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Evaluation of Pigeon Pea (*Cajanus cajan* (L.) Millsp) Genotypes for Grain Yield and Yield Components at Jinka South Omo Zone, Ethiopia

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***Abstract* – Evaluation the performance of pigeon pea genotypes for yield and yield components were not conducted in the studied area. As a result, Eighty one pigeon pea genotypes were tested in Augmented at Jinka Agricultural Research Center, Ethiopia during 2007 cropping season The analysis of variance revealed highly significant difference ($p \leq 0.01$) for all studied traits .Therefore, the present study indicated that there is sufficient genetic diversity in pigeon pea germplasm that could be used as a base for improvement of the yield and other important attributes of this crop through direct selection and hybridization. Future work may also proceed in collecting and characterizing all the pigeon pea germplasms found in Ethiopia and developing short duration and high yielding varieties.**

***Keywords* – Evaluation, Genotypes, Pigeon Pea, Yield Components, Yield.**

I. INTRODUCTION

Pigeon pea (*Cajanus cajan* (L.) is a deep rooted and drought-tolerant leguminous food crop used in several countries as a source of dietary protein [11]. Although it can grow in any warm climate, the pigeon pea is particularly popular throughout tropical and sub-tropical regions. The crop is said to have originated in both Africa and Asia.

Pigeon pea endowed with rich dietary protein in its seed provides the much needed protein requirements [5]. The seed contains 18-29% protein on dry weight basis which is about three times the value found in cereals and closer to soybean which is 34% [8], [10] The protein is also of excellent quality, being high in lysine. The crop is, therefore; an important complements to cereal and root based diet [12].

The evaluation of the yield-determining quantitative traits of crop has become primary interest in crop improvement program. Yield improvements have been achieved through directional selections for yield and contributing traits [1]. It has been found that yield contributing traits have reliable and predictable effect on grain yields in grain legumes such as, Mung bean, pea and pigeon pea [10].

A majority of legume crops in Ethiopia are grown in the highlands as cool season crops and their production is poor. On the other hand, there are vast areas of land under arid and semi arid conditions and pigeon pea is a legume suitable to drought prone areas, if we use it we may be able to reduce protein deficiency. Therefore; pigeon pea a tropical legume is the one which holds such a promise [2].

Pigeon pea research in terms of crop improvement is still at low level in Ethiopia [7]. Therefore; by considering the importance of pigeon pea in food security in the drought prone areas of South omo zone of South Nation Nationality Peoples region of Ethiopia and its potential for future Ethiopian economy, it is vital to increase its production and productivity through evaluation of genotypes for their yield and yield components. Therefore; the present study was proposed (1) to develop improved pigeon pea varieties (2) to evaluate the genotypes for future breeding programs.

II. MATERIALS AND METHODS

A field experiment was carried out at Jinka Agricultural Research Center of South Agricultural Research Institute, Ethiopia. Jinka is located at 5° 52' N, 36° 38' E, and 1450 m above sea level with an annual average rainfall and temperature of 855 mm and 22.3°C, respectively. The soil of the experimental field is sandy loam. Eighty one pigeon pea genotypes collected from Ethiopia Institute Biodiversity Conservation (IBC) and three checks were planted on September 2, 2005. Augmented design was used. Each plot consisted of four rows, 4 m long and 3 m width with spacing of 20 cm between plants and 75 cm between rows. The distance between blocks was 1 m.

For each genotype five randomly taken plants in each plot were used to record data on pods per plant, and seeds per pod. Days to flowering, days to maturity and seed yield per plot were recorded on plot basis. The data were analyzed using GLM procedure of SAS software [9].

III. RESULTS AND DISCUSSION

Results of analysis of variance of 5 characters for 100 pigeon pea genotypes and 3 checks (controls) are presented in Table I. All the characters showed significant ($p<0.01$) difference among the tested genotypes (Table I).The presence of significance among landraces indicate the presence of genetic variability for each of the characters among the tested genotypes. The ANOVA of contrast analysis between the genotypes, controls and genotypes vs controls is also presented in Table I.

Days to 50% flowering ranged from 86 to 138 for the genotype L393 and L482, respectively. Also days to maturity varied from 142(L187 and L639) to 248 (L351, L293, L659, L364 and L350). While number of pod per plant and number of seed per pod varied between 27.8(L337) to 190 (L536) and 2.1(L364, L620 and L303) to 4.1(L680 and L538), respectively. The highest grain yield of 4.3 kg/plot was recorded from the genotype L29 and genotype L199, L304 and L429 gave the low grain yield of 0.01 kg/plot. This result has confirmed the previous reports [6], [12]. Variability for days to 50% flowering, days to maturity, number of pod per plant and number of seed per pod was also reported by [3], [4] .The present investigation revealed considerable amount of variations for most of the traits studied. Such wide variations indicated the scope of improving for these traits.

Table I: Significance of mean squares for five grain yield and yield related traits for 81 pigeon pea genotypes.

Source of variation	Df	DTH	DTM	NPPP	NSPP	GY(kg/plot)
Block (Adj)	8	65.8ns	157.6ns	667.6ns	0.06ns	0.18**
Tret (Adj)	83	214.4 ***	482.2 **	1639.1***	0.1**	0.78***
Test	80	172.0 ***	396.04 ***	884.6 ns	0.20 ns	0.480823 **
Controls	2	1224.7 ***	3925.47*	9000.4***	0.15 ns	4.460366 ***
Test Vs controls	1	1560.2	493.826802 **	47282.0 **	0.03***	17.686686 ***
Error		16	62.1	114.48	0.06	0.03
CV (%)		7.5	5.20	25.4	8.3	19.3

Table II: Adjusted Mean values of five grain yield and yield related traits of 81 pigeon pea genotypes and three checks grown under rain faid condition at on station of Jinka Agricultural Research Center.

Genotypes	DTM	DTH	GY(kg/plot)	Pod/plant	NSPP
C1	225.7	124	2.5	129.7	3.3
C2	188.4	105	1.4	170.1	3.0
C3	190.8	103	1.1	107.7	3.0
L172	186.0	94	0.6	125.5	2.7
L58	186.0	92	0.7	47.5	2.7
L580	186.0	94	0.5	32.5	2.7
L592	186.0	92	0.6	58.5	1.7
L603	186.0	92	1.2	83.5	2.7
L431	186.0	94	0.8	56.5	2.7
L603	189.0	104	0.9	79.5	2.7
L267	229.0	92	0.6	69.5	1.7
L354	229.0	94	0.9	92.5	3.0
L281	187.0	102	0.8	182.5	3.0
L283	190.0	102	4.2	120.5	3.0
L289	190.0	102	0.6	138.5	3.0
L474	190.0	100	0.4	128.5	3.0
L444	190.0	100	0.7	111.5	3.0
L327	190.0	122	1.4	147.5	4.0
L372	189.0	132	0.5	115.5	4.0
L285	230.0	100	1.4	160.5	3.0
L284	229.0	112	0.8	196.5	3.0
L117	185.7	108	0.7	66.8	4.0
L337	185.7	91	0.5	27.8	4.0
L642	185.7	89	0.4	18.8	3.0
L342	185.7	95	0.6	28.9	3.0
L247	185.7	91	0.5	64.8	3.0

L572	186.7	89	0.5	59.8	3.0
L453	187.7	91	0.7	30.8	2.0
L206	187.7	91	0.4	62.8	3.0
L31	187.7	91	0.4	1.8	3.0
L24	205.7	90	0.4	64.9	3.0
L340	245.7	130	1.4	89.8	3.0
L681	205.7	93	0.6	51.8	3.0
L288	205.7	130	2.6	63.8	3.0
L637	205.7	90	0.3	29.8	3.0
L187	145.7	90	1.8	71.8	3.0
L639	145.7	130	1.4	113.8	3.0
L663	205.7	130	1.1	101.8	3.0
L501	205.7	88	0.5	137.8	3.0
L653	190.3	88	0.1	37.8	3.0
L191	189.3	93	0.2	41.8	2.7
L676	189.3	88	0.2	61.8	2.7
L199	189.3	88	0.01	39.8	2.7
L429	189.3	88	0.01	97.8	2.7
L500	189.3	88	1.1	95.8	2.7
L392	189.3	128	0.7	124.8	2.7
L211	189.3	88	0.1	63.8	2.7
L393	229.3	86	0.1	91.8	3.0
L165	232.3	129	0.7	112.5	2.1
L680	232.3	129	1.7	114.5	4.1
L543	232.3	87	0.1	102.5	3.1
L537	232.3	89	0.2	76.5	4.1
L691	232.3	95	0.1	65.5	3.1
L677	232.3	87	0.2	72.5	3.1
L538	191.3	89	0.1	57.5	3.1
L605	191.3	89	0.1	51.5	3.1
L332	192.3	87	0.3	77.5	3.1
L465	236.3	98	0.2	59.5	3.1
L304	197.3	98	0.01	39.5	3.1
L455	197.3	98	0.2	48.5	3.1
L482	237.3	138	0.6	64.5	3.1
L241	237.3	132	0.7	103.5	3.1
L160	197.3	108	0.2	69.5	3.1
L182	237.3	108	0.5	50.5	3.1
L370	207.3	108	0.5	57.5	3.1
L667	197.3	106	0.7	60.5	3.1
L156	208.0	100	0.6	94.1	3.1
L293	248.0	98	0.4	94.2	3.1
L351	248.0	100	0.4	64.2	3.1
L593	208.0	102	0.5	78.2	3.1
L528	208.0	102	2.2	76.2	3.1
L329	208.0	98	0.4	127.2	4.1
L300	248.0	98	0.4	99.2	3.1
L364	248.0	132	1.5	138.2	2.1
L659	248.0	128	1.3	137.2	3.1
L431	232.3	123	1.2	136.2	3.1
L682	192.3	99	0.1	125.2	3.1
L627	232.3	99	0.4	123.2	2.1
L29	232.3	99	4.3	139.2	3.1
L303	232.3	99	0.3	99.2	2.1
L527	230.3	109	0.6	90.2	3.1
L536	230.3	119	0.6	190.2	3.1
L309	232.3	119	0.9	116.2	3.1
L658	192.3	103	0.7	128.2	4.1

DTH = days to 50% heading, DTM= days to 95% maturity, NPPP= Number of pod per plant , NSPP=Number of seed per pod and , GY= grain yield.

Table III. Standard error and critical differences among two tests ,controls and test vs control.

Critical differences b/n	DTH		DTM		NPPP		NSPP		GY	
	SED	CD (%)	SED	CD (%)	SED	CD (%)	SED	CD (%)	SED	CD (%)
Two control treatment	3.7	10.8	5.04	14.7	11.9	34.9	0.12	0.35	0.08	0.25
Two test treatment b/n the same block	11.1	32.7	15.3	44.2	35.9	10.5	0.36	1.05	0.25	0.75
Two test treatment b/n different block	12.8	37.7	17.47	51.0	41.4	12.1	0.41	1.2	0.29	0.87
A test treatment and a control treatment	9.3	27.3	12.69	37.1	30.1	87.9	0.30	0.8	0.21	0.63

DTH= days to 50% heading, DTM= days to 95% maturity, NPPP= Number of pod per plant, NSPP=Number of seed per pod and, GY= grain yield, SED= standard error, CD= critical difference.

Critical differences were varied from 0.25(critical difference between two control treatment) to 87.9 (critical difference between a test treatment and control treatment) for the character grain yield and number of pod per plant, respectively. The character number of pod per plant was showed the highest standard error of two test treatment between different blocks with value of 41.4 and the lowest standard error of 0.08 between two control treatment was recorded from the character grain yield (Table III).

IV. CONCLUSION

From this study, its clear that the tested genotypes have a potential to increase pigeon pea production and productivity in South omo zone. Therefore, further evaluation of the selected genotypes for their yield and yield related is vital.

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