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Ram Babu Raman, Nandan Manna, Sudipta Patra and Narayan Chandra Sahu

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Research Article

Genetic analysis of yield and yield attributing characters of blackgram (*Vigna mungo* (L.) Hepper) during summer season in gangetic alluvial soil of West Bengal

Ram Babu Raman*[1], Nandan Manna[2], Sudipta Patra[3] and Narayan Chandra Sahu[4]
[1,4]Sasya Shyamala Krishi Vigyan Kendra, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI), Arapanch, Sonarpur, Kolkata-700150
[2,3]Integrated Rural Development and Management (IRDM) School of Agriculture and Rural Development, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI), Ramakrishna Mission Ashrama, Narendrapur Kolkata- 700103
E-Mail: dr.rbraman@gmail.com

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Abstract
The experiment was laid out with twenty genotypes and three replications at Instructional Farm of Ramakrishna Mission Vivekananda Educational and Research Institute, Narendrapur, Kolkata, West Bengal. Among the genotypes RSU-03 showed significantly superior for number of branches per plant (9.07), number of pods per plant (26.27), 100 seed weight (5.15 g) and yield per plant (11.53 g). The phenotypic coefficients of variation (PCV) for all the traits were higher than the corresponding genotypic coefficient of variation (GCV). High heritability coupled with high genetic advance (% of mean) was recorded for no. of pods per plant, plant height, yield per plant which indicates the predominance of additive gene effects on the expression of these traits and these can be used for further breeding programmes for improvement of these traits. Some genotypes showed high percentage of protein and carbohydrate. Based on three ISSR primers, genetic diversity was analyzed. UBC-827 showed high polymorphism (88%) followed by UBC-856 (64%) and ISSR-33 (58%). Among the seven clusters, cluster VI stands out to be the largest.

Keywords
Blackgram, Genetic Analysis, Yield and Yield attributing characters

Introduction

Blackgram (*Vigna mungo*), popularly known as "urad / uradbean" is one of the most important grain legumes crops in India. The blackgram seed contains 24.2% protein, 1.3% fat and 60.4% carbohydrate which plays important role for nutritional security of human being. Blackgram has been shown to be useful in mitigating elevated cholesterol levels and prominence in Indian diets especially for culinary preparation of Dal, Idli, Vada, Dosa, Papad.

India is the world's largest producer as well as consumer of blackgram (cultivated as fallow crop after rice cultivation but it is also well-grown in Southeast Asia (particularly in Thailand), Australia, and other Asian and South Pacific countries (Poehlman, 1991). The need for cultivating richer protein sources for cattle feed and human consumption has led to great interest in studying the diversity and pathology in blackgram. During kharif season, it is grown as a sole crop or mixed with sorghum, pearl millet and pigeon pea, but in rabi and zaid (summer) seasons, it is cultivated as a sole crop.

The assessment of genetic diversity is an important component in any crop improvement programme. The accurate estimation of genetic diversity can be invaluable in the selection of diverse parental combinations to generate segregating progenies with maximum genetic variability and introgression of desirable traits from diverse or wild germplasm into the available cultivars to broaden the genetic base. Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Evaluation of genetic diversity would promote the efficient use of genetic variations in the breeding programme (Paterson *et al*., 1991).

Materials and Methods

The genotypes for conducting the experiment were collected from Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal and some were advance elite lines developed through pedigree methods by the communicating author. Total twenty number of genotypes were evaluated with three replications in simple RBD design at the Instructional Farm of Ramakrishna Mission Vivekananda Educational and Research

Institute (RKMVERI), Narendrapur, West Bengal during summer season. The details of germplasms are presented in Table-1

Data were collected on ten randomly selected plants of each genotypes in three replication to evaluate the yield and yield attributing characters of blackgram. The traits under studies were days to 50% flowering, number of branches per plant, number of pods per plant, number of seeds per pods, plant height(cm), 100 seeds weight(gm), days to maturity and yield per plant.

Analysis of variance permits the estimation of phenotypic, genotypic and environmental coefficients of variability for each characters concerned by using following formula as suggested by Burton (1952).

Phenotypic coefficient of variation

$$PCV = \frac{\sigma^2 p}{\overline{X}} \times 100$$

Genotypic coefficient of variation

$$GCV = \frac{\sigma^2 g}{\overline{X}} \times 100$$

Where, PCV and GCV are respectively the phenotypic and genotypic standard deviations expressed as the percentage of the population mean $\overline{X}$.

Heritability (h^2) It was estimated in broad sense by using following formula as suggested by Lush (1940).

$$h2 = \frac{Vg}{Vp} \times 100$$

Where, h^2 = Heritability in broad sense Vg = Genotypic variance V_P = Phenotypic variance

In the present experiment, protein content of seeds was estimated as described by Lowry (1951) carbohydrate as described by Anthrone method.

Results and Discussions

The mean performance of genotypes (Table-2) showed that the genotype RSU-03 recorded highest number of branches per plant, number of pods per plant, 100 seed weight and yield per plant where as number of seeds per pod was recorded by genotype Sulata (WBU-109). The coefficient of variation (Table-3) revealed that the magnitude of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied which indicates the role of environment in manifestation of these traits. Heritability is good index for identification of traits. In addition to heritability, the genetic advance (GA) offers a potential parameter for selection. The characters such as number of branches per plant (0.92), plant height (0.98), yield per plant (0.97), days to 50% flowering (0.87), number of pods per plant (0.86), 100 seed weight (0.87), days to maturity (0.85) showed higher heritability estimates than other character while number of seeds per pod (0.79) showed high heritability estimates than other characters. The characters like number of pods per plant (31.64), plant height (28.02), yield per plant (39.16) were recorded higher genetic advance (%) of mean than other characters. (Fig-I) In the present study high heritability coupled with high genetic advance (%) of mean was recorded for number of pods per plant, plant height, yield per plant indicated the predominance of additive gene action in the expression of the traits and these can be used for further breeding programmes for improvement of these traits. Other traits showed high heritability coupled with moderate to low genetic advance (%) of mean suggesting the existence of non-additive gene action in the expression of the traits and may be exploited better in recombination breeding.

Protein and Carbohydrate content of Genotypes

Genotype RSU-44 (22.50%) showed highest protein content (Fig-II) followed by NDUK15-222 (22.30%) and RSU-06 (21.25%). Highest carbohydrate content (Figure-III) recorded by Genotype Sarada (57.02%) followed by Sulata and NDUK15-222.

Cluster analysis of 20 blackgram genotypes by ISSR Primers

Initially ten ISSR primers were selected but only three gave the amplification for all 20 blackgram genotypes(Fig IV-VI) Based on these three ISSR primers genetic diversity was analyzed for all the traits. UBC-827 showed high polymorphism (88%) followed by UBC-856 (64%) and ISSR-33 (58%)

It is clear from the cluster analysis (Fig-VII) that there was a wide range of diversity found among the twenty genotypes of blackgram. Seven clusters were found under dendrogram considering the Jacquard coefficient. Cluster VI has been considered as large cluster having six genotypes namely PantU-31, PU-11-25, TJU-24, Uttara, KUG-725 and TU-22. Cluster V (Goutam and RSU-03) and cluster VII (KUG-718 and NDUK15-09) were having two genotypes each. Cluster II (Shekhar-3, RSU-44, VBG12-062 and KPU12-1730) and cluster IV (RSU -06, Sulata, RSU-46 and VBG11-053) were having four genotypes each

where as cluster I (NDUK15-222) and cluster III (Sarada) were having single genotype.

It may be concluded that the advance generation elite line RSU-03 recorded highest yield through their yield attributing characters and can be used for commercial cultivation of this line after formal release and notification. However it is needed to verify the genotypes under study with specific molecular marker for better screening of genotypes for used in further breeding programmes.

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Table 1. List of genotypes used for the study

Sl. No.	Genotypes	Source
1-4	RSU-06, RSU-44, RSU-44, RSU-03	Advance elite lines
5-20	NDUK15-222, Shekhar-3, KUG-78, Sarada, Sulata, VBG11-053, NDUK15-9, VBG12-062, PantU-31, KPU12-1730, Goutam, TJU-24, KUG-725, TU-22, PU-11-25, Uttara	AICRP, MULLaRP, B. C. K. V. Mohanpur, Nadia, West Bengal

Table 2. The mean values of different yield attributing characters of the genotypes of blackgram.

Genotype	Days to 50% flowering	No. of branches per plant	No. of pods per plant	No. of seeds per pod	Plant height (cm)	100 seed weight (g)	Days to Maturity	Yield per plant (g)
NDUK15-222	36.67	7.53	16.93	5.47	25.57	3.97	67.67	7.54
Shekhar-3	35.33	6.63	17.23	5.57	24.73	4.32	66.33	7.91
KUG-718	36.33	6.80	16.13	5.80	22.37	4.29	66.00	6.21
Sarada	35.67	7.53	24.47	5.33	25.70	3.87	66.67	10.94
RSU-06	37.00	7.60	24.57	6.40	32.00	4.22	69.00	10.91
RSU-44	40.33	7.33	22.40	5.60	31.60	4.16	71.67	10.84
RSU-46	38.67	7.23	18.33	5.20	33.43	4.48	70.00	9.76
Sulata (Check)	40.67	7.03	21.53	**6.43**	33.58	4.46	72.00	10.26
VBG11-053	36.67	6.53	15.47	5.80	33.67	3.77	68.00	8.71
NDUK15-09	35.67	6.77	19.63	5.43	33.54	3.52	66.67	9.95
VBG12-062	38.67	8.50	18.30	5.70	35.58	4.47	70.33	7.16
PantU-31(Check)	42.33	6.50	22.70	5.50	33.58	3.83	72.33	7.27
KPU12-1730	36.00	7.13	17.00	5.53	34.19	4.55	65.67	7.46
Goutam (Check)	37.67	7.10	18.73	5.70	36.46	4.13	68.00	7.47
TJU-24	41.33	7.93	22.27	6.20	34.95	4.28	71.33	10.68
KUG-725	38.00	6.33	26.17	6.33	32.71	4.26	70.00	10.66
TU-22	41.00	8.33	23.13	6.20	31.52	4.09	72.67	10.86
RSU-03	35.67	**9.07**	**26.27**	5.30	31.83	**5.15**	66.33	**11.53**
PU-11-25	35.33	6.70	18.57	5.13	25.43	3.55	68.33	7.01
Uttara	37.33	6.67	17.02	5.37	25.73	3.58	70.67	7.55
SEm (±)	0.47	0.11	0.78	0.11	0.33	0.08	0.53	0.14
CD=0.05	1.36	0.33	2.23	0.33	0.97	0.24	1.54	0.41

Table 3. Genotypic coefficient variation (GCV), Phenotypic coefficient variation (PCV), Heritability and Genetic advance (% of mean) of different yield attributing characters of blackgram

Character	GCV (%)	PCV (%)	Heritability (%)	GA (%) of Mean
Days to 50 % flowering	5.75	6.14	0.87	11.09
No. of branches per plant	9.98	10.36	0.92	19.79
No. of pods per plant	16.56	17.85	0.86	31.64
No. of seeds per pod	6.84	7.69	0.79	12.35
Plant height (cm)	13.72	13.86	0.98	28.02
100 seed weight (gm)	9.33	9.99	0.87	17.96
Days to maturity	3.26	3.53	0.85	6.21
Yield per plant (gm)	19.21	19.41	0.97	39.16

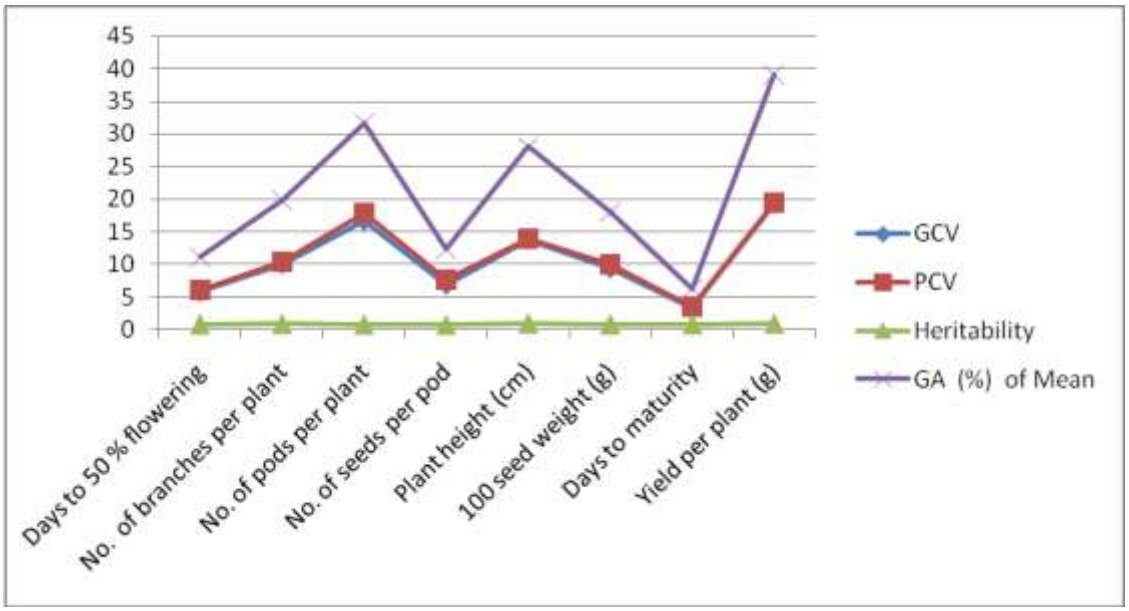

Fig. 1. Graphical representation of GCV, PCV, Heritability and Genetic Advance

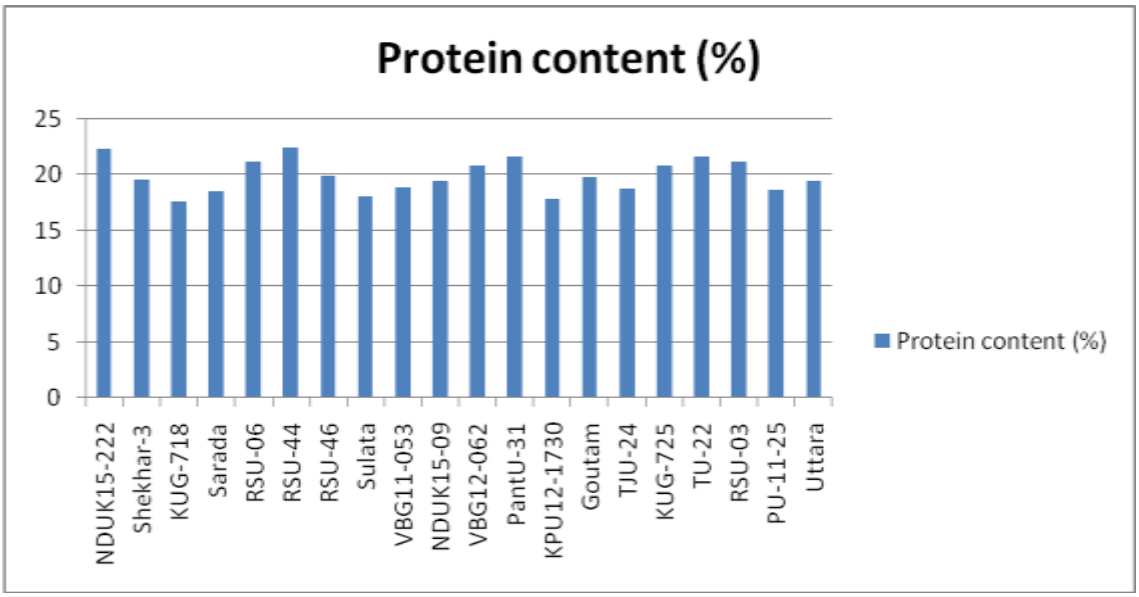

Fig. 2. Graphical representation of protein content (%) in the genotypes of blackgram

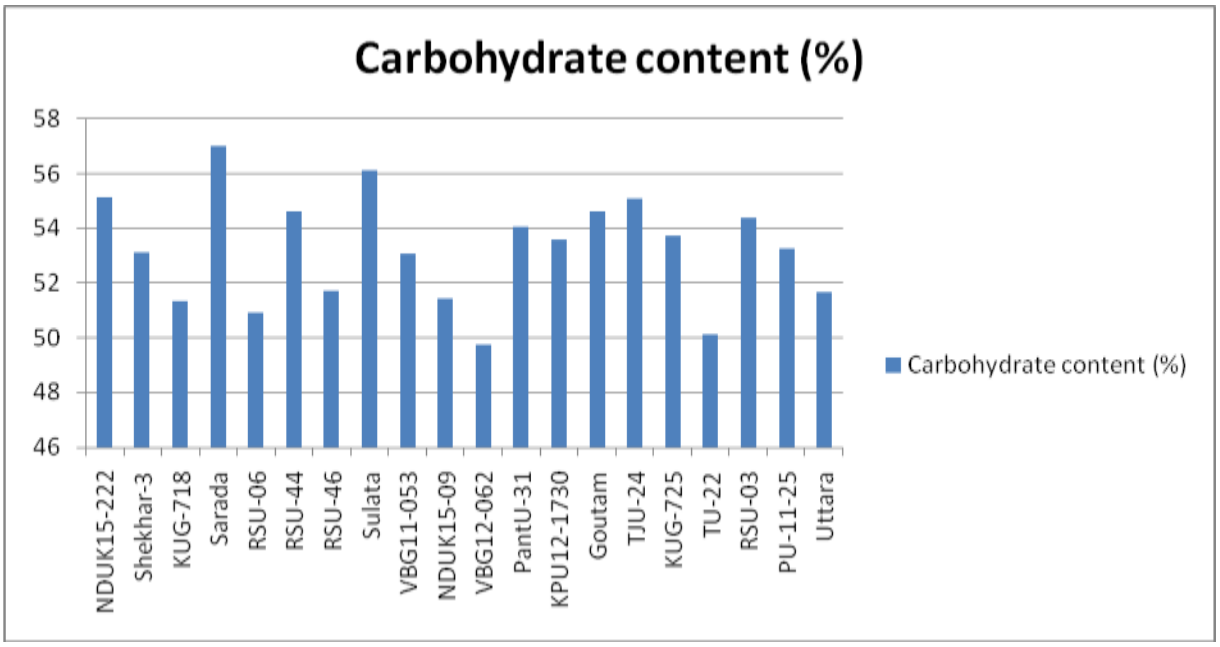

Fig. 3. Graphical representation of carbohydrate content (%) of blackgram genotypes

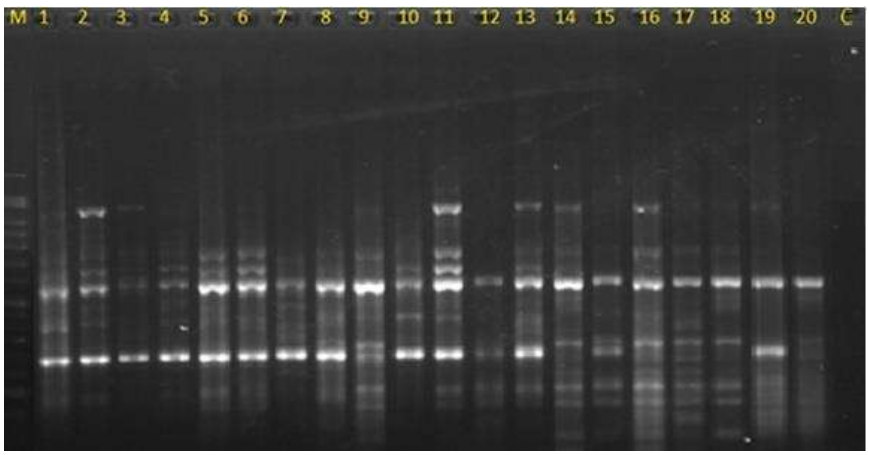

Fig. 4. Gel profile of blackgram genotypes based on the ISSR primers (using UBC-827 primer), Lane M-50 bp DNA Marker, Lane-1 to 20 (genotypes), Lane C-Control

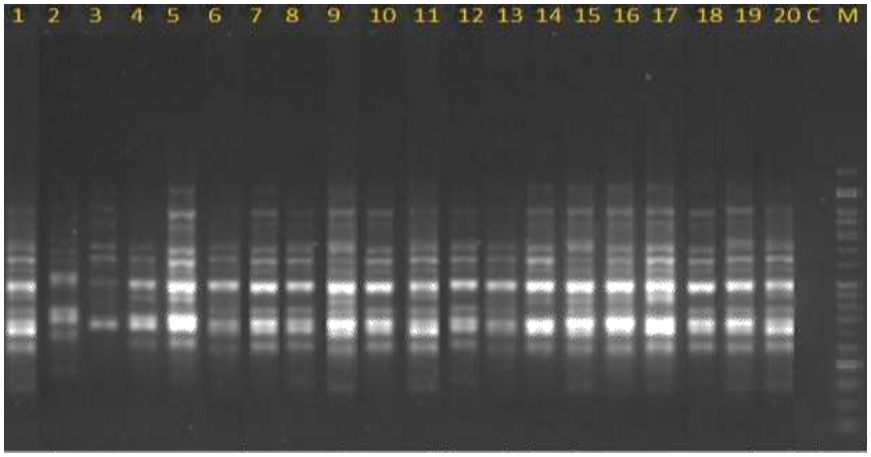

Fig. 5. Gel profile of blackgram genotypes based on the ISSR primers (using UBC- 856 primer), Lane M-50 bp DNA Marker, Lane-1 to 20 (genotypes), Lane C-Control.

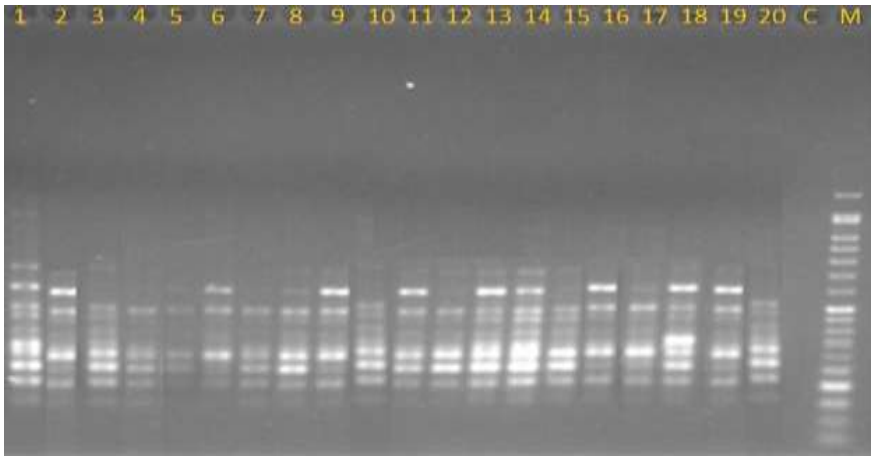

Fig. 6. Gel profile of blackgram genotypes based on the ISSR primers (using ISSR-33), Lane M-50 bp DNA Marker,Lane-1 to 20 (genotypes), Lane C-Control

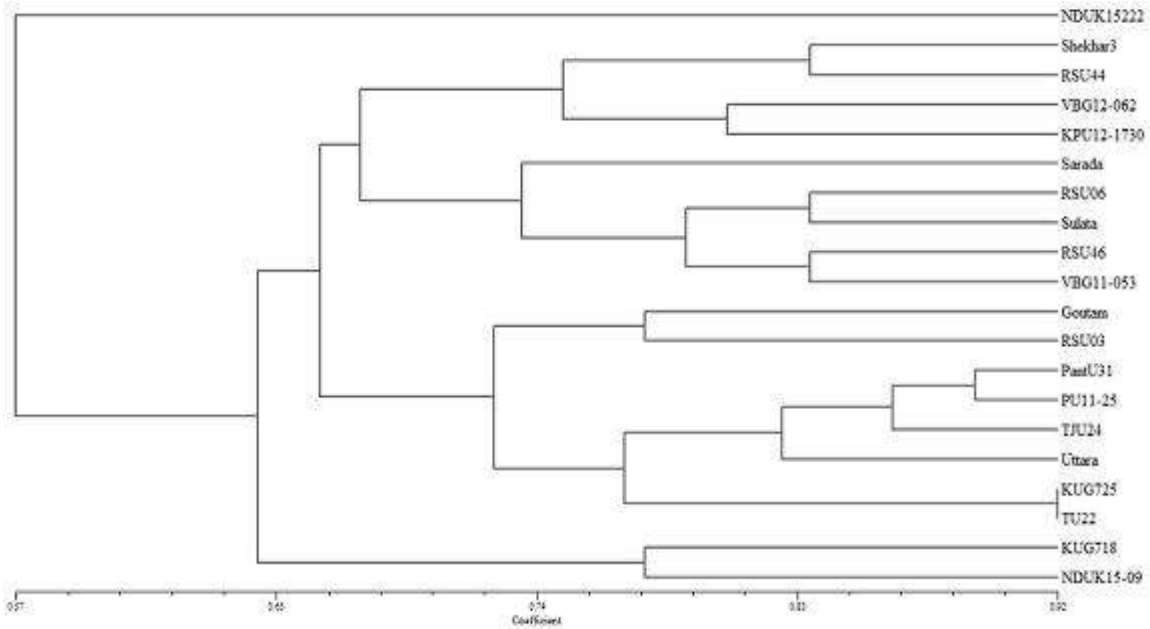

Fig. 7. Clustering of blackgram genotypes

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