Under Rainfed Effect of Foxtail Millet [*Setaria italica* (L.) *beauv*] Germplasms Evaluation on Genotypic Variance, Correlation and Path Analysis

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ABSTRACT

Background: *Setaria italica* is an essential crop in the developing world and yield levels are low. To improve the yield, the utilization of diverse germplasm in a breeding program is vital.

Methods: The present study aimed to characterize 50 genotypes in the first year and out of 50, 10 genotypes in the second year using multivariant traits. Wide variation was observed in both the qualitative and quantitative characteristics. Analysis of variance revealed the presence of significant differences for most symptoms. Higher estimates of GCV were followed for grain yields, followed by panicle lengths and organic outcomes. Higher estimates of PCV were observed for plant height and leaf length, followed by leaf width. Low GCV and PCV were recorded as leaf length, 50% flowering in days. PCV study indicated direct selection based on characters, panicle weight, test weight and strawweight showed a high and positive effect on grain yield per plant in both rainy and summer season indicating the proper relationship between these characters with grain yield per plant, which helps indirect selection for these traits thus in improving the grain yield per plant. Variability in foxtail millet germplasm allows plant breeders to effectively select specific donor lines for genetic improvement of foxtail millet.

Result: Best 5 genotypes were found to be: Kangni-7 > Kangni-1 > Kangni-6 > Kangni-5 > Kangni-4.

Key words: Correlation, Genotypic, Path analysis, Phenotypic, Variability.

INTRODUCTION

Plant genetic resources is the backbone of agriculture which is planning a crucial role in the agriculture system; it is showing a positive and unique part in developing new cultivars from the earlier to nowadays, including the restructuring of existing ones. To establish the Genotypes, selection which could stand better under biotic and abiotic pressures, gene for such traits are often available in wild species and landraces. Studies on the genetic diversity of wild crop relatives were carried out in the present experimental study. Information's is needed to formulate a breeding plan for sustainable agriculture; included in the present paper are genetic diversity, endangered plant species, species diversity and ecosystem stability, global floristic diversity in a food plant, genetic resources in India, wild collections of significant crops, plant genetic resources vis-à-vis crop breeding emphasis and conservation of plant genetic resources including new plant genetic resources. Foxtail millet is a diploid (2n=18), C4 panicoid crop. Cultivation of foxtail millet is now limited to certain pockets and in several areas, it has been replaced by other crops with irrigation. Its superior nutritional quality and low water requirement make it a climate-resilient crop suitable for cultivation under dryland agricultural systems. It has a small genome and its use as a model crop for bioenergy has created momentum with more groups working than before. This crop's floral morphology and flowering behavior make it challenging to take up crosses between the desired parents.

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Thus, we have seen many research publications to date on developing methods for crossing in foxtail millet. In this chapter, we discuss the floral biology, crossing ways and development of cytoplasmic male sterile lines (Bhat *et al.,* 2018).

MATERIALS AND METHODS

The experimental material comprised 50 germplasm accessions of the foxtail millet. These 50 germplasm accessions were collected from ICRISAT and NBPGR, New Delhi, during *Kharif* -2018. For evaluation and characterization, these 50 germplasm accessions and 3 checks varieties were grown in randomized complete block design (RBD) at Field Experimental Centre, Department of GPB, SHUATS, Prayagraj. The selection of the best 10 genotypes is based on the yield of 50 germplasm of Foxtail millet.

RESULTS AND DISCUSSION

Accessions showed variability concerning various quantitative and qualitative characters studied. Genetic parameters of 10 genotypes for 15 characters of foxtail millet. Genotypic variance is found high in plant height and low in leaf width. Phenotypic variance is maximum in plant height and minimum in leaf width. GCV maximum in economic yield and minimum in CTD. PCV maximum in economic yield and minimum in CTD. Heritability maximum in days 50% flowering and minimum in economic yield. GA maximum in plant height and minimum in harvest index. Fig 1,2 GCV and PCV ratios were high in economic yield. GCV and PCV ratios were found very low in CTD. Heritability and GA ratio was found very low in the economic yield and harvest index.

Genotypic correlation

Genotypic correlation trend of days 50% flowering, days 70% flowering, plant height, leaf length, leaf width, leaf area index, panicle length, peduncle length, stem girth, SPAD, CTD, panicle weight, biological yield per plant, seed yield per plant, harvest index, economic yield. In 50 genotypes correlation between days 70% flowering showing 1% significant genotypic correlation with 50% flowering (0.466**), economic yield with leaf width (0.184*) showing 50% significant genotypic correlation, economic yield with biological yield (0.554**) showing 1% significant GC, economic yield with Harvest index (1.059**) 1% significant GC, economic yield showing negative genotypic correlation with SPAD (-0.403), CTD (-0.037), stem girth (-0.326) and panicle length (-0.048).

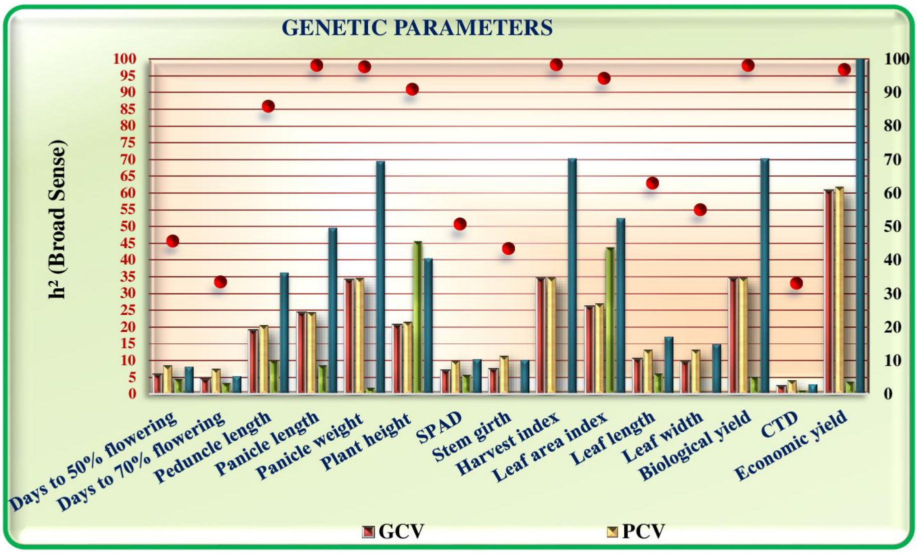

Fig 1: GCV and PCV for parameters in *Setaria italic.*

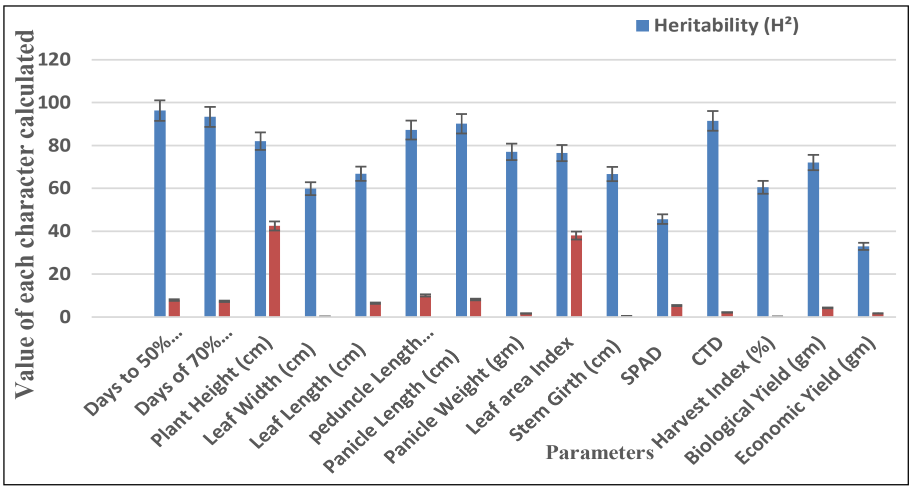

Fig 2: H^2 and GCV for parameters in *Setaria italic.*

Phenotypic correlation

Phenotypic correlation in 50 genotypes showing 1% significance with days 70% flowering, plant height, leaf area index, leaf length, leaf width, peduncle length, harvest index, biological yield, economic yield, peduncle weight, stem girth. Economic yield with the days 70% flowering (-0.015), panicle length (-0.036), stem girth (-0.023), CTD (0.043), SPAD (0.150) showing negative phenotypic correlation. Economic yield showing significant increase in positive correlation with the day 50% flowering (0.071), pant height (0.053), leaf area index (0.099), leaf length (0.117), leaf width (0.084), peduncle length (0.024), panicle weight (0.207), biological yield (0.297), harvest index (0.506), economic yield (1.000). Economic yield showing increase positive phenotypic correlation with days 50% flowering (0.071), plant height (0.053), leaf area index (0.099), leaf length (0.117), leaf width (0.084), peduncle length (0.024), panicle weight (0.297), biological yield (0.506), economic yield (1.000) and economic yield showing negative phenotypic correlation with days 70% flowering (-0.015), panicle length (-0.036), stem girth (-0.023), CTD (-0.043) and SPAD (-0.150). In 10 genotype genotypic correlation given in the Table 1 economic yield with plant height (0.915**), peduncle length (0.568**), panicle length (0.551**), panicle weight (1.028**), SPAD (0.609**), harvest index (1.062**), biological yield (1.197**) showing 1% significant genotypic correlation. Economic yield with leaf width (-0.034), stem girth (-0.273), CTD (-0.053), showing negative genotypic correlation. Economic yield showing positive genotypic correlation with days 50% flowering (0.109), days 70% flowering (0.102), plant height (0.015), leaf length (0.249), peduncle length (0.568), panicle length (0.551), leaf area index (1.028), SPAD (0.098), harvest index (0.609), biological yield (1.062), economic yield (1.197).

Phenotypic correlation in 10 genotypes given in Table 2 economic yield with plant height (0.457*) showing 5% significant phenotypic correlation, economic yield with panicle weight (0.615**), harvest index (0.553), biological yield (0.521**) showing 1% significant phenotypic correlation, economic yield with leaf width (-0.046) stem girth (-0.064), SPAD (-0.113), CTD (-0.088) showing negative phenotypic correlation. Economic yield with days 50% flowering (0.104), days 70% flowering (0.071), plant height (0.116), leaf length (0.091), peduncle length (0.304), panicle length (0.331), biological yield (0.521), economic yield (1.000), showing positive correlation. Earlier studies have also reported a significant positive association on biological yield per plant with productive panicle and peduncle length (Brunda *et al.,* 2014; Upadhyaya *et al.*, 2011 and Nirmlakumari *et al.,* 2010). The positive correlation for yield with other characters indicated that all these characters could be simultaneously improved and it also suggested that an increase in any one of them would improve other characters. Selection criteria should consider all these characters for the improvement of biological yield in foxtail millet.

Table 1: Estimation of genotypic correlation coefficient of yield component traits with yield in *Setaria italica* 2019.

Characters	Days to 50% flowering	Days of 70% flowering	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Peduncle length (cm)	Panicle length (cm)	Panicle weight (gm)	Leaf area index	Stem girth (cm)	SPAD (nm)	CTD °C	Harvest index (%)	Biological yield (gm)	Economic yield (gm)
Days to 50% flowering	1.000	0.953**	0.033	-0.457*	-0.543**	-0.230	-0.418*	-0.073	-0.456*	-0.480**	-0.004	0.534**	0.453*	-0.209	0.109
Days of 70% flowering		1.000	0.087	-0.411*	-0.541**	-0.358	-0.556**	-0.081	-0.466**	-0.290	-0.114	0.480**	0.589**	-0.264	0.102
Plant height (cm)			1.000	-0.055	0.360	-0.165	0.027	0.659**	0.128	-0.036	0.556**	-0.246	0.705**	0.634**	0.915**
Leaf width (cm)				1.000	0.842**	0.440*	0.526**	0.592**	0.949**	0.144	-0.208	-0.720**	-0.294	0.346	-0.034
Leaf length (cm)					1.000	0.460*	0.627**	0.647**	0.963**	-0.063	0.218	-0.786**	-0.212	0.612**	0.249
Peduncle length (cm)						1.000	0.945**	0.431*	0.508**	-0.539**	-0.219	-0.362*	0.078	0.593**	0.568**
Panicle length (cm)							1.000	0.540**	0.605**	-0.394*	-0.089	-0.596**	-0.030	0.662**	0.551**
Panicle weight (gm)								1.000	0.650**	-0.141	0.247	-0.292	0.595**	0.941**	1.028**
Leaf area index									1.000	-0.102	0.068	-0.654**	-0.260	0.560**	0.098
Stem girth (cm)										1.000	0.191	0.062	0.133	-0.327	-0.274
SPAD (nm)											1.000	0.211	0.004	0.388*	0.609**
CTD °C												1.000	0.043	-0.211	-0.053
Harvest index (%)													1.000	0.499**	1.062**
Biological yield (gm)														1.000	1.197**
Economic yield (gm)															1.000

Table 2: Estimation of phenotypic correlation coefficient of yield component traits with yield in *Setaria italica* 2019.

Characters	Days to 50% flowering	Days of 70% flowering	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Peduncle length (cm)	Panicle length (cm)	Panicle weight (gm)	Leaf area index	Stem girth (cm)	SPAD (nm)	CTD °C	Harvest index (%)	Biological yield (gm)	Economic yield (gm)
Days to 50% flowering	1.000	0.952**	0.037	-0.398*	-0.489**	-0.198	-0.383*	-0.048	-0.424*	-0.377*	-0.013	0.503**	0.337	-0.183	0.104
Days of 70% flowering		1.000	0.087	-0.373*	-0.497**	-0.305	-0.504**	-0.042	-0.435*	-0.217	-0.086	0.450*	0.432*	-0.237	0.116
Plant height (cm)			1.000	0.018	0.317	-0.107	0.026	0.574**	0.156	-0.078	0.334	-0.209	0.462*	0.536**	0.457*
Leaf width (cm)				1.000	0.833**	0.179	0.367*	0.371*	0.931**	-0.151	-0.112	-0.514**	-0.114	0.180	-0.046
Leaf length (cm)					1.000	0.258	0.463**	0.496**	0.937**	-0.270	0.133	-0.618**	-0.123	0.460*	0.091
Peduncle length (cm)						1.000	0.861**	0.338	0.330	-0.342	-0.199	-0.315	-0.037	0.501**	0.304
Panicle length (cm)							1.000	0.424*	0.485**	-0.277	-0.008	-0.540**	0.002	0.521**	0.331
Panicle weight (gm)								1.000	0.504**	-0.126	0.178	-0.234	0.403*	0.767**	0.615**
Leaf area index									1.000	-0.250	-0.002	-0.542**	-0.172	0.390*	0.100
Stem girth (cm)										1.000	0.095	0.036	-0.000	-0.228	-0.064
SPAD (nm)											1.000	0.176	0.035	0.211	-0.113
CTD °C												1.000	0.001	-0.159	-0.088
Harvest index (%)													1.000	0.173	0.553**
Biological yield (gm)														1.000	0.521**
Economic yield (gm)															1.000

Path coefficient analysis genotypic correlation

it revealed the role of a high positive direct effect of panicle length, days 50% flowering, plant height, leaf width, biological yield, economic yield, harvest index showing negative genotypic path coefficient analysis with plant height (-0.1375), leaf width (-0.1275), peduncle length (-0.0190), panicle length (-0.1401), panicle weight (-0.051), stem girth (-0.6868), CTD (-0.1372), SPAD (0.3700). Harvest index showing significant increase and showing positive correlation coefficient analysis with the days 50% flowering (0.0979), days 70% of flowering (0.2048), leaf area index (0.0218), leaf length (0.2456), biological yield (0.0109), economic yield (0.7547).

Phenotypic path correlation in 50 genotypes revealed the role of a high positive direct effect of plant height, leaf length, leaf width, panicle length, biological yield. HI showing negative phenotypic path correlation with the plant height (-0.0630), leaf area index (0.0032), leaf width (-0.0431), peduncle length (-0.0561), panicle length (-0.0988), stem girth (-0.0201), CTD (-0.281), SPAD (-0.1502), biological yield (-0.2820). HI showing positive phenotypic path coefficient analysis with days 50% lowering (0.0419), days 70% flowering (0.0582), leaf length (0.0740), panicle weight (0.0359) given below in Table 3 and Table 4. It suggests that selection for these traits indirectly improves the grain yield obtained by (Brunda *et al.,* 2015).

In 10 genotypes, genotypic path coefficient analysis given in the Table 3 revealed the role of high positive direct effect in harvest index, panicle weight, plant height. Genotypic path coefficient analysis showing positive genotypic path with days 50% flowering (2.364), leaf length (0.427), panicle length (0.741), leaf area index (2.747). Biological yield with days 50% flowering (0.234), days 70% flowering (0.296), stem girth (0.366), CTD (0.236) showing positive genotypic path coefficient analysis. Phenotypic path in 10 genotypes revealed given in Table 4 the role of a high positive direct effect of plant height, harvest index, biological yield. Biological yield showing positive phenotypic path with plant height (0.037), leaf width (0.012), leaf length (0.031), pedicle length (-0.034), panicle length (0.036), panicle weight (0.052), SPAD (0.027) and showing negative phenotypic path with days 70% flowering (-0.013), days 50% flowering (-0.016), stem girth (-0.016), CTD (-0.011), Harvest index (0.013), biological yield (0.016). Path analysis indicated that plant height harvest index had a high positive direct effect on grain yield. This positive direct effect of plant height and the biological yield on economic yield provides scope to increase the biomass of plants with increased yield. The direct effect of biological yield on economic yield per plant was positive and high in both the year, which indicated the true relationship of this trait and natural selection through this trait will be effective. Direct selection of biological yield in foxtail millet led to the simultaneous indirect selection of several panicles, panicle length, pedicle length, panicle weight, number of productive tillers and biological yield for increased economic yield per plant. Conducted research

Table 3: Genotypic path of yield component traits with yield in *Setaria italica* 2019.

Characters	Days to 50% flowering	Days of 70% flowering	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Peduncle length (cm)	Panicle length (cm)	Panicle weight (gm)	Leaf area index	Stem girth (cm)	SPAD (nm)	CTD °C	Harvest index (%)	Biological yield (gm)
Days to 50% flowering	2.364	-2.265	0.034	1.124	-0.379	-0.085	-0.310	-0.002	-1.252	-0.466	0.004	0.580	0.530	0.234
Days of 70% flowering	2.253	-2.377	0.089	1.011	-0.378	-0.132	-0.412	-0.003	-1.279	-0.281	0.105	0.521	0.689	0.296
Plant height (cm)	0.079	-0.207	1.024	0.136	0.251	-0.061	0.020	0.022	0.351	-0.035	-0.513	-0.267	0.825	-0.710
Leaf width (cm)	-1.079	0.977	-0.056	-2.461	0.588	0.163	0.389	0.019	2.607	0.140	0.192	-0.782	-0.344	-0.388
Leaf length (cm)	-1.284	1.287	0.368	-2.073	0.698	0.170	0.464	0.021	2.646	-0.061	-0.201	-0.854	-0.248	-0.685
Peduncle length (cm)	-0.544	0.850	-0.169	-1.084	0.321	0.370	0.700	0.014	1.396	-0.523	0.202	-0.393	0.091	-0.663
Panicle length (cm)	-0.988	1.322	0.027	-1.294	0.438	0.350	0.741	0.018	1.663	-0.383	0.082	-0.648	-0.035	-0.740
Panicle weight (gm)	-0.173	0.193	0.675	-1.456	0.452	0.159	0.400	0.033	1.785	-0.137	-0.228	-0.318	0.697	-1.053
Leaf area index	-1.077	1.107	0.131	-2.335	0.672	0.188	0.448	0.021	2.747	-0.099	-0.063	-0.711	-0.305	-0.627
Stem girth (cm)	-1.134	0.689	-0.037	-0.354	-0.044	-0.199	-0.292	-0.005	-0.281	0.971	-0.176	0.067	0.156	0.366
SPAD (nm)	-0.010	0.271	0.569	0.513	0.152	-0.081	-0.066	0.008	0.188	0.186	-0.922	0.229	0.005	-0.434
CTD °C	1.261	-1.141	-0.252	1.771	-0.549	-0.134	-0.442	-0.010	-1.798	0.060	-0.194	1.086	0.051	0.236
Harvest index (%)	1.070	-1.400	0.722	0.723	-0.148	0.029	-0.022	0.019	-0.715	0.129	-0.004	0.047	1.171	-0.559
Biological yield (gm)	-0.495	0.628	0.649	-0.852	0.427	0.219	0.490	0.031	1.538	-0.318	-0.357	-0.229	0.584	-1.119

Table 4: Phenotypic path of yield component traits with yield in *Setaria italica* 2019.

Characters	Days to 50% flowering	Days of 70% flowering	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Peduncle length (cm)	Panicle length (cm)	Panicle weight (gm)	Leaf area index	Stem girth (cm)	SPAD (nm)	CTD °C	Harvest index (%)	Biological yield (gm)
Days to 50% flowering	0.085	0.046	0.002	0.693	0.081	0.150	-0.365	-0.007	-0.819	-0.090	0.007	0.160	0.173	-0.013
Days of 70% flowering	0.081	0.048	0.004	0.649	0.082	0.232	-0.481	-0.006	-0.840	-0.052	0.049	0.143	0.222	-0.016
Plant height (cm)	0.003	0.004	0.043	-0.032	-0.052	0.081	0.025	0.086	0.301	-0.019	-0.191	-0.066	0.238	0.037
Leaf width (cm)	-0.034	-0.018	0.001	-1.741	-0.138	-0.136	0.350	0.055	1.796	-0.036	0.064	-0.164	-0.059	0.012
Leaf length (cm)	-0.041	-0.024	0.014	-1.451	-0.165	-0.196	0.442	0.074	1.808	-0.064	-0.076	-0.197	-0.063	0.031
Peduncle length (cm)	-0.017	-0.015	-0.005	-0.312	-0.043	-0.760	0.821	0.051	0.637	-0.081	0.114	-0.100	-0.019	0.034
Panicle length (cm)	-0.032	-0.024	0.001	-0.639	-0.077	-0.655	0.954	0.063	0.937	-0.066	0.005	-0.172	0.001	0.036
Panicle weight (gm)	-0.004	-0.002	0.025	-0.646	-0.082	-0.257	0.405	0.149	0.974	-0.030	-0.102	-0.075	0.208	0.052
Leaf area index	-0.036	-0.021	0.007	-1.620	-0.155	-0.251	0.463	0.075	1.930	-0.060	0.001	-0.172	-0.089	0.027
Stem girth (cm)	-0.032	-0.010	-0.003	0.264	0.045	0.260	-0.264	-0.019	-0.483	0.238	-0.054	0.011	0.000	-0.016
SPAD (nm)	-0.001	-0.004	0.014	0.196	-0.022	0.152	-0.008	0.027	-0.004	0.023	-0.573	0.056	0.018	0.014
CTD °C	0.043	0.022	-0.009	0.896	0.102	0.240	-0.515	-0.035	-1.046	0.009	-0.101	0.318	0.000	-0.011
Harvest index (%)	0.085	0.046	0.002	0.693	0.081	0.150	-0.365	-0.007	-0.819	-0.090	0.007	0.160	0.173	-0.013
Biological yield (gm)	0.081	0.048	0.004	0.649	0.082	0.232	-0.481	-0.006	-0.840	-0.052	0.049	0.143	0.222	-0.016

**Significant at 1% and *Significant at 5% level.

revealed seed yield per plant positively and significantly correlated with biological yield, panicle weight, harvest index, leaf length, leaf area index, leaf width, plant height, days to flowering and days to maturity. This means these traits are predominantly governed by additive gene action and hence natural selection for these traits will lead to simultaneous improvement in grain yield. Similar results were reported by (Kumar *et al.,* 2015) for plant height and panicle length for plant height (Fujita *et al.,* 1996) for 1000 grain weight and flag leaf blade length (Kempthorne 1957) for plant height and panicle length. Plant height, panicle length, flag leaf blade length, flag leaf blade width, plant height (Kavya *et al.*, 2017) for panicle length, plant height, 1000 grain weight (Kumari *et al.,* 2015).

CONCLUSION

Germplasm evaluation and characterization for plant breeders and multivariate statistical analysis provide a means for estimating the genotypic phenotypic parameters. The characteristics described in the pre-harvest and post-harvest observations were used to select the best 5 genotypes. PCV values were higher than GCV values which indicate the effect of environment on the expression of characters. Since results are based on data of two years, biochemical testing of these genotypes is required to confirm the consistency of these results. These genotypes Kangni-7(GS-62) > Kangni-1(GS-14) > Kangni-6(GS-55) > Kangni-5(GS-389) > Kangni-4(GS-368) cannot find anywhere except SHUATS. That is why these genotypes are named by SHUATS. These best 5 genotypes will further be analyzed by the biochemical trait analysis.

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