ABSTRACT

Comment [A1]: The abstract should bear the objective of the study. It is current form, the authors did not indicate the objective of the study. The authors should conclude the abstract section with the implications of the findings of the study and the way forward.

Introduction

Finger millet (*Eleusinecoracana*L. *Gaertn*)is commonly known as ragi which is popularamong millets in India, specifically in down south. It'shigher nutritious nature attracting the urban dwellers and playing key role in counterpart the diabetes.Finger millet is grown as minor millet belongs to a grass family, its water requirement is 30% fewer compare to rice in particular. It is good sources ofprotein (7.3g) and fiber (3.6g).The cultivated ragi is a tetraploid (2n = 4x = 36).It is mostly a self pollinated crop due to cleistogamy, but it ranges about 1% cross pollination moderated by wind(Jansen and Ong 1996; Purseglove 1972).Over the years the area under millets is in a steep decline, till the early 1970's the share of millets in the food basket is 20% but now it merely left with 6%, but the silver lining aspect in the entire sequence is that the productivity is increased by the 2.5% (Ministry of Agriculture & Farmers Welfare, Break out session; 2022). The yield trait is very complicated because it is effected by lot many other factors & traits, it is quiet important to study the direct impact of characters on yield this will further aids to improve the yield potential under variable circumstances, it is a proven fact that the proper understanding of yield associated characters helps in altering the genetic composition and ultimately leads to genetic gain in the particular gene base.

Here combination of both correlation and path analysis helps in shedding light on understandingthe relationship between the yield and associated characters.

In general, yield in finger millet grain yield is greatly influenced by the number of productive tillers per plant, number of fingers per ear head, has been illustrated with the help of both correlation and path co efficient analysis (Sapkal*et al*.2019).

Comment [A2]: That problem is the study trying to solve?
the background information is weak. The authors need to clearly state the objectives of the study and the possible implication of the findings as far as finger millet production or breeding are concerned

Material and Methods

The present experiment was carried out at the Field Experimentation Centre of the Department of Genetics and Plant Breeding. The site is located at 25.28 N latitude, 81.54 E longitude and 98 meter above the sea level. Itcomes under sub-tropical and semi-arid climate. Lies 102m above sea level. The average annual rainfall is 1042 mm. The present study consists of 20finger millet lines which were collected from IIMR, Hyderabad grown in *kharif*, 2021. The experiment was laid in a randomized block complete design (RCBD) with 20 genotypes in three replications.

Totalthirteen traits were studied *viz.,* days to 50% flowering, days to maturity, plant height, flag leaf length, number of fingers, number of tillers, finger length, peduncle length, ear head length, biological yield, test weight, harvest index and seed yield per plant (g). Thequantitative data~~e~~ of all the above traits were recorded from the average of five best plants from each plot and subjected to the following listed data analysis.

Firstly measure of variability is figured with the aid of Coefficient of variation, which is the ratio of standard deviation of a sample to its mean and expressed in percentage. In the present investigation two types of coefficient of variations were estimated *viz*., phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

Coefficient of variation (CV): It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

CV (%) = Standard deviation / Mean X 100

Comment [A3]: The formula for CV (%) should be correctly written using equation. Ie. CV(%) = (Standard deviation/Mean) x 100

The formulae used to calculate PCV and GCV were stated by **(Burton, 1952)**

PCV (%) = Phenotypic standard deviation /Grand mean X 100

GCV (%) = Genotypic standard deviation / Grand mean x 100

Comment [A4]: The formula for PCV should be written correctly written using equation. Ie. PCV(%) = (Phenotypic standard deviation/Grand mean) x 100

Comment [A5]: The formula for GCV should be written correctly written using equation. Ie. GCV(%) = (Genotypic standard deviation/Grand mean) x 100

Heritability calculated by the formula given by**Lush (1949) and Burton and Devane (1953).** CorrelationCoefficientwascalculatedaccordingtotheformulasuggestedby**Miller*et al*(1958)**. And laterused by**Gandhi*et al*(1964)**.Path coefficient analysisis normally to measures thedirectandindirecteffectsof independentvariablesonthedependentvariables.Thistechnique was firstly used by **Dewey and Lu (1959)**.

Results and Discussion

Genetic Variability

High GCV along with PCV is found in characters such as ear head length (31.10 & 31.87%) followed by in seed yield per plant (18.37 & 23.38%), while it is observed low in plant height (1.75 & 3.49%).

Comment [A6]: the authors should make reference to the tables where this information can be found in the text.

Heritability

The normal heritability (broad sense) is ranged from 25.03% (plant height) to 78.70% (number of fingers)

Genetic advance

High genetic advance as percentage of mean was found in ear head length (46.59%) followed by grain yield (39.62%), whereas reported low among others is in plant height (2.33%).

Correlation

The quantitative traits such as harvest index, plant height, number of tillers per plantobservedhavinghighly positive significant genotypic and phenotypic correlation with seed yield per plant**(0.930**, 0.769**, 0.542**)**.While positive and non-significant phenotypic and genotypic correlation exhibited between flag leaf length and seed yield per plant is **(0.035)**. Similar results were noticed in (**Gohel and Chaudhari,2018)** where seed yield having highly non-significant negative relation with days to 50% flowering (r_p= -0.154) and negative significant observed in days to 50% flowering (r_g= -0.274**) and number of fingers (r_g= -0.392**). However genotypic correlation having higher significance than phenotypic correlation. Both the genotypic and phenotypic values are clearly illustrated in Table 1.

Preliminary studies also revealed the similar results in **(gohel and chaudhari2018)** stated the significant positive genotypic relation with harvest index (0.883**) and phenotypic with harvest index (0.697**). Similarly **chavan*et al.*, (2020)** also proved phenotypic positive significant correlation between seed yield and harvest index (0.664**).

Path analysis

Path analysis in particular having the direct effect of seed yield on characters such as harvest index followed by number of effective pods per plant, plant height, days to maturity, biological yield in descending order.

At the phenotypic path coefficient analysis test weight (p = 0.493**) followed by test weight (p = 0.457**),biological yield per plant (p = 0.425**), number of tillers (ph = 0.397**)exhibited significant positive direct effect with seed yield per plant and characters such as number of fingers (ph= -0.202) followed by days to 50% flowering (ph = -0.154) and peduncle length (ph = - 133) showed potential negative indirect effect with seed yield per plant, similar results were projected by ***chavan et al.*** **(2020)** and **sapkal*et al.* (2019)**.

Table 1: Phenotypic correlation among the different traits evaluated in finger millet during *Kharif*, 2021

	DTF	DTM	PH	FLL	NF	NT	FL	PL	EHL	BY	TW	HI	GYPP
DTF	1	-0.112	-0.075	0.183	0.668**	-0.029	-0.598**	0.188	-0.765**	0.390**	-0.264*	-0.808**	-0.154
DTM		1	0.752**	-0.181	-0.269**	0.301**	0.553**	0.039	0.359**	-0.053	0.275**	0.527**	0.289**
PH			1	0.060	-0.548**	0.349**	0.543**	-0.007	0.465**	-0.004	0.255*	0.722**	0.312**
FLL				1	0.147	0.236*	-0.011	-0.341**	-0.216*	0.228*	0.429**	-0.376**	0.061
NF					1	-0.326**	-0.739**	-0.090	-0.721**	0.323**	-0.108	-0.726**	-0.202
NT						1	0.510**	0.014	0.335**	0.174	0.383**	0.563**	0.397**
FL							1	-0.133	0.943**	-0.402**	0.379**	0.847**	0.493**
PL								1	0.200	-0.338**	-0.556**	0.138	-0.134
EHL									1	-0.599**	0.119	0.889**	0.320**
BY										1	0.382**	-0.301**	0.425**
TW											1	0.100	0.457**
HI												1	0.362**
GYPP													1

*** and ** Significant at P<0.05 and P<0.01, respectively**

DF50: Days to 50% flowering, DTM: Days to 50% Maturity, PH: Plant height (cm), FLL: Flag leaf length, NF: Number of fingers, NT: No. of tillers, FL: Finger length, PL: Peduncle length, EHL: Ear head length, BY: Biological Yield (g), TW: Test weight (g), HI: Harvest index (%), GYPP: Grain yield per plant (g)

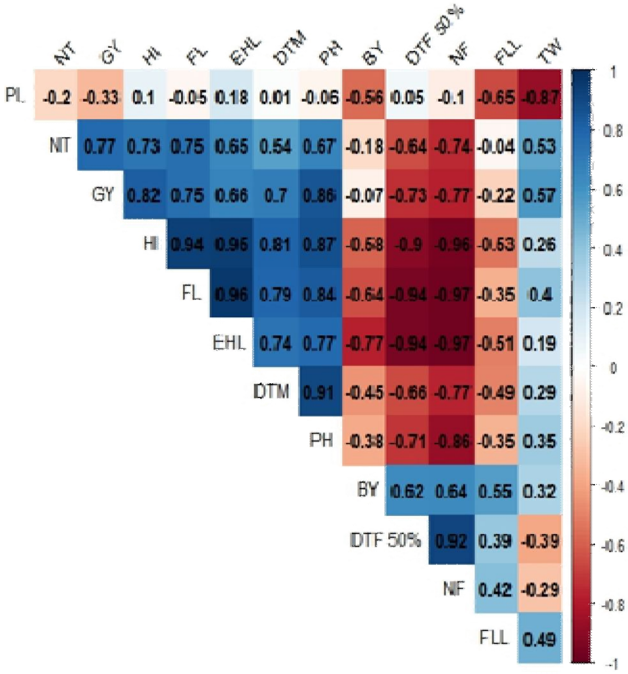

Fig. 1: Pearson's Correlation Matrix

At genotypic level especially among all the characters, harvest index showed highest direct effect (g = 1.449) on seed yield followed by number of effective pods per plant (g = 0.499), plant height (g = 0.330) and days to maturity (g = 0.197), but days to 50% flowering (g = -0.325), number of primary branches per plant (g = -0.321), seed index (g = -0.170) exhibited potential negative direct effect.

Similar results expressed by~~n~~*Negi et al.* (2017) seed yield per plant is showing consistent positive direct effect with biological yield (0.619) followed by harvest index (0.437), number of tillers per plant (0.395) but showing consistent negative direct effect with characters like days to 50% flowering (-0.179), days to maturity (-0.167). The direct and indirect effects are clearly illustrated in the table 3 and 4. The current experiment conducted under the rainfed conditions. The characters harvest index, biological yield, test weight and number of tillers manifested the higher results of effecting direct contribution on seedyield, with all the above presented results it is evi~~e~~dently conclusive that the exploitation of harvest index and number of tillers per plant will be valuable.

Table 2: Genotypic correlation among the different traits evaluated in finger millet during *Kharif,* 2021

	DTF	DTM	PH	FLL	NF	NT	FL	PL	EHL	BY	TW	HI	GYPP
DTF	1	-0.112	-0.075	0.183	0.668**	-0.029	-0.598**	0.188	-0.765**	0.390**	-0.264*	-0.808**	-0.154
DTM		1	0.752**	-0.181	-0.269**	0.301**	0.553**	0.039	0.359**	-0.053	0.275**	0.527**	0.289**
PH			1	0.060	-0.548**	0.349**	0.543**	-0.007	0.465**	-0.004	0.255*	0.722**	0.312**
FLL				1	0.147	0.236*	-0.011	-0.341**	-0.216*	0.228*	0.429**	-0.376**	0.061
NF					1	-0.326**	-0.739**	-0.090	-0.721**	0.323**	-0.108	-0.726**	-0.202
NT						1	0.510**	0.014	0.335**	0.174	0.383**	0.563**	0.397**
FL							1	-0.133	0.943**	-0.402**	0.379**	0.847**	0.493**
PL								1	0.200	-0.338**	-0.556**	0.138	-0.134
EHL									1	-0.599**	0.119	0.889**	0.320**
BY										1	0.382**	-0.301**	0.425**
TW											1	0.100	0.457**
HI												1	0.362**
GYPP													1

*** and ** Significant at P<0.05 and P<0.01, respectively**

DF50: Days to 50% flowering, DTM: Days to 50% Maturity, PH: Plant height (cm), FLL: Flag leaf length, NF: Number of fingers, NT: No. of tillers, FL: Finger length, PL: Peduncle length, EHL: Ear head length, BY: Biological Yield (g), TW: Test weight (g), HI: Harvest index (%), GYPP: Grain yield per plant (g)

Table 3: Phenotypic direct (in bold) and indirect effects of thirteen traits on seed yield in finger millet evaluated in *Kharif,* 2021

	DTF	DTM	PH	FLL	NF	NT	FL	PL	EHL	BY	TW	HI	GYPP
DTF	**0.0020**	0.0002	0.0000	0.0000	0.0005	-0.0005	-0.0006	0.0001	-0.0006	0.0003	-0.0005	-0.0003	-0.1541
DTM	-0.0047	**-0.0438**	-0.0204	0.0039	0.0094	-0.0075	-0.0172	-0.0002	-0.0143	0.0018	-0.0056	-0.0141	0.289**
PH	-0.0025	0.0804	**0.1728**	0.0125	-0.0487	0.0168	0.0350	-0.0056	0.0203	0.0060	0.0164	0.0405	0.312**
FLL	0.0015	0.0115	-0.0094	**-0.1294**	-0.0143	-0.0330	-0.0138	0.0369	0.0140	-0.0225	-0.0424	0.0232	0.0613
NF	0.0055	-0.0574	-0.1916	-0.2713	**0.0201**	-0.0828	-0.0626	0.0794	0.0077	-0.0510	-0.1012	0.0059	-0.2024
NT	-0.0257	0.0193	0.0110	0.0288	-0.0271	**0.1128**	0.0459	-0.0024	0.0296	0.0105	0.0423	0.0140	0.397**
FL	-0.1021	0.1383	0.0715	0.0377	-0.1724	0.1435	**0.3525**	-0.0408	0.2701	-0.0715	0.1440	0.1372	0.493**
PL	0.0040	0.0003	-0.0019	-0.0172	-0.0043	-0.0013	-0.0070	**0.0603**	0.0118	-0.0138	-0.0208	0.0020	-0.1335
EHL	-0.0067	0.0068	0.0024	-0.0023	-0.0115	0.0055	0.0160	0.0041	**0.0208**	-0.0076	0.0040	0.0096	0.320**
BY	0.0630	-0.0191	0.0164	0.0816	0.1394	0.0436	-0.0951	-0.1070	-0.1700	**0.4686**	0.1051	-0.0054	0.425**
TW	-0.0581	0.0318	0.0234	0.0809	-0.0026	0.0926	0.1008	-0.0853	0.0477	0.0554	**0.2469**	-0.0411	0.457**
HI	-0.0251	0.0630	0.0460	-0.0352	-0.0708	0.0244	0.0764	0.0065	0.0907	-0.0023	-0.0327	**0.1962**	0.362**

*** and ** Significant at P<0.05 and P<0.01, respectively**

DF50: Days to 50% flowering, DTM: Days to 50% Maturity, PH: Plant height (cm), FLL: Flag leaf length, NF: Number of fingers, NT: No. of tillers, FL: Finger length, PL: Peduncle length, EHL: Ear head length, BY: Biological Yield (g), TW: Test weight (g), HI: Harvest index (%), GYPP: Grain yield per plant (g)

Table 4: Genotypic direct (in bold) and indirect effects of thirteen traits on seed yield in finger millet evaluated in *Kharif*, 2021

	DTF	DTM	PH	FLL	NF	NT	FL	PL	EHL	BY	TW	HI	GYPP
DTF	**-0.3708**	0.0414	0.0276	-0.0679	-0.2476	0.0109	0.2217	-0.0695	0.2836	-0.1445	0.0977	0.2997	-0.274**
DTM	0.0348	**-0.3119**	-0.2346	0.0565	0.0838	-0.0937	-0.1723	-0.0121	-0.1121	0.0165	-0.0856	-0.1644	0.415**
PH	-0.0802	0.8092	**1.0758**	0.0644	-0.5890	0.3758	0.5845	-0.0076	0.5007	-0.0041	0.2744	0.7761	0.769**
FLL	-0.0337	0.0333	-0.0110	**-0.1839**	-0.0271	-0.0435	0.0021	0.0628	0.0397	-0.0419	-0.0790	0.0692	0.0350
NF	0.3234	-0.1301	-0.2651	0.0712	**0.4842**	-0.1576	-0.3577	-0.0436	-0.3490	0.1562	-0.0521	-0.3517	-0.392**
NT	-0.0132	0.1355	0.1575	0.1065	-0.1467	**0.4508**	0.2297	0.0062	0.1509	0.0783	0.1726	0.2536	0.542**
FL	0.5074	-0.4687	-0.4610	0.0096	0.6268	-0.4324	**-0.8484**	0.1132	-0.8000	0.3410	-0.3214	-0.7190	0.490**
PL	-0.0666	-0.0138	0.0025	0.1212	0.0320	-0.0049	0.0474	**-0.3552**	-0.0711	0.1202	0.1975	-0.0491	-0.210*
EHL	-1.0567	0.4965	0.6430	-0.2984	-0.9958	0.4625	1.3027	0.2767	**1.3815**	-0.8278	0.1637	1.2279	0.393**
BY	0.3040	-0.0412	-0.0030	0.1778	0.2517	0.1355	-0.3137	-0.2641	-0.4676	**0.7804**	0.2984	-0.2349	0.449**
TW	0.0500	-0.0521	-0.0484	-0.0816	0.0204	-0.0727	-0.0720	0.1056	-0.0225	-0.0726	**-0.1899**	-0.0191	0.460**
HI	0.1279	-0.0834	-0.1142	0.0595	0.1149	-0.0890	-0.1341	-0.0219	-0.1406	0.0476	-0.0159	**-0.1582**	0.930**

*** and ** Significant at P<0.05 and P<0.01, respectively**

DF50: Days to 50% flowering, DTM: Days to 50% Maturity, PH: Plant height (cm), FLL: Flag leaf length, NF: Number of fingers, NT: No. of tillers, FL: Finger length, PL: Peduncle length, EHL: Ear head length, BY: Biological Yield (g), TW: Test weight (g), HI: Harvest index (%), GYPP: Grain yield per plant (g)

Fig. 2: Phenotypic Path Diagram showing direct and indirect effects of different traits on seed yield

Comment [A7]: The information on the right side of figure 2 is not visible enough for readers to appreciate the values. The authors should use a more clearer diagram instead of this image. It appears the lines are too thick

Fig. 3: Genotypic Path Diagram showing direct and indirect effects of different traits on seed yield

References

Burton, G. W., and Devane, D. E. (1953). Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agr. Jour.*, 45(10): 478-481.

Chavan, B. R., Jawale, L. N., and Shinde, A. V. (2020).Correlation and path analysis studies in finger millet (*Eleusinecoracana*L. *Gaertn*) for yield and yield contributing traits. *Int. Jou. of chem. Stu.*, **8**(1): 2911-2914.

Directorate of Economics ~~A~~and Statistics, (2018-19).Ministry of Agriculture & Farmers Welfare (DAC&FW), Govt. of India; IIIrd Advance Estimate

O'Kennedy M. M., Grootboom A.,~~,~~ andShewry P. R. (2006). Harnessing sorghum and millet biotech for food and health. *Jou.ofCer. Sci.,* 44: 224–235.

Dewey, D.R. and Lu, K.H. (1959).A correlation and path coefficient analysis of component of seed production.*Agro. J*., 51: 515-518.

Fisher, R. A. (1936). The Use of Multiple Measurement in taxonomic problem. *Annals of Eugenics*, 7(2): 179-188.

Jansen, P. M. C. and Ong, H. C. (1996).*Eleusinecoracana* (L.)*Gaertner*ev. groupFinge Millet. Plant Resources of South-East Asia No 10. Cereals, *Back. Pub.Leid., Netherlands.*Pp.90-95.

Gohel, D. S. and Chaudhari, S. B. (2018).Study of correlation and path analysis in finger millet (*Eleusinecoracana*L. *Gaertn*) genotypes.*Jour.Of Phar. And Phyt., 7*(6): 1283-1288.

Manyasa, O. E., Tongoona, P., Shanahan, P., Githiri, M, and Rathore,A. (2016).correlation, path analysis and heritability for quantitative traits in finger millet (*Eleusinecoracana*L. *Gaertn*) land races. *Phili.Jou.Of Sci.,*145: 197-208.

Negi, S., Arun, B. and Kumar, V. (2017).Character association and path analysis for yield and its related traits in finger millet genotypes.Jou.Of App. And Nat. Sci. 9(3): 1624-1629.

Robinson, H. F., Comstock, R. E. and Harvey, P. H. (1951).Genotypic &phenotypic correlation in maize and their implications in selection.*Agr.Jou., 43*: 282-287.

Sneha, R, S., Bhavsar, V. V., Barhate, K. K. and Kohakade, N. (2019.)Correlation and path analysis for different characteristics in genepool of finger millet(*Eleusinecoracana*L. *Gaertn*).8(1): 1020-1027.

Comment [A8]: Replace with the correct abbreviation of the journal

Comment [A9]: Replace with the correct abbreviation of the journal

Comment [A10]: Replace with the correct abbreviation of the journal

Comment [A11]: Replace with the correct abbreviation of the journal

Comment [A12]: Replace with the correct abbreviation of the journal

Comment [A13]: Replace with the correct abbreviation of the journal

Comment [A14]: The correct abbreviation of the journal should be put here

Comment [A15]: The correct abbreviation of the journal should be put here

Comment [A16]: Name of journal missing