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Studies of correlation between yield and yield attributing characters of Kodo millet (*Paspalum scrobiculatum* L.)

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Abstract

The present experiment entitled "Characterization and Genetic Analysis in Kodo Millet (*Paspalum scrobiculatum* L.) for Rainfed Agriculture" was carried out at Instructional cum Research farm, S.G. college of Agriculture and Research Station, Jagdalpur (C.G.) in *kharif* 2107-18. 33 genotypes of kodo millet were evaluated for genetic analysis of kodo millet. Correlation studies revealed that the grain yield per plot had positive association with tillers per plant, panicle length, panicle per plant, days to flowering, days to maturity, fodder yield, test weight. Hence improving of grain yield can be achieved by improving these traits.

Keywords: Characterization and Genetic Analysis, Kodo millet, *Paspalum scrobiculatum*

Introduction

Kodo millet (*Paspalum scrobiculatum* L.) is a small grained cereal belonging to family poaceae (gramineae). It is a tetraploid ($2n=4x=40$) crop species. Kodo millet is grown for its grain and fodder purpose. Kodo millet is also known as varagu, kodo, haraka, arakalu, ditch millet, rice grass, cow grass, native paspalum, or Indian crown grass. It is grown in India, Pakistan, Philippines, Indonesia, Vietnam, Thailand and West Africa (Deshpande *et al.*, 2015)^[11]. It is widely distributed in damp habitats across the tropics and subtropics of the World. Kodo millet is indigenous to India (De Wet *et al.*, 1983)^[10]. In India area of small millet 589.6 (000) ha. with a production of 358.9 (000) metric tons and productivity of 654.9 kg/ha. (Indian Institute of Millet Research 2014). Kodo millet is gaining importance due to dual reasons like nutritional properties and stress tolerance (Kumar *et al.*, 2016)^[15]. It provides low priced protein, minerals and vitamins in form of sustainable food (Yadava *et al.*, 2006)^[29]. The millet contains a high proportion of complex carbohydrate and dietary fibre which helps in prevention of constipation and slow release of glucose to the blood stream (Kumar *et al.*, 2016)^[15]. Kodo contain water soluble fiber and this property may be utilized for maintaining or lowering blood glucose response among diabetic and cardiovascular disease patients, glycemic load (GL) representing both quality and quantity of carbohydrate in a food and allows comparison of the likely glycemic effect of realistic portion of the different foods and low glycemic index foods like kodo, have been shown to improve the glucose tolerance in both healthy and diabetic subjects (Riccardi *et al.*, 2008)^[22].

Systematic breeding efforts in this crop have so far been neglected. For starting any crop improvement work, information about the genetic variability available in the population is a prerequisite. Presence of high variability in the germplasm of this crop offers much scope for its improvement (Subramanian *et al.*, 2010)^[27]. Estimation of genetic parameters in the context of trait characterization is an essential component in developing high yielding varieties (Reddey *et al.*, 2013)^[21]. Genetic variability is a basis for any heritable improvement in crop plants. Variability can be observed through biometric parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as percent of mean in respect of nine characters.

Materials and Methods

The present study was carried out at Research cum Instructional Farm of S.G. College of Agriculture and Research Station Kumhrawand, Jagdalpur, Chhattisgarh. Jagdalpur is situated in 19°4'0" N and 82°2'0" E. The city is nestled on the Bastar Plateau and is positioned at a height of around 552 meters from the mean sea level. The investigation was conducted during *kharif* 2017-18 in randomized block design. With 80 germplasm of kodo millet in which 33 were selected for genetic analysis presented in table 1.

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The crop was sown on plot size 2.25m x 3m and the spacing between row to row is 22.5 and plant to plant is 7.5 cm. The regional crop production practices was followed. Observations were recorded on randomly chosen five plants from each genotype and both replication for 7 quantitative traits *viz.* plant height, number of productive tillers per plant, number of panicles per plant, panicle length, grain yield, fodder yield and test weight from both replications, except flowering and maturity, they were recorded on plot basis. Phenotypic and genotypic correlation co-efficient were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae suggested by Al-Jibouri *et al.* (1958) [1]. Observations were recorded on competitive and randomly chosen five plants from each genotype and from both replications, except flowering and maturity, they were recorded on plot basis. Average of the data from the sampled plants in respect of different quantitative characters was used for statistical analyses.

Table 1: List of selected 33 genotypes of kodo millet for genetic analysis

S.N.	Genotype name	S.N.	Genotype name	S.N.	Genotype name
1	BK-19	12	BK-48	23	BK-6
2	BK-20	13	BK-49	24	BK-7
3	BK-21	14	BK-50	25	BK-8
4	BK-34	15	BK-64	26	BK-9
5	BK-35	16	BK-81	27	BK-10
6	BK-36	17	PCGK-8	28	BK-11
7	BK-38	18	PCGK-12	29	BK-12
8	BK-42	19	BK-1	30	BK-13
9	BK-43	20	BK-2	31	BK-14
10	BK-45	21	BK-3	32	IK-01*
11	BK-46	22	BK-5	33	IK-02*

$$\text{Genotypic correlation co-efficient, (rg)} = \frac{\text{Cov } x \text{ } y \text{ (genotypic)}}{\sqrt{(\text{Var } x) \cdot (\text{Var } y) \text{ (genotypic)}}$$

$$\text{Genotypic variance} = \frac{\text{Treatment MS} - \text{Error MS}}{\text{Number of replication}}$$

$$\text{Genotypic covariance} = \frac{\text{Treatment Cov} - \text{Error Cov}}{\text{Number of replications}}$$

$$\text{Phenotypic correlation coefficient (rp)} = \frac{\text{Cov } xy \text{ (phenotypic)}}{\sqrt{(\text{Var } x) \cdot (\text{Var } y) \text{ (phenotypic)}}$$

The values of genotypic correlation exceeding unity should be considered as unit only (of same sign). To test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1967) at 5 per cent and 1 per cent levels of significance with (n-2) degrees of freedom, where 'n' is the number of pairs of observations used in the experiment.

Result and Discussion

The efficiency of selection for grain yield mainly depends on the direct and magnitude of correlation between yield and its components and among themselves. Correlation helps understand the nature of interrelationship among the morpho-physiological traits and their simultaneous improvement. In the present investigation, the genotypic correlation

coefficients were higher in magnitude than their corresponding phenotypic correlations for most of the characters studied indicative of the inherently strong genetic relationships among the traits once the non-heritable influence of the environment was removed (Manayasa *et al.* 2016) [18] correlations were estimated among nine quantitative traits that are closely related to grain yield in kodo millet. The results are provided in table 2

Correlation between grain yield and pre yield parameters

The pre yield parameters studied in this experiment includes productive tillers per plant, panicles per plant and panicle length. These characters play an important role in contribution to yield. Genotypes possessing more productive tillers along with more number of panicles per plant and longer panicles showed higher yield. Productive tillers per plant exhibited significant positive association with grain yield per plot (0.4035** and 0.3076*), panicle length per plant (0.3273* and 0.2945*), days to maturity (0.2839* and 0.2780*) and test weight (0.5379*** and 0.4352***) at genotypic and phenotypic level. It showed positive non significant association at genotypic and phenotypic level with days to 50% flowering (0.1862 and 0.1836), panicles per plant (0.1042 and 0.1007). Negative correlation recorded at genotypic and phenotypic level for fodder yield per plot (-0.1456 and -0.1089), increase in productive tillers will give more grain yield because more the number of tiller contain more panicles. These result were in accordance with Bezawelelaw *et al.* (2006) [6] reported positive phenotypic correlation of productive tillers per plant with test weight, Anuradha *et al.* (2013) [2] reported productive tillers per plant had positive significant association with days to maturity, Sreeja *et al.* (2014) [26] for grain yield, Chaurasiya (2014) [9] for test weight and inflorescence length and Arya *et al.* (2017) [4] for finger length in barnyard millet. Panicles per plant exhibited positive significant correlation with panicle length at genotypic level (0.3978**) and non significant association at phenotypic level (0.1502), grain yield per plot (0.1079), day to 50% flowering (0.0768), days to maturity (0.0384) and negative correlation with fodder yield per plot (-0.0882) and test weight (-0.0742) at phenotypic level. It showed positive association at genotypic level with days to 50% flowering (0.1302), days to maturity (0.0714) and it showed negative association at genotypic level with grain yield per plot (-0.0876) fodder yield (0.0882) and test weight (-0.1855). This finding is conformity with Bezawelelaw *et al.* (2006) [6] in finger millet and Sabiel *et al.* (2014) [23] for grain yield in pearl millet. Panicle length exhibited significant positive association with test weight (0.3241** and 0.2621*), days to 50% flowering (0.4338*** and 0.4055***), days to maturity (0.5075*** and 0.4682****) at genotypic and phenotypic level. It showed positive non significant association with grain yield per plot (0.0597 and 0.0835), and it negatively correlated with fodder yield (-0.3041 and -0.2260) at both level. This result had conformity with Ganapathey *et al.* (2011) for grain yield in finger millet, Chaurasiya (2014) [9] for 1000 grain weight, Brunda *et al.* (2015) [7] for days to maturity and Arya *et al.* (2017) [4] for DAS to 50% flowering in barnyard millet.

Correlation between yield and vegetative parameters

The vegetative phase in an critical in contributing to yield since vegetative growth, this phase eventually determines the end product. The vegetative parameters studied in this experiment included plant height, days to 50% flowering and

day to maturity. Plant height had significant negative association at genotypic and phenotypic level with productive tillers per plant (-0.3003* and -0.2727*), days to 50% flowering (-0.6614*** and -0.5717***), days to maturity (-0.7377*** and -0.6450***), and non significant negative association with panicle length (-0.2313 and -0.1903), test weight (-0.1564 and -0.1421), grain yield per plot (-0.1031 and -0.0303). It showed positive correlation with panicle per plant (0.3796* and 0.2246) and fodder yield per plant (0.0787 and 0.0474) at both genotypic and phenotypic level. This founding were conformity with Bezawetaw *et al.* (2006) [6] for test weight, Nandini *et al.* (2010) [19] reported negative correlation of plant height with grain yield of cross VI and VII in F₂ generation of finger millet, Chitalu (2013) [8] for negative association of productive tillers per plant with plant height, Brunda *et al.* (2015) [7] for days to flowering, Productive tillers per plant, fodder weight and test weight, and Anuradha *et al.* (2017) [3] for 50% flowering. Days to 50% flowering recorded significant positive correlation with days to maturity (0.7667*** and 0.7689***), non significant positive association with fodder yield per plot (0.0370 and 0.0156), grain yield per plot (0.1696 and 0.1289) and negative association with test weight (-0.0450 and -0.0281) at genotypic and phenotypic level. This result were accordance with Haradari *et al.* (2012) [13] and Lule *et al.* (2012) [17] for days to maturity, Prasanna *et al.* (2013) [20] for grain yield, Shinde *et al.* (2014) [25] for grain yield and test weight, Chaurasiya (2014) [9] for test weight and Kumar *et al.* (2017) [17] for fodder yield. Days to maturity recorded positive association with test weight (0.2455 and 0.2290), grain yield per plot (0.1400 and 0.1132) at genotypic and phenotypic level. It showed positive genotypic association with fodder yield per plot (0.0054), while negative association (-0.0046) at phenotypic level. This result are in conformity with Prasanna *et al.* (2013) [20] and Brunda *et al.* (2015) [7] for grain yield and test weight.

Association among grain yield and yield parameters

The yield parameters undertaken were grain yield, fodder yield and test weight. The genotypes with greater grain and fodder yield per plot along with higher test weight are selected directly due to high heritability and genetic advance. Fodder yield per plot exhibited positive correlation with grain yield per plot (0.1732 and 0.1044) and test weight (0.0824 and 0.0426) at genotypic and phenotypic level. This founding has been conformity with Prasanna *et al.* (2013) [20] in Italian millet; Sabeil *et al.* (2014) in pearl millet; Sao *et al.* (2017a) [24] in kodo millet for grain yield. Test weight exhibited positive correlation with grain yield (0.1798) at genotypic and phenotypic level. Earlier reported by Prasanna *et al.* (2013) [20] in Italian millet and Sabeil *et al.* (2014) significant association with grain yield in pearl millet. Test weight showed Positive association with grain yield per plot. This founding is conformity with Ulganathan and Nirmalakumari (2015) [28]; Bastola *et al.* (2015) [5] in finger millet, Brunda *et al.* (2015) [7] for grain yield in foxtail millet. However when the higher test weight decrease the total number of grain per panicles. The results of correlation analysis indicated that grain yield had positive correlation with productive tillers per plant, Panicles per plant, Panicle length, days to 50% flowering, days to maturity, fodder yield and test weight; therefore these character should be considered as criteria for selection for higher yield as these were positively correlated with grain yield. While the character plant height negatively associated with grain yield per plot therefore this character should be conceder along with the other character. Grain yield is the end expression of genotypes with respect to economic dry matter production which is a unique feature of genotype to produce some secondary genetic productivity factors (SPGFs) or component traits. Moreover genotype may have optimum SPFs but may not yield higher because of micro and macro environmental contributions and validate role of genetics and environment in determination of yield pathway (Kumar *et al.* 2015) [14].

Table 2: Genotypic and Phenotypic correlation coefficient of 9 character in kodo millet

S. N	Character		Plant Height (cm)	Tillers/ Plant	Panicles/ Plant	Panicle Length (cm)	Days to 50% Maturity (das)	Days to Maturity (das)	Fodder Yield kg/Plot	1000 Grain Weight (g)	Grain Yield kg/Plot
1.	Plant Height (cm)	G	1.0000	-0.3003*	0.3796	-0.2313	-0.6614***	-0.7377***	0.0787	-0.1564	-0.1031
		P	1.0000	-0.2727*	0.2246	-0.1903	-0.5717***	-0.645***	-0.0474	-0.1421	-0.0303
2.	Tillers/ Plant	G		1.0000	0.1042	0.3273*	0.1862	0.2839*	-0.1456	0.5379***	0.4035**
		P		1.0000	0.1007	0.2945*	0.1836	0.2780*	-0.1089	0.4352***	0.3076*
3.	Panicles/ Plant	G			1.0000	0.3978	0.1302	0.0714	-0.0151	-0.1855	-0.0876
		P			1.0000	0.1502	0.0768	0.0384	-0.0882	-0.0742	0.1079
4.	Panicle Length (cm)	G				1.0000	0.4338***	0.5075***	-0.3041	0.3241*	0.0597
		P				1.0000	0.4055***	0.4682***	-0.2260	0.2621*	0.0835
5.	Days to 50% Maturity (das)	G					1.0000	0.7667***	0.0370	-0.0450	0.1696
		P					1.0000	0.7689***	0.0156	-0.0281	0.1289
6.	Days to Maturity (das)	G						1.0000	0.0054	0.2455	0.1400
		P						1.0000	-0.0046	0.2290	0.1132
7.	Fodder Yield kg/Plot	G							1.0000	0.0824	0.1732
		P							1.0000	0.0426	0.1044
8.	1000 Grain Weight (g)	G								1.0000	0.1798
		P								1.0000	0.1789
9.	Grain Yield kg/Plot	G									1.0000
		P									1.0000

Concussion

The characters tillers per plant, panicles per plant, panicle length, days to 50% flowering, days to maturity, fodder yield

and test weight showed positive association with grain yield per plant, suggesting grain yield can be improved by improving these characters.

References

- Al-Jibouri HR, Miller PA, Robinson HF. Genotypic and environmental variance in an upland cotton crop of inter specific origin. *Agron. J* 1958;50:633-63.
- Anuradha N, Bhanu UK, Patro TSSK, Sharma NDRK. Character association and path analysis in finger millet (*Eleusine coracaana* L. Gaertn) association belongs to late maturity group. *Int. J of food, Agri. And Veterinary sci* 2013;3(3):113-115.
- Anuradha N, Patro TSSK, Divya M, Sandhya Rani Y, Triveni U, *et al.* Genetic variability, heritability and correlation of quantitative traits in little millet genotypes. *J. of Pharmacognosy and Phytochemistry* 2017;6(6):489-492.
- Arya R, Bhatt A, Kumar V, Singh Divya Prakash. Correlation analysis of some growth, yield and quality parameters of barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) Germplasm. *J. of Pharmacognosy and Phytochemistry* 2017;6(5):1426-1429.
- Bastola BR, Pandey MP, Ojha BR, Ghimire SK, Baral K. Phenotypic diversity of Nepalese finger millet (*Eleusine coracaana* (L.) Gaertn) accessions at iaas, Rampur, Nepal. *Int. J. Appl. Sci. Biotechnol* 2015;3(2):285-290.
- Bezaweletaw K, Sripichitt P, Wongyai W, Hongtrakul V. Genetic variation, heritability and path-analysis in Ethiopian finger millet [*Eleusine coracana* (L.) Gaertn] landraces. *Kasetsart J. (Nat. Sci.)* 2006;40:322-334.
- Brunda SM, Kamatar MY, Ramaling H, Naveenkumar KL. Studies on correlation and path analysis in foxtail millet genotypes. *Univer. of Agric. Sci. Dharwad Karnatak* 2015;6(5):966-969.
- Chitalu G. genetic characterization of pearl millet (*Pennisetum glaucum* (L.) R. Br.) genotypes in Zambia. M.Sc. Thesis, University of Zambia 2013, 46.
- Chaurasiya V. Genetic variability, association and path coefficient analysis for grain yield and its components in kodo millet (*Paspalum scrobiculatum* L.) Thesis. JNKVV, Jabalpur 2014, 38-44.
- De-Wet MJM, Prasada Rao KE, Mengesha MH, Brink DE. Diversity in kodo millet, *Paspalum scrobiculatum*. *Economic Botany* 1983;37:159-163.
- Deshpandey SS, Mohapatra D, Tripathi MK, Sadvatha RH. Kodo Millet-Nutritional Value and Utilization in Indian Foods. ICAR-Central Institute of Agricultural Engineering, Nabibagh, Berasia Road, Bhopal (M.P.), India. *Journal of Grain Processing and Storage J* 2015. homepage: www.jakraya.com/journal/jgpps
- Ganapathy S, Nirmalakumari A, Muthiah AR. Genetic variability and inter relationship analyses for economic traits in finger millet germplasm. *World J. of Agric. Sci* 2011;7(2):185-188.
- Haradari IC, Ugalat J, Nagabhushan. A study on character association, genetic variability and yield components of finger millet (*Eleusine coracana* L.). *J of Crop and Weed* 2012;8(2):32-35.
- Kumar P, Sao A, Mukherjee SC, Netam RS. Secondary genetic productivity factor (SGFs) in expression of grain yield in rainfed upland rice of Bastar Plateau. *Asian J. of Bio Sci* 2015;10(2):1-5.
- Kumar P, Sao A, Thakur AK, Netam RS, Sahu P. Kodo millet (*Paspalum scrobiculatum*) for climate change laid agriculture. Proceedings of brainstorming workshop and two days national seminar on emerging technologies for enhancing water productivity held at IGKV Raipur, India. November 2016;17-18:93-94.
- Kumar P, Sao A, Thakur AK, Yadav SC, Sahu P. Resourceful Photosynthesis System and Stem Reserve Accumulation Plays Decisive Role in Grain Yield of Kodo Millet (*Paspalum scrobiculatum*) *Int. J. Pure App. Biosci* 2017;5(2):420-426.
- Lule D, Tesfaye K, Fetene M. Multivariate analysis for quantitative traits in finger millet (*Eleusine coracna* subsp. *coracana*) population collected from eastern and southeastern Africa: detection for pattern of genetic diversity. *Int.J. of Agri. Res* 2012;7:303-304.
- Manyasa OE, Tongoona P, Shanahan P, Githiri M, Rathore A. Correlations, path coefficient analysis and heritability for quantitative traits in finger millet land races. *Philippine J. of Sci* 2016;145(2):197-208.
- Nandini B, Ravishankar CR, Mahesha B, Shailaja H, Murthy KNK. Study of correlation and path analysis in F2 population of finger millet *Int. J. of Plant Sci. (Muzaffarnagar)* 2010;5(2):602-605.
- Prasanna Laxmi P, Samba Murthy JSV, Ramakumar PV, Rao Srinivasa V. Studies on correlation and path analysis in exotic genotypes of Italian millet [*Setaria italica* (L.) Beauv]. *Ele. J. of Plant Breeding* 2013, 1080-1085.
- Reddey CV, Chandra Mohan, Reddey P VRM, Munirathnam P, Gowda J. studies of genetic variability in yield and yield attributing traits of finger millet [*eleusine coracana* (L.) Gaertn]. *Indian J Agric. Res* 2013;47(6):549-552.
- Riccardi G, Rivelluse AA, Giacco R. Role of glycemic index and glycemic load in the healthy state, in prediabetics and in diabetes. *Ameri. J. of Clinical Nutri* 2008;87:269S-74S.
- Sabiel Salih AI, Ismail Mohamed I, Abdalla Elgailani, Osman Khalid A, Ali Adam M. Genetic variation among Pearl millet genotypes for yield and its components in semi-arid zone Sudan. *Int. J of Agric. and Crop Sci* 2014;822-826.
- Sao A, Singh P, Kumar P, Pradhan A. Estimates of genetic parameters for yield and contributing traits in kodo millet (*Paspalum scrobiculatum* L.). *Res. J. of Agri. Sci* 2017;8(1):120-122.
- Shinde SR, Desai SV, Pawar RM. Genetic diversity pattern in finger millet (*Eleusine coracana* (L.) Gaertn). *Int. J. Plant Sci* 2014;9(1):13-16.
- Sreeja R, Subramanian A, Nirmalakumari A, Kannan Babu JR. Genetic analysis of yield and clum strength related trait in kodo millet (*Paspalum scrobiculatum* L.) *Trends in biosciences* 2014;7(17): 2496-2499.
- Subramanian A, Nirmalakumari A, Veerabathiran P. Trait based selection of superior kodo millet (*Paspalum scrobiculatum* L.) genotype. *Elect. J. of Plant Breeding* 2010;1(4):852-855.
- Ulagathan V, Nirmalakumari A. Finger millet germplasm characterization and evaluation using principal component analysis. *SABRAO J. Breed. Genet* 2015;47(2):79-88.
- Yadava HS, Jain AK. Advances in kodo millet research. New Delhi Directorate of Information and Publications of Agriculture, Indian Council of Agric. Res 2006. ISBN: 81:7164-062-1.