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Research Article

Morphological characterization and assessment of genetic diversity in minicore collection of pigeonpea [*Cajanus Cajan* (L.) Millsp.]

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Abstract
An investigation was undertaken to ascertain the extent of genetic diversity present among 196 pigeon pea genotypes using D^2 statistic. A wider genetic diversity was observed for nine characters as evidenced by formation of 13 clusters. Number of pods per plant contributed most (59.83%) towards divergence, followed by plant height (21.55 The highest inter cluster distance was observed between the cluster XIII and VII, followed by cluster V and XIII, II and XIII and cluster XII and VII, which indicates that the crosses among the genotypes between these clusters may result in better segregants and high heterotic combinations. Cluster mean analysis indicated that cluster V contains dwarf and early maturing genotypes and cluster XIII possess high yielding entries. Morphological characterization was also carried out for 15 traits can be used in varietal purification and seed production.

Key words: Pigeon pea, *Cajanus cajan*, mini core, genetic diversity, morphological characterization

Introduction

Pigeon pea (*Cajanus Cajana.* (L.) Millsp.) is one of the major food legume crops of both tropics and subtropics. It is drought tolerant and exhibits a large variation for physiological maturity, cultivated in a total area of 4.92 million ha, globally, with an annual production of 3.65 million tons (mt) and productivity of around 900 kg/ha. India has 3.90 mha (≈ 80% of world acreage) with a total production and productivity of 2.89 mt (≈ 79% of world production) and around 750 kg/ha respectively (http://www.faostat.fao.org). The productivity is 150 kg/ha lower compared to global average. This crop has a wider adaptation to a range of environments and cropping systems. Four maturity groups have been identified *viz.,* extra early (90-120 days), early (120-150 days), medium (150-200 days) and late (200-300 days), that has direct relevance on the survival and fitness of the crop in different agro ecological situations (Choudary *et al.,* 2011).

Germplasm collections coupled with unavailability of passport data, has resulted in lower usage (<1%) of germplasm and narrow down the genetic base in many crops. Off late, germplasm collections in many crops with almost full representation of genetic diversity in the form of minicore (~1% of the core collection) approach has been an effective methodology to enrich and enhance crop improvement programs (Upadhyaya *et al.,* 2010). The mini core provides a means for accessing the larger collections for further exploration and also helps in proper assessment of genetic diversity, population structure, association mapping and targeted gene mining. Use of mini core approach will lead to greater utilization of diverse germplasm for developing broad-based cultivars, especially in the context of climate change. However, characterization of minicore collection across environments, is a fundamental step, though seems routine, but is vital. Most often, a set of locally collected germplasm are augmented along with the minicore while assessing. This helps in identification of location specific genotypes.

Success of crop improvement program, in any crop *vis a vis* pigeon pea, depends on genetic diversity and extent of available variability, which directly affects choice of parents for hybridization and selection procedures adopted. Multivariate analysis by D^2 statistics is proved more often to be a powerful tool in quantifying the genetic divergence within a set of genotypes. The concept of genetic distances has been vital in many contexts and more so in differentiating well defined populations (Arunachalam, 1981). In addition, characterization of genotypes using morphological characters; those are stable across environments owe to oligogeneic nature. Hence, they serve as morphological marker in breeding which can be used in varietal or genotypic identification, varietal purification and even in

seed production. Keeping above points in view, the present investigation was chosen to study genetic diversity among a set of genotypes and categorize these genotypes based on morphological characters.

Material and Methods

Investigation was carried out, during *kharif* 2012-13 at Pulse Research Institute, Agricultural Research Station (ARS) Gulbarga, which is situated in North Eastern Dry Zone (Zone-2) of Karnataka between latitude (N) 17^0 35' and longitude (E) 76^0 81'. The experimental material comprised of 191 minicore collections with five check varieties viz., ICPL-87119 (Asha), WRP-1, TS3R, BSMR-736 and ICP-8863 (Maruti). This minicore consist of 94 genotypes received from International Crop Research Institute for Semi Arid Tropics (ICRISAT), Patancheru (Andrapradesh), 81 genotypes received from Indian Institute of Pulses Research Institute, Kanpur, (Uttarpradesh) and 21 local collections of Gulbarga district of Hyderabad-Karnataka region from the Pulse Research Institute, ARS, Gulbarga.

The experiment was laid out in Lattice Design (14 x 14) with two replications. Each genotype was sown in 2 rows of 4 meter length with a spacing of 90 cm and 30 cm between rows and plants respectively. Agronomic practices were adopted during the crop growth period as per the package of practice recommended by UAS, Raichur. Observations were recorded for nine quantitative traits on five randomly selected plants from each genotype, *viz.*, plant height, number of branches, pod bearing length, number of pods per plant, number of seeds/pod and seed yield per plant. While, days to 50% flowering, maturities and 100-seed weight were recorded on the plot basis. The analysis of variance was carried out for all characters individually. Multivariate analysis and clustering was carried out using WINDOSTAT ver 8.5 software developed by Indostat services, Hyderabad as per the principles of Mahalanobis (1936) and clustering by Tocher's method (Rao,1952). Morphological characterization of 15 characters (qualitative and quantitative) of all the genotypes was carried out as per the key guidelines provided by PPV & FR (Protection of Plant Varieties and Farmer Rights) Authority, New Delhi.

Results and Discussion

All 196 genotypes could be grouped in to 13 clusters Cluster I was the largest, comprising 80 genotypes (38 and 34 entries from ICRISAT and IIPR, Kanpur respectively and 8 from PRI, Gulbarga), followed by cluster III (51 genotypes) 28 from ICRISAT, 18 from IIPR, Kanpur and 5 from PRI, ARS, Gulbarga, cluster II (20 genotypes) almost equal frequencies from all institutes, cluster V (17 genotypes) most entries from IIPR, Kanpur, cluster VII (9 genotypes), cluster IV (7 genotypes) and cluster XIII (6 genotypes). Six clusters (VI, VIII, XI, X, XI, XII) had solitary entries mostly from ICRISAT (Table 1). Formation of more clusters in general and solitary clusters in particular is an indicative of existence of enormous amounts of diversity among the set of genotypes. The genotypes that fall into solitary clusters more often have some unique characters which make them divergent. Additionally, the genotypes in a single cluster exhibit narrow range of genetic diversity among them, while between clusters indicate a wider range of variability depending on the intra and inter cluster distances. Generalized distance (D) varied from 21.81 to 147.38 (Table 2) indicating enormous diversity among the genotypes. The result was in line with the observation of Katiyar *et al*. (2004), where they observed grouping of 221 genotypes into 14 clusters. Thombre *et al.* (2000), observed 15 clusters in 64 genotypes of pigeonpea.

The intra cluster distance was maximum for cluster VII (51.96), with 9 genotypes, followed by cluster XIII (45.29), cluster V (44.69), cluster III (31.16), cluster IV (30.6), cluster II (29.36) and cluster I (29.05). It was interesting that despite with 80 genotypes, the intra cluster distance of Cluster I was the least possibility of inclusion of sister lines or genetically very similar lines in the mini core collection cannot be precluded. The highest inter cluster distance (147.38) was observed between the cluster XIII and cluster VII, followed by cluster XIII and V (138.83), cluster XIII and II (138.21), Cluster XII and VII (125.03) (Table 2). It suggested that the selection of genotypes from these divergent groups would yield higher magnitude of heterosis or even a chance to recover transgressive sergregants for specific characters concerned. Crossing of genotypes from cluster XIII with genotypes of cluster VII would be ideal to realize heterosis. The lowest inter cluster distance was between cluster IX and XII (21.81), indicate the closer relationship among the genotypes between these clusters. It can be opined that for most characters there was no much phenotypic differences. Selection of genotypes with short inter cluster distance may not be desirable to get higher yield benefits and this is attributable to smaller allelic frequency differences between these genotypes, which results in lower heterotic progenies. The possibility of high inbreeding depression cannot be excluded. These results were in agreement with the earlier findings of Sreelakshmi *et al.* (2010) and Patel and Acharya (2011).

Cluster mean analysis indicated that the cluster V had dwarf, early flowering, early maturing and low test weight genotypes. Cluster XIII had entries with maximum pod bearing length, number of pods per plant and in addition to high

yielding. Cluster X and XI had entries with high test weight but were late maturing (Table 3). Based on the maximum inter cluster value and *per se* performance for seed yield, number of pods per plant and test weight, the genotypes GRG 281-1, ICP-13673 and ICPB-2043 were found desirable. Singh *et al*. (2010) and Bhadru (2011) obtained similar results as that of present for pods per plant and seed yield per plant. It was interesting that the means of clusters were exhibiting relatively large variation for characters such as days to flowering and maturity, number of pods per plant, plant height, branches/plant and pod bearing length. However, for number of seeds per pod, there was no difference between clusters mean indicate that the seed per pod has not changed through the domestication process or naturally. Further, it was exemplified that the contribution of seeds per pod towards genetic divergence is negligible (0.51). Thimmaraju (2012) was also observed low contribution (2.08 %) while Nethravathi (2013) noticed zero per cent contribution of seeds per pod towards divergence.

Among nine characters studied, number of pods per plant contributed most (59.83%) towards divergence, followed by plant height (21.77%), pod bearing length (8.08 %) and days to maturity (6.96 %). Intriguingly, these four traits could contribute up to 97% diversity. The contribution of rest of the traits was negligible (Table 4 and Fig 1). Variation for number of pods per plant is the main trait while assessing the diversity of Pigeon pea germplasm. Shreelakshmi *et al.,* (2010) reported major contribution of number of pods per plant towards divergence is in accordance with the present finding.

Morphological characterization indicated that characters like determinate growth habit can be successfully used to differentiate ICP-7148 and GC-11-39 from rest of the genotypes. Further, the oblong leaf shape could separate ICP-7148 and Gulyal (a land race from Gulbarga region of Karnataka) from rest of the entries. Anthocyanin colour on hypocotyl was observed in seven out of 196 genotypes. Similarly the characters like purple stem colour, red coloured base petal, purple pod, short plant type (<100 cm), small seed size (< 7 gram) and very large seed size (> 11 gram), absence of pod waxiness and pod stickiness were found in limited number of genotypes. Seed characters like, colour, colour pattern and seed shape can also be used to characterize genotypes (Table 5), which helps in varietal or genotype identification and serves as morphological indicators in breeding at field level. Unlike quantitative characters, morphological traits are less influenced by the environment. Hence, they may serve as morphological markers in varietal identification, thus helps in purification of a variety. Phillip (2002) evaluated 28 accessions for 23 descriptors and observed leaf pubescence in all genotypes. However, in the present set of genotypes, leaf pubescence was not observed.

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Table 1. Grouping of pigeon pea genotypes in to clusters based on the source of seed supply.

Cluster	No. of Genotypes	Source of seed supply	Genotypes
I	80	38 ICRISAT	ICP-655, ICP-939, ICP-995, ICP-1126, ICP-4317, ICP-4392, ICP-4715, ICP-6370, ICP-6668, ICP-6845, ICP-6859, ICP-7314, ICP-7869, ICP-8152, ICP-8255, ICP-8266, ICP-8700, ICP-8840, ICP-8860, ICP-8949, ICP-9336, ICP-9655, ICP-9691, ICP-9750, ICP-10228, ICP-10503, ICP-11015, ICP-11059, ICP-11320, ICP12410, ICP-13270, ICP-14638, ICP-14832, ICP-14900, ICP-14976, ICP-15049, ICP-15185, ***ICP-87119(ASHA)(check),***
		34 IIPRI, Kanpur	AK-022, AK-101, AKP-1, AKT-9913, AKT-9915, AL-1855, BPG-51-3, BSMR-853, CO-5, CORG-9701, GPHR-08-11, GT-1, IUPL-332, JPB-109B, PT-002-2, PT-002251, PUSA-2001, PUSA-991, RVK-273, RVK-281, RVK-282, RVK-284, RVK-285, RVK-286, RVK-287, RVKP-260, RVKP-261, RAJA,TAT-9903, TTB-7,TV-1,UPAS-120,VIPUL, ***WRP-1(check),***
		08 PRI, ARS, Gulbarga	CHAPLE, GC-11-39, GRG-2009-1, GRG-2009-3, GRG-333, GRG-2010, PG-12, ***TS3R (check),***
II	20	07 ICRISAT	ICP-11477, ICP-11543, ICP-13579, ICP-13633, ICP-16309, ICP-2746, ICP-3046
		07 IIPRI, Kanpur	BWR-153, GT-101, JAMADAR LOCAL, JKM-189, JKM-7, K-2, TJT-501,
		06 PRI, ARS, Gulbarga	GRG-276-1,GRG-2012, GRG-818,GRG-109,GRG-107, GRG-825,
III	51	28 ICRISAT	ICP-11910, ICP-11946, ICP-12680, ICP-1279, ICP-13304, ICP-13571, ICP-14471, ICP-14701, ICP-14722, ICP-16264, ICP-2698, ICP-4029, ICP-4167, ICP-4307, ICP-4575, ICP-4903, ICP-5142, ICP-6049, ICP-6739, ICP-6815, ICP-6929, ICP-6971, ICP-7035, ICP-7057, ICP-7148, ICP-7221, ICP-7366, ICP-7803
		18 IIPRI, Kanpur	AKT-8811, AL-1794, AL-201, BAHAR, BANAS, BPG-51-2, BRG-109, C-11, MAL-13, PUSA-9, RVK-272, RVK-274, RVK-275, RVK-277, RVK-278, RVK-279, RVK-280, RVK-283,
		05 PRI, ARS, Gulbarga	GRG-811, GRG-815, GRG-2009, GRG-822, GRG-2012,
IV	7	07 ICRISAT	ICP-1156, ICP-11690, ICP-12515, ICP-12596, ICP-12654, ICP-13191, ICP-7223
V	17	02 ICRISAT	ICP-3451, ICP-348
		14 IIPRI, Kanpur	BDN-2, BDN-2004-3, BDN-2008-1, BDN-2008-12, BDN-2008-7, BDN-2008-8, BSMR-533, LRG-38, NDA-1, PKV-TARA, PT-04-31, PUSA-2001, VKS-11-24-2, WRG-27,
		01 PRI, ARS, Gulbarga	GRG-206,
VI	1	01 IIPRI, Kanpur	IPPFC-43
VII	9	05 ICRISAT	ICP-8793, ICP-8757, ICP-14229, ICP-9414, ICP-8227
		02 IIPRI, Kanpur	BIRSA ARHAR-1, ***BSMR-736 (check),***
		02 PRI, ARS, Gulbarga	BENNUR LOCAL, GULYAL RED,
VIII	1	PRI, ARS, Gulbarga	GRG-281-1
IX	1	ICRISAT	ICP-3576
X	1	ICRISAT	ICP-14116
XI	1	ICRISAT	ICP-13673
XII	1	ICRISAT	ICPB-2043
XIII	6	03 ICRISAT	ICP-2577, ICPL-129808, ***ICP-8863 (check)***
		03 IIPRI, Kanpur	BRG-11-01, BDN-2008-9, BDN-708

Table 2. Intra (Diagonal) and Inter cluster distances (D^2 Value).

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	29.05	45.81	74.64	42.46	64.36	34.75	57.96	36.02	75.86	49.11	43.10	86.62	107.67
II		29.36	76.92	56.33	73.88	43.69	43.20	58.86	107.12	67.87	50.76	116.70	138.21
III			31.16	52.73	80.76	62.86	87.36	42.47	43.03	43.66	53.27	53.88	75.18
IV				30.60	89.70	48.67	72.29	59.72	75.55	56.43	50.67	90.54	103.42
V					44.69	56.49	75.04	57.99	107.89	88.78	84.89	111.97	138.83
VI						0.00	54.17	50.28	94.99	71.62	62.75	107.62	125.52
VII							51.96	65.18	116.35	77.0	61.74	125.03	147.38
VIII								0.00	64.85	36.74	40.30	71.26	99.23
IX									0.00	52.46	71.51	21.81	42.34
X										0.00	22.06	60.51	85.00
XI											0.00	80.02	103.28
XII												0.00	47.19
XIII													45.29

Table 3. Cluster means of 13 clusters for 9 quantitative traits in Pigeon pea.

Cluster	Plant height (cm)	Branches/ Plant	Pod Bearing Length	No. of pods /plant	No. seeds/pod	Seed Yield/plant (g)	Days to Maturity	Days to first flowering	Test weight (g)
I	148.9 ± 4.79	19.80 ± 2.19	23.7 ± 5.3	81.4 ± 8.7	3.63 ± 0.30	31.57 ± 1.7	148.4 ± 0.96	97.8 ± 0.85	9.27 ± 0.10
II	151.4 ± 4.21	20.20 ±2.39	13.6 ± 3.2	51.8 ± 7.2	3.36 ± 0.23	21.62 ± 2.0	158.6 ±1.06	107.2 ± 0.58	9.61 ± 0.12
III	148.6 ± 5.60	21.7±2.3	24.8 ± 3.2	117.9 ± 9.9	3.24 ± 0.32	35.38 ± 2.2	145.2 ±1.10	94.6 ± 1.60	8.86 ± 0.15
IV	178.8 ± 4.80	21.3±1.5	23.3 ± 2.7	88.5 ± 13.1	3.19 ± 0.35	32.16 ± 1.9	153.2 ± 0.48	101.4 ± 0.40	8.54 ± 0.04
V	110.2 ± 3.70	11.2±2.5	27.4 ± 3.7	65.5 ± 14.6	3.58 ± 0.28	25.18 ± 2.0	126.8 ± 0.43	76.7 ± 0.27	8.19 ± 0.14
VI	153.70 ± 0	14.3± 0	36.0 ± 0	62.0 ± 0	3.5 ± 0	29.30 ± 0	138.0 ± 0	88.0 ± 0	9.30 ± 0
VII	139.5 ± 3.69	14.5 ± 2.69	18.2 ± 2.6	45.7 ± 9.2	3.59 ± 0.18	23.93 ± 1.4	160.0 ± 0.89	108.89 ± 0.67	9.51 ± 0.10
VIII	123.3 ± 0	23.7± 0	24.7 ± 0	93.3 ± 0	3.80 ± 0	39.0 ± 0	151.0 ± 0	100.0 ± 0	8.43 ± 0
IX	147.7 ± 0	24.0± 0	27.8 ± 0	153.3± 0	3.50 ± 0	42.60 ± 0	151.0 ± 0	100.0 ± 0	8.70 ± 0
X	138.7 ± 0	22.7± 0	16.7 ± 0	111.0 ± 0	3.70 ± 0	37.50 ± 0	171.0 ± 0	118.0 ± 0	11.3 ± 0
XI	143.7 ± 0	19.3± 0	12.3 ± 0	92.30 ± 0	3.50 ± 0	29.50 ± 0	175.0 ± 0	119.0 ± 0	11.1 ± 0
XII	133.0 ± 0	30.3± 0	21.2 ± 0	163.3 ± 0	4.30 ± 0	34.10 ± 0	150.0 ± 0	99.0 ± 0	10.0 ± 0
XIII	158.9 ± 5.07	26.4 ± 2.9	30.7 ±3.9	179.9 ±7.9	3.42 ± 0.78	51.77 ± 1.5	150.3 ± 0.26	99.17 ± 0	8.73 ± 0.18

Table 4. Per cent contribution of each trait towards genetic divergence.

Source	Times Ranked 1st	Per cent contribution	Cumulative contribution
No. of pods per plant	11433	59.83	59.83
Plant height (cm)	4113	21.55	81.38
Pod bearing length	1544	8.08	89.46
Days to maturity	1331	6.96	96.42
Days to 50% flowering	236	1.23	97.65
Seed yield per plant (g)	216	1.15	98.8
No. of seeds per pod	95	0.51	99.31
No. of Branches/plant	94	0.49	99.80
100 seed weight (g)	48	0.20	100.00
Total percentage		100.0	

Table 5. Characterization of 196 pigeon pea genotypes based on morphological characters.

Morphological Characters	Types	No. of genotypes	Example of Varieties
Anthocyanin colour on hypocotyl	Absent	7	BDN-2008-12, BDN-2008-7, BSMR-736 *etc.*
	Present	189	Majority of genotypes had anthocaynin
Plant branching pattern	Erect ($<30^0$)	11	ICP 11320, ICP 12515,ICP 40103, ICP6845, ICP 7035, ICP8152, ICP 8860, ICP 9655 *etc.*
	Semi spreading ($30\text{-}60^0$)	122	Most genotypes were semi-spreading.
	Spreading ($> 60^0$)	63	AL 1794, AL 1855, BDN 2008-9 *etc*
Time of flowering (50% of the Plants with at least one open flower)	Very early (<60days)	4	AL-1794, AL-1855, AL-201, ICP 14229
	Early (61-90days)	36	GC-11-39, GT-1, ICP-11543 *etc.*
	Medium (90-130 days)	156	AKT-8811, AKT-9915, BSMR-853 *etc.*
	Late (131-160 days)	0	Not observed
	Very late (>160 days)	0	Not observed
Plant growth habit	Determinate	2	GC-11-39, ICP-7148
	Indeterminate	194	Genotypes had indeterminate growth habit.
Stem colour	Purple	11	BDN-2008-9, Kari togari, ICP-1156, ICP-14976, ICP-3576, ICP-4575, ICP-6152, ICP-6049, ICP-7223, ICP-8152, ICP-9336
	Green	185	Genotypes have had green stem
Leaf Shape	Oblong	194	Genotypes have had oblong leaf shape
	Obvate	2	ICP-7148 and Gulyal
	Narrowly oblong	0	None
Pubescence on lower surface of leaf	Absent	196	Absent in all 196 genotypes
	Present	0	None
Flower colour of base petal & (Standard)	Light yellow	26	AKT-8811, AKT-9915, BAHAR *etc.*
	Yellow	143	AL-1855, BDN-2008-8, AL-201 *etc.*
	Orange Yellow	15	BPG-51-3, GRG-815, GRG-2009 *etc.*
	Purple	3	ICP-14116, ICP-14229 *etc.*
	Red	9	TS-3R, ICP-3576, ICP-4575 *etc.*
Flower pattern of streaks on petal (Standard)	Absent	51	BDN-2, BDN-2008-9, BSMR-736 *etc.*
	Sparse	77	AK-022, AKT-913, BDN-708 *etc.*
	Medium	64	AK-101, AKT-8811, AKT-9915 *etc.*

	Dense	2	GC-11-39, TS-3R
	Mosaic	2	ICP-6929, Kari togari
Pod : colour	Green	4	BSMR-736,BDN-2008-12,NDA-1,ICPB2043
	Green with brown streaks	1	ICP-4167
	Green with purple streaks	189	BDN-708, Bennur local, BRG-109 *etc.*
	Purple	2	BANAS, BAHAR
	Dark purple	0	None
Pod pubescence	Absent	196	Present on all the studied genotype
	Present	0	None
Pod : waxiness	Absent	2	ICP-14976 and ICP-6815
	Present	194	Genotypes with pod waxiness.
Pod : surface stickiness	Absent	2	ICP-6815 and ICP-14976
	Present	194	Genotypes have had pod surface stickiness.
Pod feature: constriction	Slight	43	BDN-2008-1, RVK-272, RVK-283, RVK-285, ICP-11015 *etc*.
	Prominent	153	AK-022, AK-101, AKP-1, AKT-8811 etc (Majority had prominent pod constriction)
Plant height	Short (<100cm)	3	AL-1794, AL-1855 and AL-201
	Medium (100-150cm)	126	AK-022, AK-101, AKT-8811 *etc.*
	Tall (> 150cm)	67	ICPL-87119, BPG-51-2, BSMR-533 *etc.*
Seed: size (100 seed weight)	Small (<7g)	17	BIRSA ARHAR, ICP-11477, ICP-1156 and ICP-1279 *etc*.
	Medium (7-9g)	98	AK-101, AKP-1, AKT-8811 *etc*.
	Large (9-11g)	71	AKT-9913, AKT-9915, AL-1794 *etc.*
	Very Large (>11g)	10	GRG-107, MAL-13, ICP-14229, ICP-14701 *etc.*
Seed: colour	Reddish brown	72	AK 022, BDN-2008-7 etc.,
	Light brown	83	AK 101, AKP-1, AKT-8811 etc.,
	Cream	13	BANAS, BDN-2 etc.,
	White	11	BDN-2004-3, BWR-153 etc.,
	Orange	8	ICP 11320, ICP 14701 etc.,
	Dark purple	7	BDN-2008-9,ICP 3576, ICP 4575, etc.,
	Dark grey	1	Karitogari,
	Purple	1	ICP 7035
Seed: colour pattern	Plain	188	Genotypes have had plain seed colour pattern
	Speckled	4	ICP 11910, ICP 13633, ICP 14701, ICP 14976
	Mottled & Specked	3	ICP 12515, ICP 3576, ICP 7035
	Mottled	1	BDN 2008-9
Seed: shape	Globular	53	AKT 9913, BDN-2004-3 etc.,
	Oval	124	AK-022, AK 101 etc.,
	Square	19	AKT 8811, AKT 9915 etc.,