Research Paper

# DOI: 10.5281/zenodo.4957816 Adaptability study of Cowpea (Vigna unguiculata) genotypes for their agronomic performance and nutritive value in Adola district of East Guji zone of Oromia

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Abstract: The study was conducted to identify adaptable, high biomass and seed yield of Cowpea genotypes. Three Cowpea genotypes Bole, 6786 and 2351 were tested in a randomized complete block design (RCBD) with three replications. The result revealed that days to 50% flowering, days to seed maturity, plant height and seed yield was significantly (P<0.05) differ among treatments. Among the tested genotypes late matured was obtained from genotype 6786 (131) days while late genotype was obtained from 2351 (113 days). The highest value of plant height was measured from genotype 6786 (132.8 cm) whereas the short plant height was obtained from genotype 2351 (64.8 cm). The highest seed yield was produced from Bole genotype (24.18 qt/ha) whereas the lowest seed yield was obtained from genotype 6786 (6.8 qt/ha). Chemical composition indicated genotype 2351 was the highest in total ash (TASH) and neutral detergent fiber (NDF) whereas less in crude protein (CP) genotype 6786 was the highest in crude protein (CP) while Bole variety had the highest in dry matter (DM), acid detergent lignin (ADL), acid detergent fiber (ADF) and organic matter (OM). The result of this study implied that 6786 genotype was well adapted and being productive regarding the plant height (131.8 cm) and biomass yield (4.4 t/ha) which is hopeful to fill the gap of low quantity ruminant feed. In addition, the nutritional values were promising particularly the crude protein (CP) in 6786 genotype. Thus it could be possible to conclude that cowpea genotype especially 6786 used as a protein supplement. Based on its adaptability, high biomass, plant height, good CP content 6786 genotype is

recommended for further promotion in the midland of East Guji zone and similar agroecologies.

Keywords: Adaptability; Adola; Cowpea; Genotypes; Guj; Nutritive value; Cowpea

# **1. INTRODUCTION**

Feed shortage both in quantity and quality remains the leading constraint to good animal performance in Ethiopia [1]. Natural pasture and crop residues are the main feed sources (feedstuffs). Feedstuffs of such composition are insufficient to provide year round supply of adequate quantity and quality of nutrients beyond maintenance [2]. Legumes are the most important forage plants that substantially improve the feed available for livestock as they can provide the essential protein for animals, improving soil fertility, food crop production and household nutrition through a more reliable supply of milk and meat [3, 4].

Cowpea (Vigna unguiculata (L.) is a leguminous crop grown throughout West Africa, often in association with pearl millet (Pennisetum glaucum L.) and sorghum (Sorghum bicolor L.). Cowpea is well adapted to the harsh growing conditions, including low soil fertility, high temperatures, and [5]. Cowpea can fix nitrogen to improve soil fertility and cropping system productivity. Additionally, farmers feed cowpea fodder to livestock to increase income, and collect the manure produced for use in their fields thereby reduces farmers' reliance on commercial fertilizers and sustain soil fertility [3, 6].

Previous studies with cowpea [3, 4, 7, 8] indicated this legume improves soil fertility and enhances the intake and utilization of poor quality roughage consequently improves livestock production and productivity. Another important feature of cowpea is also its ability to suppress weeds particularly striga species [9]. Therefore, this experiment was conducted with the objective to evaluate and identifying adaptive, high quality yielding cowpea genotypes in midland of Guji east Guji zone.

#### 2. MATERIALS AND METHOD

#### 2.1. Description of the study area

The experiment was carried out at Adola sub-site of Bore Agricultural Research Center, Adola district, Guji Zone of Oromia. Adola district is located around at a distance of 470 km

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from Addis Ababa and 120 Km from the zonal capital city, Negele Borena. It is an area where a mixed farming and semi- nomadic economic activity takes place, which is the major livelihood of the local people. The total area of the district is 1254.56km<sup>2</sup>. The district is situated at 5°44'10" - 6°12'38" N latitudes and 38°45'10" - 39°12'37" E longitudes. The district is characterized by three agro- climatic zones, namely highland 11%, mid-land 29% and low-land 60% respectively. The major soil type of the district is nitosols (red basaltic soils) and orthic Acrosols [10].

# 2.2. Experimental treatments and design

The study was executed using Bole, 6786 and 2351 genotypes. The experiment was conducted in a randomized complete block design with three replications. Seeds were sown in rows at spacing of 30 cm with seed rate of 30 kg ha<sup>-1</sup>. Plot size of 1.8 m x 3 was used. NPS fertilizer at 100 kg ha<sup>-1</sup> was uniformly applied for all treatments at sowing time.

## 2.3. Data collection methods

Relevant data including days 50% flowering, days to seed maturity, plant height, seed yield and nutritive value were collected. Seed yield weight was calculated at 10% moisture content. Seed yield weight was calculated at 10% moisture content. At 50% flowering stage the middle rows of each plot were harvested for dry matter herbage determination and chemical analysis. Plants were harvested at ground level and fresh biomass weighed immediately using a 0.1 g scale. Then, a sub-sample of 15-20% of the total weight was separated and put into a paper bag for dry matter herbage determination. The samples were oven dried at 105 °C for 24 hours. To determine grain yield, the pods were harvested from the rest rows at optimum physiological maturity by hand picking.

# 2.4. Statistical analysis

All collected data were analyzed using general linear model procedure SAS [11] version 9.1. Means were separated with least significant difference (LSD) at 5% significant level. The statistical model for the analysis data was:  $Y_{ijk} = \mu + A_j + B_i + e_{ijk}$ 

Where;  $Y_{ijk}$ = response of variable under examination,  $\mu$  = overall mean,  $A_j$  = the jth factor effect of treatment/ cultivar,  $B_i$  = the ith factor effect of block/ replication,  $e_{ijk}$  = the random error.

#### 3. Results and Discussions

#### 3.1. Yield and yield components

Mean value of agronomic and yield parameter of cowpea genotypes are shown in table 1. The analyzed result shows that days to 50% flowering, days to maturity, plant height and seed yield was significantly (P<0.05) differ among treatments. Genotype 6786 attained early 50% flowering (72.8 days) followed by genotype 2351 (75.9 days) while genotype Bole late flowered (82.3 days) of 50% flowered as compared to other genotypes. Our results for days to 50% flowering were higher than reported by [12-14]; [15] possibly due to ecological and genetic differences.

Early matured genotype was 2351 (113 days) followed by Bole genotypes (127.9 days) while late matured genotypes were obtained from 6786 (131 days) to set seed when compared to rest genotypes. Early maturity is a relatively important agronomic characteristic and is measured by such criteria as days to flowering or days to maturity [16]. Our results for days 50% flowering and maturity were highly higher than reported by [12] who found average results of 39.5 and 51.6 days to reach 50% flowering and maturity for cow pea genotypes in Ghana, respectively. The result of current study for days to 50% flowering was higher than reported by [14] and [13] who found average results of 63 and 63.7 days, respectively, possibly due to ecological and genetic differences.

The highest plant height was measured from genotype 6786 (132.8 cm) followed by Bole genotype (66.8 cm) whereas the short plant height was obtained from genotype2351 (64.8 cm). The highest seed yield was produced from Bole genotype (24.18 qt/ha) followed by genotype 2351 (19 qt/ha) while the lowest seed yield was obtained from genotype 6786 (6.8 qt/ha). Non-significant different to biomass yield, pod per plant and seed yield was observed between treatments at (P > 0.05). However numerically had high yield was recorded among treatments. The highest biomass yield was produced from genotype 2351 (5.9 ton/ha) followed by genotype 6786 (4.4 ton/ha) while the low biomass yield was obtained from Bole variety (3.7 ton/ha). The highest pod per plant produced from genotype 6786 (12.7) followed by genotype 2351 (10.2) whereas the lowest pod per plant was obtained from Bole genotype (9.11). The highest pod length was obtained from 6786 genotype (3.27 cm) followed by Bole genotype (2.9 cm) while the short pod length was obtained from genotype 2351 (1.7 cm).

Varieties	DsM	Ррр	PoL (cm)	PH (cm)	BMY (t/ha)	SY(qt /ha)
2351	113b	10.2	1.7	64.8b	5.9a	19ab
6786	131.a	12.7	3.274	131.8a	4.4b	6.8b
Bole	127.9a	9.11	2.9	66.8b	3.7b	24.2a
Mean	124	10.7	2.6	87.7	4.7	16.6
CV	9.9	69.9	80.6	23.7	30.5	96.6
LSD (5%)	*	Ns	Ns	*	Ns	*

Table 1. Combined yield and yield attributes of three cow pea genotypes

 $^{(a,b)}$  Mean in a column within the same category having different superscripts differ (p < 0.05) DF=flowering date, DM=maturity date, Ppp=Pod per plant, PoL=Pod length centimeter, PH=plant height centimeter, BMY= biomass yield tone per hectare, SY=grain yield, Cv=Coefficient of variation, LSD= Least significant difference.\*=significant, ns=non significant.

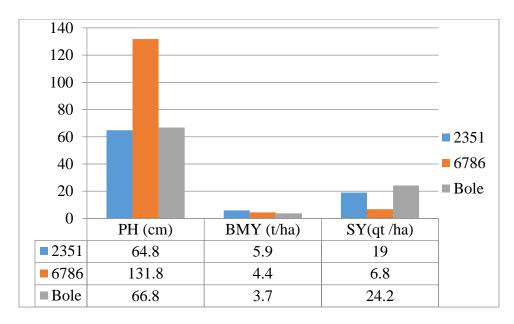


Figure 1. Mean plant height, biomass yield and seed yield of cow pea cultivars.

# 3.2. Chemical Composition

The chemical composition indicated that DM, CP, NDF, ADL, ADF, TASH and OM was not significantly (P>0.05) differ among treatments. However, numerically had high yield was recorded among treatments. Genotype 2351 was highest in TASH and NDF while less in CP, genotype 6786 was highest in CP whereas less in DM, NDF, ADL and OM, Bole variety had the high in DM, ADL, ADF and OM while less in TASH compared the rest treatments. The minimum CP content in the ruminant diet should be around 6.0 - 8.0% of dry matter for adequate activity of rumen microorganism [17] suggesting that hay CP content in investigated cowpeas are more than twice needed rations. Based on its CP% content [7] suggested that cowpea has the potential of being utilized as protein supplement for ruminants on low quality roughages. Literature [3] Realized that supplementation of dairy cows with cowpea hay stimulated the voluntary intake of maize stover which as a result could bring an increment in milk yield. Literature [18] revealed that legume supplementation is an appropriate option where protein sources such as oilseed cakes and those of animal origin are produced in limited quantities and are beyond the economic reach of most of the small holder farmers in Ethiopia. The mean CP content obtained in the present study was agreed with the reported by [14] and [20] who found that CP contents of cow pea were 20.33 and 23.9%, respectively. The maximum NDF content of diet that does not hinder production may be as high as 750 g/kg for mature beef cows and as low as 150 g/kg DM for growing or fattening ruminants [19]. NDF and ADF contents determined in present study were higher than reported for genotypes of cowpea [14]; [20]. This difference could be due to harvest time and duration of sample analyzed at the laboratory.

Genotypes	DM	СР	NDF	ADL	ADF	TASH	ОМ
2351	90.3	22	82.4	9	35.9	13.7	76.5
6786	89.2	27.4	67.1	7.5	37.3	12.8	76.4
Bole	90.4	24.8	74.1	13.1	39	12.2	78.3

Table 2 Mean chemical composition of Cowpea genotypes.

AD= Acid Detergent Fiber; AD= Acid Detergent Lignin; CP= Crude Protein; ND= Neutral Detergent Fiber and O= Organic Matter; TA=Total Ash; D=Dry matter

# 4. Conclusions and Recommendation

The result of this study indicated that genotype 6786 was well adapted and being productive regarding the plant height (131.8 cm) and biomass yield (4.4 t/ha) which is hopeful to fill the gap of low quantity ruminant feed supply of the community. In addition to the nutritional values were promising particularly the crude protein (CP) content in genotype 6786. Thus, it could be possible to conclude that the cow pea genotype 6786 used as a protein supplement for midland of East Guji. Based up on its adaptability high biomass plant height and good CP of genotype 6786 is recommended for further promotion in the midland of East Guji zone and similar agroecologies.

# 5. Acknowledgements

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