International Journal of Current Research and Modern Education (IJCRME)
Impact Factor: 6.925, ISSN (Online): 2455 - 5428
(www.rdmodernresearch.com) Volume 8, Issue 1, 2023

DIVERSITY ANALYSIS FOR BASE COLLECTION IN GREENGRAM

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Cite This Article: Pandiyan Muthaiyan, “Diversity Analysis for Base Collection in Greengram”, International Journal of Current Research and Modern Education, Volume 8, Issue 1, Page Number 58-69, 2023.

Abstract:

In the present investigation, the 18 quantitative characters of greengram germplasm for 646 accessions were evaluated. Hierarchical Cluster Analysis (HCA) and Principal Component analysis (PCA) were used for base collections. Eight distinct clusters could be recognized from the tree for base collection. The PCA revealed that the total variability cumulatively accounting for 60.47 per cent in base collections. The average range retention coresponding to all the 18 traits accounted for 88.5 per cent. The cluster VI revealed highest mean performance for many morphological characters the parents were selected from different clusters for intra specific hybridization based on the wide adaptable nature of the accessions. The selection of lines and testers were not found in the same clusters.

Introduction:

Vigna radiata (L.) wilczek, commonly known as green gram or mungbean is the most widely distributed species among the six Asiatic *Vigna* species. It is one of the predominant sources of protein and certain essential amino acids like lysine and tryptophan in vegetarian diets. It possessed certain added features compared to other pulses. It is relatively drought tolerant and well adapted to a range of soil conditions including light soils and can thrive even under limited irrigation, more over, it is suited for crop rotation and crop mixtures (Baldev, 1988 and Sadaphal, 1988). However, this crop is suffering from the yield advantage as realized in case of C4 cereals.

Presently, the yield level of green gram as like other pulses is well below the optimum level. The average yield of mungbean is very low not only in India (425 kg/ha) but in entire tropical and subtropical Asia. In Tamil Nadu it is cultivated in an area of 1.63 lakhs hectare with a production of 0.78 lakhs tonnes. Besides management factors the prime cause for the low productivity can be ascribed to the inherently low yielding potential of the cultivars coupled with susceptibility to diseases.

The core collection concept was suggested by Frankel and Brown (1984), who defined it as a representative sample of a collection where as much as possible of the diversity of the collection, is retained with minimum redundancy.

The core collection is a logical first step in the screening for desirable alleles (Holbrook and Anderson.1995). The economy of size makes it possible to increase the number of characteristics evaluated and or to promote the use of other techniques for screening such as molecular markers. Selection of parents from the core collection for hybridization program is likely to generate superior transgressive segregants

For utilizing the variability available in the secondary and tertiary gene pools it is essential to attempt interspecific crosses and to develop viable hybrids. These hybrids need to be critically evaluated as such and in the segregating generations for improvement in yield and yield components. The introgressed materials developed through wide crosses can also contribute as genetic reservoirs for novel genes apart from contributing to the improvement of yield and yield components. With a view to evaluate the available germplasm using the descriptors and form the core collection and for attempting intra and interspecific hybridization to generate segregants for better yield, this study was taken up keeping the following objectives in mind**.**

- To evaluate available germplasm of green gram
- To perform hierarchical cluster analysis and ordinate analysis of available germplasm and to establish base collection following specific scientific principles.

Materials and Methods:

This investigation was carried out during the period of 2021 to 2023 at Agriculture College and Research Institute, Tamil Nadu Agricultural University, Eachangkottai, Thanjavur, Tamil Nadu for Moon University, Western Africa.. Materials, Seeds of 646 accessions of green gram were collected from the various and utilized for the study. The details of the accessions are presented in Table 1.Methods All the 646 accessions were raised during two seasons viz., Kharif 2022 and Rabi 2022-2023 at the Agriculture College and Research Institute, Tamil Nadu Agricultural University, Eachangkottai, Thanjavur, Tamil Nadu for African Moon University, Western Africa in a randomized block design with two replications. Each genotype was sown in two single row plot each of four metre length, plants were raised at a spacing of 30 x 10 cm. The package of practices recommended inthe crop production guide were followed. Observations recorded for eeighteen quantitative traits in greengram were recorded in five randomly selected plants in each of the accession per replication.

Plant Height (cm):

Table 1: List of greengram germplasm

Acc No	Name of the Accessions	Source	Acc No	Name of the accession	Source
1	PLS.168	New Delhi	36	PLS.312	New Delhi
2	PLS.239/1	New Delhi	37	PLS.313	New Delhi
3	PLS.267	New Delhi	38	PLS.316	New Delhi
4	PLS.262	New Delhi	39	PLS.317/1	New Delhi
5	PLS.263	Punjab	40	MDU.2013/1-2/1(B)	TamilNadu
6	VBN.1-1	Tamil Nadu	41	PLS.318/1	New Delhi
7	PLS.265	New Delhi	42	PLS.318/2	New Delhi
8	PLS.267/1	New Delhi	43	PLS.326(D)	New Delhi
9	PLS.267/2	New Delhi	44	PLS.330	New Delhi
10	Paiyur.1	Tamil Nadu	45	PLS.334	New Delhi
11	PLS.272	New Delhi	46	PLS.331	New Delhi
12	PLS.274	New Delhi	47	PLS.419/1	New Delhi
13	PLS.275	New Delhi	48	AC.5	Tamil Nadu
14	PLS.276	New Delhi	49	AC.28	Tamil Nadu
15	PLS.278(D)	New Delhi	50	AC.41	Tamil Nadu
16	PLS.280	New Delhi	51	AC.147(B)	Tamil Nadu
17	AVT/AMI-2	New Delhi	52	AC.152	Tamil Nadu
18	PLS.282(B)	New Delhi	53	AC.154(S)	Tamil Nadu
19	PLS.282(D)	New Delhi	54	AC.154(D)	Tamil Nadu
20	K.851	Uttra Pradesh	55	AC.192	Tamil Nadu
21	PLS.282 (S)	New Delhi	56	AC.164(S)	Tamil Nadu
22	V.5197/1(S)	Taiwan	57	AC.164(D)	Tamil Nadu
23	PLS.287(D)	New Delhi	58	AC.171	Tamil Nadu
24	PLS.289	New Delhi	59	MDU.3486(S)/1	Tamil Nadu
25	PLS.293(S)	New Delhi	60	VRMG(g) 1	Tamil Nadu
26	PLS.294(S)	New Delhi	61	AC.196	Tamil Nadu
27	SPS.99/1	New Delhi	62	AC.198	Tamil Nadu
28	PLS.296	New Delhi	63	AC.199	Tamil Nadu
29	PLS.298	New Delhi	64	AC.204	Tamil Nadu
30	PLS.301	New Delhi	65	AC.205	Tamil Nadu
31	PLS.302	New Delhi	66	AC.241	Tamil Nadu
32	PLS.303	New Delhi	67	AC.244	Tamil Nadu
33	PLS.305	New Delhi	68	AC.348	Tamil Nadu
34	PLS.308	New Delhi	69	AC.248	Tamil Nadu
35	PLS.308/1	New Delhi	70	AC.254	Tamil Nadu
71	AC.266	Tamil Nadu	106	LM. 98 (D)	Punjab
72	AC.285	Tamil Nadu	107	LM. 103 (S)	Punjab
73	ACS.307	Tamil Nadu	108	LM.103 (D)	Punjab
74	LM.1	Punjab	109	LM.104	Punjab
75	LM.5/1	Punjab	110	LM.105(B)	Punjab
76	LM.9	Punjab	111	LM.107	Punjab
77	LM.13	Punjab	112	LM.108	Punjab
78	LM.17	Punjab	113	LM.113	Punjab
79	LM.19	Punjab	114	LM.115	Punjab
80	LM.23	Punjab	115	LM.116	Punjab
81	LM.25	Punjab	116	LM.125	Punjab
82	LM.29	Punjab	117	LM.143	Punjab
83	LM.30	Punjab	118	LM.147 (D)	Punjab
84	LM.31	Punjab	119	LM.147 (S)	Punjab
85	LM.32 (D)	Punjab	120	LM.152	Punjab
86	LM 32.(S)	Punjab	121	LM.153	Punjab

87	LM.35	Punjab	122	LM.154	Punjab
88	LM.36	Punjab	123	LM.158	Punjab
89	LM.38	Punjab	124	LM.159	Punjab
90	LM.43	Punjab	125	LM.163	Punjab
91	LM.58	Punjab	126	LM.167	Punjab
92	LM.60	Punjab	127	PLS 318/2 (S)/1	Punjab
93	LM.65	Punjab	128	LM.179 (S)	Punjab
94	LM.66	Punjab	129	LM.179 (D)	Punjab
95	LM.67	Punjab	130	LM.185	Punjab
96	LM.68	Punjab	131	LM. 189	Punjab
97	LM.73	Punjab	132	LM.196	Punjab
98	LM.75	Punjab	133	LM.197	Punjab
99	AVT/RMI-3	Taiwan	134	LM.205	Punjab
100	LM.82 (S)	Punjab	135	LM.207	Punjab
101	LM.82 (D)	Punjab	136	LM.209	Punjab
102	LM.85	Punjab	137	LM.214	Punjab
103	LM.87	punjab	138	LM.215	Punjab
104	LM.89(B)	Punjab	139	LM.216 (S)	Punjab
105	LM.98(S)	Punjab	140	LM.216 (D)	Punjab
141	LM.218(D)	Punjab	176	LM.331	Punjab
142	LM.222(S)	Punjab	177	LM.333	Punjab
143	LM.224(D)	Punjab	178	LM.334	Punjab
144	LM.224	Punjab	179	LM.336(D)	Punjab
145	LM.232(S)	Punjab	180	LM.336(S)	Punjab
146	LM.232(D)	Punjab	181	LM.338	Punjab
147	LM.233	Punjab	182	LM.344	Punjab
148	LM.234	Punjab	183	LM.346	Punjab
149	LM.235(GY)	Punjab	184	LM.352	Punjab
150	LM.236	Punjab	185	LM.354	Punjab
151	LM.251	Punjab	186	LM.358	Punjab
152	LM.253	Punjab	187	LM.359	Punjab
153	LM.255	Punjab	188	LM.360	Punjab
154	LM.263	Punjab	189	LM.365	Punjab
155	LM.269	Punjab	190	LM.369	Punjab
156	LM.272	Punjab	191	LM.384	Punjab
157	LM.274(D)	Punjab	192	LM.387	Punjab
158	LM.274(S)	Punjab	193	LM.388	Punjab
159	LM.275(D)	Punjab	194	LM.391	Punjab
160	LM.275(S)	Punjab	195	LM.392 (S)	Punjab
161	LM.279(D)	Punjab	196	LM.392 (D)	Punjab
162	LM.289	Punjab	197	LM.399	Punjab
163	LM.292	Punjab	198	LM.401	Punjab
164	LM.294	Punjab	199	LM.405	Punjab
165	LM.296	Punjab	200	LM.406	Punjab
166	LM.299	Punjab	201	LM.409	Punjab
167	LM.304	Punjab	202	LM.412	Punjab
168	LM.305	Punjab	203	LM.415	Punjab
169	LM.306	Punjab	204	LM.419	Punjab
170	LM.307	Punjab	205	LM.420 (B)	Punjab
171	LM.309	Punjab	206	LM.440	Punjab
172	LM.314	Punjab	207	LM.442	Punjab
173	LM.315	Punjab	208	LM.446	Punjab
174	LM.328	Punjab	209	LM.450	Punjab
175	LM.330	Punjab	210	LM.452	Punjab
211	LM.1	Punjab	246	MDU.2010	Tamil Nadu
212	LM.3	Punjab	247	MDU.2106	Tamil Nadu
213	LM.5	Punjab	248	MDU.2268	Tamil Nadu
214	LM.6	Punjab	249	MDU.2773	Tamil Nadu

215	LM.8	Punjab	250	MDU.89047(L)	Tamil Nadu
216	LM.10	Punjab	251	MDU. 3096	Tamil Nadu
217	LM.26	Punjab	252	MDU.3156	Tamil Nadu
218	LM.30	Punjab	253	MDU.3179	Tamil Nadu
219	LM.33	Punjab	254	MDU.3372(S)	Tamil Nadu
220	LM.62	Punjab	255	MDU.3372(D)	Tamil Nadu
221	LM.65	Punjab	256	Vellore local	Tamil Nadu
222	LM.70(S)	Punjab	257	MDU.3385(D)	Tamil Nadu
223	LM.70 (D)	Punjab	258	MDU.3387	Tamil Nadu
224	MS.9384	Maharastra	259	MDU.3404	Tamil Nadu
225	LM.131(D)	Punjab	260	MDU.3404/1(S)	Tamil Nadu
226	LM.192/1	Punjab	261	MDU.3404/1(D)	Tamil Nadu
227	LM.307	Punjab	262	MDU.3405	Tamil Nadu
228	MS.9382	Maharastra	263	MDU.3476	Tamil Nadu
229	ML.682	Punjab	264	MDU. 3484	Tamil Nadu
230	AVTM.103	Maharashtra	265	MDU.3485	Tamil Nadu
231	MS.9720/1	Maharashtra	266	MDU.3486	Tamil Nadu
232	ML.80	Punjab	267	VBN. 1	Tamil Nadu
233	MS.9720/2(D)	Maharashtra	268	MDU.3487	Tamil Nadu
234	MS.9720/2(S)	Maharashtra	269	MDU.3379	Tamil Nadu
235	MS.9721	Maharashtra	270	1735/5	Korea
236	MS.9722	Maharashtra	271	1732/2	Korea
237	MS.9723	Maharashtra	272	AVT/RMI-6/1	Uttar Pradesh
238	MS.9724(D)	Maharastra	273	1788/1	Korea
239	MS.9724(B)	Maharashtra	274	1788/2	Korea
240	MS.9583	Maharashtra	275	1789/3	Korea
241	AVT.M.108	Maharashtra	276	1790/3	Korea
242	MDU.1942	Tamil Nadu	277	1790/4	Korea
243	MDU.1944	Tamil Nadu	278	1791	Korea
244	MDU.1948(Gy)	Tamil Nadu	279	118890	Korea
245	MDU.1968	Tamil Nadu	280	118891	Korea
281	V.1972	Taiwan	316	T.3485	Uttra Pradesh
282	SPS.99/2	Taiwan	317	TT.9E	Uttra Pradesh
283	118895(B)	Korea	318	UPM.79-3-4	Uttrapradesh
284	118896	Korea	319	11/399	Uttrapradesh
285	118897(B)	Korea	320	652/4	Uttrapradesh
286	118898	Korea	321	11/395	Uttrapradesh
287	ADT.1	Tamil Nadu	322	12/333	Uttrapradesh
288	B.1	Tamil Nadu	323	78/2	Uttrapradesh
289	BPS.1-1	Tamil Nadu	324	76-5(S)	Uttra Pradesh
290	CO.2/1	Tamil Nadu	325	76-5(D)	Uttra Pradesh
291	CO.3	Tamil Nadu	326	ML.307	Punjab
292	CC.192A	Tamil Nadu	327	KM.1/1(D)	Tamil Nadu
293	CM.44/1	Tamil Nadu	328	76-17	Uttar Pradesh
294	DM.2	Tamil Nadu	329	76-18	Uttra Pradesh
295	DPI.701	Tamil Nadu	330	76-19	Punjab
296	DPI.702	Tamil Nadu	331	76-22	Uttra Pradesh
297	DPI.703	Tamil Nadu	332	76-29	Uttra Pradesh
298	G.1	Tamil Nadu	333	76-32	Uttra Pradesh
299	V.109/1(S)	Taiwan	334	76-36	Uttra Pradesh
300	HG.22	Haryana	335	76-37	Uttra Pradesh
301	SML.171/1(D)	Punjab	336	76-43	Uttra Pradesh
302	HYB.12	Andra Pradesh	337	76-47	Uttra Pradesh
303	24-Feb	Uttar Pradesh	338	76-47/1	Uttra Pradesh
304	HG.19A	Haryana	339	Pabatla	Andra Pradesh
305	KG.52	Kerala	340	Bodi.1	Tamil Nadu
306	K 851	Punjab	341	Khalikola	Tamil Nadu
307	LGG.122 (D)	Andra Pradesh	342	Kovilpatti	Tamil Nadu

308	LGG122(B)	Andra Pradesh	343	K .Pudur-1	Tamil Nadu
309	MH.1(B)	Maharashtra	344	K .Pudur-(D)	Tamil Nadu
310	MH.1(D)	Maharashtra	345	K .Pudur.2	Tamil Nadu
311	NP.36	Maharashtra	346	K .Pudur.3	Tamil Nadu
312	PANT M.103	Uttra Pradesh	347	Kopergoan	Maharastra
313	T.44	Uttra Pradesh	348	Kankeyam	Tamil Nadu
314	T.2272	Uttra Pradesh	349	Nigeriavariety	Nigerian
315	T.3484	Uttra Pradesh	350	Rajendran	Tamil Nadu
351	Pusa Riagle	New Delhi	386	MDU.3092	Tamil Nadu
352	Pusa bold	New Delhi	387	NA.10	Tamil Nadu
353	Nelambur	Tamil Nadu	388	IVT.OISM.30	Uttar Pradesh
354	Sabourcate	Tamil Nadu	389	MDU.2013/1-2	Tamil Nadu
355	Salem	Tamil Nadu	390	AC.246	Tamil Nadu
356	Sona moong	Tamil Nadu	391	AC156	Tamil Nadu
357	Tenkasi	Tamil Nadu	392	PLS.291	New Delhi
358	Thoppakunda	Tamil Nadu	393	LM.216/1(S)	Punjab
359	Thokkavadi	Tamil Nadu	394	AKM.9243	Tamil Nadu
360	T.V. Malai(S)	Tamil Nadu	395	AC.268	Tamil Nadu
361	T.V. Malai(D)	Tamil Nadu	396	AC 266	Tamil Nadu
362	Velampatti	Tamil Nadu	397	PLS.315	Punjab
363	Villathikulam	Tamil Nadu	398	LM.407	Punjab
364	IVT .OISM.29	Uttar Pradesh	399	COGG.408	Tamil Nadu
365	Agasthiyalingapuram	Tamil Nadu	400	LM.308	Punjab
366	Ilangai-1	Srilanka	401	LM.71	Punjab
367	Ilangai-2	Srilanka	402	LM.169	Punjab
368	Muthiavaraikal	Tamil Nadu	403	PLS.269(S)	New Delhi
369	V.5197	Taiwan	404	PLS.269(D)	New Delhi
370	Vellurior	Taiwan	405	PLS.304	New Delhi
371	M.980	Maharastra	406	EC.118898	Taiwan
372	M.986(S)	Maharastra	407	PLS.167	New Delhi
373	M.986(D)	Maharastra	408	V.109	Taiwan
374	K M 1	Tamil Nadu	409	AC.172	Tamil Nadu
375	H. 70/16	Haryana	410	A C.176	Tamil Nadu
376	T1	Punjab	411	COGG 236	Tamil Nadu
377	LM.14	Punjab	412	AVT/RMI-6	Uttar Pradesh
378	V.4718	Taiwan	413	LM.366	Punjab
379	EC.118889	Tiwan	414	PLS.269A	New Delhi
380	LM .171	Punjab	415	COGG.123	Tamil Nadu
381	ML.267	Punjab	416	LM.253	Punjab
382	PLS.319	Punjab	417	LM.18	Punjab
383	AC.263	Tamil Nadu	418	PLS.315A	New Delhi
384	LM.4	Punjab	419	COGG.412(GY)	Tamil Nadu
385	MS.8909	Maharashtra	420	12-Jun	Tamil Nadu
421	J.45	Tamil Nadu	456	CC.192	New Delhi
422	Hyderabad 1	Andra Pradesh	457	PLS.419/1	Punjab
423	AVRDC1785/5	Taiwan	458	Pusa.102	New Delhi
424	LM.18A	Punjab	459	S.61	New Delhi
425	LM.253	Punjab	460	824	New Delhi
426	COGG 123A	Tamil Nadu	461	S.5	New Delhi
427	CO 4	Tamil Nadu	462	PLM.50	Punjab
428	1734	Tamil Nadu	463	S.1	Punjab
429	AVT/RMI-9	Uttar Pradesh	464	Pusa.101	New Delhi
430	S.13	New Delhi	465	T.3485/1(D)	Uttra Pradesh
131	1979/1	New Delhi	466	AVT.OISM 10	Uttar Pradesh
432	1725	New Delhi	467	Pusa 196	New Delhi
433	MG.50-10G	Gujarat	468	PHM.32	Punjab
434	PBS-1	Tamil Nadu	469	M.1	Maharashtra
435	P.46	Punjab	470	PLM.501	New Delhi

436	MDU.3385	Tamil Nadu	471	Vijayapuri	Tamil Nadu
137	V.3495	Taiwan	472	LM.469	Punjab
438	Glanger	Taiwan	473	LM.228	Punjab
439	CRS .55	Taiwan	474	LM.150(Late)	Punjab
440	TAP.7(S)	Andra Pradesh	475	NA.5	Tamil Nadu
441	TAP.7(D)	Andra Pradesh	476	M.9	Maharastra
442	MG.122	Gujarat	477	ADT.2	Tamil Nadu
443	H.76-27	Haryana	478	ADT.3	Tamil Nadu
444	Madura moong	Uttra Pradesh	479	AG.2080	Taiwan
445	PS.11	New Delhi	480	EC.170300	Taiwan
446	S.28	New Delhi	481	MG.161	Gujarat
447	S.15	New Delhi	482	ML.326	Punjab
448	Pusa .103	New Delhi	483	ML.405(S)	Punjab
449	TNAU26	Tamil Nadu	484	ML.405(D)	Punjab
450	MG.143	Gujarat	485	MH.85-111	Maharastra
451	MG.123	Gujarat	486	NDM 5-3	Punjab
452	Velampatti.A	Tamil Nadu	487	PS.16 (Early)	New Delhi
453	No.822	New Delhi	488	PUM.6	Uttra Pradesh
454	S.4	New Delhi	489	PDM.2	Uttra Pradesh
455	118892(B)	New Delhi	490	PDM.54	Uttra Pradesh
491	PDM.216	Uttra Pradesh	526	VGG 4	Tamil Nadu
492	PDM.219	Uttra Pradesh	527	V.1388	Taiwan
493	PDM.84-146	Uttra Pradesh	528	AVT OISM 22	Uttar Pradesh
494	PDM.84.164	Uttra Pradesh	529	VC.1163(D)	Taiwan
495	PDM.84.178	Uttra Pradesh	530	VC.1007A	Taiwan
496	PDM.85.199(S)	Uttra Pradesh	531	WGG.2	Andra Pradesh
497	PDM.86.199(S)	Uttra Pradesh	532	WGG.19	Andra Pradesh
498	BDYR.3	Uttra Pradesh	533	WGG.37	Andra Pradesh
499	Pusa 118	New Delhi	534	WBM.202(GY)	West Bengal
500	Pusa 121	New Delhi	535	WBM.204	West Bengal
501	Pusa 122	New Delhi	536	COGG.407	Tamil Nadu
502	Pusa SR.22	New Delhi	537	AC.42	Tamil Nadu
503	Pusa 8731	New Delhi	538	ML.2	Punjab
504	Pusa 9871	New Delhi	539	PLS.276/1	New Delhi
505	Pusa 8972	New Delhi	540	PLS.4	New Delhi
506	Pusa 8973	New Delhi	541	PLS.5	New Delhi
507	Pusa 8974	New Delhi	542	PLS.339	New Delhi
508	Pusa 9031	New Delhi	543	COGB.2	Tamil Nadu
509	Pusa 9032	New Delhi	544	SPS.COGG.902	Tamil Nadu
510	Pusa 9033	New Delhi	545	ML.192/1/1(D)	Punjab
511	Pusa 9034	New Delhi	546	COGB.17	Tamil Nadu
512	LGG 50	Andra Pradesh	547	COGB 9	Tamil Nadu
513	LGG.407	Andra Pradesh	548	K 1	Tamil Nadu
514	LGG.410	Andra Pradesh	549	NARP.4	Tamil Nadu
515	LGG.450	Andra Pradesh	550	BG.62	Bungaladesh
516	RMG.266	Rajasthan	551	LM.275/1(S)	Punjab
117	MCP/BDYR-2	Rajasthan	552	AG.2016	Tamil Nadu
518	SML.100	Punjab	553	AG.2080	Tamil Nadu
519	SML.119	Punjab	554	MS.9331	Maharastra
520	SML.130	Punjab	555	V.5200	Taiwan
521	SML.134	Punjab	556	KM.1 (S)	Tamil Nadu
522	KGG.373	Tamil Nadu	557	KM.2	Tamil Nadu
523	KGG.374	Tamil Nadu	558	ML.6/1(S)	Punjab
524	TARM.22	Maharashtra	559	CO.3 (B)	Tamil Nadu
525	VGG.3	Tamil Nadu	560	CO.5 (BOLD)	Tamil Nadu
561	PDM.90.239	Punjab	591	PUSA-103	New Delhi
562	GM.8906	Gujarat	592	EC.396097	Taiwan
563	PDM.89.227	Punjab	593	EC. 396098	Taiwan

564	GM.89.10	Gujarat	594	EC396099.	Taiwan
565	GM.84.2	Gujarat	595	EC.396100	Taiwan
566	GM.86.17	Gujarat	596	EC.396101	Taiwan
567	HUM.1	Uttra Pradesh	597	EC.396102	Taiwan
568	HUM.2	Uttra Pradesh	598	EC. 396103	Taiwan
569	PDM90.237	Punjab	599	EC.396104	Taiwan
570	PDM 90.239	Punjab	600	EC.396105	Taiwan
571	PUSA M.9132	New Delhi	601	EC.396106	Taiwan
572	UPM 89.8	Uttrra Pradesh	602	EC.396107	Taiwan
573	MG.368	Gujarat	603	EC.396108	Taiwan
574	PDM.89-224	Uttra Pradesh	604	EC.396109	Taiwan
575	SML.168	Punjab	605	EC.396110	Taiwan
576	SML.171	Punjab	606	EC.396111	Taiwan
577	SML.191	Punjab	607	EC.396112	Taiwan
578	PDM.84.143	Uttra Pradesh	608	EC.396113	Taiwan
579	LGG.429/1	Andra Pradesh	609	EC.396114	Taiwan
580	LGG.429/2	Andra Pradesh	610	EC.396115	Taiwan
581	LGG 429/3	Andra Pradesh	611	EC.396116	Taiwan
582	PS.16/1	New Delhi	612	EC.396117	Taiwan
583	VGG.6	Tamil Nadu	613	EC.396118	Taiwan
584	VGG.7	Tamil Nadu	614	EC. 396119	Taiwan
585	TARM.2/2	Maharashtra	615	EC.396120	Taiwan
586	Srivilliputhur	Tamil Nadu	616	EC.396121	Taiwan
587	MGG.329/1	Andra Pradesh	617	EC.396122	Taiwan
588	TARM2/1	Maharastra	618	EC.396123	Taiwan
589	VBN.1 (D)	Tamil Nadu	619	EC.396124	Taiwan
590	PUSA -9171	New Delhi	620	EC.396125	Taiwan
621	EC.396126	Taiwan	634	PDM.54-1	Uttra Pradesh
622	NARP.3	Tamil Nadu	635	VC.6370-30-65	Taiwan
623	Parjula	New Delhi	636	RMG.226/1(S)	Rajastahan
624	S.1/1(S)	Uttra Pradesh	637	NM.94	Taiwan
625	LM.392/1(B)	Punjab	638	VC.6368(46-40-4)	Taiwan
626	1789/3/1(S)	Punjab	639	VC.6369(5397)	Taiwan
627	MGG.336	Andra Pradesh	640	KPS.2	Kerala
628	BINA MUNG-2	Maharashtra	641	VC.6370-A	Taiwan
629	BARI MUNG-2	Maharashtra	642	VC.6173 B-10	Taiwan
630	LM.214/1(D)	Punjab	643	HARSHA	Tamil Nadu
631	PDM.11	Punjab	644	MDU.3486/1	Tamil Nadu
632	SML.32	Punjab	645	VBNG(g) 2 -1	Tamil Nadu
633	SML.134	Punjab	646	RRMI-10 (AVT)	Uttra Pradesh

Number of branches per plant, Length of branch (cm), Days to initial flowering, Days to 50 per cent flowering, Number of clusters per branch, Number of clusters per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Seed length (cm), Seed breadth (cm), Hundred seed weight (g), Single plant yield (g) , Dry matter production (g), Days to initial maturity and Days to full maturity

Statistical Analysis:

Hierarchical Cluster Analysis

The data on the 18 quantitative traits for all the 646 accessions were subjected to multivariate hierarchical cluster analysis. The mean data over two seasons and replications were computed. For hierarchical cluster analysis, the computer software NTSYS pc was used (Rohlf, 1992). A phenetic tree was constructed using the TREEPLOT programme of NTSYS pc after standardization of the data.

Principal Component Analysis (PCA):

The PCA was performed as adopted by Bisht (1998) in order to confirm the diversity patterns brought out by cluster analysis. The cumulative percentage contribution to variation of different traits to Eigen vector were also computed.

Derivation of Core Collection:

The size of core collection was fixed at 65 (approximately 10 per cent of base collection), which is manageable size at a relatively low cost of maintenance. The selection of the core was done based on the combination of logarithmic strategy (L) and Relative Diversity (RD) method as described by Diwan *et al.*

(1995) which considered the variation inside the group prior to the selection of the accession. The scheme consisted of cluster analysis within a group identifying as many clusters as accession of the group correspond to be selected to constitute the core, and then one accession from each cluster is selected at random. Cluster analysis was performed using UPGMA method with the squared Euclidian distance. The steps involved in building the core were as follows

Steps:

- Fixing the size of core collection at 10 per cent level as suggested by Brown (1989 a)
- For fixing the number of accessions for each cluster resulting from cluster analysis, logarithmic strategy suggested by Brown (1989 b) was adopted. The logarithmic strategy adopted is as follow
- Performing second level of cluster analysis (cluster within cluster) for further assortment of accessions.
- Selection of accessions as fixed in step 2 from each second level cluster at random. These accession put together constitute core.

$$S = \frac{\log p^{i}}{\sum_{m}^{t=1} \log p} \times n$$

where

S – *number of accessions selected in a character*

p – *size of the cluster*

P^{i} – *proportion of* i^{th} *cluster*

n – *Number of accessions to be selected for core* (10% *base collection i.e.* 65)

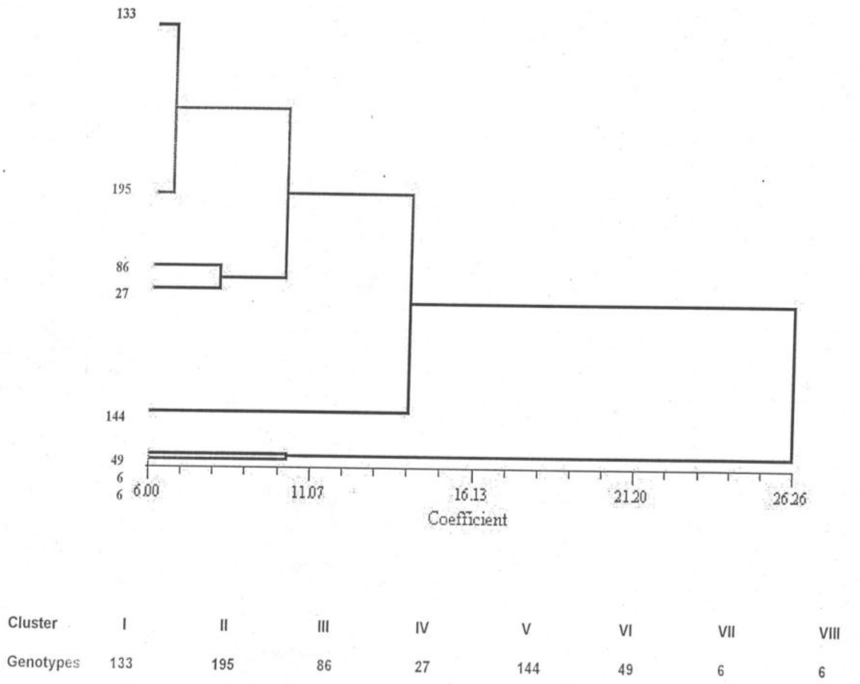
m – *total number cluster*

Calculation of Range Retention:

The principle idea of constituting a core collection is to represent maximum possible variability within a small collection of accessions. In order to assess the validity of the core collection made, it is imperative to assess the variability available in the core in relation to that of base collection which is assessed by the parameter range retention (Diwan *et al.*, 1995) .Range retention is computed as follows for all the 18 quantitative traits.

The extent of variability retained by the core for 35 qualitative traits was also assessed by Shannon diversity index (SDI) as suggested by Shannon and Weaver (1963). The SDI_i for the i^{th} qualitative characters was computed as follows

Results:



Cluster	I	II	III	IV	V	VI	VII	VIII
Genotypes	133	195	86	27	144	49	6	6

Fig 1. Phenetic tree depicting the clustering pattern of 646 greengram base collection accessions

In the present investigation, 646 greengram accessions were subjected to multivariate analysis. Distinct clusters were identified based on cluster and principal component analysis.. Parents selected from different clusters were selected and crosses were effected Genetic divergence, the germplasm 646 green gram accessions were subjected to multivariate analysis to estimate the level of genetic diversity. For this two approaches namely *viz.,* Hierarchical Cluster Analysis (HCA) and Principal Component analysis (PCA) were used. Hierarchical cluster analysis (HCA**)** the result of HCA utilizing 18 quantitative traits on 646 germplasm accessions is presented as a dendrogram (Fig 1). Eight distinct clusters could be recognized from the tree. The composition of clusters is presented in Table. 1. The cluster II, V and I were large with 195, 144, and 133 accessions respectively while the cluster III, VI and IV were medium sized with 86, 49 and 27 accessions respectively. The cluster VII and VIII were the smallest with 6 accessions each.

$$SDI^{i} = \sum_{j=1}^{d_i} p_{ij} \log p_{ij}$$

d_i – being the descriptor state for i$^{\text{th}}$ descriptor

p_{ij} – the proportion of accessions for j$^{\text{th}}$ descriptor state of i$^{\text{th}}$ descriptor.

Table 1: Distribution of 646 accessions of greengram base collection for different clusters

Cluster	No. of Accession	Accession Number
I	133	1,564,24,341,386,511,21,524,25,351,530,172,354,324,334,3,497,456,500,150,153,507,312,336,399,29,290,174,184,358,408,175,343,385,640,498,187,361,582,369,333,335,368,402,583,512,2,631,137,628,120,322,390,494,163,340,419,84,128,227,140,633,180,431,364,585,565,611,26,178,183,209,328,103,323,533,392,421,30,296,303,307,586,32,119,382,233,302,91,319,96,186,367,243,38,79,448,105,225,215,542,301,393,434,240,253,460,355,372,379,136,255,377,4,164,210,213,501,627,562,383,489,514,645,510,529,156,315,531,23,19, 46,403
II	195	203,239,223,374,366,320,332,20,159,220,237,550,625,48,196,459,234,569,622,95,346,115,289,363,144,201,316,130,297,398,375,405,33,360,477,106,182,45,587,247,362,413,304,99,236,216,147,329,580,339,291,61,493,257,345,526,581,139,321,389,151,211,305,350,86,87,88,342,629,451,444,50,160,12,344,35,195,551,418,121, 443,188,254,561,55,485,574,480,420,185,238,59,85,544,577,97,296,54,63,472,337,70,7,18,27,194,414,251,349,404,464,94,559,537,357,454,7,10,82,198,547,56,424,57,126,108,425,423,463,566,48,646,11,436,34,432,435,468,433,563,356,299,505,541,482,539,76,83,536,560,567,430,6,124,310,427,13,338,40,4,14,473,78,232,326,540,44,51,170,318,387,47,441,179,438,245,409,571,327,401,380,437,36,447,412,442,426,453,538,553,58,117,546,249
III	86	578,407,42,110,330,570,53,104,113,395,90,522,446,161,400,548,568,219,579,572,17,65,67,9,231,294,557,347,428,197,248,222,226,417,12,406,77,235,410,73,308,92,242,306,359,370,317,49,429,623,31,260,348,277,449,15,101,43,141,41,66,93,112,397,440,116,252,64,123,131,39,556,462,80,470,545,250,543,584,37,552,75,16, 122,230,411
IV	27	132,8,206,176,626,193,177,415,624,558,60,102,158,644,143,246,309,488,373,554,166,157,259,169,589,276, 261
V	144	266,62,129,146,461,69,72,125,465,450,452,535,28,313,311,515,314,643,516,481,142,528,457,154,171,325,590,165,635,384,518,466,394,492,487,591,612,532,149,479,504,156,168,513,467,509,98,228,388,549,597,608,641,214,523,109,189,474,300,598,221,458,639,471,200,439,602,642,293,609,576,118,603,615,52,207,422,114,376,555,81,107,445,217,490,573,378,506,575,476,22,416,190,371,138,181,204,630,241,396,508,525,588,111,212,224,331,455,148,191,496,202,258,288,475,527,495,68,519,520,521,517,192,292,391,502,134,365,208,135,167,127,173,133,353, 155,483,486,499,607,610,491,503,613
VI	49	595,643,601,268,534,218,484,617,618,632,619,244,592,638,636,599,637,593,594,600,606,605,620,621,614,596, 616,89.100,145,298,469,256,273,275,283,269,279,265, 285,281,282,278,280,286,604,287,199,205
VII	6	262,263,267,229,271,264
VIII	6	284,270,272,274,381,352

Principal Component Analysis:

The PCA revealed that the first three principal components accounted for 33.61, 15.69 and 11.16 per cent of the total variability respectively, cumulatively accounting for 60.47 per cent (Table. 2). Principal component analysis scatter plot of first three PCA axes is shown in Fig.2. The distribution of accession along this axes confirmed the grouping obtained through hierarchical cluster analysis.

Table 2: Extraction of principal component for base collection

PC Axes	Eigen Value	Variance (%)	Cumulative Eigen Value	Cumulative Variance (%)
I	6.05	33.61	6.05	33.61
II	2.82	15.69	8.87	49.31
III	2.00	11.16	10.88	60.47

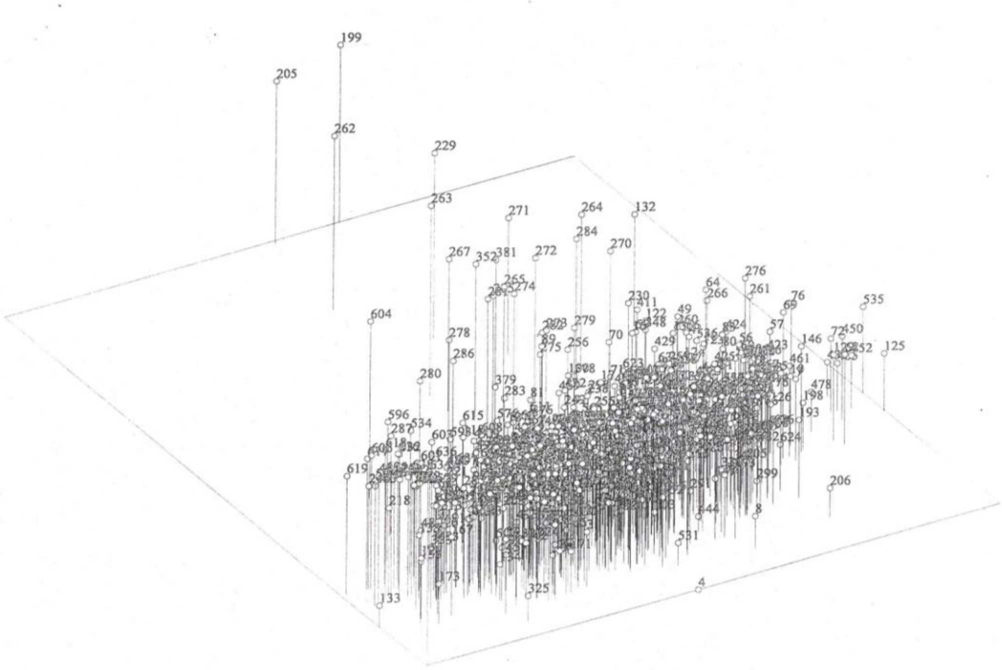


Fig 2. Three dimentional ordination of 646 greengram germplasm accessions

The size of the core collection was fixed at 65 (approximately 10 per cent of the base collection) which is a manageable size at a relatively low cost. Selection of accession to form the core was worked out using the relative diversity method, which consisted cluster analysis within the clusters of the base collection and then identifying as many clusters as that of the number of accession of the group corresponding to the selected, to constitute the core and then selection of one accession from each cluster at random. For fixing the number of accessions the logarithmic strategy was adopted. The results of the cluster analysis performed within the first level clusters along with the accessions selected adopting logarithmic strategy. Ten accessions selected each from cluster I and III ,11 accessions each from cluster II and V and four accessions each from cluster VII and VIII were selected a apice. The remaining fifteen accessions were selected from cluster IV and VI, and this constituted a total of 65 accessions in the core collection.

Table 6: Original cluster size and log value of each cluster for selection of core collection

Cluster	Original size	Log value	Proportions of log value	No. of accessions to be selected	No. of second level cluster formed	No. of accession selected from each cluster	Accession number
I	133	2.12	0.16	10	10	1	21,23,32,38,128,164,240,377,582,645
II	195	2.29	0.17	11	11	1	130,162,198,374,412,418,427,436,505,526,560,
III	86	1.93	0.14	10	10	1	16,67,93,131,330,348, 406,411,543,548

IV	27	1.43	0.10	7	7	1	8,60,132,259,276,488,558
V	144	2.15	0.16	11	11	1	28,62,68,72,133,138,207,224,266,293,523,
VI	49	1.69	0.12	8	4	2	89,205,256,280,287,285,619,620,
VII	6	0.77	0.05	4	2	2	229,262,264,267
VIII	6	0.77	0.05	4	2	2	270,272,352,381
Total	646	13.18		65			65

Discussion:

The present investigation for evaluation of the existing germplasm collections for qualitative traits for base and establishment of a base collection for this germplasm representing wide genetic diversity. The genetic diversity an improvement in yield and quality of a self pollinated crop like greengram is normally achieved through selection of genotypes with desirable characters from the germplasm or by creating variability through hybridization. Among these two approaches, the latter is widely followed by the pulse breeders, as it is possible to combine desired characters and develop superior ideotypes with maximum yield. The success of hybridization programme depends upon selection of suitable parents which are genetically diverse from the existing germplasm. Hence for selection of genetically diverse parents from the germplasm it is essential that the collection should be systematically characterized using descriptors encompassing both quantitative and qualitative traits. In addition to this systematic characterization, the development of a core collection or working germplasm representing maximum diversity in the base collection will be of immense practical utility for mungbean improvement. Hence a core collection was established in this investigation, following recommended scientific principles.

The core collection concept was first suggested by Frankel and Brown (1984) who defined it as a representative sample of the base collection where, as much as possible of the diversity in the base collection is retained with minimum redundancy. For developing a core collection from the existing germplasm a number of methods has been proposed by many workers. Among them, the method suggested by Diwan *et al.*, (1995) which combine the logarithmic method of stratification and relative diversity principle of selection that takes into account the morphological diversity of different strata has been recommended as the best approach for developing better core with maximum diversity by Malosetti and Abade (2001).

By applying this strategy in the existing 646 germplam accessions a core collection consisting of 65 (approximately 10 per cent) diverse accessions were constituted in this investigation. Constituted core collection was tested for proportion of variability of the base collection, represented by two statistical parameters *viz.*, average range retention and Shannon diversity index (Shannan and Weaver, 1963). Computed values of average range retention for quantitative traits suggested by Diwan *et al.* (1995) as well as Shannon diversity indices for qualitative traits were high indicating that the established core collection represented majority of genetic variation present in base collection.It is envisaged (Marshall, 1989) that core collection concept will receive priority in evaluation and characterization, so that in a short time, a large number of traits would be evaluated at different locations. This could lead to a better understanding of genetic structure of the crop and promote the exchange of information and material, thus facilitate the use of the core collection. Mackay (1995) has discussed the practical application of core collection and the possible inclusion of core collection principles into gene bank information management systems.

Conclusion:

With the objectives to constitute a core collection the available 646 germplasm accessions of greengram were characterized for 18 quantitative traits. Two multivariate statistical approaches *viz.*, Hierarchical cluster analysis and Principal component analysis were utilized of the base collection). The value of average range retention for quantitative traits were high in magnitude indicating that the core represented the majority of variability of the base collection.The cluster mean performance for 18 quantitative characters in the core revealed high mean performance for the characters namely plant height, number of branches per plant , length of branch, number of clusters per branch, number of clusters per plant and number of pods per plant registered by cluster VI among the nine clusters. The cluster IV exhibited highest mean value for the characters, length of pod, seed length and seed breadth. Among the nine clusters, the cluster VII registered the highest mean performance for many traits namely number of seeds per pod, dry matter production, protein content, days to initial flowering, days to 50 per cent flowering, days to initial maturity and days to full maturity. Clusters VIII and I registered highest mean value for hundred seed weight and single plant yield respectively. Hence the accessions of these clusters can be utilized for hybridization programme.

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