

ADVISORY COMMITTEE



CERTIFICATE-II

This is to certify that the thesis entitled “**Character association, path analysis and genetic diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes**” submitted by **Pratikshya Mishra, Adm. No. 191222106** to the **Odisha University of Agriculture and Technology, Bhubaneswar** in partial fulfilment of the requirements for the degree of **Master of Science in Agriculture (Plant Breeding and Genetics)** has been approved/disapproved by the students’ advisory committee and the external examiner.

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ACKNOWLEDGEMENT

Firstly, I would express my sincere gratitude, reverence and indebtedness to Dr. T.K. Mishra, Professor, Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar and Chairman of the my Advisory Committee, for his guidance, constant supervision, sustained interest, dynamic thought, constructive criticism, steady encouragement and whole hearted co-operation during the entire tenure of post-graduation for the successful completion of my dissertation.

I express my heartfelt gratitude to Dr. B. Pradhan, Professor and Head, Department of Plant Breeding and Genetics, OUAT, Bhubaneswar and member of my Advisory committee for providing the necessary facilities for the present investigation and preparation of this manuscript.

I am highly obliged to Dr. Manasi Dash, Assistant Professor, Department of Plant Breeding and Genetics and Dr. K.C Samal Professor of Department of Agricultural Biotechnology, OUAT, Bhubaneswar for constructive discussion, execution of plan of work and improving the manuscript.

I feel greatly indebted and convey my deep sense of gratitude to my esteemed professors Dr S.R. Das, Honorary Professor, Dr. D. Lenka, Professor, Dr. S. Sahu, Professor, Dr. P.N. Jagdev, Professor and Dr. B. Baisakh, Professor, Department of Plant Breeding and Genetics, OUAT, Bhubaneswar for giving their valuable and constructive suggestions, constant support and tremendous encouragement during the course of study and for timely completion of my thesis work.

My heartiest thanks to my seniors for their guidance and especially for providing necessary technical suggestions during my research pursuit. I feel thankful to all my friends and well-wishers for their encouragement and sincere co-operation.

I am also thankful to the staff of EB-I section, Mr. Barik and Mrs. Geetanjali Department of Plant Breeding and Genetics, OUAT for their sincere and timely assistance during my thesis work.

Lastly, I deeply acknowledge my beloved father Mr. Ramesh Chandra Mishra, mother Mrs. Puspanjali Mishra and brother Pratyush for being there for me in all good and bad times for constant support, encouragement and blessings.

I express my heartfelt gratitude to my grandparents and my uncle late Mr. Shubhranshu Shekhar Mishra, for their blessings and my entire family for being there with me throughout the journey and to encourage me for perusing higher studies.

And finally; I solicit benedictions before “The Almighty” for the progress and prosperity and thank Him for everything.

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ABBREVIATIONS

%	:	Per cent
ANOVA	:	Analysis of variance
CD	:	Critical difference
CV	:	Coefficients of variation
Fig.	:	Figure
FYM	:	Farmyard manure
GA	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic coefficient of variation
h^2		Heritability
<i>i.e.</i>	:	That is
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized Block Design
S. E. (d)	:	Standard error of difference
S. E. (m)	:	Standard error of mean
viz.	:	Namely

ABSTRACT

The present investigation on “**Character association, path analysis and genetic diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes**” was undertaken with the objective to determine the nature and extent of genetic variability, character association among yield and yield components, direct and indirect effects of various independent traits on grain yield and the extent of genetic diversity among the test genotypes of finger millet. In the present investigation, 30 promising genotypes of finger millet including two checks were taken and the experiment was conducted during Kharif, 2020 in the EB-II section, Department of Plant Breeding and Genetics, OUAT, Bhubaneswar with 3 replications using Randomised Block Design (RBD). From the analysis of variance, significant differences were observed among the genotypes for all the traits under study, indicating the presence of high degree of variability among the genotypes. A high GCV and PCV were recorded for the trait like grain yield/plant and number of ears/plants suggesting that these traits are under the direct influence of genotype of the plant. The characters grain yield/plant and number of ears/plants exhibited high GCV, PCV and moderate heritability coupled with high genetic advance. The maximum positive and significant association was found in between grain yield and number of ears per plant followed by days to 50% flowering, days to maturity and finger length, both at phenotypic and genotypic levels. Hence, these traits are truly associated with grain yield and selection of these traits may be rewarding to obtain higher yielding genotypes from the crosses in the crop. Path coefficient analysis revealed the highest positive direct effect of grain yield/plant on number of ears/plants followed by days to 50% flowering, finger length, number of fingers/ears and days to maturity while the maximum negative direct effect on grain yield were observed for 1000-seed weight followed by plant height, at both genotypic and phenotypic level. The Mahalanobis D^2 analysis grouped the thirty genotypes under study into five distinct clusters, cluster I having the maximum and cluster II and V having the minimum genotypes each. The maximum intra cluster distance was recorded in cluster III, while the minimum in cluster IV. The highest inter-cluster distance was present in between cluster IV and V followed by cluster III and IV, while minimum between cluster II and III. It implies that cluster IV and V are more distantly related than the rest of the others. As a result, these distantly related genotypes can be used as parents in a hybridization programme to obtain desirable transgressive segregants for crop improvement programme.



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CERTIFICATE OF ANTI-PLAGIARISM

This is to certify that the M.Sc. (Ag.) thesis of **Pratikshya Mishra**, Adm. No. **191222106**, Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar has been checked for anti-plagiarism by using Turnitin web portal and similarity index was found within 15% level (from Abstract to Summary & Conclusion) as prescribed by OUAT.

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INTRODUCTION

Eleusine corocana, commonly known as finger millet is a significant minor millet crop of India. It is widely accepted coarse cereal crop in the arid and semiarid zones in Asia and Africa. It holds fourth position in the list of important millet crop in the world after sorghum followed by pearl millet and barley. It is an annual herbaceous cereal (monocotyledonous) crop commonly known to have originated around five thousand years ago in the highlands of eastern Africa *i.e.*, from western Uganda to Ethiopia. It belongs to family Poaceae and is commonly known as Ragi (Hindi), mandua or mandia (Odia).

Finger millet is a C₄ short-day plant which is tolerant to drought and quite resistant to diseases and pests. It is found to be grown in warm temperate regions of the world. Ragi (*Eleusine coracana* L.) is an allotetraploid crop having chromosome number $2n=4x=36$ (AABB). Popularly, it is known as the poor man's crop. Out of the total area under the cultivation of millets which is around 38 million hectares, finger millet occupies 12% of it, covering more than twenty-five countries in Asia and Africa. Finger millet is cultivated in India in an area of 1.19 million hectares with a production and productivity of 1.98 million tonne and 1661 kg per ha, respectively. In Odisha, it is cultivated in an area of 1.16 million hectares with a production of 10.05 lakh quintals. It is a self-pollinated crop, but cross-fertilization has been reported to contribute less than 1% of the pollination. The branches of the inflorescence are slender to robust and sometimes may have secondary branches. Each spikelet has 6 to 9 flowers each of which are 6–10 mm long and are mostly organized in two rows along each side of the rachis. After the removal of the pericarp, the grains may be black, brown, red or white in colour. After ripening, the grains are visible between the florets in the non-shattering spikelets.

Agronomically, it is a sustainable crop which can be grown on high altitudes, marginal lands and can easily survive drought and saline environments. It has a much less requirement of irrigation and other inputs as compared to other crops. In India, finger millet is generally grown in rabi crop (cool and dry). Karnataka and Tamil Nadu are the most leading Ragi growing states in India, followed by Andhra Pradesh, Maharashtra, Uttar Pradesh, Uttarakhand, Rajasthan, Bihar and Odisha. It has high

yield potential more than 10-ton ha⁻¹ under optimum irrigated conditions. It can be grown on a wide range of soil from alluvial to lateritic soils. Besides, it can tolerate soil salinity up to some extent and can withstand water logging. Finger millet can be grown in the pH range of 5 to 8.2 and hence can tolerate moderately acidic to alkaline soils. It faces less risk to storage pest attack and can be stored for a long time (up to 5 years).

Ragi is crop of high nutraceutical values. The grains of finger millet are easily digestible, highly nutritious and can be cooked like rice, ground to make flour or used to make many traditional dishes. Sprouted grains are recommended for infants and elderly people. Finger millet is also used to make traditional liquor and its by-products are used as livestock feed. It can be used as a backup (famine) food and can be used as animal feed/fodder. It is gluten-free, rich in mineral and fibers that helps with weight loss and diabetes. It is full of calcium, good carbohydrates, amino acids and Vitamin D. It consists of a notable amount of niacin and a minimal level of fats. On an average, per it contains approximately 72 g of carbohydrates, 7.3 g of protein, 1.3 g of fats, 3.6 g of crude fibre and 2.7 g of mineral matters per 100 g of finger millet grain. It contains a very high concentration of calcium (344 mg per 100 g of grain) which is readily bio available and relatively high amount of phosphorus (238 mg per 100 g of grain) (Directorate of millet development, 2016). The grains are a rich source of protein (5.6 to 12.7%) proportionately higher in brown seeded than in white seeded genotypes. The grains contain high level of essential amino acids with 44.7% lysine, threonine and valine above the 33.9% of FAO. Besides, finger millet has sulphur containing amino acids that are crucial for human health and rich source of minerals like calcium, iron, zinc with manganese (Bhatt *et al.*, 2003, Singh and Srivastava, 2006).

In terms of research, however, this important nutri-cereal has long been neglected and often categorized as an orphan crop. Finger millet is one of the most neglected coarse cereal crops due to the reasons *viz.*, floral morphology and breeding behaviour, very small florets, not amiable for hand emasculatation and hybridization. Moreover, it is difficult to undertake breeding activities like genetic improvement through hybridization techniques due its extremely small inflorescence. These barriers have been the possible reasons for the unexplored genetic variability of finger millet.

Hence, it is of prime importance to screen the existing landraces and cultivars under cultivation for explain the existence of genetic variability for an efficient and rapid system of varietal improvement.

Reasonable variability has been stated in finger millet for the several traits such as days to maturity plant height, days to maturity, days to 50% flowering, finger related traits and disease reaction, which had not been fully exploited in breeding programmes. Hence, there is need to study the broad spectrum of genetic variability in the available finger millet genotypes to improve upon the characters contributing to grain yield. The major objective of any crop improvement programme is to breed for high yielding varieties in that crop. Yield being a polygenic character can not be selected directly based on any one or more morphological characters. Hence, genetic improvement in yield components would be more effective to improve yield. For achieving the above, the study of degree and direction of association of various components characters and with that of grain yield would be of paramount importance.

The major objective of plant breeding in any field crop is to create new improvement in genotypes with traits that contribute to higher yield potential, improved quality traits and higher yield stability (Poehlman and Sleper, 1995). In order to make the hybridization programme effective, genetically diverse parents are selected to achieve the target of combining traits of two different genotypes.

Based on the above facts, an investigation entitled **“Character association, path analysis and genetic diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes”** was carried out to study the following objectives.

1. To estimate the variability present in the genotypes of finger millet
2. To estimate the nature and magnitude of character association among yield and yield components
3. To access the direct and indirect effects of yield contributing characters on grain yield
4. To examine the genetic diversity among the test genotypes of finger millet

REVIEW OF LITERATURE

The knowledge on genetics of grain yield and other component characters is essential to formulate the effective breeding programme to bring about improvement in the crop yield. The successful exploitation of potentiality however, is dependent on the existence of variability at genetic level in the crop. For an effective plant breeding programme aimed to bringing improvement in complex characters like yield, an efficient selection and skilled management of experimental material would be of vital importance. Besides, that a comprehensive review of material in the domain concerned would also be of helpful in planning a strategy to achieve the aim. Studies pertaining to the present investigation are reviewed under the following headings.

2.1 Genetic variability

In order to initiate any breeding programme for crop improvement, the evaluation of genetic variability existing in the crop is of prime importance. Selection is only effective if the variation is heritable and a character is heritable only if it is under the influence of genetic control. Johnson *et al.* (1955) stated that heritability estimates give hints for selection based on phenotypic character and the heritability along with the genetic advancement should be considered together to attain a more reliable inference. Hence, in order to identify superior genotypes, genetic variability, heritability and genetic advance as percent of mean play a significant role. The comprehensive review of literature on coefficient of variability, heritability and genetic advance of finger millet as follows:

Nandini *et al.* (2010) examined the F₂ generation of 4 crosses of finger millet to enumerate the variability, heritability and genetic advances created for some quantitative characters. Maximum broad sense heritability detected for height of the plant, tillers/plant. Days to 50% flowering, finger length and 1000 seed weight showed moderate to high broad sense heritability.

Shet *et al.* (2010) recorded maximum GCV and PCV values for grain yield/plant, height of the plant and days to 50% flowering. High broad sense heritability accompanied with high genetic advance is detected in traits like plant height, length of the finger, test weight and grain yield/plant.

Dhamdhare *et al.* (2011) observed that genetic coefficient of variation was the main element of phenotypic variation. However, GCV was always less than PCV for most of the traits under study. High PCV was observed for crude content, ear weight and grain yield while lowest PCV was observed for plant height. High heritability and high genetic advance were recorded for ear weight, straw weight and total biomass while low heritability observed for plant height, tillers/plant and finger number/ear, leaf number/plant.

Two hundred and thirty germplasms of finger millet were examined by Ganapathy *et al.* (2011) and they found out that number of tillers/plant exhibited high GCV and PCV. Days to maturity showed significantly low GCV and PCV. High heritability and high genetic advance were recorded for traits like days to 50% flowering, plant height, finger length, tillers / plant, numbers of finger/ear and seed yield/plant.

Lule *et al.* (2012) studied 144 landraces of finger millet to evaluate the extent of genetic variability present in the quantitative traits under study. PCV were always higher than GCV for all the characters under study. High heritability and genetic advance were recorded for traits like, finger length, 1000 seed weight and grain yield/plant.

Extensive studies were undertaken for studying the presence of genetic variability in one thousand genotypes of finger millet for eleven polygenic traits by Haradari *et al.* (2012). For most of the traits a close association was found between GCV and PCV. Plant height, finger length and days to 50% flowering showed high heritability. Maximum genetic advance was observed for length of finger, no. of tillers/plant, grain yield/plant and plant stature.

Manjunath *et al.* (2013) analysed sixty-four accessions of white seeded finger millet for genetic variability for no. of productive tillers, finger length and 1000 seed weight high GCV and PCV was documented. Traits like days to 50 % flowering shows low PCV and GCV. For traits like days to fifty % flowering, finger length and 1000 seed weight showed high heritability and high genetic advance. Simple methods of selection can be applied due to fixable additive gene effects.

A study on sixty-five germplasms of finger millet for the presence of genetic variability was done by Karad and Patil (2013). The maximum values of GCV and PCV was observed for iron % and lowest was recorded for days to maturity. High heritability along with high genetic advance was observed for fodder yield/plant, days to 50% flowering, days to maturity and plant stature.

Analysis of eleven germplasms of finger millet under three environments for genetic variability of yield and yield contributing traits were undertaken by Patil and Mane (2013). Traits like number of productive tillers/plant and weight of ear contributed highly towards GCV and PCV. Characters like panicle weight, number of tillers/ plant and length of the main finger showed high heritability along with high genetic advance as percent of mean demonstrating the presence of additive gene action for these traits and selection of these traits can help improve the crop.

Reddy *et al.* (2013) analysed eighteen germplasms of finger millet to find out the extent of genetic variability present in them. Maximum value of PCV and GCV was noted for no. of fingers/ear. High broad sense heritability and genetic advance were noticed for traits like yield/plant, finger length and number of fingers/ear. Low heritability and genetic advance were recorded for threshing percentage.

Savitha *et al.* (2013) assessed twenty-one hybrids of finger millet along with their parents for genetic variability. Traits like number of fingers/ear and iron content recorded the maximum value of GCV and PCV. Traits like plant height, no. of productive tillers/plant, number of fingers/ear, harvest index (HI) and single plant yield showed high heritability along with high genetic advance demonstrating the presence of additive gene action for these characters and selection of these characters can prove to be effective.

Wolie and Dessalegn (2013) studied genetic variability in eighty-eight varieties of finger millet for some characters. High GCV and PCV has been recorded in traits like number of ears/plant, number of fingers/ear, finger length and grain yield/plant. Traits like number of ears/plant, number of fingers/ear, finger length, days to heading and 1000 grain weight showed high heritability along with high expected genetic advance per cent of mean denoting the presence of additive gene effects and

selection of these traits can be utilised for improvement of the crop due to its fixable nature of additive gene effects.

Thirty-five germplasms of finger millet were analysed for genetic variability by Chaudhart *et al.* (2014). Traits like straw yield, plant stature, days to 50% flowering and days to maturity showed high PCV and GCV. Medium PCV and GCV was observed for grain yield and total fingers/plant and the traits like tillers/plant, fingers/main ear, finger length and test weight showed low PCV and GCV.

Evaluation of one hundred and five germplasms of finger millet for 13 quantitative traits to evaluate the extent of variability and characters association was undertaken by Ulaganathan and Nirmalakuman (2014). Grain yield/plant and number of tillers/plant showed maximum values for PCV and GCV. All the traits under study recorded high heritability ranged from indicating that these traits were relatively less predisposed to environment and selection of these traits can be utilised for improvement of the crop.

Suryanarayana *et al.* (2014) assessed for the extent of genetic variability in thirty-five genotypes of finger millet for seven polygenic traits for genetic variability. For traits like high for grain yield/plant, number of tillers/plant and finger length, the GCV and PCV were reported to be high. For seed yield/plant and length of the finger, high heritability with high genetic advance were detected.

Shinde *et al.* (2014) examined forty-one germplasms of finger millet for variability, heritability and character association. High GCV and PCV were witnessed for number of tillers/plant and grain yield/plant. A high approximation of heritability was obtained for all the traits studied except protein content. For traits like tillers/plant, seed yield/plant and iron content showed high heritability along with high genetic advance as per cent of mean and selection on the basis of these characters is likely to be more effective in the segregating generations.

Saundarya and Satish (2015) observed thirty-five varieties of finger millet and recorded high PCV and GCV along by high heritability and genetic advance as percent of mean for traits like, number of fingers/ear, grain yield/plant, harvest index, tillers/plant, 1000 seed weight and days to 50% flowering demonstrating the presence

of additive gene action for these characters and selection based on phenotypic for these traits would likely to be more useful.

Rani *et al.* (2015) observed forty diverse germplasms of finger millet for genetic variability for eleven polygenic characters. Maximum genetic gain was observed for seed yield/plant followed by seed protein content and weight of ear/plant representing the existence of additive gene action in the inheritance of these traits.

Manjunath *et al.* (2015) examined two-hundred and seventy-four finger millet genotypes. High values of PCV and GCV was observed for tiller number/plant, finger length and test weight. Days to 50% flowering, plant height, finger length and test weight showed high heritability coupled with high genetic advance which specifies the prevalence of additive gene effects in these characters hence, selection of these traits can be utilised for improvement of the crop due to its fixable nature of additive gene effects.

Eric *et al.* (2016) examined 340 landraces varieties of finger millet from Uganda, Kenya and Tanzania and eighty global mini core accessions from ICRISAT Gene bank. Traits like fingers/ear, tillers/plant, 1000 seed weight and finger length showed high broad-sense heritability representing the possibility for their enhancement through selection.

Jyothana *et al.* (2016) observed that GCV for all the traits under study of the 25 genotypes of finger millet were lesser than the PCV indicating the genotypes with environment. For traits like seed yield/plot and straw yield/plot high heritability coupled with high genetic advance (GA) was detected. This represented the significance of additive gene effect in governing the inheritance of these traits.

Genetic variability in fifteen genotypes of finger millet were examined by Sao *et al.* (2016a). High PCV and GCV were recorded for finger length whereas low PCV and GCV were recorded for days to maturity and plant height. High heritability along with high genetic advance was observed for days to 50% flowering, days to maturity, finger length and grain yield/plant. Simple selection of these traits is effective as they are highly under the influence of additive gene effects.

Sao *et al.* (2016b) studied twenty-six finger millet high yield varieties to reveal the genetic variability present in the characters under study. High GCV and PCV were documented for finger length and number of fingers/ear. Traits like days to 50% flowering, finger length, days to maturity and grain yield/plant showed high heritability. Thus, Simple selection of these traits is effective as they are highly under the influence of additive gene effects.

Auti *et al.* (2017) compared sixty-four landraces of finger millet and two cultivars for yield contributing and agro-morphological characters. Maximum genotypic and phenotypic coefficient of variation was recorded for number of tillers/plant. The characters which were influenced by environment showed higher PCV. High and low heritability were observed in 1000 seed weight and plant height, respectively. Thousand seed weight showed high heritability along with small genetic advance.

Mahanthesha *et al.* (2017) recorded the high values of GCV and PCV for characters like grain yield/plot, grain yield/plant, number of tillers/plant, main ear width and length of the finger. For characters like plant stature, number of tillers/plant, ear length, ear width, finger length and grain yield/plant high heritability along with high genetic advance as percent of mean was noticed. Hence, these traits are under the influence of additive gene effects and selection of these characters can be effective.

An experiment was done by Devaliya *et al.* (2018) with sixty-eight varieties of finger millet evaluate the extent of genetic variability, heritability (h^2bs) and genetic advance (GA) for yield and yield contributing characters. Grain yields showed high GCV and PCV. Traits like grain yield/plant, number of productive tillers/plant and finger length showed high heritability along with high genetic advance at per cent of mean and hence are involved in additive gene action and phenotypic selection on the basis of these characters is likely to be more effective in the segregating generations.

Anuradha *et al.* (2019) analysed ten genotypes of finger millet for variance. ANOVA showed substantial variation for many characters under study. For these traits GCV ranged from medium to low. High heritability with moderate genetic advance at per cent of mean was observed in traits like days to fifty % flowering, days to maturity, finger length, finger width and leaf length signifying occurrence of both

additive and non-additive gene action. High heritability with moderate GAM indicates the presence of both additive and non-additive gene action. Although, the grain yield showed moderate heritability with moderate GAM. This indicated the presence of both additive and non-additive gene action affecting the grain yield and hence, can respond to selection moderately.

Patel *et al.* (2020) studied thirty finger millet germplasms which consisted of 29 landraces and 7 commercial varieties were assessed for 12 morphological characters. Moderate GCV and PCV was obtained for traits like number of fingers/ear, grain yield/plant, finger length, ears/plant and harvest index. Low GCV and PCV was recorded for days to 50% flowering, days to maturity, plant stature and 1000 grain weight signifying low variability for these traits. High heritability was observed for days to 50% flowering, days to maturity, plant stature, number of tillers/plant, fingers/ear, main ear head length, finger length, 1000 grain weight, and grain yield/plant. As a result, these features are impacted more by additive gene action than by the environment.

2.2 Character association and path analysis

Correlation coefficient analysis measures the mutual relationship between various agronomic characters and determines the component characters of grain yield on which selection can be based to bring about genetic improvement in yield. But path analysis on the other hand specifies the cause and permits the separation of correlation into two measures of direct and indirect effects and describes the relative importance of casual factors in producing the end products.

Experiment on sixty primitive varieties of finger millet along with two check varieties for fifteen characters in Ethiopia was done by Bezawelelew *et al.* (2006). Maximum and minimum range was observed in grain yield/plant and days to maturity, respectively. High heritability was recorded for finger length and width. Leaf blade and culm thickness had the strongest positive relationship, whereas 1000 seed weight and finger number had the weakest. Grain yield/plant was favourably related to productive tillers, 1000 seed weight, and finger number, but days to maturity was adversely connected. The 1000 seed weight, finger number, and

productive tillers were found to be the key contributors to grain yield/plant in the correlation and path-coefficient study.

Nandini *et al.* (2010) studies F2 generation of finger millet for correlation and path analysis. They concluded that, a significantly strong positive association prevailed in between grain and characters like yield/ear, 1000 seed weight and tiller/plant. Positive direct effect of weight of ear and 1000 seed weight is observed on grain yield.

Anuradha *et al.* (2013) observed positive significance association for traits like number of fingers/ear and days to maturity. From path analysis it was concluded that number of fingers/ears and days to maturity displayed positive correlation and positive direct effect towards the grain yield.

Ali *et al.* (2013) investigated variability, heritability, and character association among key yield contributing features in 140 finger millet germplasms. They found high heritability with moderate genetic advance for days to maturity and days to 50% flowering, as well as high heritability with moderate genetic advance for days to 50% flowering and days to maturity. The most significant positive correlation was found between total fingers/plant and the number of productive ears/plant at both the genotypic and phenotypic levels, while the most significant negative association was found between harvest index and biological output.

Kumar *et al.* (2014) experimented with 140 germplasms of finger millet for ten polygenic characters. From the analysis of variance, it was concluded that significant variability was present among the germplasms. From path coefficient analysis, positive and direct effects were detected for tillers/plant and no. of fingers/ear on grain yield at genotypic and phenotypic levels. Selection for these traits can be useful for improving the finger millet genotypes.

Singh *et al.* (2014) experimented with 15 germplasms of finger millet. From the correlation studies it was concluded that yield/plant was associated positively and significantly with weight of the ear/plant. While yield was reported to be negatively and significantly associated with days to maturity and days to 50% flowering. The path analysis revealed the maximum positive and direct effect of ears/plant.

Jadhav *et al.* (2015) studied character association in germplasms of finger millet and recorded at both genotypic and phenotypic levels, a significant positive association of grain yield/plant with traits like thousand seed weight, number of fingers/ear, ear length, days to maturity, tillers/plant, days to 50% flowering and plant height. By path analysis estimations, a true relationship was observed for traits like that thousand seed weight, number of fingers/ear, days to maturity, finger length and days to 50% flowering with seed yield/plant thus, implying a significant positive association and high positive direct effect.

Jyothsna *et al.* (2016) observed the GCV for all the traits under study were less than PCV. This indicates the presence of interaction between the genotype and the environment. From correlation analysis the plant height and finger length were found to be positively correlated with grain yield/plot at genotypic and phenotypic levels. By path analysis at both genotypic and phenotypic levels, plant height and finger length exhibited close association by establishing positive association and direct effect on grain yield/plant.

Evaluation of thirty-five germplasms of finger millets was done by Saundarya Kumari *et al.* in (2016). Outcomes from correlation studies showed that grain yield/plant revealed significant positive association with harvest index, number of tillers/plants, grain weight of main panicle and thousand grain weight. Although, days to maturity and days to 50% flowering showed negatively association with grain yield/plant. This implies that early genotypes yielded less. Path coefficient analysis disclosed that highest positive direct effect was shown by harvest index, number of ears/plants, grain weight of main panicle, thousand grain weight and number of fingers/panicles.

Investigation was done to find out the correlation and path coefficient analysis of 15 finger millet germplasms by Sao *et al.* (2016). Grain yield was found to have a substantial positive connection with features like productive tillers/plant and finger length. Days to maturity, days to 50% blooming, and length of finger all demonstrated positive significance at the genotypic level. The results of path analysis revealed that factors like days to maturity and fodder weight/ear had a favourable direct effect on seed output.

Thirty-five genotypes of finger millet for fourteen quantitative traits using RCBD design were analysed by Negi *et al.* (2017). They found out a robust affirmative correlation among grain yield/plant and biological yield, harvest index, productive tiller number and 1000 seed weight both at genotypic and phenotypic level. According to path-coefficient analysis, biological yield/plant and harvest index (HI) were found to be major contributors towards yield/plant at phenotypic and genotypic level. Thus, the traits identified above helps in selection of finger millet for developing high yielding varieties.

Devaliya *et al.* (2017) used estimated correlation and path coefficient analysis in 68 genotypes of finger millet for thirteen morphological traits. Grain yield/plant had a highly positive and significant relationship with the number of productive tillers/plant, main ear head length, and protein content at both genotypic and phenotypic levels, and calcium content had a highly significant correlation with grain yield/plant at genotypic level, indicating that these traits were primarily affecting the phenotypic level. Days to 50% flowering, 1000-grain weight, and protein content all had a direct positive effect on grain output, according to path analysis.

Gohel *et al.* (2018) studied 30 germplasms of finger millet for character association and path analysis. A significant positive association was found in traits like grain weigh/main ear, harvest index, number of productive tillers/plants, biological yield/plant and panicle length towards grain yield/plant at both phenotypic and genotypic level. Path coefficient analysis exposed that grain weight/ear had the highest direct positive effect towards the grain yield followed by number of productive tillers/plant, ear length, days to 50% flowering, harvest index and biological yield/plant.

From the correlation analysis conducted by John *et al.* (2018) on various genotypes of finger millet for certain characters, it is observed that yield/plant has a positive correlation with days to 50% flowering, days to maturity, finger length, fingers/ear productive and ears/plant. As a result, because these traits were linked to grain yield, they may be used as selection criteria for higher yielding plants. Days to 50% flowering had a significant positive correlation with days to maturity (0.9700), fingers/ear (0.4290), and finger length (0.2932), as well as a non-significant positive

correlation with plant height (0.2772), fodder weight/plant (0.2342), tillers/plant (0.1536), and grain yield/plant (0.1439).

Mahanthasha *et al.* (2018) examined character association and path coefficient analysis, for 48 finger millet germplasms. Grain yield/plant has a substantial positive relationship with number of tillers/plants, fingers/ear and ear length, according to correlation analysis. According to path analysis, productive tillers/plant had the greatest positive direct effect on grain yield/plant, followed by ear length.

Keerthana *et al.* (2019) examined 120 strains of finger millet under sodic soil condition. From path analysis, it was concluded that of productive tiller/plant, days to 50 % flowering, ear length, plant height and thousand grain weight has a direct effect on seed yields. The above characters were significantly and positively associated with grain yield. Thus, the above traits can be used for yield enhancement in finger millet.

Studies on forty genotypes of finger millet in RBD for correlation coefficient and path analysis were undertaken by Sapkal *et al.* (2019). A positive and significant correlation was observed for number of tillers/plant, finger length and number of fingers/plant. Direct effect was observed in number of tillers/plants, number of tillers/plants, length of finger and number of fingers/ears along with highly significant correlation in the desirable direction towards grain yield/plant indicated real relationship between the grain yield and these traits.

Vidhate *et al.* (2020) experimented with one hundred and fifty-eight germplasms of finger millet using randomized block design with 2 replications. Correlation analysis aims at understanding the interrelationship among various yield components at genotypic and phenotypic levels. It revealed that traits like thousand grain weight, finger length and number of fingers/ear, showed positive association with grain yield. Path coefficient analysis aims at understanding the direct and indirect effect of the various quantitative traits towards grain yield/plant. From these studies it was concluded that days to 50% flowering, finger number/panicle, finger length, finger width, days to maturity, thousand grain weight, calcium content and iron content contributed significantly towards grain yield/plant. Selection for one of the above traits can hence, significantly increase the economic yield of the plant.

Chavan *et al.* (2020) investigated path association and correlation in 15 genotypes of finger millet using RBD (Randomized Block Design) with three replications. By path coefficient analysis, harvest index followed by straw yield/plant, number of fingers/ear, number of tillers/plant, plant height seemed as the chief factors that has the maximum effect of grain yield/plant both at genotypic level and phenotypic level. A positive correlation was observed in between plant height, days 50% flowering, number of ears/plant, number of fingers/ear, length of finger (cm), test weight (g), straw yield/plant (g) and harvest index (%) and grain yield/plant (g) at genotypic and phenotypic levels. Positive correlation was observed in between days to maturity and grain yield/plant only at phenotypic levels.

Nagar *et al.* (2020) observed GCV and PCV to be high for days to 50% flowering but moderate for features like plant height, days to maturity, tillers/plant and 1000 seed weight. Days to 50% flowering, days to maturity, plant height, tillers/plant and 1000 grain weight all had high heritability. Days to 50 % flowering, tillers/plant, plant height, days to maturity and flag leaf length all had high estimates of genetic advance. Grain yield/plant was found to have a highly substantial and positive phenotypic association with harvest index, length of inflorescence, biological yield/plant and peduncle length. Path analysis revealed that the biggest positive direct effect on grain yield/plant was by number of ears/plant followed by days to 50% flowering, biological yield/plant, peduncle length, 1000 grain weight, length of inflorescence and tillers/plant.

2.3 Genetic divergence

The prevalence of genetic diversity in the population is essential for the success of any crop improvement programme. Selection within a population is useless without genetic variability. The Mahalanobis D^2 statistical analysis is used to determine the genetic diversity existing among different germplasms. This analysis helps to group the genotypes into distinct clusters. The more the inter cluster distance the more diversely they are related and hence, hybridization work can be taken up in between the distantly related genotypes.

Investigation of 37 genotypes of Ragi to study the extent of genetic diversity present in the genotypes was done by Bedis *et al.* (2007). Mahalanobis D^2 statistics

was done and it was found out that the 37 genotypes had a significant amount of genetic diversity. These varieties were gathered into 7 clusters. Out of them, cluster I has the highest number (12) of genotypes. Genetic divergence was highest between clusters III and V as the intra-cluster distance between them was maximum.

Satish *et al.* (2007) conducted an experiment involving 178 finger millet genotypes. These strains were found to be grouped under ten clusters. In between cluster II and V, the maximum inter-cluster was recorded. They concluded that the genetic diversity is not associated with geographic origin. Florets number/spikelet added maximum towards the genetic divergence. Cluster VI showed maximum cluster mean. Choice of parental lines for crossing programme to get alluring recombinants has been anticipated.

Prabhu *et al.* (2008) examined genetic divergence in 150 germplasms of finger millet for twelve traits. A highly substantial difference was observed among the germplasms for all the twelve traits under study. For no. of tillers and single plant yield, High heritability and genetic advance were recorded. This increases the likelihood of improvement for these characters by simple selection. Cluster analysis was done using Mahalanobis D^2 statistics which resulted in 18 clusters out of which 14 mono-genotypic clusters were superior. Hybridization between strains of these genetically diverse clusters would result into heterosis in the F1 and segregating generations for the development of high yielding commercial varieties. The conventional breeding techniques can utilize only the genetic variability and diversity present in the parent population. Hence, it is desirable to evaluate the genetic divergence of the germplasms to bring about desirable hybridization and get desirable traits in the subsequent generations.

Kadam (2008) revealed that an experiment was done with seventy germplasms of finger millet for 15 traits to evaluate the genetic diversity and variability using Mahalanobis D^2 analysis. The genotypes eventually were found to be grouped into 8 clusters. Cluster I had the maximum number of germplasms (38). The highest inter cluster distance was detected between cluster VIII and V. Cluster III had most elevated mean values for grain yield/plant. He revealed that plant tallness and days to half blooming contributed greatest towards the total genetic divergence. Parallelism

has been detected between geographical diversity and genetic diversity. While undertaking plant breeding programme, it is advisable to take genotypes with high yields and those with high genetic divergence as parents for hybridization to produce wide-ranging variability for the improvement of yield in Ragi.

An experiment was conducted with one-hundred and forty diverse strains of finger millet for ten polygenic characters by Kumar *et al.* (2010). They classified these one hundred and forty diverse genotypes into 10 distinct clusters, based upon the non-hierarchical Euclidean cluster analysis. Cluster I had the maximum number of genotypes (31) followed by cluster V (28). The inter-cluster distance was highest in between clusters X and I lowest in between cluster III and VIII.

Analysis of genetic diversity in 30 genotypes of finger millet utilizing Mahalanobis's D^2 statistics, out of which 10 were already released varieties, was undertaken by Sahu and Pradhan (2012). These strains got arranged in 12 clusters. Cluster II comprised of the maximum (seven) genotypes. The highest inter cluster distance was found in between cluster IV and VII subsequently by cluster IV and XII. Cluster X (OEB 71) and cluster VI showed the highest means for grain yield. Cluster VIII (Neelachal) was recorded to give the maximum number of productive tillers/plants. Cluster XII (VL 149) had the most noteworthy mean for plant stature, fingers/ear and finger length.

Lule *et al.* (2012) presented their views on rapid change in the climatic conditions, especially in the rainfall distribution pattern along the tropical and sub-tropical regions. This has necessitated switching over to some climate resilient hardy crops like finger millet. Evaluating genetic diversity is a vital for development of good climate resilient varieties and for the conservation of genetic resources. They collected 144 finger millet primitive varieties from various provinces of Ethiopia. Results of D^2 analysis showed strong resemblance among the finger millet germplasms taken from neighbouring areas of Ethiopia, neighbouring African nations and proximity in altitude classes. Principal component analysis showed that traits like seed yield/plant, 1000-seed weight and days to maturity played major role towards the contribution genetic variability. Hence, it was inferred that selection of these characters can help achieve the goal.

An experiment with a set of 65 strains of finger millet was done by Karad and Patil (2013). They took into consideration 12 phenotypical traits for the analysis of the extent of genetic divergence by the use of Mahalanobis D^2 statistics. They detected variations for the characters under study. D^2 statistics showed the presence of genetic diversity within the genotypes. Those 65 genotypes were grouped under 5 clusters. The highest 50 genotypes were present under Cluster I succeeded by cluster II (11) and cluster III (2). The mono-genotypic clusters were IV and V. After D^2 analysis, they recommended KOPN 161, KOPN 370, VL 149, KOPN 387, PR 202, PES 110, KOPN 495, KOPN 892 and KOPN 926 to be the most diverse genotypes. These genotypes could be exploited to enhance, widen the genetic base and for plant hybridization programme to improve the grain yield of finger millet.

Shinde *et al.* (2013) gathered forty-one genotypes of ragi from different areas and assessed the genetic divergence of the genotypes by using D^2 statistics. Undergoing D^2 analysis, the genotypes grouped under 7 clusters. In between clusters II and VII maximum inter-cluster distance was observed. Thus, these can be used as parents in crossing programme. Their studies revealed, iron content trait contributed utmost towards divergence succeeded by height of the plant, days to physiological maturity and days to half blooming.

Wolie and Belete (2013) stated that finger millet is a cereal crop of prime importance in Ethiopia and ranks sixth in terms of total production within Ethiopia. To assess the genetic divergence indigenous genotypes of variable origins were taken. Multivariate analysis using Mahalanobis's D^2 statistics was done to analyse the Genetic divergence. The strains of finger millet got grouped into 8 clusters. They recorded the highest intra cluster D^2 in cluster VIII and maximum inter-cluster distance was in between cluster VII and VIII. The investigation revealed that the genotypes collected showed an unparallel behaviour for genetic divergence and geographical diversity. Thus, hybridization and subsequent selection of desirable traits is suggested as an essential tool to utilize the wide spectrum of variability present among the germplasms to produce superior high yielding and good quality commercial varieties.

Jain and Patel (2013) examined genetic divergence in one hundred and eight strains of sorghum by using Mahalanobis D^2 statistics. the strains got partitioned into eleven clusters out of which cluster I had the maximum number of genotypes (23)

followed by cluster II (17). The maximum inter-cluster values were recorded between cluster XI and V cluster followed by VI and III. Towards the total variation green and dry fodder yield contributed significantly. Hence, the extensive degree of divergence has been observed in the sorghum genotypes.

Kumari and Singh (2015) conducted an experiment with 35 varieties of ragi to find out extend of genetic diversity utilizing D^2 analysis, in randomized block design (RBD) with 3 replications. Observations were recorded on 11 quantitative characters. On the basis of Tocher's method, the germplasms of finger millet were congregated into 6 clusters. A high degree of genetic divergence was exhibited by cluster IV and VI. For grain yield/plant, 1000-seed test weight, seed yield of main panicle and harvest index (HI) Cluster III was found to be appropriate.

Analysis of genetic divergence among thirty-three strains of black gram out of which 26 were mutant lines, 3 parental and 4 check varieties was done by Das *et al.* (2016). On the basis of D^2 statistics, by using Tocher's method these thirty-three strains were partitioned into 6 clusters. Cluster-III showed the maximum intra cluster distance while the highest inter-cluster distance was recorded between cluster V and VI. Cluster V gave exceptionally good results for yield/plant and thousand seed test weight. Whereas for seeds/pod and pods/plant, in cluster IV gave outstanding results. Therefore, crossing between strains belonging to cluster V with cluster IV is recommended for development of high yielding cultivars.

Analysis was undertaken for genetic divergence in forty-eight stains of finger millet for eleven quantitative traits by using D^2 statistics by Mahanthesha *et al.* (2017). They observed that cluster I had the maximum number of germplasms followed by cluster II. The extreme intra-cluster distance was observed in cluster VI. Utmost genetic divergence was detected between cluster VI and VIII. Among the polygenic traits considered, seed yield/plant was the utmost important trait contributing maximally towards divergence trailed by main ear width. For improving finger millet, worth of parents has been recognized based on genetic divergence. Clusters VI, II and IV had high yielding genotypes. They concluded that not a single genotype within any cluster had all the desirable characters. Therefore, no genotype can be directly selected for immediate use. Therefore, to achieve the desirable combination of traits, crossing between the genotypes from distinct clusters is indispensable.

Investigation for the presence of genetic diversity in thirty-five varieties of finger millet for 14 phenotypical traits using Mahalanobis D^2 analysis was done by Negi *et al.* (2017). From the studies they concluded that genotypes under study were genetically diverse. From the analysis, the 35 genotypes under study were grouped into six distinct clusters. The geographic diversity and genetic diversity were found to be unrelated. The maximum number of genotypes were present in cluster I and VI (8) followed by cluster II and V (4). Having the maximum inter-cluster distance, cluster IV and V were more diverse and hence can be recommended to be used in potential crossing programme. They suggested, hybridization of genotypes within cluster IV with that of cluster V and VI would be productive for attaining transgressive segregants in F2 generations. This could help in the development of superior high yielding varieties in finger millet.

Devaliya *et al.* (2017) revealed that the presence of genetic variability, genetic divergence and the correlation among different traits is indispensable for the fruitfulness of any plant breeding programme. Conventional breeding approach can utilise only the genetic variability and genetic divergence present within the germplasms. And for efficient utilization of these germplasm resources, it is essential to recognize superior genotypes by proper characterization & evaluation. Among the multivariate procedures, Mahalanobis (1936) D^2 statistics has been employed widely. They examined sixty-eight germplasms of finger millet (*Eleusine coracana* (L.) for thirteen polygenic characters to assess the extent of genetic divergence. D^2 analysis showed that the germplasms studied were genetically distinct. These germplasms were arranged into 8 clusters, cluster I having the highest numbers of genotypes (60). In between cluster-VIII and III, highest inter-cluster distance was recorded. They recommended that germplasms from different clusters could be used in crossing programme for enriching the yield efficiency of finger millet.

Mahanthesha *et al.* (2017) examined forty-eight germplasms of finger millet for genetic divergence using D^2 analysis. The D^2 statistic divided the genotypes into 8 clusters, cluster I having the majority of germplasms (24) followed by cluster II (24). Maximum inter-cluster distance was observed between cluster VI and VIII, indicating the maximum degree of genetic divergence among the lines present in these clusters. Cluster VI, II and IV were identified to be high yielding groups. Out of the eleven

polygenic characters analysed, the most significant feature contributory to the genetic divergence was grain yield/plant followed by total number of tillers/plant, number of fingers on the main ear and width of the finger. Parents from diverse groups are selected to get better heterosis in the subsequent generations, hence improving the productivity of finger millet.

Damtie *et al.* (2019) conducted a study to investigate genetic divergence among twenty-four genotypes of finger millet for 10 morphological characters in randomized complete block design (RBD). The aim was to examine and select high yielding and blast tolerant germplasms. The variance analysis of revealed the presence of highly significant ($P < 0.01$) variation among strains for all examined characters. This infers the feasibility of selection for these characters present in the germplasm for imminent improvement of the finger millet varieties. For logging, finger length, head blast and grain yield elevated genotypic and phenotypic coefficients of variations were observed. High genetic advance was detected for finger length; seed yield and head blast score. The principal component analysis demonstrated the first three principal components elucidated most of the variability detected in the data set. Traits like days to blooming, days to maturity, blast score, and grain yield contributed significantly towards the genetic variability. From cluster analysis, highly substantial inter-cluster distance was recorded to be present in between four clusters. Under cluster II stress resistant and high yielding strains were observed. Hence, the genotypes under cluster II can be significantly used as parents in the plant breeding improvement hybridization programme.

Suryanarayana *et al.* (2019) examined 30 strains of finger millet for genetic diversity using D^2 statistics. These strains were assembled into 12 distinct clusters, cluster I having the highest number of strains (6) followed by cluster XI (4). The inter cluster distance was found to be highest between cluster VII and XI. According to inter cluster distance, cluster II, VII and XI were found to be genetically more diverse and hybridization within these clusters was recommended to get the desirable transgressive segregants. Trait like grain yield, no. of tillers/plant and finger length contribution towards genetic divergence in a descending order, respectively. They suggested the use the genotypes of these diverse cluster as parents to develop good high yielding cultivars.

Mahalanobis D^2 statistical analysis for forty germplasms of finger millet was carried out by Sapkal *et al.* (2019). The variance analysis indicated that significant variation is present among strains for all the characters. Of the 6 clusters formed, cluster I has the highest number of genotypes (23) followed by cluster II (8). No evidence of any relationship was found in between the genotypic clusters showing more divergence can be crossed to exploit more heterosis and produce required transgressive segregants in segregating generations for improvement of the crop breeding programme. In between cluster II and VI, highest inter-cluster distance was found. The variance for cluster means were maximum for grain iron content, followed by seed yield/plant, finger length. On the basis of above analysis, they concluded that the following genotypes were diverse and unique viz., DHFM-13, DHFM-36, DHFM-3, DHFM-12, DHFM-18. Hybridization among these genotypes can ensure promising results.

An experiment on genetic diversity was conducted to study thirty-three germplasm of finger millet using D^2 statistical analysis by Subramanya and Ravikumar (2020). These 33 strains were arranged into 10 clusters. Cluster II and IV had 9 strains each while cluster I had 8 strains. Rest of the clusters were mono-genic. The maximum inter cluster distance was found in between cluster VII and VIII and followed by cluster VII and cluster II. Towards the genetic divergence, Days to 50% flowering contributed maximally. Grain yield was highest for cluster VII (GE4568). The strains having the most divergent genotypes with higher mean per se performance for many of the yield and yield associated traits were GE4568 and GE5118 and these can be efficiently exploited in hybridization programme to generate greatly variable segregating population to produce superior commercial varieties.

Patel *et al.* (2020) did genetic diversity analysis by using 36 finger millet strains. They took into consideration 12 polygenic characters. As per Tocher's method, the genotypes were arranged into 7 clusters. Cluster I had the maximum number of strains (26). The maximum inter-cluster distance was observed in between clusters VI and VII hence, they are more genetically diverse groups. The outcomes validated the absence of any significant relationship between genetic diversity and geographic origin, as germplasms from the various geographical regions were present in the same clusters and the genotypes of same geographical regions were present in the different clusters.

MATERIALS AND METHODS

The present investigation on “**Character association, path analysis and genetic diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes**” was carried out at EB-II section, Department of Plant Breeding and Genetics, OUAT, Bhubaneswar during Kharif season in 2020. This section comprises of a complete elaboration of the location of the experiment, experimental material, design, layout, observations recorded and statistical techniques followed for analysis of data.

3.1 Location of experiment

The experiment was conducted during Kharif season 2020 in the OUAT Farm, EB-II sections, Department of Plant Breeding and Genetics, OUAT, Bhubaneswar. The experimental site is located at 20°15' N and 85°52' E latitude and longitude, respectively with an elevation of 45 m above the mean sea level or 148 ft above the mean sea level.

3.2 Experimental material

The experimental material comprised of 28 promising cultures of finger millet along with 2 check varieties (Table 1). The experiment was conducted using Randomized Block Design (RBD) with 3 replications.

3.3 Experimental designs and field layout

The seeds were sown in the nursery on 30th June, 2020 and were transplanted into the main field on 28th July, 2020. The research was performed using Randomized Block Design (RBD) with 3 replications. The area of the plot was 826-meter square with the dimensions of 28 m length and 29.5m width. The plot was subdivided into 9 subplots each consisting of 5 rows with each row having 30 plants. The spacing was maintained at 20 cm x 10 cm. The fertilizer dose of N:P:K @ 40:20:20 kg/ha was applied to the experimental field with whole potassium and phosphorous as basal at the time of transplanting. The rest 50% nitrogen fertilizer was applied at the time of land preparation, as top dressing at tillering stage. Farm yard manure @10 tons/ha was applied. Other suggested agronomical packages of practices were followed during the experimental process to raise a good crop.

3.4 Recording experimental data

Five plants were randomly selected from each entry in each replication. The plants were tagged before harvest of each entry. Observations were recorded on the following characters.

1. Days to 50% flowering
2. Days to maturity
3. Plant height (cm)
4. Ear length (cm)
5. Number of fingers/ear
6. Number of ears/plant
7. 1000-seed weight (g)
8. Grain yield/plant (g)

The data on the following traits were recorded in each replication

1. **Days to 50% flowering:** Period in number of days recorded from the day of sowing in nursery to the days when the 50% of ear emergences from the main tiller in each entry was observed.
2. **Days to maturity:** It involves the number of days from the date of sowing to till 80% of the plant reaches physiological maturity.
3. **Plant height (cm):** It represents the length of the plant from the ground level to the tip of the inflorescence at dough stage. The measurement was taken in centimetre.
4. **Ear length (cm):** At the dough stage, the length measurement from the basal node to the tip of the longest spike of the main tiller is taken. Observation was taken only for the tagged plants.
5. **Number of fingers/ear:** At the dough stage, the number of fingers in the main ear head is taken into account. The average number of fingers per ears was calculated.
6. **Number of ears/plant:** No. of ears per tagged plant was counted and their average was taken
7. **1000-seed weight (g):** 1000 seeds were counted randomly from the tagged plants and their weight was taken in grams up to 3 decimal points.

- 8. Grain yield/plant (g):** The total amount of seed obtained from each tagged plant was weighed using an electrical balance. Then the average of the five tagged plants was calculated.

Table 1. List of genotypes of finger millet used in investigation

Sl. No.	Name of cultures/genotypes	Sl. No.	Name of cultures/genotypes
1	Mut-3	16	G39-GG-2-3
2	Mut-4	17	GPU-157
3	V3-VG-3	18	PR-202
4	V21-VE-3-7	19	P5-400
5	MR-33	20	RES-110
6	BM-107-2	21	RAU-8
7	BM-110-2	22	SRS-2
8	MG-1-3	23	VL-149
9	G5-GG-2-1	24	VL-322
10	G18-GG-2-2	25	VR-708
11	G20-GG-2-4	26	VR-768
12	G22-GE-3-2	27	VR-822
13	G24-GE-3-4	28	VR-849
14	G26-GN-1-2	29	Suvra
15	G30-GN-2-2	30	Nilanchala

3.5 Statistical analysis

The replication wise mean values of each entry for various traits were subjected to statistical analysis. The statistical analysis based on their mean values like analysis of variance (ANOVA), phenotypic and genotypic variances, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability (h^2_{bs}), genetic advance (GA), genetic advance as per cent mean, genotypic and phenotypic correlation coefficients, path coefficients and genetic divergence was carried out.

3.5.1 Analysis of variance (ANOVA)

The mean values for the polygenic characters under study in 30 genotypes of finger millet were subjected to statistical analysis. As per Panse and Sukhatme (1961) the mean, standard error and coefficient of variation were computed. By utilising the formula of Panse and Sukhatme (1985), standard error (SE) and critical difference (CD) at 1 and 5 percent level of significance were investigated. Analysis of variance was conducted for all the characters. The linear model for randomised block design is as follows.

Table 2. Analysis of variance with expectations mean sum of square

Source of variation	d.f.	SS	MSS	EMS	F value
Replication	(r-1)	P	M_r	$\sigma_e^2 + t\sigma_r^2$	M_r/M_e
Treatments	(t-1)	Q	M_t	$\sigma_e^2 + r\sigma_t^2$	M_t/M_e
Error	(r-1)(t-1)	R	M_e	σ_e^2	
Total	rt-1				

d.f.: degrees of freedom; **SS:** sum of squares; **MSS:** mean sum of squares

Where,

- r = Total number of replications
- t = Total number of genotypes or treatments
- P = Sum of squares of replications
- Q = Sum of squares of treatment
- R = Sum of squares of error
- M_r = Replication mean sum of square
- M_t = Genotype mean sum of square
- M_e = Error mean sum of square

Against the corresponding error degrees of freedom by the use of 'F' Test (Fisher and Yates, 1967), the significance of mean sum of squares for each trait under observation was examined.

$$\text{Standard error of mean (SE}_m) = \frac{\sigma_e^2}{r}$$

$$\text{Critical Difference (CD)} = \text{SE}_{(m)} \times t \text{ at error degree of freedom (1\% or 5\% level of significance)}$$

$$\text{Coefficient of variation (CV)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

Where,

t = Table value for error degree of freedom at 5 per cent or 1 per cent level of significance

r = number of replications

Mean

Sum of all the observations divided by the total number of observations is equal to the mean of a data set.

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

Where,

$\sum_{i=1}^n X_i$ = Summation of the observations

n = Number of observations

m = Mean value of the character

Range

The difference between the highest and lowest value in a set of observations for a character is equal to range.

Range = Highest value of the observations – Lowest value of the observations

Variance

The square of standard deviation is defined as variance. In other words, it can be stated as mean minus the sum of square of the deviation of all the observations, whole divided by (n-1).

$$\text{Variance} = \frac{\sum X^2 - \sum (X)^2}{n}$$

Where,

X_i = i^{th} observation of a population

n = Total number of observations

Standard deviation

$$\text{Standard deviation (SD)} = \frac{\sum d^2}{n} = \sqrt{\text{Variance}}$$

Where,

d = Deviation of the individual values from the mean

n = Total number of observations

Standard error

It is the variation caused in a sample due to the measures which cannot be controlled. Standard deviation divided by the square root of a number of observations in the sample gives an estimate of standard error (SE).

$$SE = \frac{SD}{\sqrt{n}}$$

Where,

SD = Standard deviation

n = Total number of observations

3.5.2 Assessment of genetic variability parameters

Under this heading, discussion will be made under the following sub-heading i.e., genotypic and phenotypic variances, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability (in broad sense), genetic advance and genetic advance as percent mean.

3.5.2.1 Genotypic and phenotypic variances

As per the methodologies of Johnson *et al.* (1955) the genotypic variance (σ_g^2) and phenotypic variances (σ_p^2) were evaluated.

$$\text{Genotypic variance } (\sigma_g^2) = \frac{M_t - M_e}{r}$$

Where,

M_t = Genotype mean sum of square

M_e = Error mean sum of square

r = Total number of replications

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where,

σ_g^2 = Genotypic variance

σ_e^2 = Error variance

Error variance (σ_e^2) = M_e

Where,

M_e = Mean sum of square due to error

3.5.2.2 Coefficient of variation

According to Burton and De Vane (1953) all the components of variance *viz.*, phenotypic variances, genotypic variances and environmental variances were employed all the characters under study to evaluate the coefficient of variation (CV) at both phenotypic and genotypic levels.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

As per Burton and De Vane (1953) the genotypic and phenotypic coefficients of variation were analysed based on the results of genotypic and phenotypic variances.

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

\bar{X} = General mean of the character

GCV and PCV have been categorized as high (>20%), moderate (10-20%) and low (<10%).

High = 20.1% and above

Moderate = 10-20%

Low = 0-10%

Heritability (broad sense)

The ratio of genotypic variance to phenotypic variance gives the estimate of heritability in broad sense and is expressed in percentage. Following formula given by

Singh and Choudhary (1977) was used for estimating heritability in percent in broad sense.

$$\text{Heritability } h_{(bs)}^2 = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

As suggested by Robinson *et al.* (1949) the range of heritability was classified as:

High = 60.1% and above

Moderate = 30.1-60%

Low = Below 30%

Genetic advance

According to the methods provided by Johnson *et al.* (1955) the genetic advance estimated.

$$\text{Genetic advance (GA)} = K \times h^2 \times \sigma_p$$

Where,

K = Standardized selection differential at 5 per cent selection intensity (2.06)

h^2 = Heritability

σ_p = Phenotypic standard deviation

Genetic advance as percent of mean

Genetic advance estimated by based on the formula given below:

$$\text{Genetic advance as percent of mean} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

\bar{X} = General mean of the character

As suggested by Johnson *et al.* (1955) the range of genetic advance as a percentage of mean was classified as follows:

High = 20.1% and above

Moderate = 10-20%

Low = 0-10%

3.5.3 Correlation coefficient

As per the formula given by Miller *et al.* (1958) the genotypic and phenotypic correlation coefficients between each pair of characters were estimated. As per

Robertson (1959), the coefficient of correlation was analysed utilizing tabulated value at $n - 2$ degree of freedom, at 5% and 1% probability level, where n is the total number of treatments.

Phenotypic correlation coefficient

$$r_p(x,y) = \frac{\text{Cov}_p x,y}{\sqrt{\sigma_p^2 x \sigma_p^2 y}}$$

Where,

$\text{Cov}_p x,y$ = Phenotypic covariance between character x and y

$\sigma_p^2 x$ = Phenotypic variance of character x

$\sigma_p^2 y$ = Phenotypic variance of character y

Genotypic correlation coefficient

$$r_g(x,y) = \frac{\text{Cov}_g x,y}{\sqrt{\sigma_g^2 x \sigma_g^2 y}}$$

Where,

$\text{Cov}_g x,y$ = Genotypic covariance between character x and y

$\sigma_g^2 x$ = Genotypic variance of character x

$\sigma_g^2 y$ = Genotypic variance of character y

3.5.4 Path coefficient analysis

Path coefficient analysis expresses the cause-and-effect relationship among the variables. Path coefficient analysis is a standardized partial regression coefficient. As demonstrated by Dewey and Lu, 1959, it measures the direct effect of one variable upon another and permits the partitioning of the correlation coefficients into components of direct and indirect effects. This analysis helps estimate significant components of a variable, on the basis of their direct and indirect influences. By taking grain yield per plant as a dependent variable, the direct and indirect effects both at genotypic and phenotypic level were assessed.

The equations formed for the path analysis are given below

$$P_{01} + P_{02}r_{12} + \dots\dots\dots P_{0p}r_{1p} = r_{01}$$

$$P_{01} r_{21} + P_{02}r_{22} + \dots\dots\dots P_{0p}r_{2p} = r_{02}$$

$$P_{0p} r_{1p} + P_{0p}r_{2p} + \dots\dots\dots P_{0p} = r_{0p}$$

Where,

$P_{01}, P_{02}, \dots, P_{0p}$ is the direct path effect of variables 1, 2, 3, ..., p on the dependent variable 0.

$r_{12}, r_{13}, \dots, r_{1p}, \dots, r_{(p-1)}$ are the possible correlation coefficients between various independent variables and $r_{01}, r_{02}, \dots, r_{0p}$ are the correlations of the independent variable with dependent and independent variables.

The indirect effect of the i^{th} variable via j^{th} variable derived as $P_{0j} \times r_{ij}$

From the above equations, it is indicative that the correlation coefficient is the sum of the direct and indirect path coefficients.

The influence of the remaining unknown factors was estimated as the residual factor and estimated as below:

$$P^2_{0x} = (1 - (P^2_{01} - 2^2_{01} - 2P^2_{03} + \dots + P^2_{0n} + 2P_{01}P_{02} r_{12} + 2P_{01}P_{09}r_1 + \dots P^2_{02} + P_{02}r_{29} + \dots P^2_{p0}))$$

$$\text{Residual factor} = \sqrt{(p^2_{0x})}$$

3.5.5 Genetic divergence analysis

The genetic divergence between thirty genotypes of finger millet was estimated using Mahalanobis D^2 analysis (Mahalanobis, 1936). From this analysis, the genotypes were grouped into distinct clusters and their inter and intra-cluster distances were estimated.

The distance D from the sample was estimated using the formula given below.

$$D^2_p = d^1 S^{-1} d$$

Where,

D^2_p = Square of distance considering p variables

D = Vector observed differences of the mean values of all the characters ($x_{i1} - x_{i2}$)

S^{-1} = inverse of variance and covariance matrix

3.5.5.1 Clustering of the D^2 values

By using Tocher's method (Rao, 1952) all the genotypes used were clustered into different groups. The intra and inter-distance were also computed. The criterion used in clustering to the same cluster should at least on the average, show a smaller D^2 values than those belonging to different clusters.

The device suggested by Tocher (Rao, 1952) was started with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average D^2 value from the first three and so on. If at any stage increase in average D^2 value exceeded the average of already included, because of the addition of new genotypes, then that genotype was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those that were already included in the former cluster and grouping them into different cluster.

3.5.5.2 Intra-cluster distance

As per the formula given by Singh and Chaudhary (1977) the average intra-cluster distances were estimated.

$$\text{Square of intra-cluster distance} = \Sigma D_i^2/n$$

Where,

ΣD_i^2 = sum of distance between all possible combinations

n = number of all possible combinations

3.5.5.3 Inter-cluster distance

As per the formula given by Singh and Chaudhary (1977) the average inter-cluster distances were estimated.

$$\text{Square of inter-cluster distance} = \Sigma D_i/n_i n_j$$

Where,

ΣD_i^2 = sum of distance between all possible combinations ($n_i n_j$) of the entries included in cluster study

n_i = number of entries in cluster i

n_j = number of entries in cluster j

3.5.5.4 Contribution of individual characters towards genetic divergence

As per the formula given by Singh and Chaudhary (1977) contribution of individual characters towards genetic divergence was estimated.

In all the combination, each character is classified on the basis of $d_i = y_i^j - y_i^k$

Where,

d_i = mean deviation

y_i^j = mean value of the j^{th} genotype for the i^{th} character

y_i^k = mean value of the k^{th} genotype for the i^{th} character

EXPERIMENTAL RESULTS

The present investigation was carried out in finger millet (*Eleusine coracana* L.) to evaluate the thirty genotypes including two checks for assessing variability, correlation, path coefficient analysis and genetic diversity analysis with respect to different morphological characters. Thirty genotypes were evaluated in Randomised Block Design with three replications. The outcomes of the present study are under the following sub headings.

- 4.1 Genetic variability studies
- 4.2 Correlation coefficient analysis
- 4.3 Path coefficient analysis
- 4.4 Genetic divergence

4.1 Genetic variability studies

Any breeding programme for genetic improvement can be undertaken only if sufficient amount of genetic variability exists within the population. Selecting parents from genetically diverse population and crossing among them leads to production of superior progenies with respect to yield or other quality characters in the subsequent generations. In addition, the knowledge of heritability and genetic advance helps in selection of desirable traits and hence to develop suitable breeding techniques.

4.1.1 Analysis of variance

Before the conduct analysis of variance, mean table was formulated and has been demonstrated as Table 3. From the analysis of variance significant level of differences were observed among the genotypes for all the traits under study, indicating the presence of high degree of variability among the genotypes. It has been shown in Table 4. The genetic variability i.e., mean, range, PCV, GCV, heritability (in broad sense) and genetic advance (as % of mean) for quantitative traits including grain yield has been shown in Table 5. The same has been represented graphically in Figure 1. A notable amount of variation was observed for all the eight characters indicating an immense opportunity in bringing about improvement in the required way.

Table 3. Mean performance of different genotypes of finger millet for yield and yield contributing traits

Sl. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Finger length (cm)	Number of fingers/ear	Number of ears/plant	1000-seed weight (g)	Grain yield/plant (g)
1	Mut-3	84.33	111.67	103.94	6.50	6.13	2.67	3.04	14.56
2	Mut-4	85.67	110.67	97.65	7.50	6.67	3.33	2.94	21.48
3	V3-VG-3	88.33	119.33	97.89	9.30	5.67	3.00	2.64	17.10
4	V21-VE-3-7	69.33	99.00	88.63	5.90	5.40	2.33	2.46	7.43
5	MR-33	67.33	98.67	84.51	6.20	4.53	2.33	3.00	7.53
6	BM-107-2	68.33	100.00	107.41	7.00	6.33	3.00	2.77	14.85
7	BM-110-2	67.33	98.33	105.68	6.67	6.27	2.00	2.67	8.39
8	MG-1-3	66.33	98.33	90.98	6.80	6.33	1.33	2.75	4.60
9	G5-GG-2-1	78.33	110.33	104.91	8.53	6.13	1.67	2.79	9.81
10	G18-GG-2-2	81.67	110.67	107.37	8.57	6.13	2.67	2.29	15.33
11	G20-GG-2-4	83.67	119.67	113.88	7.97	9.20	1.00	2.92	5.16
12	G22-GE-3-2	85.33	111.67	104.70	8.80	5.60	2.33	2.96	12.28
13	G24-GE-3-4	81.33	112.33	111.03	7.07	5.47	3.00	3.06	15.39
14	G26-GN-1-2	81.00	111.67	99.83	8.63	6.13	3.33	2.65	16.74
15	G30-GN-2-2	83.67	111.67	99.23	7.77	6.00	4.00	2.79	22.31
16	G39-GG-2-3	65.33	96.67	97.06	5.67	5.60	2.67	2.86	8.96
17	GPU-157	77.33	110.00	107.32	8.07	6.00	2.00	3.13	10.07

18	PR-202	78.33	109.67	108.85	6.77	6.60	3.00	2.62	14.01
19	P5-400	79.33	110.00	112.75	7.47	6.13	2.67	2.99	11.40
20	RES-110	78.67	109.33	114.55	7.13	6.87	2.67	2.93	11.60
21	RAU-8	65.67	96.67	109.29	7.30	6.93	3.33	2.92	16.16
22	SRS-2	67.33	95.67	112.51	6.63	5.43	2.33	2.51	8.01
23	VL-149	70.67	101.67	108.77	6.77	4.97	1.33	2.90	4.22
24	VL-322	80.67	112.00	116.01	8.30	8.00	3.00	2.82	15.12
25	VR-708	78.33	109.00	114.54	5.23	4.47	1.33	2.63	4.36
26	VR-768	79.00	110.00	115.89	6.90	7.10	3.00	2.96	12.86
27	VR-822	86.67	116.00	116.50	10.20	6.67	2.33	2.74	14.75
28	VR-849	86.67	117.67	117.33	9.40	6.80	3.00	2.82	14.84
29	Suvra	82.67	113.33	115.41	8.90	6.40	2.33	3.02	10.65
30	Nilanchala	83.67	114.33	115.68	8.07	6.53	3.67	2.87	17.27
Mean		77.74	108.2	106.67	7.53	6.22	2.56	2.82	12.24
CV (%)		7.79	7.13	8.17	8.02	7.01	7.42	7.14	7.47
SEm		3.5	4.45	5.03	0.35	0.25	0.11	0.12	0.53
CD at 5%		9.9	12.61	14.25	0.99	0.71	0.31	0.33	1.49
CD at 1%		13.17	16.78	18.96	1.31	0.95	0.41	0.44	1.99
Minimum		65.33	95.67	84.51	5.23	4.47	1	2.29	4.22
Maximum		88.33	119.67	117.33	10.2	9.2	4	3.13	22.31

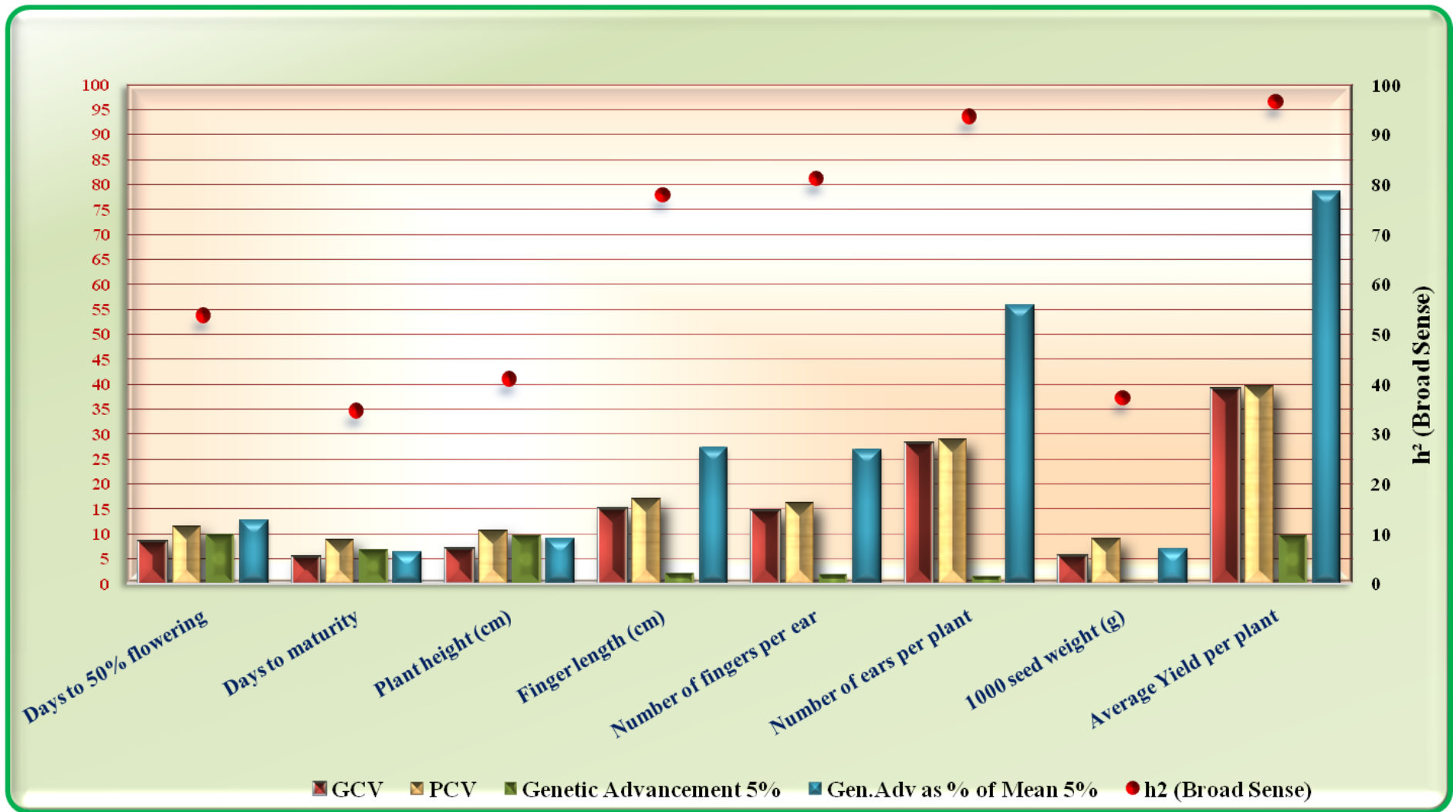


Fig. 1. Graphical representation of mean, range and genetic parameter estimates for the traits of finger millet [*Eleusine corocana* (L.)]

4.1.2 Variability of characters

The mean, range and coefficient of variation for all the traits were evaluated and presented in Table 4. The table below showed the existence of substantial amount of variability for majority of traits.

Table 4. ANOVA (analysis of variance) for various traits

Sl. No.	Source (Degrees of freedom)	Replication (2)	Treatment (29)	Error (58)
1	Days to 50% flowering	32.643	163.740**	36.665
2	Days to maturity	82.242	153.439**	59.529
3	Plant height (cm)	31.307	233.282**	75.999
4	Finger length (cm)	0.006	4.195**	0.365
5	Number of fingers/ear	0.060	2.622**	0.190
6	Number of ears/plant	0.108	1.571**	0.036
7	1000 seed weight (g)	0.015	0.112**	0.040
8	Gran yield/plant (g)	0.429	68.866**	0.837

** Significant at 1% level

4.1.2.1 Days to 50 % flowering

The mean days to 50% flowering ranged from 65.33 days to 88.33 days with a general mean of 77.74 days. The maximum days taken for 50% flowers to reach anthesis has been observed in V3-VG-3 (88.33 days) whereas the minimum number of days was taken by G39-GG-2-3 (65.33 days). In comparison to the general mean, 20 genotypes out of 30 showed early flowering.

4.1.2.2 Days to maturity

With a mean of 108.20 days, the days to maturity ranged from 95.67 to 119.67 days. Genotype SRS-2 showed the minimum days to maturity that is 95.67 days demonstrating it to be an early variety whereas the maximum number of days is taken by genotype G20-GG-2-4 (119.67 days) and hence it is a late variety.

4.1.2.3 Plant height (cm)

For thirty genotypes under the experiment, the mean plant height in the ranged from 84.51 to 117.3 cm with a general mean of 106.67 cm. The tallest germplasm was recorded to be VR-849 with a height of 117.3 cm whereas the shortest of all was MR-33 with a height of 84.51 cm.

4.1.2.4 Ear length (cm)

Mean ear length (cm) in the genotypes under study ranged from 5.23 to 10.20 cm with a mean of 7.53 cm. Genotype VR-822 showed the maximum ear length (10.20 cm) whereas the minimum ear length was shown by genotype VR-708 (5.23).

4.1.2.5 Number of fingers/ears

From 4.47 to 9.20 is the range of the mean number of fingers/ear with a mean of 6.22. The maximum number of finger/ears was observed for genotype G20-GG-2-4 (9.20) whereas the minimum number of fingers/ear genotypes was observed for genotypes VR-708 (4.47).

4.1.2.6 Number of ears/plants

With a general mean of 2.56, the mean number of ears per plant ranged from 1 to 4. The maximum number of ears per plant was recorded in genotype G30-GN-2-2 with 4 ears per plant and the minimum in G20-GG-2-4 with 1 ear per plant.

4.1.2.7 1000-seed weight (g)

The mean value of 1000-seed weigh ranged from 2.29 to 3.13 g with a general mean of 2.82 g. The maximum 1000-seed weight was observed in culture GPU-157 (3.13 g) and a minimum in culture G18-GG-2-2 (2.29 g).

4.1.2.8 Grain yield/plant (g)

With a general mean of 12.24 g, the mean grain yield per plant ranged from 4.22 to 22.31 g. The maximum grain yield was observed in genotype G30-GN-2-2 with a yield of 22.31 g per plant while the minimum amount of yield per plant was observed in genotype VL-149 with a yield of 4.22 g.

4.1.3 Coefficient of variation

The coefficient of variation both at genotypic and phenotypic levels for yield and yield affecting traits along with physiological characters of thirty elite finger millet genotypes are depicted in Table 5.

The analysis on the coefficient of variations (CV) in different traits ranged from 7.01% for number of fingers per ear to 8.17% for plant height. The coefficient of variation was less than 8% for majority of traits under study. On the contrary a higher value of CV (more than 8 %) was recorded only for plant height and finger length.

For the traits under studied, the GCV ranged from 5.171% for days to maturity to 38.901% for grain yield/plant. PCV ranged from 8.808% for days to maturity to 39.612% for grain yield/plant. For all the characteristics, the genotypic and phenotypic coefficients of variance in different traits-maintained agreement. The majority of the features between PCV and GCV showed just minor differences. The phenotypic coefficient of variance was, on average, greater than the genotypic coefficient of variation. Both, GCV and PCV were observed to be high (more than 20%) for the trait grain yield/plant with PCV (39.612%) and GCV (38.901%) and number of ears/plants with PCV (28.957%) and GCV (27.989%).

4.1.4 Heritability and genetic advance

The heritability in broad sense (h_{bs}^2) and genetic advance (as % of mean) analysed for all the polygenic traits are presented in Table 5. The heritability values assessed for different traits varied from 96.422 % for grain yield/plant to 34.463% for days to maturity. Maximum number of traits under study showed high heritability *i.e.*, grain yield/plant followed by number of ears/plants, number of fingers/ears and finger length while moderate heritability was observed for the trait days to 50% flowering, plant height, 1000-seed weight and days to maturity in the descending order, respectively.

Table 5. Estimates of mean, range and genetic parameters for the quantitative traits including yield for finger millet

Sl. No.	Traits	Mean	Range	CV (%)	GCV (%)	PCV (%)	h^2_{bs} (%)	Genetic Advance at 5%	Genetic Advance (as % of Mean 5%)
1	Days to 50% flowering	77.74	65.33 - 88.33	7.79	8.37	11.43	53.60	9.82	12.63
2	Days to maturity	108.2	95.67 -119.67	7.13	5.17	8.81	34.46	6.77	6.25
3	Plant height (cm)	106.67	84.51 - 117.33	8.17	6.79	10.62	40.82	9.53	8.93
4	Ear length (cm)	7.53	5.23 - 10.2	8.02	15.00	17.01	77.78	2.05	27.25
5	Number of fingers/ear	6.22	4.47 - 9.2	7.01	14.48	16.09	81.04	1.67	26.86
6	Number of ears/plant	2.56	1 - 4	7.42	27.99	28.96	93.43	1.42	55.73
7	1000-seed weight (g)	2.82	2.29 - 3.13	7.14	5.48	9.00	37.05	0.19	6.87
8	Grain yield/plant(g)	12.24	4.22 - 22.31	7.47	38.90	39.61	96.44	9.63	78.70

Genetic advance expressed as percentage of mean varied from 6.253% for days to maturity to 78.697 for grain yield/plant. High genetic advance expressed as percentage of mean was observed for grain yield/plant followed by number of ears/plants, finger length and number of fingers/ears and while moderate genetic advance expressed as percentage of mean was observed for the trait days to 50% flowering. Low genetic advance expressed as percentage of mean was observed for plant height, 1000-seed weight and days to maturity in the descending order respectively.

In view of the importance of GCV value along with heritability and genetic advance in increasing the reliability and response of selection, efforts were also made to indicate both heritability and genetic advance values along with GCV for various traits during the present studies. The characters grain yield/plant and number of ears/plants exhibited high GCV, PCV, heritability coupled with high genetic advance expressed as percentage of mean. While the traits finger length and number of fingers/ears exhibited moderate GCV, PCV and high heritability coupled with high genetic advance expressed as percentage of mean. Low GCV, PCV and high heritability coupled with high genetic advance expressed as percentage of mean was observed for days to maturity.

4.2 Correlation coefficient analysis

The nature and magnitude of the association of different component characters with grain yield is provided by the estimate of correlation coefficient. The interrelationship among the traits under study is also exploited through it. In general, the estimates of phenotypic correlation were always less than genotypic correlation, suggesting the influence of environmental effects on the genotypic correlation hence reducing the reliability of phenotypic correlations. The main objection of correlation coefficient analysis is to enhance the selection tactics to improve the economic yield of the crop.

Analysis for correlations at both genotypic and phenotypic level were computed for different pairs of morphological characters including grain yield/plant in order to find out the degree and direction of association in between grain yield and the other component characters and also among themselves. The results obtained from the study of correlations at both genotypic and phenotypic level thirty genotypes of finger millet are presented in Table 6.

Table 6. Estimates of phenotypic and genotypic correlation coefficients among eight quantitative traits in finger millet

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Ear length (cm)	No. of fingers/ear	No. of ears/plant	1000-seed weight (g)	Grain yield/plant (g)
Days to 50% flowering	r _p	1	0.567**	0.212*	0.512**	0.252*	0.218*	0.139	0.433**
	r _g	1	0.922**	0.556**	0.812**	0.348**	0.320**	0.139	0.622**
Days to maturity	r _p		1	0.243*	0.473**	0.287**	0.132	0.125	0.314**
	r _g		1	0.701**	0.927**	0.546**	0.204	0.243*	0.539**
Plant height(cm)	r _p			1	0.272**	0.326**	0.022	0.186	0.077
	r _g			1	0.382**	0.550**	0.012	0.096	0.081
Ear length (cm)	r _p				1	0.321**	0.192	0.031	0.420**
	r _g				1	0.436**	0.217*	0.018	0.489**
No. of fingers/ear	r _p					1	0.076	0.144	0.197
	r _g					1	0.096	0.153	0.234*
No. of ears/plant	r _p						1	0.020	0.865**
	r _g						1	0.013	0.916**
1000-seed weight(g)	r _p							1	0.021
	r _g							1	0.046
Grain yield/plant (g)	r _p								1
	r _g								1

* Significant at 5% level

** Significant at 1% level

r_p : Phenotypic correlation

r_g : Genotypic correlation

4.2.1 Correlation between grain yield and its component traits

The maximum positive and significant association was found in between grain yield/plant and number of ears/plant (0.865, 0.916) followed by days to 50% flowering (0.433, 0.622), days to maturity (0.314, 0.539) and finger length (0.420, 0.489) at both phenotypic and genotypic levels respectively. While a positive and non-significant association was observed in between grain yield/plant and fingers/ear (0.1973, 0.234), 1000-seed weight (0.0211, 0.0461) and plant height (0.0766, 0.0810) at both phenotypic and genotypic levels, respectively.

4.2.2 Inter correlation among yield components

Days to 50% flowering exhibited a significant and positive association with days to maturity (0.567, 0.922), ear length (0.512, 0.812), fingers/ear (0.252, 0.348), number of ears/plant (0.218, 0.320) and plant height (0.212, 0.556) where as a non-significant and positive association with 1000-seed weight (0.1390,0.1388).

A significant and positive association was displayed by days to maturity displayed with ear length (0.473, 0.927), number of fingers per ear (0.348, 0.287) and plant height (0.243, 0.701) in a descending order. Though, it showed a non-significant and positive association was recorded with the trait number of ears per plant (0.1323, 0.2039) and 1000-seed weight (0.1245, 0.243). Plant height exhibited a significant and positive association with number of fingers per ear (0.326, 0.550) and ear length (0.272, 0.382) in the descending order. Although, it showed a non-significant and positive association was recorded with the trait number of ears per plant (0.0223, 0.0120) and 1000-seed weight (0.1864, 0.0957). A significant and positive association was shown by ear length with number of fingers per ear (0.321, 0.436) while it showed a non-significant and positive association was recorded with the trait number of ears per plant (0.1923, 0.217) and 1000-seed weight (0.0306, 0.0184).

The trait fingers/ear displayed a non-significant and positive association was recorded with the trait number of ears per plant (0.0758, 0.0958) and 1000-seed weight (0.1442, 0.1525). Whereas, the trait number of ears per plant exhibited a non-significant and positive association was recorded with the trait 1000-seed weight (0.0197, 0.0126) only.

4.3 Path coefficient analysis

Path coefficient analysis was undertaken taking the grain yield as a dependent character. It is used to split up the observations of the correlation coefficient (between the grain yield per plant and its component traits) into direct and indirect effects.

The results obtained from the study of direct and indirect effects of yield affecting characters on grain yield at both genotypic and phenotypic level in thirty genotypes of finger millet are presented in Table 7.

4.3.1 Direct effect of yield contributing traits on yield

A positive and direct effect on grain yield was displayed by five out of eight characters viz., days to 50 per cent flowering (0.1500, 0.1879), days to maturity (0.0447, 0.1504), ear length (0.1650, 0.0594), number of fingers per ear (0.0505, 0.1065), number of ears per plant (0.7917, 0.8047) at both genotypic level and phenotypic levels. While negative direct effects were observed on grain yield by traits like plant height (-0.0404, -0.2176) and 1000-seed weight (-0.0257, -0.0231). The highest positive direct effect was recorded for number of ears/plants (0.7917, 0.8047) while the maximum negative direct effect on grain yield were observed for 1000- seed weight (-0.0257, -0.0231). The genotypic and phenotypic path diagram indicating cause and effect relation between yield affecting attributes and grain yield/plant has been demonstrated through Figure 2 and 3, respectively.

4.3.2 Indirect effects of yield components on grain yield

4.3.2.1 Days to 50 % flowering

At both genotypic and phenotypic and levels, the character days to 50 % flowering exhibited positive and indirect effects on the grain yield/plant through days to maturity (0.0254, 0.2157), ear length (0.0845, 0.0482), no. of fingers/ear (0.0127, 0.0370) no. of ears/plant (0.1726, 0.2573). Whereas, negative indirect effects were observed on the grain yield through plant height (-0.0086, -0.1211) and 1000-seed weight (-0.0036, -0.0032).

Table 7. Direct (diagonal) and indirect effects of various traits on grain yield/plant in finger millet genotypes by path coefficient analysis

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Ear length (cm)	No. of fingers/ear	No. of ears/plant	1000-seed weight(g)	Grain yield/plant (g)
Days to 50% flowering	rp	0.150	0.085	0.032	0.077	0.038	0.033	0.021	0.433**
	rg	0.188	0.270	0.105	0.153	0.065	0.060	0.026	0.622**
Days to maturity	rp	0.025	0.045	0.011	0.021	0.013	0.006	0.006	0.314**
	rg	0.216	0.150	0.105	0.139	0.082	0.031	0.037	0.539**
Plant height(cm)	rp	-0.009	-0.010	-0.040	-0.011	-0.013	-0.001	-0.008	0.077
	rg	-0.121	-0.152	-0.218	-0.083	-0.120	-0.003	-0.021	0.081
Ear length(cm)	rp	0.085	0.078	0.045	0.165	0.053	0.032	0.005	0.420**
	rg	0.048	0.055	0.023	0.059	0.026	0.013	0.001	0.489**
No. of Fingers/ear	rp	0.013	0.015	0.017	0.016	0.051	0.004	0.007	0.197
	rg	0.037	0.058	0.059	0.046	0.107	0.010	0.016	0.234*
No. of Ears/plant	rp	0.173	0.105	0.018	0.152	0.060	0.792	0.016	0.865**
	rg	0.257	0.164	0.010	0.175	0.077	0.805	0.010	0.916**
1000-seed weight(g)	rp	-0.004	-0.003	-0.005	-0.001	-0.004	-0.001	-0.026	0.021
	rg	-0.003	-0.006	-0.002	0.000	-0.004	0.000	-0.023	0.046
Grain yield/plant (g)	rp	0.433**	0.314**	0.077	0.420**	0.197	0.865**	0.021	1.000
	rg	0.622**	0.539**	0.081	0.489**	0.234*	0.916**	0.046	1.000
Partial R2	rp	0.065	0.014	-0.003	0.069	0.010	0.684	-0.001	
	rg	0.117	0.081	-0.018	0.029	0.025	0.737	-0.001	

* Significant at 5% level

** Significant at 1% level

r_p : Phenotypic correlation

rg : Genotypic correlation

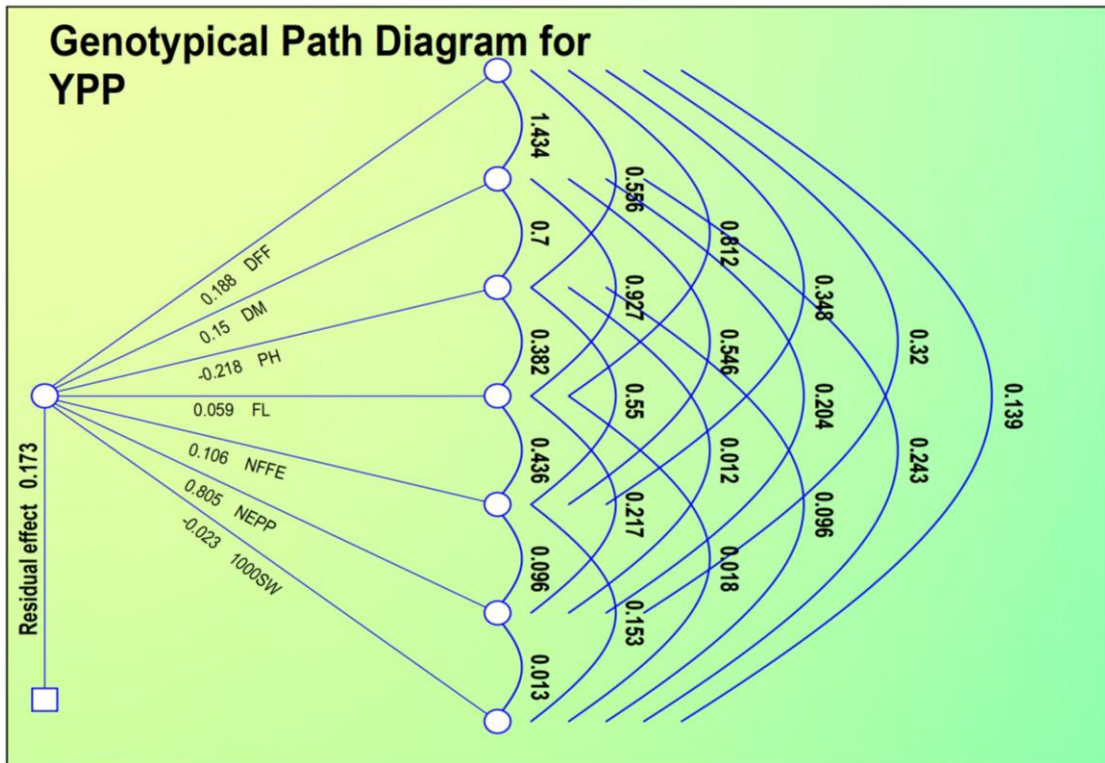


Fig. 2. Genotypic path diagram indicating cause and effect relation between yield affecting attributes and grain yield/plant in *Eleusine corocana* (L.)

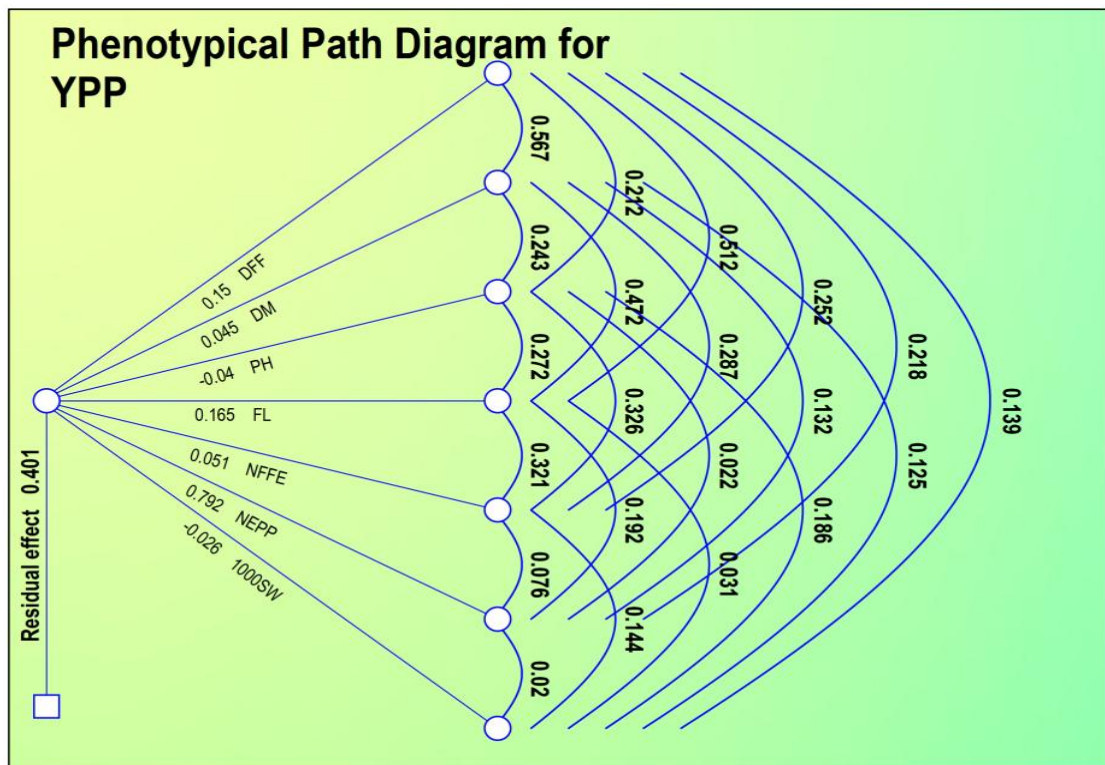


Fig. 3. Phenotypic path diagram indicating cause and effect relation between yield affecting attributes and grain yield/plant in *Eleusine corocana* (L.)

4.3.2.2 Days to maturity

A positive and indirect effects was displayed by days to maturity on the grain yield/plant through days to 50% flowering (0.0850, 0.2695), ear length (0.0780, 0.0551), no. of fingers/ear (0.0145, 0.0582), no. of ears/plant (0.1048, 0.1641) at phenotypic and genotypic levels respectively. Although, negative indirect effects were observed on the grain yield through plant height (-0.0098, -0.1524) and 1000-seed weight (-0.0032, -0.0056).

4.3.2.3 Plant height (cm)

On the grain yield/ plant, the trait plant height exhibited a positive and indirect effects through days to 50% flowering (0.0319, 0.1046), days to maturity (0.0109, 0.1054), ear length (0.0449, 0.0227), no. of fingers/ear (0.0165, 0.0585), no. of ears/plant (0.0177, 0.0096), while on the other hand, negative indirect effects were observed on the grain yield through 1000-seed weight (-0.0048, -0.0022) at phenotypic and genotypic levels, respectively.

4.3.2.4 Ear length (cm)

Ear length displayed positive and indirect effects on the grain yield/plant through days to 50% flowering (0.0768, 0.1525), days to maturity (0.0211, 0.1394), no. of fingers/ear (0.0162, 0.0464), no. of ears/plant (0.1522, 0.1750) while negative indirect effects were observed on the grain yield through plant height (-0.0110, -0.0831) and 1000-seed weight (-0.0008, -0.0004) at phenotypic and genotypic levels, respectively.

4.3.2.5 Number of fingers/ear

A positive and indirect effects on the grain yield/plant was exhibited by number of finger/ears through days to 50% flowering (0.0378, 0.0654), days to maturity (0.0128, 0.0822) ear length (0.0530, 0.0259) no. of fingers/ear (0.0600, 0.0771) whereas, negative indirect effects were observed on the grain yield through plant height (-0.0132, -0.1196) and 1000-seed weight (-0.0037, -0.0035) at phenotypic and genotypic levels, respectively.

4.3.2.6 Number of ears/plant

On the grain yield/plant, the trait number of ears/plants exhibited positive and indirect effects through days to 50% flowering (0.0327, 0.0601), days to maturity (0.0059, 0.0307), ear length (0.0317, 0.0129), fingers/ear (0.0038, 0.0102) while negative indirect effects were observed on the grain yield through plant height (-0.0009, -0.0026) and 1000-seed weight (-0.0005, -0.0003) at phenotypic and genotypic levels, respectively.

4.3.2.7 1000-seed weight (g)

The trait 1000-seed weight (g) showed a positive and indirect effects on the grain yield/plant through days to 50% flowering (0.0208, 0.0261), days to maturity (0.0056, 0.0365), ear length (0.0050, 0.0011), no. of fingers/ear (0.0073, 0.0162), no. of ears/plant (0.0156, 0.0101) although negative indirect effects were observed on the grain yield through plant height (-0.0075, -0.0208) at phenotypic and genotypic levels, respectively.

4.4 Genetic divergence

The Mahalanobis D^2 statistics was utilized for the estimation of genetic divergence for the traits under study among thirty genotypes of finger millet and are presented in various tables.

4.4.1 Composition of clusters

As per the Torcher's method, the thirty genotypes under study were grouped into five distinct non-overlapping clusters and different genotypes included in each cluster are presented in Table 8. The same has been represented *via*, dendrogram in Figure 4. Observations regarding inter and intra-cluster distances were recorded. The more the distance, the more is the genetic diversity present within the genotypes present in each cluster. This knowledge can be explored to select parents from different origins. The cluster diagram has been depicted in Figure 5.

The presence of maximum numbers of genotypes has been observed in cluster I (18 genotypes) followed by cluster III (8 genotypes), cluster IV (2 genotypes) and cluster II and V having 1 genotype each.

Table 8. Clustering patters of the genotypes of finger millet

Cluster	No. of Genotypes	Name of Genotypes
I	18	P5-400 (19), RES-110 (20), VR-768 (26), PR-202 (18), Mut-3 (1), BM-107-2 (6), G24-GE-3-4 (13), G18-GG-2-2 (10), G22-GE-3-2 (12), VR-849 (28), VL-322 (24), Suvra (29), VR-822 (27), G26-GN-1-2 (14), V3-VG-3 (3), RAU-8 (21), Nilanchala (30), GPU-157 (17)
II	1	G5-GG-2-1(9)
III	8	BM-110-2 (7), SRS-2 (22), V21-VE-3-7 (4), G39-GG-2-3 (16), MR-33 (5), MG-1-3 (8), VL-149 (23), VR-708 (25)
IV	2	Mut-4 (2), G30-GN-2-2 (15)
V	1	G20-GG-2-4 (11)

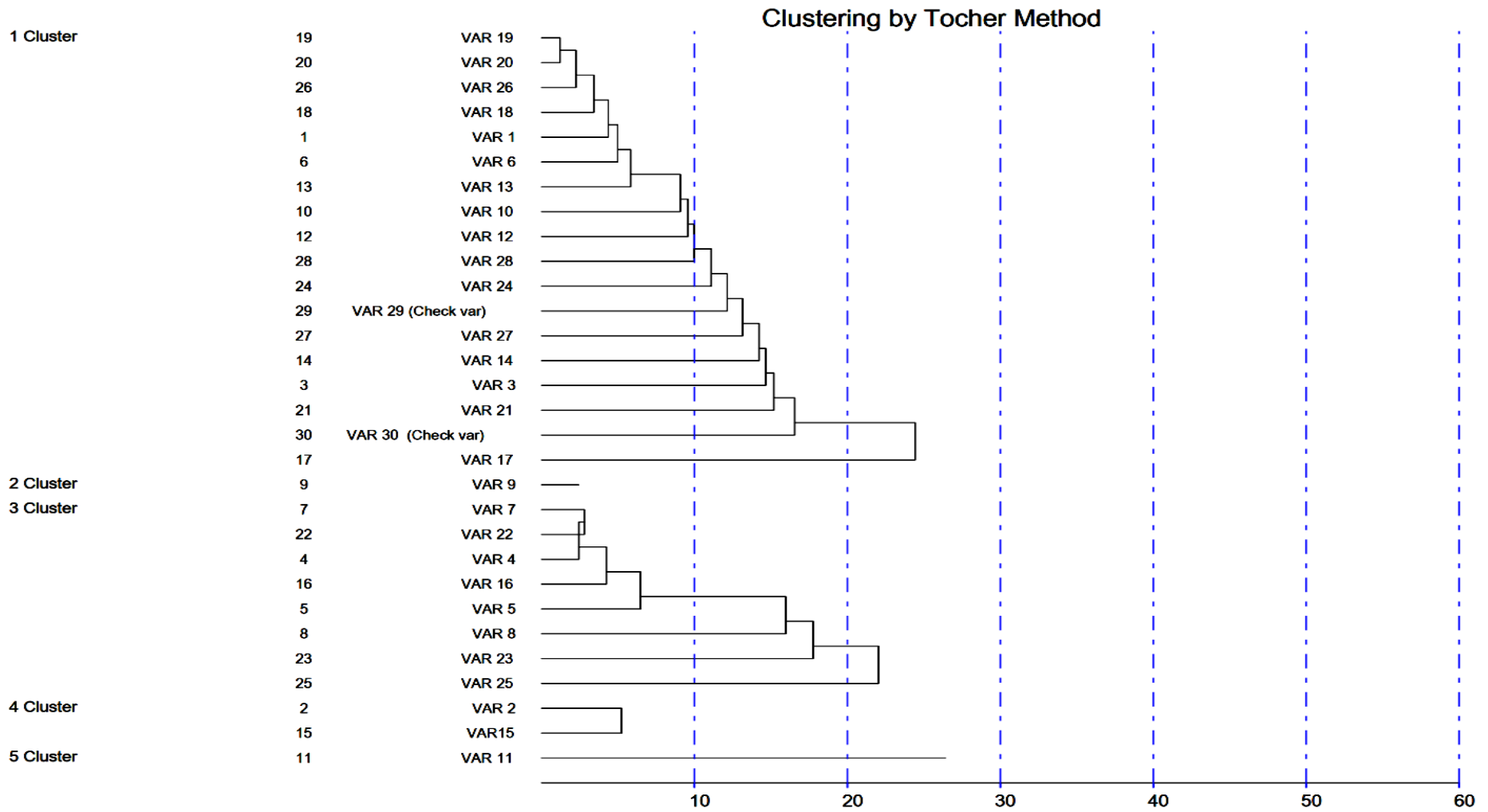


Fig. 4. Dendrogram of thirty genotypes of *Eleusine corocana* (L.)

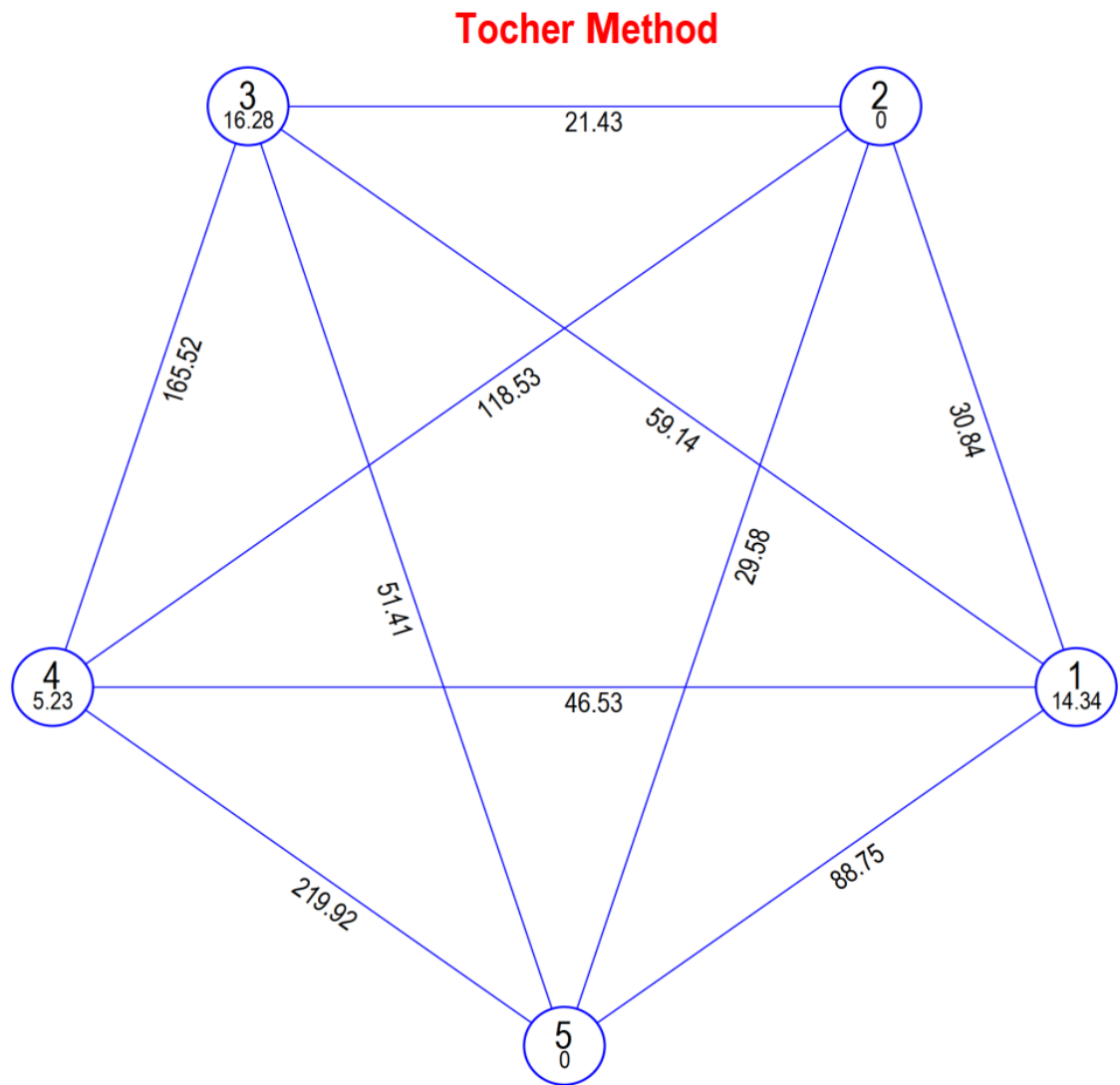


Fig. 5. Intra and inter cluster distances among 5 clusters in thirty genotypes of finger millet

4.4.2 Intra and inter-cluster distances

The average D^2 values are used to find out the inter and intra cluster relations within the clusters. From Table 9, the average D^2 values of the inter and intra cluster relations has been recorded. The range of intra-cluster values is from 0 to 16.28. The maximum intra cluster distance was recorded for cluster III (16.28) followed by cluster I (14.34) while the minimum in cluster IV (5.23). For the clusters II and V, the intra cluster distances were recorded to be zero. The highest inter-cluster distance was present in between cluster IV and V (219.92) followed by cluster III and IV (165.52), cluster II and IV (118.53), cluster I and V (88.75), cluster I and III (59.14), cluster III and V (51.4), cluster I and IV (46.53), cluster I and II (30.84), cluster II and V (29.58) while minimum between cluster II and III (21.34).

Table 9. Average D^2 intra and inter cluster distances of treatments (Intra cluster distance in diagonal)

Clusters	I	II	III	IV	V
I	14.34	30.84	59.14	46.53	88.75
II		0	21.43	118.53	29.58
III			16.28	165.52	51.41
IV				5.23	219.92
V					0

4.4.3 Cluster means analysis for different characters

For the eight quantitative traits under study, the cluster means in five clusters are present in Table 10. For most of the characters under study, significant differences between the clusters were detected.

4.4.3.1 Days to 50 % flowering

For days to 50 per cent flowering the highest mean value of (84.67 days) was observed in cluster IV while the lowest mean value of (69 days) has been recorded in cluster III. So, cluster III has genotypes for early flowering trait.

4.4.3.2 Days to maturity

In cluster V the highest mean value for days to maturity was observed *i.e.*, (119.67 days) while the lowest mean value was observed in cluster III (99.67 days). Therefore, in cluster III early maturing genotypes is present.

Table 10. Mean performance of different clusters for various characters in finger millet

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Finger length (cm)	Number of fingers/ear	Number of ears/plant	1000-seed weight (g)	Grain yield/plant (g)
I	80.5	110.91	110.1	8.02	6.42	2.83	2.85	14.17
II	78.33	110.33	104.91	8.53	6.13	1.67	2.79	9.81
III	69	99.67	100.33	6.23	5.38	1.96	2.72	6.69
IV	84.67	111.17	98.44	7.63	6.34	3.67	2.86	21.9
V	83.67	119.67	113.88	7.97	9.2	1	2.92	5.16

4.4.3.3 Plant height (cm)

For plant height, the highest mean value of (113.88 cm) was observed in cluster V, while the lowest mean value of (98.44 cm) in cluster IV.

4.4.3.4 Ear length (cm)

Ear length exhibited the highest mean value of (8.53 cm) in cluster II while the lowest mean value has been recorded in cluster III *i.e.*, (6.23). Hence, in order to get genotypes with more ear length, selection needs to be done from cluster II.

4.4.3.5 Number of fingers/ear

The highest mean value for number of fingers/ears was observed in was observed in cluster V (9.2) and the lowest mean value of (5.38) in cluster III. Therefore, in order to get genotypes with a greater number of fingers/ears, selection needs to be done from cluster V.

4.4.3.6 Number of ears/plant

For the trait number of ears/plants, the highest mean value of (3.67) was observed in cluster IV and lowest mean value of (1) in cluster V. So, to have a germplasm with a greater number of ear/plants, selection needs to be done from cluster IV.

4.4.3.7 1000-seed weight (g)

The highest mean value of (2.92 g) was observed in cluster V and lowest mean value of (2.72 g) in cluster III for 1000-seed weight. The test weight is quite comparable in the above two clusters.

4.4.3.8 Grain yield/plant (g)

For grain yield/plant, the highest mean value of (21.9 g) was observed in cluster IV and lowest mean value of (5.16 g) in cluster V. In order to select plant for the trait high grain yield/plant selection needs to be done from cluster IV.

DISCUSSION

Finger millet (*Eleusine corocana*), is a widely accepted coarse cereal crop in the arid and semi-arid zones in Asia and Africa. It is the fourth most important millet crop in the world after Sorghum followed by Pearl millet & Barley and is the third most cultivated coarse cereal crop after Jowar and Bajra in India. Karnataka and Tamil Nadu are the leading Ragi growing states in India, followed by Andhra Pradesh, Maharashtra, Uttar Pradesh, Uttarakhand, Rajasthan, Bihar and Odisha. It has high yield potential more than 10 ton ha⁻¹ under optimum irrigated conditions. It is a rich source of macro and micronutrients. It contains a very high concentration of calcium (344 mg/100 g of grain), phosphorus (238 /100 g of grain) and protein (5.6 to 12.7%). However, it is often designated as an orphan crop due to the extreme negligence of the crop in terms of increasing genetic improvement for grain yield through selection and hybridization for the presence of extremely small inflorescence. These barriers have been the possible reasons for the unexplored genetic variability of finger millet. There is a need to undertake improvement programme for the crop to generate a high and consistent yield. Increasing the grain yield is the main objective of any breeding programme. But grain yield is a polygenic trait and is governed many genes, each contributing a small and cumulative effect on the yield. And hence selection of the plants only on the basis of yield of the plant may not be regarding, rather selecting the component characters for yield through study of their association with yield.

To make an effective selection, variability must be sufficiently present in the population. Hence, the study of genetic variability in the existing population is the first and foremost step of any breeding procedure. As per Burton, 1952, the amount of genetic gain expected from selection might be better estimated if genetic variability and heritability calculations were combined. Heritability estimates, combined with genetic progress are more useful than heritability estimates alone in estimating the gain under selection. Although, as per Johnson *et al.*, 1955, it not essential that a trait exhibiting high heritability will also show high genetic advance. For a successful crop improvement programme, a full grasp of the relationship between quantitative characters and yield as well as among themselves, is an absolute requirement. It allows the breeder to control the expression of these features in order to improve crop

yield. The direction and amplitude of link between yield and its components as well as among themselves determine the efficiency of grain yield selection. Path coefficient analysis (Wright, 1921) unlike correlation coefficient values, which quantify the amount of a link, assist in dividing the correlation coefficient into direct and indirect effects *via*, other components.

Genetic variability in finger millet gathered over years has less exploited for bringing about improvement in the crop. Aside from their availability, genetic resources must be characterised in order to be used effectively in crop improvement efforts. Divergence analysis-based knowledge among genotypes, usually aids a breeder in selecting variable parents for a breeding programme. The amount of genetic diversity present in a crop species with respect to yield as well as their association, reveals the kind and degree of interaction between any two measurable characters for attaining genetic improvement in that crop. As a result, in this study, variability parameters as well as character association, direct and indirect effects between yield and its attributing traits were assessed in this investigation and are outlined below.

5.1 Variance analysis and genetic variability parameters

Analysis of variance for yield and its component traits for thirty genotypes of finger millet. The result revealed an existence of was conducted and a significant difference among all genotypes with respect to the eight traits under study.

5.1.1 Mean performances of genotypes

Mean performances of the genotypes for various characters including grain yield showed that SRS-2 is the earliest maturing variety among the thirty genotypes under study taking about 95.67 days on an average for attaining maturity. Variety G30-GN-2-2 showed the highest grain yield/plant (22.31 g/plant). G30-GN-2-2 had the maximum number of ears/plant *i.e.*, 4 ears/plant, while variety G20-GG-2-4 showed maximum number of fingers/ear (9.20). Maximum ear length was recorded in VR-822 and the highest 1000- seed weight has been recorded in GPU-157 (3.13 g).

5.1.2 Coefficients of variation

Range is based on the two extreme values of the data set and hence can not sufficiently exhibit the total variance present in the genotypes under study. The real

values of variance are thus obtained from the studies of GCV and PCV. The higher is the values of this parameter, the more is the variability present in the population. The lower the difference in between PCV and GCV, the lesser is the influence of environmental factors on the character. Between PCV and GCV for the majority of the attributes exhibited a smaller difference. The PCV were generally higher than the GCV, indicating that the environment has an impact on the expression of these traits. High PCV and GCV has been observed in traits like number of ears/plants and grain yield/plant. This suggests that these traits are under the influence of genotypes and is under the influence of lesser environmental effects. As a result, these characters may be relied on and simple selection can be used to improve further. These observations are in accordance with the findings of Wolie and Dessalegn (2013). High PCV and GCV were recorded for grain yield/plant by Devaliya *et al.* (2018); Shinde *et al.* (2014) and Mahanthesha *et al.* (2017). The presence of high GCV and PCV for any trait indicates the presence of higher level of variability and hence selection of these traits can prove to be effective in crop improvement programme.

5.1.3 Heritability and genetic advance

The broad sense heritability gives an estimate of the heritable portion of the variation out of the total variation present in a given trait. As per Johnson *et al.* (1955), in order to increase the selection efficiency, genetic gain along with heritability estimates could prove to be useful. Hence, it is crucial to use the expected genetic advance as well as the heritability estimate, as a tool in the selection process to improve efficiency.

High heritability along with high genetic advance as per cent of mean were observed for grain yield/plant followed by number of ears/plants, number of fingers/ears and finger length. This suggests that the expression of these features was least influenced by the environment and that selection can be useful to improve them. The above result is in accordance with Shet *et al.* (2010), Ganapathy *et al.* (2011), Haradari *et al.* (2012), Lule *et al.* (2012), Sao *et al.* (2016a) and Mahanthesha *et al.* (2017) for the traits like yield/plant and ear length. Similar results were also found by Ganapathy *et al.* (2011), Eric *et al.* (2016), Reddy *et al.* (2013), Savitha *et al.* (2013) and Wolie and Dessalegn (2013) for number of ears/plant and number of fingers/ears, whereas moderate heritability along with moderate genetic advance as percent of

mean were observed for the traits like days to 50% flowering. Similar findings were recorded by Nandini *et al.* (2010) and Ali *et al.* (2013).

5.2 Character association

The genetic basis of character association is regarded to be either due to linkage or pleiotropy. The association formed by coupling phase linkage is more resistant to selection pressure than the association formed by repulsion phase linkage. Pleiotropic effects, on the other hand, contribute to strong character association. If the traits related are both desirable and complementary, such linkages are useful. Long years of selection pressure on auto-gamous crops like finger millet have resulted in the establishment of both beneficial and antagonistic associations between grain yield and its component characters.

Selection for grain yield/plant is frequently unreliable, hence, selecting indirectly through component traits becomes critical for the final results. As a result, traits association studies not only aid in comprehending the character association, but also provide insight into the nature and direction of selection. As a result, during the current study, an attempt was made to quantify the nature and amount of character pair correlation, in order to aid genotypic selection in order to get enhanced production. For easier understanding, the results of such relationships are presented below.

5.2.1 Correlation of grain yield with other component characters

The results of this study showed that genotypic correlation coefficients, in general were higher than phenotypic correlation coefficients, indicating that the observed relationships between various traits were due to genetic causes and thus lowering the reliability of phenotypic correlation for breeding improvement. The above information has been illustrated in Table 6. This is also in agreement with the findings of Dhamdhare *et al.* (2011) and Lule *et al.* (2012).

The maximum positive and significant association was found in between grain yield and number of ears/plant followed by days to 50% flowering, days to maturity and finger length at both phenotypic and genotypic levels. This is in accordance with the findings of Vidhate *et al.* (2020), Chavan *et al.* (2020), Keerthana *et al.* (2019),

Anuradha *et al.* (2013) and Jadhav *et al.* (2015). This shows that these characters should be taken into account while selecting genotypes for increased grain yield.

While a positive and non-significant association was found in between grain yield/plant and number of fingers/ears and plant height at both phenotypic and genotypic levels respectively. This is in accordance to the findings of John *et al.*, (2018).

5.2.2 Correlation among component characters

Days to 50% flowering was found to be positively and significantly associated with grain yield/plant. This is in accordance with the results of Chavan *et al.* (2020) and Keerthana *et al.* (2019). It showed positive and significant association with days to maturity, ear length, fingers/ear, number of ears/plant and plant height. Therefore, this trait can be used effectively to undertake selection for yield improvement. Number of ear/plants also associated positively and significantly with grain yield/plant. The above observation is in agreement with the results published by Chavan *et al.* (2020), Kumar *et al.* (2014) and Jadhav *et al.* (2015).

For the character like days to maturity, a positive and significant association was observed with grain yield/plant. This is in accordance with the results of Anuradha *et al.* (2013) and Jadhav *et al.* (2015). It showed positive and significant association ear length, number of fingers/ear and plant height.

Ear length and number of finger/ears also showed a positive and significant association with grain yield/plant. The following observations can be stated according to the results of Chavan *et al.* (2020), Sapkal *et al.* (2019) and Jadhav *et al.* (2015). On the other hand, a significant and negative association was recorded for the traits 1000-seed weight, plant height and fingers/ears. Hence, selection for the above traits may not give fruitful results during the crop improvement programme.

Hence, it can be concluded that, yield/plant had a positive association with days to 50% flowering, ears/plant, and days to maturity, ear length and number of finger/ears from the results of the correlation study. Since, these traits are associated with grain yield, they may be used as a selection criterion for obtaining high yielding plants.

5.3 Path coefficient analysis

As per Dewey and Lu, 1959, path coefficient values assess the amount of direct and indirect effects of characters on complex dependent traits like yield and assist the breeders to make the best decisions about the relevant component characters during selection. The partitioning of correlation coefficient into direct and indirect impacts using path coefficient analysis is critical for understanding the direct and indirect effects of each character on grain yield and applying selection pressure more effectively for yield enhancement. The route coefficients calculated for different sets of characters as well as different cultural contexts reveal significant differences in the direct and indirect effects of the component characters on grain yield.

From the path coefficient analysis, it was detected that the highest positive direct effect was recorded for number of ears/plants followed by days to 50% flowering, finger length, number of fingers/ears and days to maturity, while the maximum negative direct effect on grain yield were observed for 1000-seed weight followed by height of the plant, at both genotypic and phenotypic level.

Of the characters under study, number of ears/plants, finger length, number of fingers/ears, days to 50% flowering and days to maturity showed maximum indirect effect on the dependable character grain yield/plant *via.*, other characters. Hence, these characters may be considered essential selection factors for achieving high and reliable yields in finger millet. These findings of Vidhate *et al.* (2020), Keerthana *et al.* (2019), Nagar *et al.* (2020), Jadhav *et al.* (2015) and Mahanthesha *et al.* (2018) are in accordance with the above observations.

The direct influence of traits like days to 50% flowering, finger length, fingers/ear and days to maturity is more or less the same, demonstrating that correlation is present in the underlying association and that direct selection using these attributes would be effective. A negative character association and positive direct effect was found for the traits like number of fingers/ears. The indirect effect may be considered to be the cause of correlation for the above attributes thus, implying to the need for the consideration of indirect factors during selection. In these cases, a restricted selection model is used, in which limits are established to exclude undesirable indirect effects so that direct effects can be used.

5.4 Genetic divergence studies

For the accomplishment of any crop improvement programme, the presence of genetic diversity in the population is an absolute requirement for effective selection of parents. To find out the genetic diversity present among different germplasms, the Mahalanobis D^2 statistical analysis is done. This analysis uses second degree statistics and requires replicated data. It reveals the presence of genetic divergence in the germplasm under study by dividing them into distinct clusters. The distance between the clusters implies the degree of genetic divergence and the more the distance the more is the divergence.

5.4.1 Studies on nature of genetic divergence

It is now possible to divide biological populations into various groups and examine how different component features contribute to total divergence. It is a well-known fact that choosing parents based on genetic diversity is a good indicator for generic manipulation in the genotypes. As a result, during the current study, an attempt was made to analyse the nature and magnitude of genetic divergence by including simultaneous alterations in all eight features of thirty elite finger millet genotypes in order to detect varied genotypes for upcoming breeding programmes. The results are discussed in the following paragraphs.

5.4.2 Composition of clusters

Following Tocher's method, the thirty genotypes of finger millet were genotypes into five clusters based on the relative magnitude of D^2 values. Cluster I was the major group, with eighteen genotypes followed by cluster III (8 cultures), cluster IV (2 cultures). But cluster II and V are mono-clusters having one genotype each. Cluster I have grouped a large number of cultivars due to similar selection pressure favoring identical expression of characters contributing to grain yield during selection. The genotypes within a cluster is considered to have common evolutionary ancestors and thus are less likely to be diverse from one another. The hybridization programme undertaken within the genotypes of a cluster are not expected to give superior hybrids as there is less genetic diversity present among the members of the cluster. But successful crossing works can be done among the genotypes belonging to different clusters as they turn up showing high heterosis in the F_1 crosses and the segregating generations.

Out of the five clusters obtained from thirty genotypes of finger millet, the maximum intra cluster distance has been recorded for cluster III (16.28) indicating the presence of more divergence within the cluster. While the minimum intra cluster distance has been recorded in cluster IV (5.23). Intra cluster distance in clusters II and V was found to be zero.

The highest inter-cluster distance was present in between cluster IV and V (219.92) followed by followed by cluster III and IV (165.52) and cluster II and IV (118.53) which implied the presence of high genetic diversity among the genotypes present within these clusters. Hence, while undertaking hybridization work, it would be useful criteria to select parents from these diverse clusters to get desirable segregants in the F₁ and subsequent generations. On the other hand, minimum inter cluster distance has been noted in between cluster II and III (21.34) indicating less diverse genotypes and the presence of close relationship between them.

As a result of the previous observations, genotypes in divergent clusters had considerable disparities among themselves for a greater number of characters, whereas genotypes in near clusters had genotypes that were more or less similar for the majority of features. Selecting divergent groups from the above clusters would result in a wide range of diversity in yield and yield attributing attributes, allowing for additional selection and genetic improvement. Within the limit of compatibility of these clusters, crosses developed from selected genotypes may produce desirable transgressive segregates that could be valuable in finger millet breeding. As a result, it is advised that in the current study, parents be picked from the most divergent groups, *i.e.*, cluster IV and cluster V, for hybridization and that these parental pairings should produce transgressive segregants for better yield performances in the finger millet crop. This is in accordance to Negi *et al.* (2017), Lule *et al.* (2012), Bedis *et al.* (2007), Devaliya *et al.* (2017), Patel *et al.* (2020), Suryanarayana *et al.* (2019) and Sapkal *et al.* (2019). However, selecting parents from each of these distinct groups on the basis of per se performance or component features that complement each other for the expression of ultimate output would be the most practicable choice.

5.4.3 Analysis of cluster means

A review of data from cluster average mean values revealed that different clusters performed better for different characters and no single cluster could be found

as promising for integrating all of the desirable traits. It was observed that cluster III had genotypes with minimum days to 50% flowering, days to maturity, ear length, fingers/ear and 1000-seed weight. Cluster V had genotypes for maximum number of fingers/ear, days to maturity, plant height and 1000-seed weight while minimum for number of ears/plant and yield/plant. Cluster VI has genotypes for minimum plant height and maximum days to 50% flowering, ears/plant and yield/plant. Cluster II has genotypes for maximum finger length.

To summarise, Cluster III produced the majority of lower values, whilst Cluster V offered maximum highest values for the characters described above. Furthermore, crosses involving parents from divergent clusters are expected to exhibit higher heterosis and better recombinants in segregating generations, resulting in increased finger millet production. Anantharaju and Meenakshiganesan (2008), Prabhu *et al.* (2008), Subramanya and Ravikumar (2020), Suryanarayana *et al.* (2019) and Mahanthesha *et al.* (2017) revealed a quite consistent results on genetic divergence studies in finger millet. As a result, it's important to point out that when computing cluster means, the superiority of one genotype over another in terms of a specific character is diluted by other genotypes that are related and grouped in the same cluster but are inferior or intermediary for that character. As a result, in addition to selecting genotypes for hybridization from clusters with a large inter-cluster distance, one may consider selecting genotypes depending on the extent of genetic divergence in a particular character of interest. It is indicated that for increasing grain yield genotypes can be chosen from substantially from divergent genotypes with respect to these characters.

SUMMARY AND CONCLUSION

Eleusine corocana, commonly known as finger millet is a significant minor millet crop of India and is popularly grown in Odisha. Being a C₄ short-day plant, it hardy and is resistant to biotic and abiotic stresses. Besides, it can tolerate soil salinity up to some extent and can withstand water logging. Finger millet can be grown in the pH range of 5 to 8.2 and hence can tolerate moderately acidic to alkaline soils. It faces less risk to storage pest attack and can be stored for a long time without any risk of storage damage. In Odisha, it is grown in an area of 1.16 hectares with a grain production of 10.05 lakh quintals. It is a crop of high nutraceutical values and contains a very high concentration of calcium (344 mg per 100 g of grain) and relatively high amount of phosphorus (238 mg per 100 g of grain). The grains are a rich source of protein (5.6 to 12.7%), proportionately higher in brown seeded than in white seeded genotypes. Besides, finger millet has amino acids rich in sulphur that are crucial for human health and rich source of minerals like calcium, iron, zinc with manganese. It is gluten-free, rich in mineral and fibers that helps with weight loss and diabetes. It is also used to make traditional liquor and its by-products are used as livestock feed. It can be used as a backup (famine) food in time of natural calamities.

Taking into account the importance of finger millet especially in dry and drought prone areas as it prevails in the Odisha agroclimatic conditions. The present investigation was carried out to evaluate thirty genotypes of finger millet including two checks for eight characters to access the presence of genetic variability, character association in terms of yield, path analysis and genetic divergence analysis among the genotypes to select the most helpful and promising genotypes for potential application in future breeding programmes. The present investigation was conducted during Kharif season 2020 in the OUAT Farm, EB-II sections, Department of Plant Breeding and Genetics, OUAT, Bhubaneswar. The experiment was conducted using Randomized Block Design (RBD) with 3 replications using 30 promising cultures of finger millet including 2 checks. The seeds were sown in the nursery on 30th June, 2020 and were transplanted into the main field on 28th July, 2020. The plot was of dimensions of 28 m length and 29.5m width and was subdivided into 9 subplots each consisting of 5 rows with each row having 30 plants. The spacing was maintained at 20 cm x 10 cm. The fertilizer dose of N:P:K @ 40:20:20 kg/ha was applied to the

experimental field with whole potassium and phosphorous as basal at the time of transplanting. The rest 50% nitrogen fertilizer was applied at the time of land preparation, as top dressing at tillering stage. Farm yard manure @10 tons/ha was applied. Other suggested agronomical package of practices was followed during the experimental process to raise a good crop.

From the analysis of variance, a significant level of differences was observed among the genotypes for all the traits under study, indicating the presence of high degree of variability among the genotypes. For the most of the attributes studied, the mean and range values suggested presence of significant amount of variability. A wide range of variation was also observed for all the eight traits, evident from different genetic parameters indicating an immense opportunity in bringing about improvement for the required crop. The genotypic and phenotypic coefficients of variance for all the characters in different attributes remained consistent. In-between PCV and GCV, very little differences were observed for the majority of traits. The phenotypic coefficient of variance was, on average, greater than the genotypic coefficient of variation. For traits like grain yield/plant and number of ears/plants, both GCV and PCV were found to be high (> 20%) implying that these traits are controlled by genotype of the plant to a much greater extent and less influenced by environmental factors.

For the majority of the traits studied, heritability estimates were found to be high. The heritability estimates for different characters varied from 96.422 % for grain yield/plant to 34.463% for days to maturity. High heritability was observed in the traits like grain yield/plant followed by number of ears/plants, number of fingers/ears and finger length while moderate heritability was observed for the trait days to 50% flowering followed by plant height, 1000-seed weight and days to maturity. High genetic advance expressed was observed for traits like grain yield/plant followed by number of ears/plants, ear length and number of fingers/ears and while moderate genetic advance was observed for the trait days to 50% flowering. Low genetic advance was observed for plant height, 1000- seed weight and days to maturity in the decreasing order, respectively.

Grain yield/plant and number of ears/plants exhibited high GCV, PCV, heritability along with high genetic advance, while the traits like finger length and

number of fingers/ears exhibited moderate GCV, PCV and high heritability coupled with high genetic advance. Low GCV, PCV and high heritability coupled with high genetic advance was observed for days to maturity. Generally, genotypic correlation estimates were greater than phenotypic correlation estimates showing that environmental factors influenced the genetic origin of correlation, lowering the reliability of phenotypic correlation for genetic improvement. However, estimates of phenotypic and genotypic correlations followed a nearly same pattern for all the characters.

The trait like grain yield/plant exhibited a positive and significant association with number of ears/plants followed by days to 50% flowering, days to maturity and finger length. While a positive and non-significant association was found in between grain yield/plant and number of fingers/ears, 1000-seed weight and plant height at both phenotypic and genotypic levels respectively.

The results of this study showed that in general, phenotypic correlation coefficients were lower than genotypic correlation coefficients, indicating that the observed relationships between various traits were due to genetic causes and thus lowering the reliability of phenotypic correlation for breeding improvement. The maximum positive and significant association was found in between grain yield and ears/plant followed by days to 50% flowering, days to maturity and finger length at both phenotypic and genotypic levels. While a positive and non-significant association was found in between grain yield/plant and number of fingers/ears and plant height at both phenotypic and genotypic levels respectively.

Days to 50% flowering was found to be positively and significantly associated with grain yield/plant. It showed positive and significant association with days to maturity, ear length, number of fingers/ear, number of ears/plant and plant height. Therefore, this trait can be used effectively to undertake selection for yield improvement. Number of ear/plants is also associated positively and significantly with grain yield/plant. For the character like days to maturity, a positive and significant association was observed with grain yield/plant. It showed positive and significant association ear length, number of fingers/ear and plant height. The traits ear length and number of finger/ears also showed positive and significant association with grain yield/plant. On the other hand, a significant and negative association was

recorded for the traits like 1000-seed weight, plant height and number of fingers/ears. Hence, selection for the above traits may not give fruitful result during the crop improvement programme.

Hence it can be concluded that yield/plant had a positive association with days to 50% flowering, ears/plant, and days to maturity, ear length and number of finger/ears from the results of the correlation study. Since, these traits are associated with grain yield, they may be used as a selection criterion for obtaining higher yielding genotypes.

From the path coefficient analysis, it was detected that the highest positive direct effect was recorded for number of ears/plants followed by days to 50% flowering, finger length, number of fingers/ears and days to maturity, while the maximum negative direct effect on grain yield were observed for 1000-seed weight followed by plant height, at both genotypic and phenotypic level.

The characters like number of ears/plants, days to 50% flowering, finger length, number of fingers/ears and days to maturity showed maximum indirect effect on the dependable character yield/plant *via.*, other characters. Hence, these characters may be considered essential for selection to achieve high and reliable yields in finger millet. The direct influence of features like days to 50% flowering, finger length, number of fingers/ears, and days to maturity is more or less the same, demonstrating that correlation is present in the underlying association and that selection of these traits directly would be more rewarding. A negative character association and positive direct effect was found for the traits number of fingers/ears. The indirect effect may be considered to be the cause of correlation for the above attributes thus, indicating the need for the consideration of indirect factors during selection. In these cases, a restricted selection model may be used, in which limits are established to exclude undesirable indirect effects so that direct effects can be used.

The thirty genotypes under study were grouped into five distinct clusters. The presence of maximum numbers of genotypes has been observed in cluster I with 18 genotypes followed by cluster III with 8 genotypes, cluster IV with 2 genotypes, and cluster II and V having one genotype each G5-GG-2-1 and G20-GG-2-4 respectively. The average D^2 values are used to find out the inter and intra cluster relations within

the clusters. The maximum intra cluster distance was recorded for cluster III followed by cluster I while the minimum in cluster IV. For the clusters II and V, the intra cluster distances were recorded to be zero. The highest inter-cluster distance was present in between cluster IV and V followed by cluster III and IV, II and IV, I and V, I and III, III and V, I and IV, I and II and cluster II and V, while minimum between cluster II and III. It implies that cluster IV and V are more distantly related than the rest of the others. As a result of the previous observations, genotypes in divergent clusters had considerable differences among themselves for a greater number of characters, whereas genotypes in close Clusters had genotypes that were more or less similar for the majority of features.

In the views of the average mean values of different clusters, cluster III produced the majority of lower values, whilst Cluster V offered maximum highest values for the characters described above. Furthermore, crosses involving parents from divergent clusters are expected to exhibit higher heterosis and better recombinants in segregating generations, resulting in increased finger millet production. Divergent Clusters had genotypes with considerable differences for a greater number of characters, whereas Clusters with closeness contained genotypes that were more or less similar for the majority of attributes. Hence, in order to get desirable transgressive segregants for the required traits, hybridization works can be undertaken using superior genotypes.

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