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Original Research Article

Genetic variability for yield and related traits among wild accessions of cowpea and cross-compatibility with cultivated accessions

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Abstract

Cowpea is an important legume, and its wild relatives could be reliable sources of favorable alleles for genetic diversity and improvement of important traits. The study aimed to evaluate wild accessions of cowpea for genetic variability, identify important traits focused on yield and yield components, and assess wild and domesticated cowpea genotypes for cross-compatibility. Forty-four accessions of wild relatives and domesticated cowpeas were used for the study. Forty wild accessions were evaluated for genetic variability, and selected accessions were crossed with domesticated cowpea accessions. The experiment was laid out in a randomised complete block design with three replicates. The data collected were subjected to analysis of variance (ANOVA), and correlation coefficients between characters were calculated. Furthermore, data were subjected to factor analysis, step-wise regression, and selection criteria were calculated. The genotypic effect was significant ($p < 0.01$; $p < 0.05$) for most of the measured characters except the number of branches per plant. Factor analysis showed that seed yield and number of pods per plant mainly contributed to the observed variations among the wild relatives. The number of pods per plant was among the characters that had positive and significant phenotypic and genotypic correlations with seed yield. Step-wise regression identified the number of pods per plant as the main contributor to variations in seed yield. NGB001071 was identified as one of the top accessions by the classical selection index, largely due to its relatively higher number of pods per plant and seed yield. Crosses between wild accessions and domesticated cowpea were successful. The potential of introgression of favourable alleles from wild forms to domesticated cowpea was documented. This finding suggests that leveraging wild germplasm could enhance the resilience and genetic diversity of cowpeas for measured characters, ultimately improving yield and adaptability to changing environmental conditions.

Keywords: alleles; classical selection index; factor analysis; genotypic correlation; legume; path analysis; phenotypic correlation; step-wise regression; variations; wild relatives

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is one of the most important food and forage legume crops worldwide (Singh, 2005; Timko et al., 2007). It is a rich source of proteins, calories, minerals, and vitamins. Cowpea seed contains 25% protein and is low in anti-nutritional factors (Rangel et al. 2003). This crop complements the cereal diet in countries that grow it as a major food crop (Phillips et al. 2003). Cowpea can fix atmospheric nitrogen through its root nodules, growing well in poor soils with more than 85% sand, less than 0.2% organic matter, and low phosphorus content (Singh et al. 2003). In addition, it is shade-tolerant and compatible as an intercrop with maize, millet, sorghum, sugarcane, and cotton.

Though the crop has high economic and agricultural importance, cowpea yields are relatively low in West Africa. The low yields are caused by several factors, including a narrow genetic base, several abiotic (drought, heat), and biotic (insect pests and diseases) factors limiting its production and the interaction of the genotype with the environment. Thus, genetic improvement through breeding plays a critical role in improving the overall yield potential of the crop in the region. According to Kapazoglou et al. (2023), crop wild relatives constitute a highly valuable resource of genetic diversity, and by exploiting the full potential of this extra allele pool, new traits conferring abiotic stress tolerance may be introgressed into cultivated varieties, leading to superior and resilient genotypes. Boukar et al. (2020) attributed the narrow genetic diversity of cowpea partly to the limited gene flow between the wild and cultivated types, possibly contributing to the plateauing in cowpea grain yield, thereby compromising genetic gains.

According to Boukar et al. (2020), cross-compatible cowpea wild relatives have been sparsely used in variety development because breeders shy away from them due to their tiny seed size, unattractive seed coat colour and texture, pod shattering, and susceptibility to viruses.

Several studies on genetic diversity and intercharacter relationships have been done toward cowpea improvement (Fatokun et al., 2001; Omoigui et al., 2006; Manggoel et al., 2012; Olayiwola et al., 2023a). However, little research has focused on exploiting the potential of wild relatives in cowpea breeding. This research addressed a critical gap concerning the underutilisation of wild relatives, which could potentially broaden the genetic base of cowpeas for improvement. Ng et al. (1985) proposed that cowpea was native to West Africa, with both wild and weedy forms in the sub-region. Pasquet (1997) reported that the species *V. unguiculata* includes domesticated forms, *V. unguiculata* ssp. *unguiculata* var. *unguiculata*, wild annual forms ssp. *unguiculata* var. *spontanea* (Schweinf.) Pasquet, and ten wild perennial subspecies. The author based this classification on phenotypic, allozyme, and cpDNA study results (Padulosi, 1993; Pasquet, 1999; Vaillancourt et al., 1993; Vaillancourt and Weeden, 1992). Furthermore, Padulosi and Ng (1997) and Pasquet (1999) suggested that *V. unguiculata* ssp. *unguiculata* var. *spontanea* (also called ssp. *dekindtiana sensu* Verdc.) was the likely progenitor of the domesticated cowpea.

Wild relatives of crops are reliable sources of favourable alleles for genetic diversity and for improving important traits and adaptation to a wide range of growing conditions and resistance to insects and diseases (Parker and Riches, 1993; Mammadov et al., 2018). Padulosi and Ng (1990) submitted that wild forms and closely related cowpea species are relevant germplasm pools for cowpea improvement programs. For instance, Fatokun et al. (2001) reported that due to the presence of hairs on the plants, members of the var. *pubescens* conferred some degree of insect resistance on cowpea. Some of the seeds and leaves of these wild forms have also been found to be important in human diets in Africa and thus contribute to food security in the region (www.biodiversityinternational.org).

Reports of successful and viable crosses between wild and the weedy subspecies of cowpea (V. *unguiculata* subsp. *dekindtiana*, *stenophylla,* etc.) and the cultivated forms have been documented by different authors (Baudoin and Marechal, 1985; Ng, 1990; Fatokun et al., 1997), and heterosis have been observed among the hybrids (Mohammed et al., 2009). However, Rawal et al. (1976) reported that such crosses were only successful when the wild forms were made the pollen source. Thus, the cross-compatibility and reproductive potential need to be ascertained to utilise wild relatives of cowpea effectively for cultivar improvement. Furthermore, the magnitude of genetic variability within wild relatives of cowpea must be extensively studied for a deeper understanding of their potential as sources of sustainable genetic enhancement for domesticated cultivars. Moreover, the scope of genetic variation within wild cowpea relatives remains understudied, further necessitating in-depth studies to reveal their full potential for the sustainable improvement of domesticated cultivars.

Ba et al. (2004) characterised the genetic variation within domesticated cowpea and its wild progenitor using Random Amplified Polymorphic DNA (RAPD) and found more polymorphic bands in the domesticated cultivars than in the wild forms. Coulibaly et al. (2002) studied the variation among and within domesticated cowpea and wild forms based on geographical distribution using Amplified Fragment Length Polymorphism (AFLP) and reported that the wild annual cowpea (ssp. *unguiculata* var. *spontanea*) was more diverse than the domesticated form. They also concluded that the var. *spontanea* could have originated from East Africa and that intense gene flow existed between the two cowpea forms across Africa. However, resources are scarce on genetic variability studies aiming to improve this wild relative, and the cross-compatibility with recently developed domesticated cowpea genotypes remains relatively unknown. Plant breeders have used several techniques to study genetic variability within and among genotypes of different crops (Lal et al., 2014; Nwangburuka et al., 2012; Sarr et al., 2021). Factor analysis has been used to understand the pattern of variability and the contribution of traits to the observed variation (Akbar, 2016; Rameeh, 2012). Furthermore, correlation and stepwise regression analyses have been widely used to study inter-trait relationships to identify important traits directly or indirectly related to the primary traits of interest (Ajala et al. 2018; Hannachi et al. 2013; Huang et al. 2013). This information guides breeders in developing a reliable and efficient selection index that could accelerate gains in selection. The current study aimed to evaluate genetic variability of accessions of wild relatives of cowpea for yield and yield-related characters, and identify key characters for improvement of the wild relatives using multivariate statistics. The level of cross-compatibility between the wild accessions and domesticated cowpea genotypes was also determined using controlled hybridization. Thus, we tested various hypotheses on inadequate genetic variability among accessions of cowpea wild relatives for yield and related characters, inter trait relationships, cross-compatibility among domesticated cowpea genotypes and accessions of wild relatives of cowpea.

MATERIALS AND METHODS

Experimental material

Forty-four accessions of *Vigna* spp., including 40 accessions of the wild relative, *V. unguiculata* ssp. *unguiculata* var. *spontanea,* and four accessions of domesticated cowpea were used in the study. The accessions were sourced from the Germplasm units of the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, International Institute of Tropical Agriculture (IITA), and the University of Agriculture, Makurdi (Table 1).

Field evaluation

Experimental site and field layout

The *V. unguiculata* ssp. *unguiculata* var. *spontanea accessions* were evaluated at the Teaching and Research Farm of the Federal University of Agriculture, Abeokuta. Abeokuta is located between latitudes 7°10′N and 7°58′N and longitudes 3°20′E and 4°37′E. The location is characterised by annual rainfall of 1,250 mm to 1500 mm and an average temperature of 27 °C. The experiment was carried out during the late season of 2014–2015. The experimental field was laid out in a randomised complete block design with three replicates. The blocks, 4 m × 24 m, were separated by a 1 m alley, and each block contained 40 single-row plots. The rows were 4 m long and spaced at 0.60 m. The seeds were sown on the single-row hill at a spacing of 0.40 m.

The coat of the seeds was scraped using a scalpel to ensure quick germination of the accessions. Two seeds were sown per hole, and the emerged seedlings were thinned to one plant per hole at two weeks after sowing (2WAS). A total of 10 plant stands were thus established per plot. Weeding was done manually as necessary, and Cyperforce (Cypermethrin) was sprayed at a dose of 40 ml per 15 L of water to control insect pests. The insecticide was sprayed at 3WAS and subsequently at 10-day intervals. The plants were then staked at 6 WAS.

Data collection

Five plants were randomly selected from among the competitive plants while excluding the non-competitive plants within the single-row plots. Sixteen quantitative characters which included number of days to emergence, number of days to 50% flowering, vine length at flowering (cm), leaf length at flowering (cm), leaf width at flowering (cm), number of leaves at flowering, pod length (cm), peduncle length (cm), number of branches per plant, vine length at maturity, number of peduncles per plant, number of pods per plant, number of seeds per pod, pod weight per plant (g), 100-seed weight(g) and seed yield per plant (g). Randomly selected plants had the vines unwind from their stakes and then measured along the length using a 100 m ruler. All measurements were done following the descriptor of the International Plant Genetic Resources Institute (IPGRI, 1983)

Assessment of cross-compatibility between accessions of *V. unguiculata* ssp. *unguiculata* var. *spontanea* and *V. unguiculata*

The assessment of the compatibility between *V. unguiculata* ssp. *unguiculata* var. *spontanea* and *V. unguiculata* were carried out at the designated crossing block in the greenhouse of the Department of Plant Breeding and Seed Technology, Federal University of Agriculture, Abeokuta. Four accessions of *V. spontanea* and *V. unguiculata* were used for the evaluation. The *V. spontanea* accessions were selected based on a number of days to 50% flowering.

Each cowpea genotype was sown in five pots filled with 5 kg of soil. Genotypes of *V. unguiculata* were sown

Table 1. Accessions, source and origin of *Vigna* spp. evaluated in the study

S/No.	Accession	Species	Origin	Source
1	NGB001051	*V. spontanea*	-	NACGRAB
2	NGB001053	*V. spontanea*	Kano	NACGRAB
3	NGB001071	*V. spontanea*	Sokoto	NACGRAB
4	NGB001082	*V. spontanea*	Adamawa	NACGRAB
5	NGB001086	*V. spontanea*	Borno	NACGRAB
6	NGB001087	*V. spontanea*	Sokoto	NACGRAB
7	NGB001090	*V. spontanea*	Jigawa	NACGRAB
8	NGB001106	*V. spontanea*	Taraba	NACGRAB
9	NGB001108	*V. spontanea*	Taraba	NACGRAB
10	NGB001110	*V. spontanea*	Taraba	NACGRAB
11	NGB001116	*V. spontanea*	Yobe	NACGRAB
12	NGB001120	*V. spontanea*	-	NACGRAB
13	NGB001123	*V. spontanea*	Kaduna	NACGRAB
14	NGB001126	*V. spontanea*	Borno	NACGRAB
15	NGB001129	*V. spontanea*	-	NACGRAB
16	NGB001132	*V. spontanea*	-	NACGRAB
17	NGB001133	*V. spontanea*	-	NACGRAB
18	NGB001135	*V. spontanea*	Niger	NACGRAB
19	NGB001136	*V. spontanea*	Adamawa	NACGRAB
20	NGB001140	*V. spontanea*	Kano	NACGRAB
21	NGB001141	*V. spontanea*	Yobe	NACGRAB
22	NGB001142	*V. spontanea*	Yobe	NACGRAB
23	NGB001143	*V. spontanea*	Taraba	NACGRAB
24	NGB001148	*V. spontanea*	Adamawa	NACGRAB
25	NGB001150	*V. spontanea*	-	NACGRAB
26	NGB001151	*V. spontanea*	Borno	NACGRAB
27	NGB001152	*V. spontanea*	Bauchi	NACGRAB
28	NGB001153	*V. spontanea*	-	NACGRAB
29	NGB001160	*V. spontanea*	-	NACGRAB
30	NGB001163	*V. spontanea*	Kaduna	NACGRAB
31	NGB001164	*V. spontanea*	Kaduna	NACGRAB
32	NGB001166	*V. spontanea*	Kano	NACGRAB
33	NGB001167	*V. spontanea*	Adamawa	NACGRAB
34	NGB001168	*V. spontanea*	Yobe	NACGRAB
35	NGB001169	*V. spontanea*	Yobe	NACGRAB
36	NGB001170	*V. spontanea*	Niger	NACGRAB
37	NGB001171	*V. spontanea*	Kaduna	NACGRAB
38	NGB001173	*V. spontanea*	Yobe	NACGRAB
39	NGB001174	*V. spontanea*	Sokoto	NACGRAB
40	NGB001177	*V. spontanea*	Niger	NACGRAB
41	IT98K-573-2-1	*V. unguiculata*	-	IITA
42	IT99K-529-2	*V. unguiculata*	-	IITA
43	IT07K-298-15	*V. unguiculata*	-	IITA
44	UAM1055-6	*V. unguiculata*	-	UAM

National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan
International Institute of Tropical Agriculture (IITA), Ibadan
University of Agriculture, Markurdi (UAM)

Table 2. Method of crossing between *V. sponatanea* and *V. unguiculata*

	V. unguiculata				*V. spontanea*			
Parent	**IT98K-537-2-1 (P_1)**	**IT99K-529-2 (P_2)**	**IT07K-298-15 (P_3)**	**UAM1055-6 (P_4)**	**NGB001071 (P_5)**	**NGB001120 (P_6)**	**NGB001171 (P_7)**	**NGB001174 (P_8)**
P_1	-	-	X	X	X	X	-	X
P_2	X	-	X	X	X	X	X	X
P_3	X	X	-	X	X	X	-	X
P_4	X	X	X	-	X	X	X	X
P_5	-	-	X	X	-	-	-	-
P_6	X	-	X	X	-	-	-	X
P_7	-	X	-	-	-	-	-	-
P_8	X	-	X	-	X	X	-	-

Crossed (x), Not crossed (-)

Table 3. Mean squares obtained from the analysis of variance of forty accessions of *V. spontanea*

Source of variation	DF	DTE	DTF	LWF (cm)	LLF (cm)	NLF	VLF (cm)	LP (cm)	NPEP	NBP	POL (cm)	NSP	NPOP	PWP (g)	VLM (cm)	100SW (g)	SY (g)
Accession	39	31.83**	55.04*	18.41**	24.46**	8866.21**	43594.88**	52.91*	516.19**	0.2	1.43**	10.78**	11056.86**	3106.32**	65325.79**	0.05**	1120.00**
Block	2	1.22	27.82**	0.73**	1.40**	477.13*	1259.03**	23.87	57.18*	0.14	0.76**	1.68*	708.12	195.73	2152.65**	0.30**	74.18
Error	77	0.8	12.12	0.38	0.65	277.88	636.92	15.78	32.95	0.14	0.23	0.97	538.86	162.2	1065.67	0.01	49.44
CV		6.68	64.79	6.41	9.01	99.3	192.74	24.15	14.76	4.24	9.63	14.69	39.88	20.39	278.89	2.51	11.41

*,** significant at $p < 0.05$ and $p < 0.01$, respectively

CV: Coefficient of variation; DF: degree of freedom; DTE: days to 50% emergence; DTF: days to 50% flowering; LWF: leaf width at flowering; LLF: leaf length at flowering; NLF: number of leaves at flowering; VLF: vine length at flowering; LP: length of peduncle; NPEP: number of peduncles per plant; NBP: number of branches per plant; POL: pod length; NSP: number of seeds per pod; NPOP: number of pods per plant; PWP: pod weight per plant; VLM: vine length at maturity; 100SW:100 seed weight; SY: seed yield

Table 4. Mean performance of forty accessions of *Vigna spontanea* for the sixteen characters

	Accession	DTE	DTF	LWF (*cm*)	LLF (*cm*)	NLF	VLF (*cm*)	LP (cm)	NPEP	NBP	POL (*cm*)	NSP	NPOP	PWP (*g*)	VLM (*cm*)	100SW (*g*)	SY (*g*)
1	NGB001051	6.33	64.00	6.53	9.05	84.67	195.27	26.59	10.20	4.20	9.43	13.67	46.67	21.19	273.53	2.57	13.04
2	NGB001053	6.33	64.67	6.50	9.45	106.33	205.33	22.63	13.73	4.40	8.91	14.00	38.73	15.71	293.50	2.13	12.36
3	NGB001071	6.33	59.33	5.75	9.37	94.93	233.53	27.65	18.40	4.00	11.03	15.80	60.93	25.17	310.43	3.18	23.05
4	NGB001082	7.33	64.33	6.01	8.79	107.53	196.87	26.50	18.77	4.00	9.19	14.73	50.20	14.07	284.00	2.64	14.93
5	NGB001086	6.33	65.00	6.29	9.54	95.13	184.13	27.51	11.90	4.33	9.20	14.27	27.87	22.04	261.27	2.47	8.71
6	NGB001087	6.67	65.00	6.29	9.32	116.53	172.00	27.09	12.80	4.00	9.65	14.87	30.13	16.04	268.30	2.52	8.85
7	NGB001090	7.67	64.67	6.43	8.21	90.93	169.53	20.25	11.73	4.00	8.85	13.40	29.20	13.38	257.27	2.95	8.87
8	NGB001106	7.00	62.67	6.72	10.19	121.27	211.80	24.97	17.47	4.47	9.85	14.27	43.47	30.53	287.97	3.22	15.04
9	NGB001108	7.00	63.00	6.57	10.03	97.07	204.87	24.89	20.26	4.27	9.62	14.53	65.47	29.09	282.67	2.49	15.32
10	NGB001110	6.00	68.00	5.97	9.01	92.13	204.33	27.69	18.67	4.27	9.99	15.13	54.27	34.98	286.03	2.54	17.24
11	NGB001116	7.33	65.00	6.56	8.79	116.27	216.73	25.60	17.32	4.20	10.03	14.53	52.07	20.25	312.80	2.66	14.86
12	NGB001120	6.00	60.67	6.04	8.27	74.53	195.80	24.81	18.34	4.07	9.46	13.80	51.20	29.30	267.77	2.38	14.05
13	NGB001123	6.33	63.33	6.69	8.67	115.13	192.27	29.09	16.10	4.07	10.50	14.80	51.53	19.67	274.83	3.58	20.05
14	NGB001126	6.33	67.67	6.33	8.65	114.40	230.13	25.62	12.03	4.13	9.48	15.73	28.40	9.91	319.60	2.52	8.12
15	NGB001129	8.00	68.33	7.19	10.34	119.07	191.67	27.94	15.10	4.27	9.47	15.27	58.87	29.56	295.27	2.43	16.17
16	NGB001132	6.33	64.67	6.89	9.96	96.60	196.40	31.11	14.19	4.00	10.48	14.73	42.47	31.60	245.47	2.37	14.98
17	NGB001133	8.33	72.33	6.17	8.01	91.73	175.47	23.90	12.82	4.53	9.07	13.07	29.53	8.71	262.53	2.44	7.19
18	NGB001135	7.33	68.50	6.83	9.01	90.40	196.87	20.77	11.32	4.20	8.29	14.30	28.10	10.69	291.10	2.09	5.72
19	NGB001136	7.33	66.33	6.73	9.31	104.07	210.20	22.27	13.33	4.60	9.91	14.87	33.20	14.37	325.53	2.59	7.99
20	NGB001140	6.67	67.00	6.27	10.01	97.60	194.87	21.23	13.20	4.73	10.01	15.40	31.93	14.97	285.80	2.13	9.77
21	NGB001141	6.33	62.00	6.04	9.10	75.93	163.67	23.36	9.00	4.53	9.61	14.53	20.20	10.70	253.00	2.25	5.44
22	NGB001142	6.67	67.33	6.35	8.33	106.47	199.87	21.16	11.47	4.20	9.84	16.27	25.53	12.68	296.83	2.10	6.23
23	NGB001143	6.33	68.67	7.29	9.70	105.20	204.00	21.78	9.84	4.20	8.95	14.47	24.00	11.69	300.73	2.29	6.38
24	NGB001148	6.00	61.00	6.27	8.31	107.67	195.47	24.60	9.90	3.80	9.99	15.73	21.80	14.14	269.13	2.32	5.65
25	NGB001150	5.67	61.00	6.44	8.39	89.47	170.27	28.17	18.40	4.33	10.23	16.07	45.80	21.62	257.43	2.15	11.49
26	NGB001151	7.00	70.33	6.89	9.21	110.13	229.53	21.71	9.50	4.27	9.47	13.87	22.67	28.29	304.53	2.48	5.05
27	NGB001152	5.67	64.00	7.03	9.54	117.33	191.80	18.61	16.27	4.53	9.33	14.53	46.60	14.77	301.03	2.25	11.82
28	NGB001153	6.33	65.33	6.16	9.63	102.60	193.67	25.09	12.80	4.33	9.79	14.80	26.67	26.35	284.20	2.33	8.26
29	NGB001160	7.67	67.67	6.15	7.77	102.20	182.80	20.99	12.06	4.07	8.95	14.13	20.40	5.74	271.37	2.34	2.81
30	NGB001163	6.00	64.67	7.05	9.01	99.53	200.00	21.10	25.62	4.40	9.24	14.20	52.00	22.08	293.60	2.49	11.37
31	NGB001164	6.00	62.00	5.61	8.91	90.67	179.40	20.03	16.27	4.00	9.64	15.13	44.53	19.52	265.17	2.54	10.21
32	NGB001166	6.33	60.67	5.82	9.13	101.60	169.53	23.09	17.60	3.93	10.16	15.00	56.73	29.91	220.50	2.68	16.99
33	NGB001167	7.00	69.67	6.46	9.43	95.33	199.27	24.04	13.60	4.40	9.45	14.00	35.00	34.94	316.07	2.65	9.66
34	NGB001168	6.67	64.67	6.40	7.93	89.73	167.33	21.70	11.23	4.00	9.39	14.33	24.73	16.72	262.57	2.30	4.53
35	NGB001169	6.33	67.00	6.66	8.99	108.07	215.20	22.52	13.33	4.47	9.41	14.00	33.13	21.34	315.50	2.97	11.20
36	NGB001170	8.00	63.67	6.23	8.91	74.73	187.13	20.65	12.80	4.40	10.03	13.93	30.67	15.67	252.87	2.65	7.74
37	NGB001171	6.67	61.33	6.10	8.53	94.40	184.27	25.13	23.45	4.00	9.98	15.20	75.80	22.58	271.80	2.60	19.65
38	NGB001173	6.67	62.33	7.37	9.05	100.20	184.73	25.53	27.42	4.20	9.57	15.00	78.20	36.64	264.70	2.61	19.60
39	NGB001174	6.67	59.33	4.77	7.25	69.60	121.47	23.93	8.73	4.27	9.58	15.87	20.53	14.73	190.67	2.46	4.72
40	NGB001177	6.33	64.00	6.63	9.25	104.73	192.13	24.79	15.46	4.47	9.88	15.47	41.93	25.54	278.27	2.09	11.20
	LSD (0.05)	1.45	5.65	1.00	1.31	27.09	41.01	6.45	9.33	0.62	0.78	1.61	37.71	20.70	53.03	0.17	11.42
	Mean	6.68	64.79	6.41	9.01	99.30	192.74	24.15	14.76	4.24	9.63	14.69	39.88	20.39	278.89	2.51	11.41

Table 5. Genetic parameters for yield-related traits evaluated on *Vigna spontanea*

Component	DTE	DTF	LWF (cm)	LLF (cm)	NLF	VLF (cm)	LP (cm)	NPEP	NBP	POL (cm)	NSP	NPOP	PWP (g)	VLM (cm)	100SW (g)	SY (g)
Vg	10.34	14.31	6.01	7.94	2862.78	14319.32	12.38	161.08	0.02	0.40	3.27	3506.00	981.37	21420.04	0.01	356.85
Vp	11.14	26.43	6.39	8.59	3140.66	14956.24	28.16	194.03	0.16	0.63	4.24	4044.86	1143.57	22485.71	0.02	406.29
H	0.93	0.54	0.94	0.92	0.91	0.96	0.44	0.83	0.13	0.63	0.77	0.87	0.86	0.95	0.57	0.88
GCV	48.15	5.84	38.25	31.27	53.88	62.09	14.57	85.99	3.34	6.57	12.31	148.47	153.64	52.48	4.60	165.56
PCV	49.97	7.93	39.44	32.52	56.44	63.45	21.97	94.37	9.43	8.24	14.02	159.48	165.85	53.77	6.09	176.66

DTE: days to 50% emergence; DTF: days to 50% flowering; LWF: leaf width at flowering; LLF: leaf length at flowering; NLF: number of leaves at flowering; VLF: vine length at flowering; LP: length of peduncle; NPEP: number of peduncles per plant; NBP: number of branches per plant; POL: pod length; NSP: number of seeds per pod; NPOP: number of pods per plant; PWP: pod weight per plant; VLM: vine length at maturity; 100SW:100 seed weight; SY: seed yield

Table 6. Variance, factor loadings and communalities rates of sixteen characters evaluated in *V. spontanea*

Character	Factor				Communalities
	I	II	III	IV	
Days to 50% emergence	−0.28	0.30	−0.48	0.43	0.58
Days to 50% flowering	−0.32	0.78	−0.04	0.14	0.73
Leaf width at flowering (cm)	0.32	0.75	−0.12	−0.23	0.73
Leaf Length at flowering (cm)	0.50	0.51	0.13	−0.20	0.57
Number of leaves at flowering	0.38	0.57	0.33	0.19	0.61
Vine length at flowering (cm)	0.46	0.64	0.29	0.27	0.78
Length of peduncle (cm)	0.55	−0.26	0.17	0.18	0.43
Number of peduncles per plant	0.76	−0.13	−0.34	−0.14	0.73
Number of branches per plant	−0.16	0.43	0.02	−0.17	0.24
Pod length (cm)	0.56	−0.42	0.44	0.19	0.72
Number of seeds per pod	0.25	−0.40	0.70	0.18	0.74
Number of pods per plant	0.87	−0.16	−0.33	−0.08	0.90
Pod weight per plant (g)	0.72	−0.06	−0.15	−0.11	0.56
Vine length at maturity (cm)	0.25	0.77	0.29	0.23	0.79
100-seed weight (g)	0.43	−0.12	−0.18	0.75	0.79
Seed yield	0.92	−0.19	−0.16	0.15	0.93
Eigen value	5.09	3.73	1.61	1.47	
Variation (%)	28.25	20.71	8.92	8.15	
Cumulative (%)	28.25	48.96	57.88	66.03	

two weeks earlier than *V. spontanea*. The five pots of the *Vigna* spp. were planted at one-week intervals. The sowing was staggered to synchronize the days to the flowering of the *Vigna* species. At flowering, emasculation was carried out as appropriate before crosses were made between the *Vigna* spp. as presented in Table 2. Ten crosses were made within each crossing pattern to evaluate the cross-compatibility between the *Vigna* spp. Observations were then made on several successful crosses and the number of seeds per pod.

Data analysis

Data were subjected to analysis of variance to determine significant differences among the accessions of *V. spontanea* for the characters evaluated, and means were separated using the least significant difference (LSD). Phenotypic, genotypic, and environmental variances were determined from the expected mean squares, and the phenotypic and genotypic coefficients of variation, as well as broad-sense heritability were calculated. Furthermore, the variance components were used to compute the phenotypic, genotypic, and environmental correlation coefficients as outlined by Singh and Choudhary (1985). Factor analysis was used to describe the variability among the interrelated characters and to identify homogenous characters that can be used to determine genetic groups among the cowpea accessions (Cattell, 1965). Step-wise multiple regression analysis was performed to determine the characters contributing most to variation in seed yield (Draper and Smith, 1981). The selection index developed by Smith (1936) using the discriminate function of Fisher (1936) was used to discriminate the performance of the genotypes based on all the characters. Phenotypic and genotypic variances and covariances were calculated from the means of observation (Falconer, 1989). Selection indices (Smith, 1936) were calculated as outlined by Singh and Chaudhary (1985). Seed yield was assigned an economic value of 1.5, and other characters were assigned an economic weight of unity (1). A selection index based on phenotypic performance was defined for each character. Selection criteria were then calculated for each genotype using the defined selection index. The expected genetic advance was calculated (Hanson et al., 1956; Johnson et al., 1955), whereas the response to selection was estimated as detailed by Singh and Chaudhary (1985).

RESULTS

Mean squares of the sixteen characters evaluated among 40 accessions of *V. unguiculata* ssp. *unguiculata* var. *spontanea* are presented in Table 3. Significant ($p < 0.01$; 0.05) variation existed among the forty accessions for all the characters measured except the number of branches per plant. The coefficient of variation ranged from low to high for 100-seed weight and vine length at maturity, respectively.

The mean performances of the 40 accessions of *V. unguiculata* ssp. *spontanea* for the sixteen characters are presented in Table 4. Early days to 50% emergence were recorded for NGB001150 and NGB001152, while NGB001133 was late for days to 50% emergence. However, NGB001174 was early for days to 50% flowering, had short leaf length at flowering, and leaf width at flowering. The accession was also low for number of leaves at flowering and the number of peduncles per plant. NGB001106 was high for number of leaves, while NGB001029 was high for leaf length at flowering. NGB001173 was high for number of peduncles per plant, leaf width at flowering, number of pods per plant, and pod weight per plant. Vine length at maturity ranged from 325.53 cm for NGB001136 to 190.67 cm for NGB001174. NGB001123 and NGB001071 had high values for 100-seed weight and seed yield, respectively.

Estimates of the genetic parameters (Table 5) revealed higher phenotypic than genotypic variances as well as higher phenotypic (PCV) than genotypic coefficients of variation (GCV) for all measured traits. Genotypic variances ranged from 0.01 to 21420.04 for 100-seed weight and vine length at maturity, respectively, while phenotypic variance ranged from 0.02 to 22485.71 for the same order of traits. Heritability estimates were lowest (0.13) for NBP, while the highest heritability of 0.96 was observed for VLF. The lowest GCV and PCV estimates of 3.34 and 6.09 were observed for NBP and 100SW, respectively, while the estimates were highest (165.56 and 176.66) for seed yield in the same order.

The total variance and eigenvalues of the first four-factor loadings explained 66% of the overall variance and were considered important for the sixteen characters evaluated (Table 6). The first factor had the highest eigenvalue, accounting for 28.25% of the total variation. Factors II, III, and IV explained 20.71%, 8.92%, and 8.15% of the total variation, respectively. Characters that loaded Factor I were the length of the peduncle, number of peduncles, pod length, number of pods, pod weight, and seed yield. Factor II was loaded with days to 50% flowering, leaf width, leaf length, vine length at flowering, and vine length at maturity. Factors III and IV were characterised by the number of seeds per pod and 100-seed weight, respectively. The proportion of the character variances that were explained by the factors (commonalities) ranged from 0.24 to 0.93. High

Table 7. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among quantitative characters evaluated in *V. spontanea*

Character	DTE	DTF	LWF (*cm*)	LLF (*cm*)	NLF	VLF (*cm*)	LP (*cm*)	NPEP	NBP	POL (*cm*)	NSP	NPOP	PWP (*g*)	VLM (*cm*)	100SW (*g*)	SY(*g*)
DTE		0.28	0.07	–0.07	0.02	–0.04	–0.15	–0.20	0.11	–0.45**	–0.56**	–0.15	–0.24	0.04	0.07	–0.2
DTF	0.85**		0.25	0.15	0.44**	0.30	0.03	–0.05	0.38*	0.88**	0.72**	–0.14	0.12	0.42**	0.39*	–0.12
LWF (*cm*)	0.19	0.34*		0.51**	0.52**	0.45**	–0.02	0.17	0.22	–0.34*	–0.39*	0.16	0.17	0.52**	–0.09	0.10
LLF (*cm*)	–0.19	0.43**	0.49**		0.42**	0.47**	0.20	0.16	0.34*	0.15	–0.03	0.27	0.45**	0.40**	0.03	0.35*
NLF	0.27	0.99**	0.70**	0.64**		0.52**	0.12	0.14	–0.01	0.15	0.25	0.13	0.06	0.58**	0.25	0.21
VLF (*cm*)	0.26	0.59**	0.53**	0.50**	0.58**		0.09	0.15	0.08	0.12	–0.09	0.17	0.21	0.85**	0.20	0.27
LP (*cm*)	–0.02	–0.11	–0.10	0.33*	–0.09	0.04		0.25	–0.26	0.69**	0.47**	0.41**	0.48**	–0.11	0.35*	0.57**
NPEP	–0.57**	–0.06	0.22	0.13	–0.33*	–0.12	0.12		–0.07	0.55**	0.40**	0.92**	0.57**	0.07	0.37*	0.78**
NBP	0.84**	0.75**	–0.26	0.83**	–0.72**	–0.22	–0.89**	–0.87**		–0.10	–0.15	–0.16	–0.04	0.27	–0.20	–0.19
POL (*cm*)	–0.48**	–0.04	–0.85**	0.19	0.02	–0.04	0.92**	0.58**	–0.82**		0.78**	0.60**	0.67**	–0.15	0.91**	0.77**
NSP	–0.94**	–0.70**	–0.81**	–0.04	0.48**	–0.42**	0.78**	0.52**	–0.95**	0.74**		0.38*	0.31*	–0.14	0.43**	0.41**
NPOP	–0.51**	–0.01	0.25	0.29	–0.35*	–0.04	0.60**	0.80**	–0.90**	0.96**	0.69**		0.65**	0.05	0.42**	0.94**
PWP (*g*)	–0.83**	0.88**	0.49**	0.74**	–0.08	0.64**	0.88**	0.72**	0.88**	0.61**	0.62**	0.76**		0.01	0.36*	0.65**
VLM (*cm*)	0.30	0.80**	0.82**	0.50**	0.96**	0.87**	–0.37*	–0.09	0.72**	–0.34**	–0.45**	0.12	–0.02		0.06	0.08
100SW (*g*)	0.28	–0.01	–0.17	0.05	0.32*	0.26	0.54**	0.50**	–0.79**	0.88**	0.19	0.81**	0.91**	0.08		0.63**
SY(*g*)	–0.57**	0.19	0.01	0.38*	–0.07	0.21	0.97**	0.84**	–0.97**	0.89**	0.87**	0.82**	0.92**	0.15	0.96**	

*,** significant at 5% and 1% level of probability, respectively.
DTE: days to 50% emergence; DTF: days to 50% flowering; LWF: leaf width at flowering; LLF: leaf length at flowering; NLF: number of leaves at flowering; VLF: Vine length at flowering; LP: length of peduncle; NPEP: numbers of peduncles per plant; NBP: numbers of branches per plant; POL: pod length; NSP: number seeds per pod; NPOP: number of pods per plant; PWP: pods weight per plant; VLM: vine length at maturity; 100SW:100 seeds weight; SY: seed yield

Table 8. Table 8. Stepwise selection of characters contributing to seed yield in *V. spontanea*

	Step				
	1	2	3	4	5
Intercept	0.53**	−10.44**	−17.88**	−20.90**	−27.89**
Days to 50% emergence	-	-	-	-	-
Days to 50% flowering	-	-	-	-	-
Leaf width at flowering (cm)	-	-	-	-	-
Leaf length at flowering (cm)	-	-	0.87**	0.85**	0.82**
Numbers of leaves at flowering	-	-	-	-	-
Vine length at flowering (cm)	-	-	-	-	-
Length of peduncle (cm)	-	-	-	0.17**	0.14**
Number of peduncles per plant	-	-	-	-	-
Number of branches per plant	-	-	-	-	-
Pod length (cm)	-	-	-	-	0.94**
Number of seeds per pod	-	-	-	-	-
Number of pods per plant	0.29**	0.28**	0.26**	0.26**	0.25**
Pod weight per plant (g)	-	-	-	-	-
Vine length at maturity (cm)	-	-	-	-	-
100-seed weight (g)	-	4.11**	4.22**	4.00**	3.64**
Seed yield (g)	-	-	-	-	-
Partial R^2	0.87	0.02	0.01	0.01	0.004
Model R^2	0.87	0.90	0.91	0.91	0.92

*,** significant at 5% and 1% level of probability, respectively, R^2 – coefficient of determination

commonalities were recorded for the number of pods per plant and seed yield.

Genotypic correlation coefficients were similar in direction to phenotypic correlation but higher than phenotypic correlation coefficients in magnitude for the measured characters (Table 7). Leaf length at flowering, length of peduncle, number of peduncles per plant, pod length, number of seeds per pod, number of pods per plant, pod weight per plant, and 100-seed weight all had positively significant phenotypic and genotypic correlations with seed yield. Significant and negative genotypic correlations were observed between days to emergence, number of branches per plant, and seed yield, but the corresponding phenotypic correlations with seed yield were not significant. Furthermore, days to 50% flowering, length of peduncle, and the number of peduncles per plant had positive and significant genotypic correlations with pod length. Significant and positive genotypic correlations were observed among days to 50% flowering, length of peduncle, the number of peduncles/plant, pod length, and the number of seeds per pod. Leaf length at flowering, length of peduncle, number of peduncles, pod length, and the number of pods per plant had significant and positive genotypic correlation with pod weight per plant.

The number of branches/plant had a significant and negative genotypic correlation with the number of leaves, peduncle length, peduncles per plant, pod length, pod number per plant, pod weight, and 100-seed weight. However, the corresponding phenotypic correlations were not significant. Negative and significant genotypic correlations were observed between days to 50% emergence and the number of peduncles per plant, pod length, number of seeds per pod, number of pods per plant, and pod weight. Still, they had a positive correlation with the number of branches. Also, days to 50% flowering had a negative genotypic correlation with the number of seeds per plant and a positive correlation with leaf length, number of branches, and pod weight. Pod length had a negative and significant genotypic correlation with leaf width and the number of seeds/plant. However, a positive genotypic correlation was observed between leaf width and pod weight.

Generally, the characters' environmental correlation coefficients (Table not shown) were lower than the genotypic correlation coefficients.

Parameter estimates of characters contributing to seed yield in *V. spontanea* obtained from step-wise regression analysis are presented in Table 8. The five steps generated from the step-wise regression analysis explained a total of 92% of the linear variation in seed yield. Only the number of pods per plant, the 100-seed weight, leaf length at flowering, length of peduncle, and pod length met the significance entry level to be retained in the regression model. The characters included in the regression model had a positive relationship with seed yield, with most of the traits recording high regression coefficients (gradient).

V. unguiculata ssp. s*pontanea* genotypes ranking according to selection criteria that included all five characters that were included for the regression on seed yield are presented in Table 9. The top 10% performers were NGB001123, NGB001106, NGB001071 and NGB001108 while in the lowest 10% were NGB001135, NGB001053, NGB001142, and NGB001160. The highest genetic gains were recorded for the number of pods per plant and seed yield.

Tests of compatibility between *V. unguiculata* and *V. unguiculata* ssp. *spontanea* are presented in Table 10. Thirty-six crosses were made, of which eighteen interspecific crosses were successful and produced at least three pods. Generally, a higher number of F^1 seeds were obtained from intra-specific crosses than inter-specific crosses. However, high pollination rates were observed for the following inter-specific crosses: IT99K-529-2 / NGB001071, UAM1055-6 / NGB001174, NGB001174 / IT07K-298-15, IT99K-529-2 / NGB001120, UAM1055-6 / NG001120, IT07K-298-15 / NGB001120, IT07K-298-15 / NGB001071, UAM1055-6 / NGB001071, and NGB001174 / IT99K-529-2. Although the crosses IT99K-529-2 / NGB001071 and UAM1055-6 / NGB001174 showed equally high pollination rates, the most successful cross was UAM1055-6 / NGB001174 since it combined the high pollination rates with a better seed set.

DISCUSSION

The significant accession effect on most of the studied characters underscored the presence of large variability among the wild relatives of cowpea and their potential to serve as sources of favourable alleles, and therefore, provides an opportunity for developing and selecting desirable accessions that can be utilised for breeding improved cowpea varieties.

The early days to flowering associated with NGB00174 indicated that the accession could be a source of early maturing genotypes. Accessions NGB001123 and NGB001071 had high values for 100-seed weight, seed yield, and pod length, implying that they could be valuable for seed production. The large number of peduncles per plant exhibited by NGB001173 indicated that it could produce more pods and, consequently, a higher seed yield (Adetiloye et al., 2017). Factor analysis captured the variability among the accessions of cowpea wild relatives and identified seed yield, number of pods per plant, length, and number of peduncles as the major contributors to the observed variation. These traits could thus be targeted in measuring genetic diversity among wild relatives of cowpea.

Intercharacter associations among the traits were determined using phenotypic, genotypic, and environmental correlations. Since most selections are based on phenotyping, a significant genotypic correlation without a corresponding significant phenotypic correlation may be of low practical value. Similarly, a significant phenotypic but non-significant genotypic correlation may not be repeatable and could be misleading (Sharma and Prasad, 2010; Olayiwola and Ariyo, 2015). The significant and positive genotypic and phenotypic correlations observed for leaf length at flowering, length of peduncle, number of peduncle per plant, pod length, number of seeds per pod, number pods per plant, pod weight per plant, 100-seed with seed yield is an indication that the traits could be considered for selection index focused on improving seed yield in cowpea (Ahmed et al., 2020; Rambabu et al., 2019). However, correlations are to be interpreted cautiously, particularly when most of the traits identified as important to a trait of interest are correlated *inter se* (Rodriquez et al., 2017; Ajala et al., 2018). Interdependence sets in, and since correlation does not capture functional relationships, it becomes less reliable in practical plant breeding under such circumstances (Olayiwola et al., 2023b). This necessitated using a stepwise regression analysis, which reveals the functional relationship between the trait of interest and the contributing characters. The coefficient of determination from the regression showed that the number of pods per plant chiefly accounted for the total variation in seed yield, followed by the 100-seed weight. Though leaf length at flowering, length of peduncle, and pod length were also cut, their contribution was not pronounced. Thus, a higher selection weight could be allotted to the number of pods per plant than to the other traits in improving the seed yield in *V. unguiculata* ssp. s*pontanea* (Ahmed et al. 2020; Ariyo, 1995).

The classical selection index identified NGB001123, NGB001106, NGB001071, and NGB001108 as the top four accessions. These accessions had above-average values for all traits, particularly the number of pods per plant and seed yield, and thus indicated their worth as sources of favourable alleles in the cowpea improvement programme.

Table 9. *Vigna spontanea* genotypes ranked according to classical selection index

Genotype	Leaf length (cm)	Length of peduncle (cm)	Pod length (cm)	Number of pods per plant	100-seed weight (g)	Seed yield (g)	Selection criterion
NGB001123	8.67	29.09	10.50	51.53	3.58	20.05	282.78
NGB001106	10.19	24.97	9.85	43.47	3.22	15.04	275.69
NGB001071	9.37	27.65	11.03	60.93	3.18	23.05	274.01
NGB001108	10.03	24.89	9.62	65.47	2.49	15.32	263.91
NGB001173	9.05	25.53	9.57	78.20	2.61	19.60	260.43
NGB001136	9.31	22.27	9.91	33.20	2.59	7.99	259.14
NGB001116	8.79	25.60	10.03	52.07	2.66	14.86	258.66
NGB001171	8.53	25.13	9.98	75.80	2.60	19.65	258.40
NGB001129	10.34	27.94	9.47	58.87	2.43	16.17	258.13
NGB001132	9.96	31.11	10.48	42.47	2.37	14.98	257.92
NGB001170	8.91	20.65	10.03	30.67	2.65	7.74	256.93
NGB001169	8.99	22.52	9.41	33.13	2.97	11.20	256.87
NGB001167	9.43	24.04	9.45	35.00	2.65	9.66	256.40
NGB001166	9.13	23.09	10.16	56.73	2.68	16.99	256.31
NGB001087	9.32	27.09	9.65	30.13	2.52	8.85	255.71
NGB001051	9.05	26.59	9.43	46.67	2.57	13.04	253.91
NGB001110	9.01	27.69	9.99	54.27	2.54	17.24	252.65
NGB001164	8.91	20.03	9.64	44.53	2.54	10.21	252.36
NGB001163	9.01	21.10	9.24	52.00	2.49	11.37	251.12
NGB001151	9.21	21.71	9.47	22.67	2.48	5.05	250.54
NGB001086	9.54	27.51	9.20	27.87	2.47	8.71	250.14
NGB001082	8.79	26.50	9.19	50.20	2.64	14.93	249.65
NGB001126	8.65	25.62	9.48	28.40	2.52	8.12	249.38
NGB001150	8.39	28.17	10.23	45.80	2.15	11.49	248.79
NGB001153	9.63	25.09	9.79	26.67	2.33	8.26	248.55
NGB001090	8.21	20.25	8.85	29.20	2.95	8.87	247.81
NGB001148	8.31	24.60	9.99	21.80	2.32	5.65	246.13
NGB001174	7.25	23.93	9.58	20.53	2.46	4.72	242.35
NGB001141	9.10	23.36	9.61	20.20	2.25	5.44	242.12
NGB001120	8.27	24.81	9.46	51.20	2.38	14.05	241.81
NGB001177	9.25	24.79	9.88	41.93	2.09	11.20	241.75
NGB001133	8.01	23.90	9.07	29.53	2.44	7.19	241.07
NGB001140	10.01	21.23	10.01	31.93	2.13	9.77	240.20
NGB001168	7.93	21.70	9.39	24.73	2.30	4.53	239.95
NGB001143	9.70	21.78	8.95	24.00	2.29	6.38	238.96
NGB001152	9.54	18.61	9.33	46.60	2.25	11.82	238.00
NGB001160	7.77	20.99	8.95	20.40	2.34	2.81	237.29
NGB001142	8.33	21.16	9.84	25.53	2.10	6.23	234.26
NGB001053	9.45	22.63	8.91	38.73	2.13	12.36	226.90
NGB001135	9.01	20.77	8.29	28.10	2.09	5.72	226.45
Mean of all individual	9.01	24.15	9.62	40.03	2.51	11.16	
Means of selected individual (10%)	9.17	25.84	9.64	49.13	2.63	15.84	
Selection differential (10%)	0.16	1.69	0.02	9.10	0.12	4.69	
Heritability	0.54	0.34	0.70	0.24	0.98	0.33	
Genetic gain for 10%	0.08	0.57	0.01	2.18	0.12	1.56	
10%	20.86						

Table 10. Successful crosses between four lines, each of *V. spontanea* and *V. unguiculata*

Female	Male parents	Successful pollination (%)*	Number of seeds per pod (F_1)
V. unguiculata			
IT07K-298-15	NGB001120	50 (5)	7
	NGB001174	30 (3)	15
	NGB001071	50 (5)	12
	IT98K-573-2-1	30 (3)	12
	UAM1055-6 (*V. unguiculata*)	0 (0)	0
	IT99K-529-2 (*V. unguiculata*)	0 (0)	0
IT98K-537-2-1	NGB001071	0 (0)	0
	NGB001174	30 (3)	12
	NGB001120	0 (0)	0
	IT07K-298-15 (*V. unguiculata*)	30 (3)	9
	UAM1055-6 (*V. unguiculata*)	30 (3)	13
IT99K-529-2	NGB001120	60 (6)	8
	NGB001071	70 (7)	5
	NGB001171	0 (0)	0
	NGB001174	30 (3)	12
	IT98K-537-2-1 (*V. unguiculata*)	0 (0)	0
	IT07K-298-15 (*V. unguiculata*)	0 (0)	0
	UAM1055-6 (*V. unguiculata*)	0 (0)	0
UAM1055-6	NGB001174	70 (7)	12
	NGB001071	50 (5)	17
	NGB001120	60 (6)	9
	NGB001171	0 (0)	0
	IT99K-529-2 (*V. unguiculata*)	0 (0)	0
	IT98K-537-2-1(*V. unguiculata*)	30 (3)	6
	IT07K-298-15 (*V. unguiculata*)	0 (0)	0
V. spontanea			
NGB001120	IT07K-298-15	0 (0)	0
	IT98K-573-2-1	0 (0)	0
	UAM1055-6	30 (3)	9
	NGB001174 (*V. spontanea*)	0 (0)	0
NGB001174	IT07K-298-15	60 (7)	8
	IT98K-573-2-1	0 (0)	0
	IT99K-529-2	50 (5)	8
	NGB001120 (*V. spontanea*)	30 (3)	12
	NGB001071 (*V. spontanea*)	0 (0)	0
NGB001071	UAM10055-6	0 (0)	0
NGB001171	IT99K-529-2	0 (0)	0

* Number of pods produced from ten crosses in parentheses

The successful crosses recorded between selected accessions of *Vigna spontanea* and accessions of domesticated cowpea *Vigna unguiculata* implied that the accessions were inter-fertile and that *V. unguiculata* ssp. *unguiculata* var. *spontanea* indeed belonged to the subspecies of *Vigna unguiculata*. It is noteworthy that the characteristics contributing to observed variations in domesticated cowpea and its wild relatives are similar. The potential of introgression of favorable alleles for resilience to biotic and abiotic stresses from *V. unguiculata* ssp. *unguiculata* var. *spontanea* into *Vigna unguiculata* could then be explored (Boukar et al., 2020). The most successful combinations, IT99K-529-2 / NGB001071 and UAM1055-6 / NGB001174, may provide useful insights into the hybrid vigor, particularly in terms of seed or pod production and development of resilient cowpea genotypes. The high seed output indicates potential for substantial yield improvements, which may be beneficial for future breeding programs aiming to increase productivity.

CONCLUSION AND RECOMMENDATION

The study revealed large variability among accessions of cowpea wild relatives (*V. spontanea*). This variability could be explored to broaden the genetic base of domesticated cowpea. The number of pods per plant and other traits were identified as important contributors to seed yield and could be targeted in the cowpea improvement programs. Crosses between accessions of cowpea wild relatives and domesticated cowpea were successful. These interspecific hybrids should be validated through marker-assisted breeding and tested under prevailing stresses (e.g., drought, *striga*, insect) across locations to determine their genetic merits as potential sources of novel quantitative trait loci for desirable traits originating from the wild relatives.

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CONFLICT OF INTEREST

The authors declared no conflicts of interest concerning the research, authorship, and publication of this article.

ETHICAL COMPLIANCE

The authors have followed ethical standards in conducting the research and preparing the manuscript.

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