Original Research Paper

Analysis of Parent Offspring Regression of Selected Cowpea (*Vigna unguiculata* [L]. Walp.) Agronomic Traits in Phosphorus Limiting Soil.

ABSTRACT

Cowpea is a significant grain legume pulse, vegetable, and fodder crop. However, due to biotic and abiotic stresses, yields have been consistently low. Phosphorus (P) deficiency-related yield losses are one of the major abiotic stresses. The objectives therefore were i) to evaluate the mean performance response of selected cowpea traits across genotypes in optimum and P- limiting soil media and ii) to determine the cowpea heritability response of agronomic traits in P-limiting soil. Twenty cowpea genotypes comprising of 12 F_1 crosses and eight progenitors were evaluated at the University of Zambia Greenhouse in Lusaka, using a completely randomized design with three replications and two-level sets of phosphorus (i.e. 0 kg P_2O_5 and 60 kg P_2O_5). The 60 kg P_2O_5 level set was used as a control. The results showed that the mean performance across genotypes for all measured traits was higher in control experiment at an applied rate of 60kg P_2O_5/ha than at applied rate of 0Kg P_2O_5/ha experimental sets. Significant better performances were obtained with plant height, shoot biomass, plant biomass and yield measured traits. The narrow sense heritability for measured traits ranged from 11- 35 % and 12 - 72% for 0 Kg P_2O_5 and 60 Kg P_2O_5 experimental set respectively. The highest narrow sense heritability scores in experimental set were pod length (h^2= 0.35) and root biomass (h^2= 0.28) while in the control set the variable yield (h^2= 0.72) had the highest score. This implies that the identified trait (pod length) with high narrow sense heritability in P-limiting soil can initially be used to aid in selecting for high performing genotypes in P limiting soil. However, this should be supplemented by yield response especially in late generation selection (F_5 onwards).

***Keywords:** Parent offspring regression, Phosphorus, Narrow sense and Vigna unguiculata*

1. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is an essential economic crop, native to Africa and belongs to the family Fabaceae. It is rich in diverse nutrients, with high levels of protein, vitamins, fiber, macro and micronutrients (i.e. protein, carbohydrates, vitamins, and minerals) [1,2,3,4]. Cowpea is multifunctional future smart climate-resilient crop contributing to food and nutritional security to resource poor farmers. Importantly, cowpea forms symbiosis with the root nodule bacterium, *Rhizobium*, and fixes 70 to 350 kg/ ha of atmospheric nitrogen and some 40 to 80 kg of this is deposited into soils as a natural source of mineral nitrogen, which contribute to soil health [5].

Global production of cowpea is estimated to be 7.4 million tons per annum on a 12.5 million hectare land [6]. The mean grain yield of cowpea in sub-Saharan Africa is less than 700 kg/ ha which is far less than the potential yield of 3000 kg/ha [7,8]. The yield gap is attributable to a multitude of biotic and abiotic stresses. Among the abiotic stresses, yield losses due to phosphorus (P) deficiency is an important factor. Phosphorus is one of the most important plant nutrients, accounting for 0.05 % to 0.5 % of plant dry weight [9]. However, P is one of the least available plant nutrients and is deficient in many soils of the world [10]. Presently, the use of P-formulated fertilizers by some farmers appears to be a quick and easy fix for P deficient soils. However, the current option has not been widely adopted by most smallholder cowpea growers because it is expensive, neither sustainable nor environmentally safe. Therefore, the most sustainable strategy is to develop and choose cowpea genotypes that have high yield in P-limiting soil and are easily adopted by low-resource farmers.

Knowledge on narrow sense heritability of the agronomic variables is key in understanding a breeding strategy to employ in screening for cowpea genotypes in P-limiting soils. As an indicator of selection effectiveness and a measure of the likelihood that advantageous additive genes will be passed down from progenitor to their progeny, information on narrow-sense heritability is crucial to breeders [11]. It is important because of the effectiveness of selection is dependent on the additive components of genetic relative to total variance [12,13]. However, heritability estimates are usually specific to the trait, population, and environment being investigated [14]. This allows breeders to develop the best breeding techniques and selection criteria for desirable trait. This research endeavors to generate fundamental knowledge for utilization in breeding cowpea varieties efficient at utilizing P in P-limiting soils. Therefore, the objectives of this study were i) to evaluate the mean performance response of selected cowpea traits across genotypes in optimum and P- limiting soil media, and ii) to determine the cowpea heritability response of agronomic traits in P-limiting soil.

2. MATERIALS AND METHODS

2.1 Experimental site, material used and experimental details.

Twenty genotypes comprising of 12 F1 crosses and eight progenitors were used for this study. The F_1 crosses were generated as by Chikalipa *et al*. [15] (**Table 1**). The study was conducted at the University of Zambia, Green house in Lusaka (15°23’S and 28°25’E, at 1250 m above sea level). Soil samples used in the study were collected from the top layer (0–30 cm) at Liempe Farm (15^o 22’ S and 28^o 26’ E, at 1171m above sea level) in Chongwe District, as described by [15]. It contained 7.30 mg/kg available phosphorus, 1.92 % organic matter, 0.34 % nitrogen (N) and 0.28 cmol//kg potassium (K). The average pH was measured to be 5.25.

Table 1. Genotype used in the study

Genotypes Codes	Genotypes	Type
AXH	LT 3-8-4-6 X LT 11-3-3-13	Cross
BXG	LT 11-5-1-1 X LT 10-7-1-12	Cross
AXD	LT 3-8-4-6 X LT 4-2-4-1	Cross
CXE	LT 11-5-2-2 X LT 3-8-4-1	Cross
DXA	LT 4-2-4-1 X LT 3-8-4-6	Cross

EXB	LT 3-8-4-1 X LT 11-5-1-1	Cross
FXE	LT 16-7-2-5 X LT 3-8-4-1	Cross
AXE	LT 3-8-4-6 X LT 3-8-4-1	Cross
GXC	LT 10-7-1-12 X LT 11-5-2-2	Cross
CXG	LT 11-5-2-2 X LT 10-7-1-12	Cross
EXD	LT 3-8-4-1 X LT 4-2-4-1	Cross
HXA	LT 11-3-3-13 X LT 3-8-4-6	Cross
A	LT 3-8-4-6	Parent
B	LT 11-5-1-1	Parent
C	LT 11-5-2-2	Parent
D	LT 4-2-4-1	Parent
E	LT 3-8-4-1	Parent
F	LT 16-7-2-5	Parent
G	LT 10-7-1-12	Parent
H	LT 11-3-3-13	Parent

The study was a two-set experiment and laid out as a completely randomized design (CRD), with three replications. The experimental plot was 15cm diameter polythene plastic bags filled with 3kg of soil and Single Super Phosphate (SSP) was applied three weeks after planting. The quantity of SSP added was calculated to achieve the soil P at two levels 60kg P_2O_5/ha (optimal) was added to control set while 0kg P_2O_5/ha (suboptimal) was added to experimental set. However, the recommended quantities of potassium (K) (30 kg K/ha) and nitrogen (N) (20 kg N/ha) was applied as basal dressing in form of potassium sulphate and urea (46% N) fertilisers at the rates of 64 kg/ha and 25 kg/ha respectively. In each bag, three identical genotypes were planted which were later thinned to two plants per bag at the true-leaf stage. Other crop management practices were carried out as per the best agronomic practices recommended for cowpea production.

2.2 Data collection

The following variables were collected on each experimental unit in both sets; Plant height(cm); Shoot biomass(g); Root biomass(g); Plant biomass(g); 100 Seed weight (g) was calculated in grams from hundred sampled seeds; Pod Length (cm); Root length (cm); Number of pods per plant were counted at harvest maturity; Number of seeds per pod were counted at harvest maturity; Yield/ha; Yield per hectare was estimated on a plot basis and converted the plot yield of the seed dry weight to kg/ha.

2.3 Statistical Data Analysis

Heritability in the narrow sense was estimated by regressing mid-parent means on the progeny means as suggested by Falconer and Mackay [11]. The equation being;

$$\boldsymbol{Y = bX + C}$$

Where; $\mathbf{Y}$ is the average performance of progeny, $\mathbf{b}$ is the gradient representing narrow sense heritability estimate, $\mathbf{X}$ is the average performance of mid-parent, and $\mathbf{C}$ is the constant.

Mean genotypic performance for each measured variable in each experimental set was recorded and the standard error bars were computed in excel. Data analysis was performed using GenStat (18th edition) and excel statistical software.

3. RESULTS

3.1 Genetic evaluation of traits

The results showed that the mean performance across genotypes for all measured traits was higher in control experiment at an applied rate of 60kg P_2O_5/ha than at applied rate of 0Kg P_2O_5/ha (Figure 1).

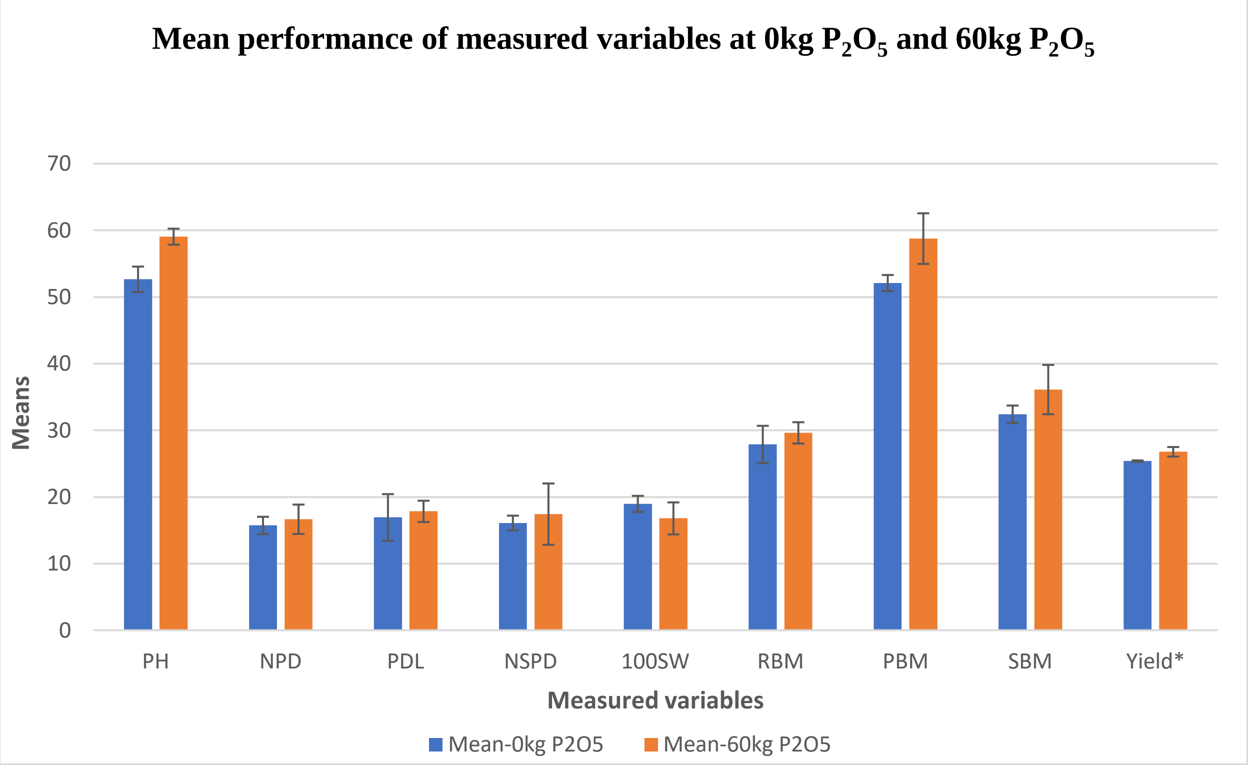

Figure 1. Mean performance of measured traits at P- limited and optimum medium PH=Plant Height (cm), **NDP**= Number of Pods per Plant, **PDL**= Pod Length (cm), **NSPD**= Number of Seed per Pod, **100SW**=Hundred seed weight (g), **RBM** =Root Biomass (cm), **PBM**= Plant Biomass (g), **SBM**=Shoot biomass (g), **Yield***= Yield Kg x 10^2/ ha.

The mean genotypic responses of measured variables exhibited varying narrow sense heritability (h^2) ranging from 11- 35 % and 12-72 % for 0 Kg P_2O_5 experimental trial and 60 Kg P_2O_5 control trial respectively across measured traits (**Table 2**).

Table 2. Narrow sense heritability of measured variables

Measured variables	**h^2 0Kg P_2O_5**	**h^2 60Kg P_2O_5**
PH	0.19	0.12
NPD	0.13	0.22
PDL	0.35	0.16
NSPD	0.11	0.46
100SW	0.12	0.24

RBM	0.28	0.16
PBM	0.12	0.38
SBM	0.13	0.37
Yield	0.11	0.72

h^2=Heritability, **PH**=Plant Height, **NDP**= Number of Pods per Plant, **PDL**= Pod Length, **NSPD**= Number of Seed per Pod, **100SW**=Hundred seed weight, **RBM** =Root Biomass, **SBM**=Shoot biomass, **PBM**= P lant Biomass, **Yield**= Yield Kg/ha.

4. DISCUSSION

Cowpea production is usually constrained by both biotic and abiotic factors. Among the biotic stresses, yield losses due to phosphorus deficiency is an important factor. In this study, mean poor performance of genotypic response of measured variables in P-liming medium compared to medium with optimum P attest to that fact.

4.1 Genetic evaluation of traits

Significant better performances were obtained with plant height, shoot biomass, plant biomass and yield measured traits. This implies that Phosphorous plays a key role in plant productivity, cowpea inclusive. Previous studies have demonstrated that phosphorous is an important element in leguminous crop [16,17].

The narrow sense heritability for agronomic traits ranged from 11-35 % and 12-72% for 0 Kg P_2O_5 and 60 Kg P_2O_5 respectively (**Table 2**). Narrow sense heritability estimates in crops are classified as high (>0.20), medium (0.10 - 0.20), and low (<0.10) [18]. The narrow-sense heritability observed in the experimental trial, suggest that there is potential for improvement through progeny selection and advancement [14]

Estimates for narrow sense heritability obtained are similar to reported narrow sense heritability ranging from 20-85% in cowpea [19, 20]. In the experimental set (0 Kg/ ha P_2O_5) variables, pod length (h^2= 0.35) and root biomass (h^2= 0.28) had the highest heritability values while in the control set, the variable yield (h^2= 0.72) had the highest value. The results entail that selection for yield in P-limiting medium may be challenging for breeders especially if applied in early generation selection and efforts may be boosted through applying genomics or marker-assisted breeding [21, 22, 23]. Responses to pod length (PDL) and root biomass (RBM) could be used as an indirect selection criteria for advancing cowpea crosses in P-limiting soil especially at early generation selection. Early generation selection can be applied to traits that have high heritability. However, for yield (h^2= 0.11) under P-limited soil, late generation selection (F_5 onwards) screening should be employed as heritability for yield was found to be low. Previous studies have shown that PDL and RBM can be used as an indirect selection criteria for dry bean agreeing with our finding [24]. The higher yield heritability value (h^2= 0.72) in control set (**Table 2**) could be due to sufficient P which permitted optimal expression of genes associated with yield [18].

5. CONCLUSION

In this study, results showed that the mean performance across genotypes for all measured traits was higher in optimum than the limiting soil medium. Significant better performances were obtained with plant height, shoot biomass and plant biomass traits. The narrow sense heritability for measured traits ranged from 11- 35 % and 12-72% for 0 Kg P_2O_5 and 60 Kg P_2O_5 experimental set respectively. The highest narrow sense heritability scores in a limiting P soil medium were for pod length (h^2= 0.35) and root biomass (h^2= 0.28) while in the control set (optimum soil medium) the yield trait (h^2= 0.72) had the highest score. This implies that the identified variable (pod length) with high narrow sense heritability in P-limiting soil can initially be used to aid in selecting for high performing genotypes in P limiting soil during early generation selection. However, this should be supplemented by yield response especially at late generation selection (non-segregating generations), F5 onwards.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

AUTHORS' CONTRIBUTIONS

This work was carried out in collaboration among all authors. Emmanuel Chikalipa designed and undertook the study, performed the statistical analysis, interpreted the data and writing of the manuscript. Langa Tembo helped in planning for execution of research, guided the analyses, interpretation process and proof read the manuscript. All authors read and approved the final manuscript.

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