

## Evaluation of Foxtail genotypes in Nagaland ecosystem for yield and yield related traits

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### ABSTRACT

Foxtail millet (*Setaria italica*) is one of the least studied crops in terms of genetic resource characterisation and genetic enhancement while compared to major cereals. Hundred foxtail millet lines representing the national collection were evaluated at Medziphema, Nagaland University in summer-2022. Fodder yield per plant exhibited high estimates of phenotypic coefficient of variation and genotypic coefficient of variation followed by biological yield, grain yield per plant, total number of tillers per plant, flag leaf width, panicle length and panicle width. All the characters under study showed high heritability coupled with high values of genetic advance as percent mean (except days to 50% flowering and days to maturity) which indicates that the traits were mostly governed by additive gene action. Grain yield per plant showed positive and significant association with panicle length, flag leaf length, flag leaf width, peduncle length, total tiller numbers per plant, panicle width, biological yield, harvest index, fodder yield per plant. Path analysis identified days to 50% flowering, peduncle length, total number of tillers, panicle width, biological yield and harvest index exhibited positive direct effects on grain yield/plant indicating their significant role during selection in yield improvement program.

### 1. Introduction

Millets are a genus of small-seeded grasses primarily produced in dry regions of Asia and Africa. They are frequently referred to as "Nutri-Cereals" due to their high nutritional value. Sorghum, pearl millet, finger millet, proso millet, foxtail millet, teff, and numerous minor varieties are among them (Amarnath *et al.*, 2018). Foxtail millet (*Setaria italica* (L.) Beauv.) belongs to family Poaceae and subfamily Panicoideae. Foxtail millet is a significant crop that is grown for silage and hay throughout South and North America as well as dry and semi-arid regions of China, some part of India, and Japan. It is also used as a staple food in many other parts of the world (Upadhyaya *et al.*, 2011). One of the oldest crops in existence, foxtail millet was first grown in the Yellow River Valley of northern China between 7,400 and 7,900 years ago, according to the earliest archaeo-botanical macro remnants found there (Tyagi *et al.* 2011).

Millets are not new to Nagaland; it was part of its history. Blended with a diverse range of nutrient-rich value, the crop is indeed a keystone crop which survives through climate variations. Traditionally millets were commonly known for brewing and are an integral part of community

diet. Millets have long been cultivated in the hilly terrain of the Eastern part of Nagaland. However, the crop was not grown much in the foothill and plain in Nagaland so far.

Breeding for high yielding crops requires knowledge of the extent of numerous genetic characteristics, such as PCV, GCV, broad sense heritability and genetic progress on which the breeding procedures are formed for its future improvement. The first step to be taken into account when making a selection is genetic variability. Heritability indicates transmissibility of a character in future generations (Prasanna *et al.*, 2013). Foreseeing genetic increase is more accurate when high heritability is combined with strong genetic progress (Reddy *et al.*, 2015). It is frequently bad decision making to select simply for yield. As a result, it's critical to understand the connection between yield and the components of yield, which is determined by correlation analysis. Path Coefficient analysis is used to quantify each yield component trait's direct and indirect influence on yield

The nature and magnitude of genetic variability present in the genetic resources indicates the possible extent of genetic improvement for the concerned trait through selection. Existence of genetic variability is of paramount

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importance for agro-biodiversity because it provides greater adaptability to environmental fluctuations. Considering the above facts, examining the genetic variability, heritability and genetic advance is very much important for formulating an efficient breeding programme. Therefore, the current investigation was undertaken to examine the nature and extent of genetic variability present in different genotypes of foxtail millet. In addition, correlation and path coefficient were also studied, which may be useful in selecting the desirable traits during future breeding programmes.

## 2. Materials and Methods

Hundred foxtail millet germplasm accessions including checks obtained from IIMR, Hyderabad were evaluated in the present study. The trial was conducted during *Summer*, 2022 at Department of Genetics and Plant Breeding farm of SASRD Nagaland University, Medziphema, India. Augmented block design was used to set up the trial along with four checks. For morphological characterization and evaluation, each accession was planted in a single one-meter-long row with spacing of 22.5cm row to row and 10 cm plant to plant. Over the course of the experiment, the suggested agronomic packages of practices were used. Thirteen quantitative characters were recorded on five randomly sampled plants on each genotype as per the standard protocol of *Setaria italica*. Data were recorded on days to 50% flowering (DF), days to maturity (DM), plant height (PH), panicle length (PL), flag leaf length (FL), flag leaf width (FW), peduncle length (PDL), total tiller numbers per plant (NT), panicle width (PW), biological yield (BY), harvest index (HI), fodder yield per plant (FY) and grain yield/plant (GY). The data were subjected to statistical analysis. Analysis of variance, coefficient of variation, correlation and path analysis were done by using *R*-software (2015).

## 3. Results and Discussion

The Analysis of variance showed significant difference among the genotypes for all the traits studied which specifies a high degree of variability in the material. The estimates of phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the characters studied (Table-1). Similar findings were earlier reported by Bheemesh *et al.*, (2017). High PCV and GCV were observed for fodder yield per plant followed by biological yield, grain yield per plant, total number of tillers per plant, flag leaf width, panicle length and panicle width. Similar results were also obtained for days to 50 % flowering, panicle width, days to maturity, grain yield per plant and flag leaf length by Jyothsna *et al.*, 2016, Kavya *et al.*, 2017, Nandini *et al.*, 2018 and Nirmalakumari *et al.* 2010.

Broad sense heritability is the ratio of genotypic variance (VG) to the total phenotypic variance (VP), which

helps in improving the selection efficiency of the complex quantitative traits. Heritability when accompanied with high genetic advance may still increase the reliability of selection rather than, heritability estimates alone (Johnson *et al.* 1955). High broad sense heritability along with high genetic advance indicates that genetic improvement is possible through phenotypic selection. In the current study, high heritability along with high genetic advance as percent of mean were recorded for Plant height, panicle length, flag leaf length, flag leaf width, peduncle length, total number of tillers, panicle width, biological yield, harvest index, fodder yield per plant and grain yield per plant. Thus, phenotypic selection for these characters may help in accumulating more additive genes and which will lead to further improvement in their performance in foxtail millet breeding programme. Similar results were reported by Prasanna *et al.*, 2013, Reddy *et al.*, 2015 and Sapkota *et al.*, 2016 for plant height, biological yield, panicle length and panicle width.

Correlation coefficient is an excellent statistical measure which is often used to discover the mutual relationship between various traits, through which efficient phenotypic selection can be made to improve yield. This measure helps to identify traits or a combination of traits, which might be useful indicator to find the high yielding genotype. In other words, an estimate of correlation coefficient among traits provide better understanding of yield components that aids the plant breeder during selection (Johnson *et al.*, 1955). The link between yield and yield contributing traits was investigated by correlation analysis. The current study revealed simple correlation co-efficient among the 13 characters of hundred foxtail millet genotypes (Table 2).

Grain yield per plant showed positive and significant association with panicle length, flag leaf length, flag leaf width, peduncle length, total tiller numbers per plant, panicle width, biological yield, harvest index, fodder yield per plant and grain yield/plant. Total tiller numbers per plant had positive significant association with grain yield per plant and tillers with a higher number of heading capacity contribute directly to grain yield. Tillering provides the crop with the requisite number of stalks for good output, which might be the cause for this. This has been earlier supported by Bheemesh *et al.*, 2017. Flag leaf area had positive significant association with grain yield per plant; higher assimilates accumulation owing to increased photosynthetic area might be the cause of this. This has been earlier supported by Jyothsna *et al.*, 2016. Panicle length and panicle width had positive significant association with grain yield per plant. This has been earlier supported by Kavya *et al.*, 2017. There were no significant relationships between days to 50% flowering and days to maturity which might be attributed to increased assimilate build up as growth length increases.

This was supported by Nandini *et al.*, 2018.

Using grain yield as a dependent character and yield characteristics as independent characters, path coefficient analysis was performed at the phenotypic level from un-replicated data. Each component acts in to two different ways, directly affecting yield and indirectly affecting component characters, two actions that were not shown by correlation research (Ashok *et al.*, 2016). In this study at phenotypic level, days to 50% flowering, flag leaf length, peduncle length, total number of tillers, panicle width, biological yield and harvest index had positive direct effects on grain yield per plant indicating their importance during selection in yield improvement program (Table 3.). Similar results were reported by Ayesha *et al.*, 2018 for panicle width, biological yield and harvest index; Jyothisna *et al.*, 2016 for total number of tillers, flag leaf length and peduncle length.

#### 4. Conclusion

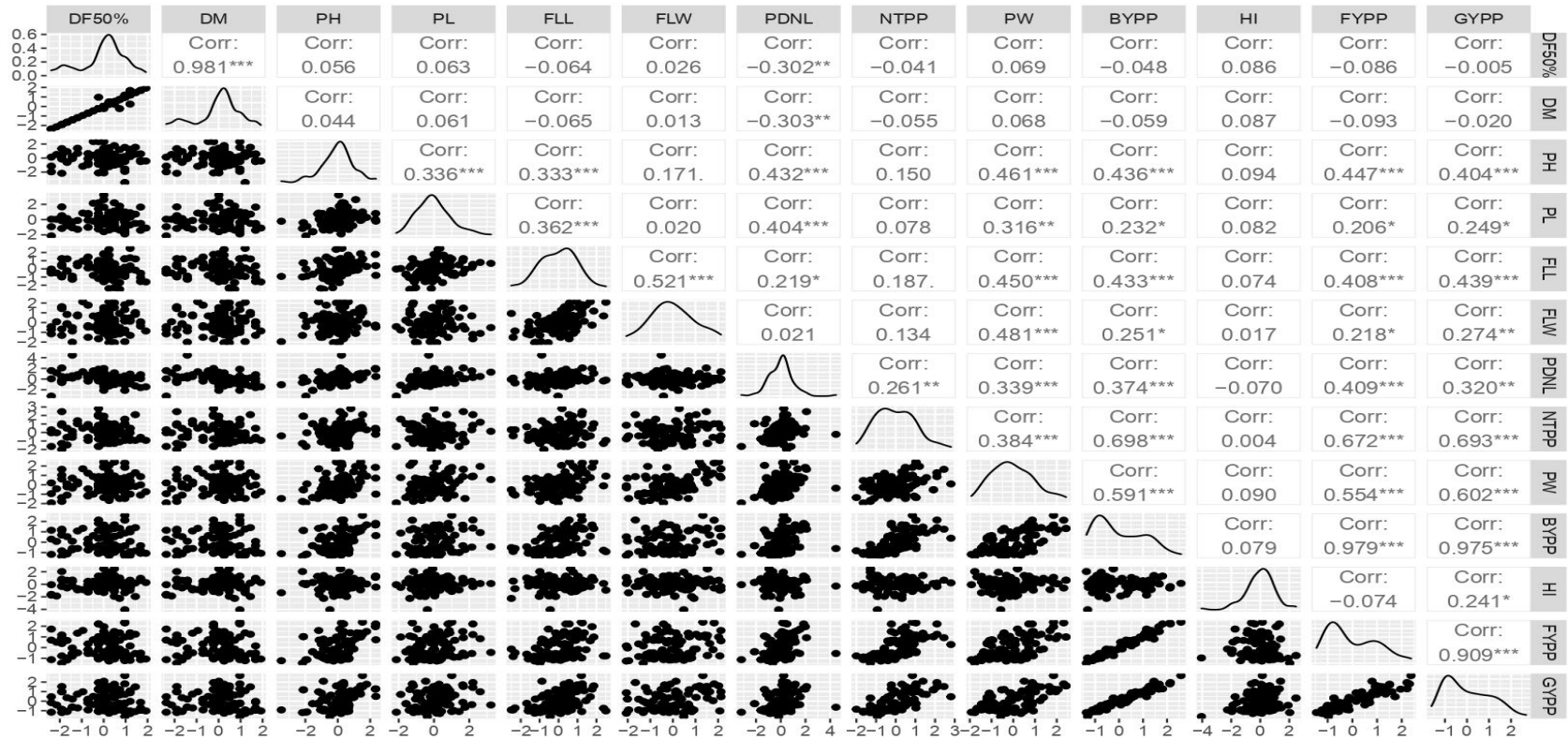
Genotypes G2(IC. No. IC0622071 from Tamil Nadu), G5 (IC. No IC 0622113 from Tamil Nadu), G10 (IC 0618597 from Maharashtra), and G27 (IC 0621991 from Andhra Pradesh) showed low mean values for days to 50% flowering, days to maturity, plant height and high mean values for panicle length, flag leaf length and peduncle length, biological yield, fodder yield and grain yield per plant. From the above it is recommended that Genotypes G2, G5, G10, G27 can be used for general cultivation under Nagaland conditions and these materials could be used in further breeding programs. Present study suggests that while selection, emphasis should be given on peduncle length, total number of tillers, panicle width, biological yield and harvest index (HI) for improvement of yield.

**Table 1.** Genetic parameters for different traits in foxtail millet

Trait	Mean	PV	GV	EV	GCV	GCV. category	PCV	PCV. Category	ECV	hBS	hBS. category	GA	GAM	GAM. category
Days to 50% flowering	69.88	17.42	16.74	0.69	5.85	Low	5.97	Low	1.19	96.06	High	8.27	11.84	Medium
Days to maturity	109.7	17.56	17.3	0.26	3.79	Low	3.82	Low	0.47	98.5	High	8.52	7.76	Low
Plant height	115.25	224.48	219.53	4.96	12.86	Medium	13	Medium	1.93	97.79	High	30.23	26.23	High
Panicle length	13.24	9.85	8.29	1.56	21.75	High	23.7	High	9.43	84.17	High	5.45	41.16	High
Flag leaf length	21.23	9.73	9.72	11.16	14.51	Medium	14.69	Medium	15.74	83.12	High	5.85	27.25	High
Flag leaf width	1.7	0.16	0.14	0.02	21.76	High	23.61	High	9.15	84.97	High	0.7	41.39	High
Peduncle length	20.43	16.34	14.32	2.02	18.52	Medium	19.79	Medium	6.96	87.63	High	7.31	35.77	High
Total tiller numbers	3.44	1.26	1.15	0.12	31.08	High	32.62	High	9.93	90.74	High	2.1	61.07	High
Panicle width	1.55	0.15	0.11	0.04	21.24	High	24.85	High	12.89	73.08	High	0.58	37.46	High
Biological yield	22.44	137.34	129.13	8.21	50.64	High	52.23	High	12.77	94.02	High	22.73	100	High

Harvest index	49.4	42.38	33.69	8.69	11.75	Medium	13.18	Medium	5.97	79.5	High	10.68	21.61	High
Fodder yield/ plant	11.45	38.63	36.41	2.23	52.72	High	54.31	High	13.03	94.24	High	12.08	100	High
Grain yield/plant	10.99	33.42	30.57	2.85	50.29	High	52.58	High	15.36	91.47	High	10.91	99.22	High

**Table 2.** Estimates of simple correlation co-efficient among different quantitative traits in hundred foxtail millet genotypes



Days to 50% flowering (DF), days to maturity (DM), plant height (PH), panicle length (PL), flag leaf length (FLL), flag leaf width (FLW), peduncle length (PDNL), total tiller numbers per plant (NTPP), panicle width (PW), biological yield (BYPP), harvest index (HI), fodder yield per plant (FYPP) and grain yield/plant (GY).

**Table 3.** Direct and indirect effect of different characters on grain yield per plant in foxtail millet genotypes

	<b>DF50%</b>	<b>DM</b>	<b>PH</b>	<b>PL</b>	<b>FL</b>	<b>FW</b>	<b>PDL</b>	<b>NT</b>	<b>PW</b>	<b>BY</b>	<b>HI</b>	<b>FY</b>	Correlation with grain yield per plant
<b>DF50%</b>	<b>0.1115</b>	0.1094	0.0057	0.0065	-0.0069	0.0011	-0.0285	-0.0036	0.0108	-0.0048	0.0100	-0.0079	-0.0040
<b>DM</b>	-0.1017	<b>-0.1037</b>	-0.0035	-0.0060	0.0068	-0.0008	0.0270	0.0054	-0.0095	0.0063	-0.0090	0.0087	-0.0275
<b>PH</b>	-0.0004	-0.0003	<b>-0.0081</b>	-0.0028	-0.0027	-0.0013	-0.0033	-0.0013	-0.0033	-0.0036	-0.0007	-0.0038	0.4187
<b>PL</b>	0.1000	0.1000	-0.0002	<b>-0.0005</b>	-0.0002	0.1000	-0.0002	0.1000	-0.0002	-0.0001	0.1000	-0.0001	0.2543
<b>FL</b>	-0.0002	-0.0002	0.0009	0.0010	<b>0.0028</b>	0.0014	0.0006	0.0005	0.0012	0.0012	0.0002	0.0011	0.4380
<b>FW</b>	-0.0002	-0.0002	-0.0031	-0.0002	-0.0092	<b>-0.0187</b>	-0.0007	-0.0027	-0.0092	-0.0048	-0.0006	-0.0040	0.2727
<b>PDL</b>	-0.0017	-0.0018	0.0027	0.0027	0.0014	0.0003	<b>0.0068</b>	0.0017	0.0022	0.0024	-0.0004	0.0026	0.3194
<b>NT</b>	-0.0003	-0.0005	0.0014	0.0007	0.0016	0.0013	0.0022	<b>0.0087</b>	0.0037	0.0061	0.1000	0.0058	0.6917
<b>PW</b>	0.0032	0.0030	0.0136	0.0096	0.0141	0.0164	0.0106	0.0139	<b>0.0332</b>	0.0189	0.0017	0.0178	0.5862
<b>BY</b>	-0.0743	-0.1035	0.7693	0.4088	0.7380	0.4385	0.6139	1.1880	0.9746	<b>1.7129</b>	0.1172	1.6721	0.9742
<b>HI</b>	0.0045	0.0044	0.0046	0.0037	0.0044	0.0015	-0.0026	0.0002	0.0026	0.0034	<b>0.0503</b>	-0.0039	0.2289
<b>FY</b>	0.0555	0.0657	-0.3648	-0.1694	-0.3122	-0.1669	-0.3062	-0.5190	-0.4198	-0.7637	0.0601	<b>-0.7823</b>	0.9063

## 5. References

- Amarnath, K., Prasad, A.V.S.D., Reddy, C.V.C.M., & Sreenivasulu, K.N. 2018. Genetic variability in Indian foxtail millet genetic resources [*Setaria italica*(L.) Beauv]. *Green Farming*, 9(4), 612-614.
- Ashok, S., Patro, T.S.S.K., Jyothsna, S and Divya, M. 2016. Studies on genetic parameters, correlation and path analysis for grain yield and its components in foxtail millet (*Setaria italica*). *Progressive Research*. 11 (3):300-303.
- Ayesha, M. D. and Babu, D. R. 2018. Estimation of genetic diversity in foxtail millet [*Setaria italica*(L.) Beauv.] germplasm using principle component analysis. *International Journal of Chemical Studies*, 6(5):2580-2583.
- Bheemesh, S. J. 2017. Studies on genetic divergence and character association for yield and drought related traits in foxtail millet (*Setaria italica*L.). M.Sc. Thesis. Acharya N.G.Ranga Agricultural University, Guntur.
- Johnson RE, Robinson HW, Comstock HF. Estimates of genetic and environmental variability in soybean. *Agron. J.* 1955;47(7):314-318
- Jyothsna, S., Patro, T. S. S. K., Ashok, S., Rani, Y. S., and Neeraja, B. 2016. Studies on genetic parameters, character association and path analysis of yield and its components in finger millet (*Eleusine coracana* L. Gaertn). *International Journal of Theoretical and Applied Sciences*, 8(1), 25.
- Kavya, P., Sujatha, M., Pandravada, S. R., and Hymavathi, T. V. (2017). Variability Studies in Foxtail Millet [*Setaria italica*(L.)P.Beauv]. *International Journal of Current Microbiology and Applied Sciences*. 6(9),955-960.
- Nandini, C., Sujata, B., and Tippeswamy, V. (2018). Characterization of foxtail millet (*Setaria italica*(L.) Beauv.) germplasm for qualitative and quantitative traits to enhance its utilization. *Academia Journal of Agricultural Research*, 6(5), 121-129.
- Nirmalakumari, A., and Vetriventhan, M. (2010). Characterization of foxtail millet germplasm collections for yield contributing traits. *Electronic Journal of Plant Breeding*, 1(2), 140-147.
- Prasanna, P. L., Murthy, J. S. V. S., Ramakumar, P. V., & Rao, S. V. (2014). Studies on correlation and path analysis in Indian genotypes of Italian millet [*Setaria italica* (L.) BEAUV]. *International Journal of Genomics and Proteomics*, 5(1), 95. R Core Team, "R: A language and environment for statistical computing", R Foundation for Statistical Computing, Vienna, Austria, 2015.
- Reddy, C. V. C. M., Pullibai, P., Manjunath, J., and Munirathnam, P. (2015). Genetic diversity and genotype by trait analysis for yield & yield attributing traits in foxtail millet (*Setaria italica*(L.) Beauv.). *International Journal of Agriculture Innovations and Research*, 3(6), 1726-1731.
- Sapkota, M., Pandey, P. M and Thapa, B. D. 2016. Agromorphological characterization of foxtail millet (*Setaria italica*L. beauv) at Rampur, chitwan, Nepal. *International Journal of Applied Sciences and Biotechnology*. 4(3):298-307.
- Tyagi, V., Ramesh, B., Kumar, D., & Pal, S. (2011). Genetic architecture of yield contributing traits in foxtail millet (*Setaria italica*). *Current Advances in Agricultural Sciences*, 3(1), 29-32.
- Upadhyaya, H D and Ravishankar, C R and Narasimhudu, Y and Sarma, N D R K and Singh, S K and Varshney, S K and Reddy, V G and Singh, Sube and Parzies, H K and Dwivedi, S L and Nadaf, H L and Sahrawat, K L and Gowda, C L L (2011) *Identification of trait-specific germplasm and developing a mini core collection for efficient use of foxtail millet genetic resources in crop improvement*. *Field Crops Research*, 124 (3). pp. 459-467.