

New pigeon pea (*Cajanus cajan*) hybrids with desirable forage traits

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Introduction Pigeon pea is a tropical forage legume usually sown in mixed pastures with tropical forage grasses. Most of the available cultivars shows erect and tall plants with poor tillering potential, breakable thick stems, low leaf/stem ratios (fresh/dry matter) and low persistence under animal grazing. It shows a high dry matter production, due to low leaf/stem ratios (Barnes & Addo, 1997). Pigeon pea shows good crude protein levels/dry matter (ranging from 14-23%) and regular *in vitro* digestibility indexes (52-58%) (Karachi & Matata, 1996); animal consumption is affected by high tannin levels of young leaves. Being a self-pollinated species, the variability for forage traits occurs **among** cultivars available at germplasm banks. No significant variation is observed for any forage character **within** a given population. Effective selection and releasing of new genetic materials bearing desirable morpho-agronomic and forage traits is mostly dependent on increases of genetic variation, which may be accomplished through artificial crossings between selected parentals. This research work was aimed at the synthesis of new pigeon pea hybrids, hopefully bearing new desirable forage characters.

Materials and methods Sixteen pigeon pea accessions, available at germplasm banks, were genetically characterized through the RAPD methodology. The 6 most divergent ones were chosen as parentals, aiming to get a broadest genetic variability in F₂ and subsequent generations, so making effective the selection of individual genotypes carrying desirable forage traits (Sidhu et al., 1996). Hand-made artificial crossings were carried out under greenhouse-controlled conditions during the 2002-growing season. The F₁ hybrid seeds of each crossing were sown to get F₁ hybrid plants, from which were picked up F₂ hybrid seeds, during the 2003-growing season. Eight segregant F₂ populations were established at 3 different experimental sites, during the 2004-growing season. Superior genotypes were chosen **within** each F₂ population. The following traits were scored: plant height and growth habit, number of basal and lateral branches, stem thickness and flowering cycles.

Results Evaluation results are presented in Table 1. Significant variation for plant height was detected, ranging from <1.0m up to >3.0m. However, most of the genotypes were concentrated in the interval 1.6-3.0m. Most of the individuals showed only one basal branch, though 2-3 basal branches were not rare events. On the other hand, remarkable variability as to the number of lateral branches was recorded, ranging from <15 to >30; as this parameter is closely related to fresh and dry matter yielding potential, indirect selection might be feasible. A broad variation was also observed for stem diameter, with a significant frequency of individuals with thin stems. Considerable variation on growth habit and flowering cycle was observed but there was the occurrence of new and desirable types never detected before in the available pigeon pea cultivars, like individuals showing prostrated growth habit and/or very late flowering cycle.

Table 1 Frequency distributions of 6 morpho-agronomic traits scored in 8 segregating F₂ populations of pigeon pea (*Cajanus cajan*)

SP	NI	Morpho-agronomic trait																										
		PH (m)						NBB			NLB					GH			CD (mm)					FC				
		<1	1-1.5	1.6-2	2.1-2.5	2.6-3	>3	1	2	3	<15	15-20	21-25	26-30	>30	E	SE	P	2-4	5-6	7-8	9-10	>10	E	M	L	VL	
1	38	-	-	10	9	19	-	29	5	4	3	14	11	7	3	13	22	3	14	12	8	4	-	4	13	12	9	
2	30	1	1	6	4	16	2	18	12	-	6	13	2	5	5	8	18	4	10	7	7	5	1	2	15	4	9	
3	17	-	-	7	8	2	-	10	6	1	4	10	1	2	-	7	9	1	4	5	5	3	-	3	5	9	-	
4	12	-	-	4	6	2	-	5	4	3	3	4	2	-	3	5	6	1	3	5	2	2	-	4	5	3	-	
5	17	-	5	3	3	6	-	12	3	2	2	1	2	5	7	6	5	6	-	-	2	2	16	9	2	3	3	
6	20	8	5	2	4	1	-	17	3	-	5	3	3	6	3	5	8	7	4	2	3	1	7	7	4	6	3	
7	20	1	-	-	4	13	2	17	3	-	2	3	3	3	9	10	8	2	12	3	2	1	2	11	4	2	3	
8	8	-	-	1	6	1	-	8	-	-	-	-	4	3	1	1	7	-	-	-	-	-	2	6	2	4	-	2

Observations: SP = segregating F₂ population; NI = number of individuals; PH = plant height; NBB = number of basal branches; NLB = number of lateral branches; GH = growth habit (E = erect; SE = semi-erect; P = prostrated); CD = stem diameter; FC = flowering cycle (E = early; M = medium; L = late; VL = very late).

Conclusions Effective selection of superior individuals is now feasible due to broad genetic variation detected.

References

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