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Research Note

Morphological characterization and discriminant function analysis in mungbean [*Vigna radiata* (L.) Wilczek] germplasm

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Abstract
The present investigation was conducted with 104 accessions of mungbean during summer 2012-13. Morphological characterization of accessions indicated high level of variation among gene pool. High GCV, PCV, heritability coupled with high genetic gain of agro-morphological traits viz., number of primary branches per plant, number of secondary branches per plant, peduncle length, leaf pubescence density, stem pubescence density, petiole pubescence density, number of clusters per plant and harvest index, indicating that selection will be effective for these traits. The genotypes were grouped in to various groups based on qualitative and quantitative traits, indicating the diversity of genotypes. This study may give better chance to select the genotypes with different weight for mungbean improvement.

Key words: Mungbean, characterization, heritability, genetic advance, selection score, agro-morphological traits

Characterization of germplasm helps to form the groups with specific traits and also gives the idea about those traits which may be used for distinguishing the genotypes from each other. Lee et al. (2004) and Piyada et al. (2010) also gave the emphasis on morphological characterization to assess the variability and classify the crop germplasm. Some of the agro-morphological traits may be used as morphological marker in crop improvement. The grouping of genotypes based on these traits can be easily detected by the naked eyes and used in mungbean breeding program for improving the seed physical quality. It also helps in assessment of genetic variability and diversity present in available germplasm.

Beside this, assessment of quantitative variation is also important because yield is the ultimate objective of any crop improvement program. Yield is a complex trait which always depends on its yield component traits and also affected by the environment. Thus, knowledge on gene action and inheritance of these traits is much important. Heritability coupled with genetic advance as percent of mean can be used to formulate the effective breeding program for mungbean improvement.

Besides the trait(s) identification, isolation of suitable genotypes is also required to initiate the hybidization breeding programmes (recombination/ transgressive breeding). Thus, giving the weight to agro-morphological traits, indices analysis is the best method to isolate the suitable/ diverse genotypes for recombination breeding. Keeping the above facts under consideration the present investigation was conducted to characterize the mungbean germplasm to formulate the trait specific groups and their effective utilization; to assess the variability parameters among germplasm and grouping of genotypes for mungbean improvement.

One hundred and four mungbean genotypes including four checks (Table 1) were received from Pulse Breeding Section, Department of Plant Breeding and Genetics, Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar. The experiment was conducted in Augmented design at Research Farm of TCA, Dholi during summer 2012-13. The experimental plot was divided in five blocks and each block contained 24 genotypes (20 genotypes + 4 checks). Each entry was grown in 4 rows of 4m row length. The spacing was maintained at 30 x 10 cm inter row and inter plant, respectively. Recommended agronomic practices were done time to time.

A total 16 descriptive and 26 quantitative traits were recorded during summer 2012 for morphological characterization. Leaf area was calculated by formula as per Yoshida et al. (1972). Grouping of genotypes based on scores was done by using statistical package NTSYS-pc version 2.21. Quantitative traits were recorded during summer 2012-13 and were subjected to pooled analysis of variance, variability parameters and index scoring was done by using computer package Windostat version 9.1.

Descriptive trait variation among germplasm**:** Scores on 17 morphological traits are presented in Table 2. Based on these scores genotypes were categorized in various groups and frequency distribution has been presented in Table 3. Morphological characterization helps in effective utilization of germplasm in crop improvement programmes. For example, hypocotyl anthocianin pigmentation has great importance in cross based

breeding program to detect the pure crosses due to its monogenic dominant inheritance pattern (Khattak et al., 2000; Mukherjee and Pradhan, 2002). This trait can be used as a morphological marker for screening of breeding material at seedling stage. Similarly stem color, petiole color and pod color can also be used for identification of material at post seedling stage. In present investigation, only 5.77% genotypes had green hypocotyls. Yimram et al. (2009) also give the emphasis on genotypes with green hypocotyls to purple ones for bean sprout industry. On the basis of stem color 95.19% genotypes were found with green stem, whereas 3.85 and 0.01% genotypes were found with greenish purple and purple stem color, respectively. But the proportion of genotypes with green, greenish purple and purple were found as 3.85, 94.23 and 0.02%, respectively indicated that it is not necessary the presence of anthocianin on all the plant parts. None of the genotypes were of glabrous nature. Black mature pod color were found in 63.46% of total germplasm evaluated which may be helpful to protect the discoloration of seeds under field condition however it affects the consumer preferability. Seed physical characters may also used as markers. Consumers prefer the green/ yellow, shiny and bold seeds over spotted/ black, dull and small seeds. Seed color also determines the phytic acid (PA) content. Tajoddin et al. (2011) reported the yellow seeded mungbean had low phytic acid content which can be used as a donor for quality improvement of mungbean seeds. Sompong et al. (2010) reported the two major genes at two different loci govern this trait. They also found the transgressive segregation for PA in F_2 population revealing modifying gene action among progenies of normal PA mungbean lines. Thus, crossing among yellow seeded mungbean lines may give opportunity to develop the varieties with desirable amount of PA content. Seed size is based on their 100 seed weight and affects the seed yield. Several researchers viz., Venkateswarlu (2001), Khajudparn and Tantasawat (2011) reported the positive association between SI and SYP. In present investigation, most of the genotypes were found with medium seed size followed by small and large. Thus, genotypes with different seed size may be included in breeding program for bold seeded mungbean varieties. Most of the genotypes (61) were noted for medium duration, whereas 43 genotypes were found with early flowering.

Multivariate cluster analysis was done based on similarity among the genotypes which gave the relative position of genotypes in group (Fig 1). Singh et al. (2010) gave emphasis on high genetic divergent genotypes for yielding better results. Therefore, genotypes may be choosen from dendrogram based on genetic diversity for crossing to improve the mungbean. Based on diversity G32 was found most divergent with other genotypes. Hence these genotypes may be crossed with for mungbean improvement by getting desirable segregents.

The analysis of variance revealed that genotypes and checks were significant for all the agro-morphological traits studied, indicating the presence of ample amount of genetic variation among the population. The high (>20%) estimates of GCV and PCV was recorded for NSBP, PedL, LPD, SPD, PetPD, NCP, BL, HI and SYP (Table 4). The high estimates of GCV and PCV for various traits has earlier been reported by Suresh et al. *(*2010) for SYP; Singh et al.(2009) for SYP, HI and SI; Narasimhulu et al. *(*2013b) for HI and SYP. Whereas, Tabasum et al. (2010) observed moderate GCV and PCV magnitude for SYP, SI & NSBP and low for HI & NPBP. This deviation indicated that the genetic variation of the traits also depends upon the breeding material. Rest traits viz., PH, LA, NMS, AIL, NPBAMS, NFPP, PAP, PPD, NCP, PL, NSP, SI and BYP showed intermediate (10-20%) GCV and PCV estimates except DFFO and DM. DFFO and DM exhibited low (<10%) estimates of GCV and PCV. Similar findings has earlier been reported by Gadak et al. (2013).

Knowledge of heritability of the traits helpful for planning of selection/ breeding methods. All the agro-morphological traits showed high (>70%) estimates of h^2bs (except LA), heritability icated the variation is arises due to genetic effect. LA exhibited moderate (50-70%) h^2bs. Heritability coupled with GAM may give good idea about selecting the traits for implication in breeding programmes. In present study, four traits viz., DFFO, DM, LA and NSP exhibited low to moderate estimates of GAM, whereas rest traits were noted for high h^2 coupled high GAM. The traits with high h^2 coupled high GAM indicating greater role of additive gene effects on the expression of these traits which is in agreement with Singh et al. (2009), Rahim et al. (2010) and Baisakh et al. (2013). Therefore, these agro-morphological traits may be added in mungbean improvement program by simple plant selection methods. Yimram et al. (2009) suggested that due to quantitative nature of these agro-morphological traits, the GV, PV, h^2 and GA of the breeding material must be considered together in choosing of traits for crop improvement. Thus, agro-morphological traits viz., NPBP, NSBP, PedL, LPD, SPD, PetPD, NCP, BL, HI and SYP were fall on this scale, indicating the role of additive genetic effect in governing the expression of traits and these traits may be included in mungbean improvement for outstanding response by applying the selection pressure. The high additive genetic effect of pubescence traits may be helpful to develop the insect tolerant varieties is broadly

agreement with Dwivedi and Singh (1986), Elden *et al.* (1986), Gunashige *et al. (*1988), Fatokun and Singh (2001) and Mohammed *et al., (*2010) in various crops.

Grouping of genotypes based on discriminant function: With identification of agro-morphological traits, isolation of suitable genotype(s) is also important. Several researchers gave more emphasis on involvement of diverse parents in crossing program for high heterotic response as well as transgressive segregants in early segregating generations for high seed yield and other targeted trait(s). Katiyar et al. (2009), Piyada et al. (2010), Narasimhulu et al. (2013a) also suggested that use of diverse parents gives better chance to develop the superior varieties. Behl et al. (1985) suggested that the incensement in heterosis occurs within a restricted range of diversity. Shukla and Singh (2006), Yadav et al. (2007) observed that negative association between between F_1 performance and genetic distance (except some traits). Parameshwarappa et al. (2009) suggested that moderate genetic diversity is expected to throw heterotic hybrids. Thus, the parents with both high and moderate diversity can be included in breeding programme to isolate the good recombinants. Thus, grouping of genotypes was done on the basis of selection scores. Equal economic weight was given to all the agro-morphological traits to calculate the selection scores for each genotype. The selection score (SC) ranged from 733.80 (x) – 1007.91 (y) with grand mean of 836.48 (m) and standard deviation (s) of 70.64. The grouping of genotypes with SCs has been presented in Table 5. These four groups wre formed as < m –s (group I), m –s < and < m (group II), m < and <m+s (group III) and > m+s (group IV). The group I consisted 18 genotypes with very high SC followed by group II (35 genotypes) with high SC, group III (33 genotypes) with moderate SC and group IV (18 genotypes) with low SC. The selection of genotypes from high to moderate SC groups may be included in breeding programmes to isolate the transgressive segregents in early segregating generation.

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Table 1. List of mungbean germplasm used in present investigation during *summer* 2012-13

Code	Genotype Name	Code	Genotype Name	Code	Genotype Name
G1	HUM-12	G37	IPM 02-19	G73	EC 398885
G2	IPM-02-14	G38	ML 515	G74	UPM 02-17
G3	NDM-09-18	G39	PDM 288	G75	UPM 98-1
G4	ML-1666	G40	PDM 11	G76	EC 30400
G5	DM 05-12-1-42-3	G41	IPM 03-1	G77	EC 39889
G6	DMS 01-34-2	G42	PDM 262	G78	ML 935
G7	DMS 03-17-2	G43	ML 729	G79	SM 47
G8	DM 99-11-5	G44	IPM 02-3 (Black)	G80	SM 48
G9	SML-668	G45	IPM 02-3	G81	EC 391178
G10	DMC 17	G46	IPM 02-14	G82	PM 4
G11	Meha	G47	Pusa Ratna	G83	EC 398894
G12	Sona	G48	ML 682	G84	ML 1059
G13	IPM 2K-14-9	G49	PDM 87	G85	PM 3
G14	DM 05-74-11	G50	IPM 02-17	G86	EC 393407
G15	IPM 99-01-10	G51	PDM 139	G87	EC 470096
G16	PM 2	G52	IPM 99-3	G88	ML 1257
G17	Pusa 1131	G53	PDM 84-143	G89	ML 1256
G18	DMS 02-11-4	G54	IPM 03-3	G90	GM 4
G19	IPM 99-1-6	G55	P 9871	G91	GM 9926
G20	Pusa 1232	G56	IPM 02-3 (Green)	G92	EC 399223
G21	Pusa Vishal	G57	P 871	G93	GM 9925
G22	Pusa 1231	G58	IPM 03-2	G94	EC 398897
G23	IPM2K-15-4	G59	PDM 281	G95	SML 191
G24	PM 08-2	G60	IPM 02-3 (DSS)	G96	EC 470096
G25	NDM12-308	G61	P Bold 2	G97	EC 398886
G26	DMS 02-11-13	G62	PDM 191	G98	EC 581523
G27	IPM 312-394	G63	ML 5	G99	EC 398891
G28	SML 1186	G64	P 9972	G100	EC 393410
G29	PM 5	G65	PDM 54	G101	TMB-37 (Check 1)
G30	SML 1151	G66	PDM 178	G102	HUM-16 (Check 2)
G31	P. Bishakhi	G67	ML 818	G103	P 9531 (Check 3)
G32	AKM 8803	G68	IPM 02-16	G104	Samrat (Check 4)
G33	DMC 4	G69	IPM 02-10		
G34	DMC 7	G70	P 9072		
G35	ML 512	G71	EC 520011		
G36	P 672	G72	EC 496841		

Table 2. List of qualitative and quantitative traits recorded during investigation

Trait name	Measurement
A. Descriptive traits (Qualitative)	
Hypocotyl Anthocianin pigmentation (AP)	1= Absent, 9= Present
Plant growth habit (GH)	3= Erect, 5= Semi-erect, 7= Spreading
Stem colour (SC), Petiole colour (PetC)	1= Green, 2= Green with purple splashes, 3= Purple
Stem pubescence (SPub), Leaf pubescence (LPub), Pod pubescence (PPub), Petiole pubescence (PetPub), Leaflet lobe (LL)	1= Absent, 9= Present
Mature pod colour (MPC)	1= Brown, 2= Black
Pod curvature of mature pod (PC)	1= Straight, 2= Curved
Seed colour (SCol)	1= Yellow, 2= Green, 3= Mottled, 4= Black
Seed lusture	1= Shiny, 2= Dull
B. Descriptive traits (Quantitative)	Based on five random plants
Flowering time	3= Early (<40 Days), 5= medium (40-50 days), 7= Late (>50 days)
Plant height	3= Short (<50 cm), 5= Medium (50-70 cm), 7= Tall (>70 cm)
Pod length	3= Short (<8 cm), 5= Medium (8-10 cm), 7= Long (>10 cm)
Seed size	3= Small (<3 g), 5= Medium (3-5 g), 7= Large (>5 g)
C. Quantitative traits	
Days to first flower opening (DFFO), Days to maturity (DM)	Plot Basis
Plant height (PH), Number of primary branches per plant (NPBP), Number of secondary branches per plant (NSBP), Petiole length (PetL), Leaf area (LA), Number of nodes on main stem (NMS), Average intermodal length (AIL), Primary branch angle with main stem (PBAMS), Number of first productive peduncle from base (NFPP), Peduncle length (PedL), Pod angle with peduncle (PAP), Stem pubescence density (SPD), Leaf pubescence density (LPD), Pod pubescence density (PPD), Petiole pubescence density (PetPD), Number of clusters per plant (NCP), Number of pods per cluster (NPC), Pod length (PL), Beak length (BL), Number of seeds per pod (NSP), Seed index (SI), Biological yield per plant (BYP), Harvest index (HI), Seed yield per plant (SYP)	Based on five random plants

Characterization was done as per description of National Test Guidelines for conducting the test for DUS of mungbean and urdbean.

Table 3. Frequency distribution and per cent variation of various characters of mungbean germplasm during *summer* 2012

Trait		Frequency	Percentage
Hypocotyl colour	Green	6	5.77
	Purple	98	94.23
Plant growth habit	Erect	4	3.85
	Semi-erect	94	90.38
	Spreading	6	5.77
Stem colour	Green	99	95.19
	Green with purple splashes	4	3.85
	Purple	1	0.01
Petiole colour	Green	4	3.85
	Green with purple splashes	98	94.23
	Purple	2	0.02
Pod colour	Brown	38	36.54
	Black	66	63.46
Stem pubescence	Absent	Nil	-
	Present	104	100
Leaf pubescence	Absent	Nil	-
	Present	104	100
Pod pubescence	Absent	Nil	-
	Present	104	100
Petiole pubescence	Absent	Nil	-
	Present	104	100
Leaflet lobe	Absent	104	100
	Present	Nil	-
Pod curvature	Strait	60	57.69
	Curved	44	42.31
Seed colour	Yellow	4	3.85
	Green	99	95.19
	Mottled	1	0.01
	Black	Nil	-
Seed lusture	Shiny	85	81.73
	Dull	19	18.27
Time of flowering	Early	43	41.35
	Medium	61	58.65
	Late	Nil	-
Plant height	Dwarf	46	44.23
	Semi dwarf	58	55.77
	Tall	Nil	-
Pod length	Small	88	84.62
	Medium	15	14.42
	Long	01	0.01
Seed size	Small	10	9.62
	Medium	87	83.65
	Large	07	6.73

Table 4. Variance components and genetic parameters on various agro-morphological traits in mungbean during *summer* 2012-13

Tratis	GCV	PCV	h^2 (bs)	GA	GAM
DFFO	8.53	9.39	82.61	8.44	15.98
DM	4.65	5.25	78.54	6.18	8.49
PH	18.09	19	90.79	15.1	35.52
NPBP	22.93	27.83	67.86	1.01	38.91
NSBP	33.71	37.71	79.9	1.38	62.07
PetL	11.93	12.72	87.97	2.71	23.05
LA	14.44	19.69	53.78	9.16	21.82
NNMS	16.41	17.78	85.22	3.2	31.21
AIL (cm)	17.66	18.58	90.29	1.47	34.56
PBAMS	17.48	18.01	94.23	22.82	34.95
NFPP	11.55	12.63	83.65	1	21.77
PedL	20.87	21.27	96.23	3.57	42.17
PAP	15.77	15.86	98.78	29.42	32.28
LPD	29.27	29.58	97.91	42.67	59.67
SPD	27.64	29.86	85.64	59.48	52.68
PPD	13.6	13.8	97.07	38.74	27.59
PetPD	27.23	27.5	98.04	40.08	55.53
NCP	23.23	27.01	73.93	2.81	41.14
NPC	14.53	16.71	75.63	1.06	26.04
PL	9.97	11.08	80.85	1.39	18.46
BL	33.53	34.34	95.32	3.02	67.43
NSP	9.82	10.73	83.73	2	18.5
SI	12.91	14.4	80.42	0.91	23.85
BYP	16.78	17.81	88.79	8.82	32.57
HI	33.44	35	91.26	15.5	65.81
SYP	28.89	30.85	87.65	3.38	55.71

GCV= Genetic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2bs= Heritability in broad sense, GAM= Genetic advance as % of mean, DFFO= Days to first flower opening, DM= Days to maturity, PH= Plant height, NPBP= Number of primary branches/ plant, NSBP= Number of secondary branches/ plant, PetL= Petiole length, LA= Leaf area, NMS= Number of nodes on main stem, AIL= Average intermodal length, PBAMS= Primary branch angle with main stem, NFPPP= Node of first productive peduncle, PedL= Peduncle length, PAP= Pod angle with peduncle, LPD= Leaf pubescence density, SPD= Stem pubescence density, PPD= Pod pubescence density, PetPD= Petiole pubescence density, NCP= Number of clusters/ plant, NPC= Number of pods / cluster, PL= Pod length, BL= Beak length, NSP= Number of seeds/ pod, SI= Seed index, BYP= Biological yield/ plant, HI= Harvest index, SYP= Seed yield/ plant

Table 5. Distribution of genotypes in various groups based on selection scores

Group	Number of genotypes	Genotypes#
I	18	G5 (1007.91), G85 (993.82), G46 (968.33), G87 (959.38), G41 (948.22), G74 (944.97), G15 (939.10), G8 9930.67), G104 (930.11), G17 (929.35), G98 (926.62), G25 (923.72), G33 (922.77), G97 (921.46), G71 (921.30), G22 (920.42), G40 (918.78), G13 (911.25)
II	35	G45 (905.01), G30 (904.40), G101 (902.05), G26 (898.93), G44 (894.33), G35 (890.07), G50 (884.05), G83 (881.93), G16 (881.74), G36 (878.03), G54 (876.03), G19 (875.47), G6 (873.380, G18 (867.07), G48 (866.84), G43 (865.57), G47 (864.70), G73 (863.81), G28 (863.16), G69 (862.45), G102 (856.14), G39 (854.68), G10 (853.71), G67 (852.66), G62 (848.68), G7 (848.38), G49 (848.26), G42 (845.72), G99 (845.66), G55 (844.54), G84 (842.83), G82 (842.49), G89 (840.21), G72 (839.100, G27 (837.08)
III	33	G14 (834.87), G24 (832.28), G9 (831.38), G60 (830.68), G37 (827.59), G66 (826.28), G4 (825.91), G1 (825.01), G57 (822.51), G3 (822.33), G53 (821.02), G70 (819.07), G59 (816.94), G86 (815.40), G100 (813.94), G11 (812.99), G64 (812.97), G91 (810.46), G51 (804.88), G81 (803.07), G34 (800.69), G103 (797.28), G93 (796.81), G80 (793.74), G38 (792.21), G29 (791.98), G92 (791.93), G68 (789.20), G 20 (786.03), G75 (786.02), G79 (784.77), G77 (769.25), G61 (766.82)
IV	18	G32 9763.84), G12 (762.51), G31 (756.58), G95 (754.06), G76 (753.23), G56 (745.04), G88 (743.06), G63 (743.03), G96 (740.57), G52 (739.63), G90 (739.47), G2 (733.80), G65 (714.63), G78 (709.83), G58 (705.57), G21 (703.21), G23 (681.23), G94 (631.34)

#Name of genotypes as per listed in Table 1. Selection scores of each genotype are given in parenthesis.

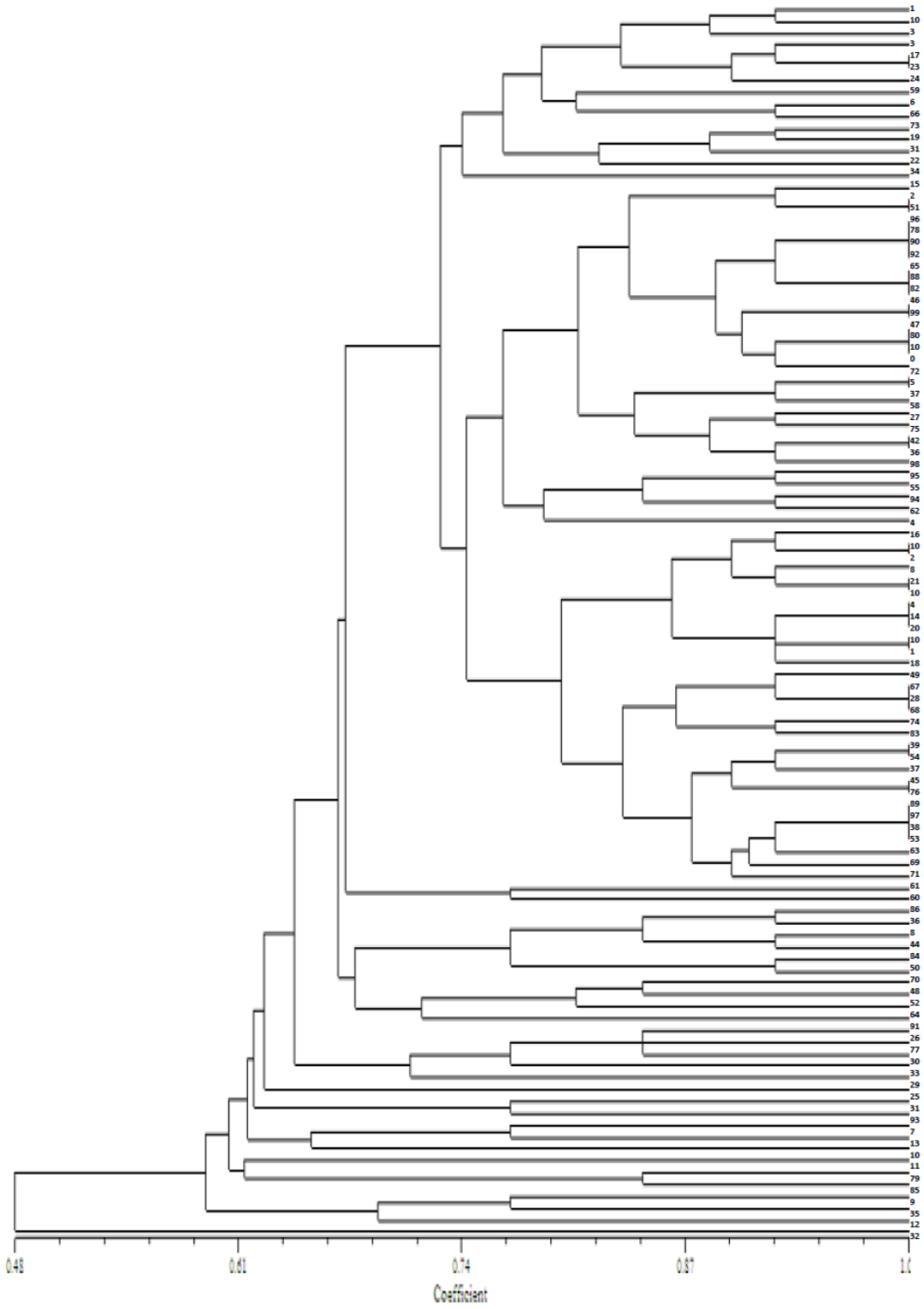

Fig 1: Dendrogram representing similarity among mungbean genotypes based on Euclidean distance