

## **Original Research Article**

### **Genetic Variability, Heritability and Genetic Advance of Yield and Yield Contributing Characters in Putative M2 Dolichos Bean (*Lablab purpureus* L.) Accessions.**

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#### **ABSTRACT**

Dolichos bean (*Lablab purpureus* L.) is a multipurpose, orphan leguminous crop in Kenya. It is characterized with narrow genetic diversity and low yield output. Use of nuclear techniques such as gamma ray induction in breeding for improved genetic variability is an effective approach in improvement of this important crop. Studies on genetic variability estimates of two Kenyan dolichos bean accessions were undertaken as the prerequisites for selection of potential high yielding putative accessions for production. This study was conducted between May 2020 and October 2020 at biotechnology department, University of Eldoret research field, Kenya. 0gy, 300gy and 400gy mutant accessions of Eldo maridadi and Eldo black I respectively were raised in Randomized Complete Block Design (RCBD) with three replications. Data was collected either on plot basis or from randomly taken 3 plants on days to 50% flowering, leaf length, number of flower buds per race, raceme length (cm), plant height (cm), number of nodes per raceme, pod length (cm), 100 seed weight (g), dry seed yield (g). The data collected for each quantitative trait was subjected to analysis of variance (ANOVA) for simple lattice design. There was high PCV and GCV coupled with high heritability in, raceme length (cm), plant height (cm), number of nodes per raceme, pod length (cm), 100 seed weight (g), dry seed yield per plant (g) in Eldo black I accession traits than in Eldo maridadi. The different accession following mutation did exhibit difference in trend of genetic variability estimates. An indication of genotypic differences, response to mutation, lesser influence of environment in expression of the traits, prevalence of additive gene action in their inheritance and amenability of the traits to simple selection. Eldo maridadi accessions exhibited high to low heritability with low genotypic advance as percent of mean in evaluated traits thus direct selection on these traits may not be beneficial. Other traits or further improvements on yield potentiality and yield traits on the accessions of this genotype are suggested by creating variation and selection.

*Keywords: Accessions, Lablab purpureus L., Mutation, Genetic variability, Heritability, Yield components*

#### **INTRODUCTION**

Dolichos bean (*Lablab purpureus* L. (Sweet)), with  $2n=22$  chromosomes belongs to the family *Fabaceae* and is one of the most ancient crops among cultivated plants [23]. Phylogenetically, *Lablab purpureus* L. (Sweet) *lablab* is related closely with common beans.

The legume species grows in the tropic and the sub-tropic regions and favourably in arid, semi-arid and humid climates of altitude ranges from sea level to 2500 meters above sea level (masl) [7, 8 and 20]

Dolichos bean is a multipurpose legume, a pioneer legume species primarily used as food crop both as a pulse or a vegetable, a forage feed in livestock production and in soil fertility and soil organic profile improvement as green manure or cover crop. Other habituated uses included being utilized as an ornamental vine or medicinal functions amongst communities [6] and [12]. In Kenya Dolichos lablab morphotypes have been collected across the country from Lamu county at the coast region to western Kenya. Lamu county is the major dolichos growing region in Kenya [13, 14]. Although dolichos lablab is significantly important in food and nutritional security in the country. The genotypes have low variability in respect of morphological, biochemical and genetic traits indicating existence of low genetic variability. Variability is a very important feature for any plant breeder for improving the efficiency of selection in a breeding population. Economically important plant characters associated with yield are usually polygenic in nature and are highly influenced by environment, it therefore becomes challenging to conclude whether the observed variability is heritable or is due to environmental factors. Local Kenyan genotypes yield between 800-900kg/ha<sup>1</sup> and are also characterized as having varying growth types, prolonged days to maturity, stay green effect, and unsynchronized maturity [17, 25]. The few improved dolichos cultivars in Kenya mainly the KAT/DL varieties from Kenya Agricultural Livestock Research Organization and Eldo KT varieties from University of Eldoret yield between 1000-3000kg/ha in most subsistence farms compared to potential yield of 5T/Ha in research stations. Success in widening genetic variability of Kenyan dolichos beans is premised on the speed of production new varieties or improvement existing ones to meet societal needs. This success can be achieved through use of mutation induction and selection of putative mutative for yield and yield associated traits. Variability, genetic diversity, expected genetic advances and heritability of the traits are key basis for genetic improvement of these polygenic traits. Heritability is the proportion of variation due to dissimilarities between genotypes to the total phenotypic difference for a character in a population and how the character is transferred to future generations [1]. Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than heritability alone. In addition relationship between yield and yield attributing traits are important for direct and indirect selection of traits to which contributes to yield. Therefore, the study was undertaken to know information on variability, heritability, genetic advance of two Kenyan dolichos lablab genotypes and their accessions following with 300gy and 400gy gamma ray mutagenesis.

## **MATERIAL AND METHODS**

The experiment was conducted at the biotechnology department research field, at the University of Eldoret (0°34'N, 35°18'E), the location has an elevation of 2153 meters above sea level (masl) predominantly a LH3 zone and experiences one rainfall season between march and September. The annual average rainfall is 1085 mm and mean temperatures range between 11-24°C. The soils are *rhodic ferralsols* [10]. Two Kenyan genotypes (Eldo KT Maridadi and Eldo KT Black I) were irradiated with gamma radiations of a cobalt 60 (<sup>60</sup>Co) source at Plant Genetics and Breeding Laboratories (PGBL) in Seibersdorf laboratories, Vienna, Austria in 2018. The mutation treatments include 0 kgy, 300 kgy and 400 kgy of gamma rays. A sample per each variety were of irradiated seeds were grown as M1 at University of Eldoret biotechnology research field to produce M2 seed for field trials which was used for this experiment. 10 M2 accessions per 100gy, 300gy and 400gy, were used as test materials of the study from two genotypes (Eldo maridadi and Eldo black I). The trial was laid out randomly complete block design. Each accessions were planted in a plot

size of 1.80 m<sup>2</sup> (3 rows, 1.5m row length, 50 cm between rows and 60 cm between plants within row and spacing of 1,1.5 m between plots and blocks, respectively. Data was collected either on plot basis or from randomly taken 3 plants on days to 50% flowering, leaf length, number of flower buds per race , raceme length (cm) , plant height (cm), number of nodes per raceme , pod length (cm), 100 seed weight (g), dry seed yield per plant (g). The data collected for each quantitative trait was subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2 (SAS, 2008). Treatment means were tested for significance (LSD) at 0.5% probability levels (SAS, 2008).The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by [5] as follows:

$$\text{Environmental variance } (\sigma^2_e) = \text{Mse}$$

$$\text{Phenotypic variance } (\sigma^2_p) = (\sigma^2_g + \sigma^2_e)$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{Mse} - \text{Mst}}{r}$$

Where:

Mse = Mean square error

Mst = Mean square treatment

r = Replication

Phenotypic coefficients of variation (PCV)

$$\text{PVC} = \frac{\sqrt{\delta_p^2}}{\mu} \times 100$$

Where  $\mu$  is the grand mean value of the trait.

Broad sense heritability ( $H^2$ ) in percentage was estimated in each character using variance components as described by DeLacy *et al.*,(1996).

$$h^2_B = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where:

$\sigma^2_p$  = Phenotypic variance

$\sigma^2_g$  = Genotypic variance

x = Grand mean of a character

Genetic Advance (GA) and percentage of the mean (GAM) assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by [13] as:

$$GA = \frac{K \times \sqrt{\sigma^2_p} \times \sigma^2_g}{\sigma^2_p}$$

Where:

GA = Expected genetic advance

k = Standardized selection differential at 5% selection intensity (K = 2.063)

$\sigma^2_p$  = Phenotypic variance

$\sigma^2_g$  = Genotypic variance

The genetic advance as percentage of mean (GAM) was computed as:

$$GAM(\%) = \frac{GA}{x} \times 100$$

Where:

GAM = Genetic advance as percentage of mean

GA = Expected genetic advance

x = Grand mean of a character

Heritability values was classified according to [26]S, greater than 80% as very high, values from 60-79% as moderately high, values from 40-59% as medium and values less than 40% are low.

Genetic advance as percentage of mean (GAM) were classified according to [13]; values from 0-10% are low, 10-20% are moderate and 20% and above are high.

## RESULTS AND DISCUSSION

The genetic estimates of Eldo maridadi genotypic and phenotypic variances, percent genotypic and phenotypic coefficient of variation (GCV%, PCV%), % heritability, genetic advance (GA) and % genetic advance of the mean (GAM%) are given in the table 1 below. The phenotypic variances were higher than genotypic variance among the three accessions (0gy, 300gy and 400gy) of Eldo maridadi. Higher phenotypic variation (PCV) was

observed for number of nodes per raceme (27.05%) at 0gy, number of racemes per plant (25.16%), number of nodes per raceme (20.91%) at 300gy and number of raceme per plant (35.38%), raceme length (21.09%) and plant height (32.68%) at 400gy whereas leaf length (10.75%), number of raceme per plant (12.01%), raceme length (11.78%), pod length (15.04%), dry seed yield per plant (14.22%) at 0gy, raceme length (18.29%), pod length (11.92%), plant height (14.27%), and dry seed yield per plant (11.33%) in 300gy, leaf

length (15.23%), number of nodes per raceme (16.27%) and pod length (14.60%) in 400gy showed medium phenotypic coefficient of variation. 100 seed weight, plant height and days to flowering in 0gy, leaf length, days to flowering and 100 seed weight in 300gy and days to 50% flowering, 100 seed weight and dry seed yield per plant in 400gy showed low phenotypic coefficient of variation.

Medium genotypic coefficient of variation was recorded in number of racemes per plant 15.71%, 14.025 and 16.75% at 0gy, 300gy and 400gy respectively, number of nodes per raceme at 0gy (17.56%) and 300gy (11.38%), plant height 0gy (13.45%), 400gy (18.63%) and raceme length (10.29%) in 300gy the remaining traits showed low genotypic coefficient of variation (<10%). Large difference between PCV and GCV was produced in 0gy on leaf length (10.78% and 5.82%), pod length (15.04% and 8.68%), seed weight (9.04% and 4.59%) and dry seed yield per plant (14.23% and 7.94%). The same trend was noted in 300gy on pod length (11.92% and 5.90%), plant height (14.27% and 7.02%) seed weight (8.04% and 2.19%). On 400gy leaf length (15.53% and 7.00%), number of raceme per plant (35.38% and 16.75%), raceme length (21.09% and 7.34%) number of nodes per raceme (16.27% and 8.60%) pod length (14.60% and 7.84%) and plant height (32.68% and 18.63%)

High heritability was only observed for 0gy in number of racemes per plant (171.05%) and plant height (250.08%). Medium heritability was recorded in raceme length (30.26%), number of nodes per racemes (42.05%), pod length (33.33%) and dry seed yield per plant (31.18%) in 0gy, number of racemes per plant (31.03%), raceme length (31.67%), number of nodes per raceme (32.28%) and days to flowering (32.64%) in 300gy and days to flowering (33.15%), plant height (32.50%), 100 seed weight (33.01%) and dry seed yield per plant (36.20%) in 400gy. The rest of the traits recorded lower heritability values <30%. In the present study moderate genetic advance as percent of mean was estimated for grain yield  $\text{kg ha}^{-1}$

(11.98%) and other traits showed low genetic advances (<10%). High genetic advance of GAM was only recorded in at 0gy in the number of nodes per raceme (36.26%). Moderate (10-20%) GAM was recorded in number of racemes per plant (13.42%) in 0gy and number of nodes per raceme (10.04%) in 300gy. 400gy produced low GAM in the traits

Table 1.Genetic estimates of Eldo maridadi accessions

	TRAITS	$\sigma^2P$	$\sigma^2G$	%PCV	%GCV	%H	GA	%GAM
0gy	LL	1.19	0.35	10.78	5.82	29.11	0.65	6.46
	NRPP	4.94	8.45	12.01	15.71	171.05	2.48	13.42
	RLC	17.98	5.44	11.78	6.48	30.26	3.18	8.85
	NNR	2.64	1.11	27.08	17.56	42.05	2.18	36.26
	DTF	1.47	0.44	1.91	1.05	29.93	0.79	1.25
	PL	0.42	0.14	15.04	8.68	33.33	0.17	3.96
	PH	31.05	77.65	8.51	13.45	250.08	2.38	3.63
	SW	5.61	1.32	9.47	4.59	23.46	1.32	5.28
	DSYPP	133.00	41.47	14.23	7.94	31.18	4.75	5.85
300gy	LL	0.95	0.23	9.44	4.64	24.21	0.49	4.71
	NRPP	24.07	7.47	25.16	14.02	31.03	0.74	3.80
	RLC	40.26	12.75	18.29	10.29	31.67	1.49	4.29
	NNR	1.91	0.62	20.91	11.88	32.28	0.66	10.04
	DTF	12.58	4.11	5.66	3.23	32.64	0.77	1.22
	PL	0.27	0.07	11.92	5.90	24.53	0.10	2.24
	PH	74.56	18.05	14.27	7.02	24.21	0.20	0.33
	SW	4.27	0.32	8.04	2.19	7.39	0.03	0.12
	DSYPP	86.34	24.85	11.33	6.08	28.78	0.08	0.10
400gy	LL	2.71	0.55	15.53	7.00	20.30	0.69	6.49
	NRPP	52.09	11.68	35.38	16.75	22.42	0.79	3.85
	RLC	70.80	8.58	21.09	7.34	12.12	0.75	1.89
	NNR	1.61	0.45	16.27	8.60	27.95	0.53	6.76
	DTF	10.91	3.62	5.28	3.04	33.15	0.73	1.16
	PL	0.30	0.09	14.60	7.84	28.81	0.12	3.23
	PH	417.18	135.59	32.68	18.63	32.50	0.64	1.03
	SW	1.03	0.34	3.87	2.23	33.01	0.07	0.26
	DSYPP	37.51	13.58	7.31	4.40	36.20	0.07	0.08

LL: Leaf length (cm), NRPP: Number of Raceme per plant, RLC: Raceme length (cm), NNR: Number of nodes per raceme, DTF: Days to flowering, PL: Pod length (cm), PH: Plant height (cm), SW: Seed weight (grams) and DSYPP: Dry seed yield per plant.

The coefficients of variation and heritability estimates of the traits of Eldo black I are summarized in Table 2.0. The phenotypic coefficient of variation (PCV) and the genotypic coefficients of variation (GCV) were positive for all the traits. High PCV and GCV were observed in dry seed yield per plant (24.77 and 33.81) in 0gy , number of nodes per raceme (25.56 and 22.25), pod length 106.60 and 150.76) in 300gy and leaf length (74.18 and 39.22),number of nodes per raceme (54.16and 35.71) ,days to flowering (141.37and 51.22) pod length (213.98 and 111.75) and 100 seed weight (117.56 and 64.28) in 400gy per plant (144.8 and 141.6),weight of seeds per plant (82.8 and 74.3). Low phenotypic (PCV) and genotypic (GCV) coefficient of variations were observed in leaf length (9.00 and 6.15), number of days to 50 % flowering (2.06 and 1.52) pod length (5.76 and 2.26) plant height (6.93 and 9.60) and 100 seed weight (6.19 and 2.92) in 0gy. Plant height (6.14 and 8.57) and dry seed yield per plant (4.52 and 6.27) in 300gy. While number of raceme per plant (9.29and 8.57) plant height (6.27 and 6.67) and dry seed yield per plant (4.41 and 2.26) in 400gy.

Traits with high heritability estimates were number of raceme per plant (196.27%), raceme length (97.20%),number of nodes per raceme (61.11%),plant height (192.16%),dry seed yield per plant (186.34%) in 0gy , number of racemes per plant (75.78%),pod length (200%),plant height (185.96%),100 seed weight (159.09%) and dry seed yield per plant (192.45%) in 300gy.Number of raceme per plant (85.01%) and plant height (113.25%).Moderate heritability 30-60% were recorded in leaf length (46.58%) and days to flowering (54.29%) in 0gy.Number of raceme per plant (37.59%) and number of nodes per raceme(43.48%) in 300gy and 400gy respectively.

Table 2. Genetic estimates of Eldo black I accessions

	TRAITS	$\sigma^2P$	$\sigma^2G$	%PCV	%GCV	%H	GA	%GAM
0GY	LL	0.91	0.43	9.01	6.15	46.58	0.41	3.83
	NRPP	10.73	21.05	16.05	22.49	196.27	68.94	337.93
	RLC	21.89	21.28	11.73	11.56	97.20	99.53	249.46
	NNR	1.80	1.10	17.42	13.62	61.11	1.48	19.17
	DTF	1.75	0.95	2.06	1.52	54.29	1.26	1.95
	PL	0.07	0.01	5.76	2.26	15.38	0.00	0.06
	PH	31.88	61.25	6.93	9.60	192.16	345.80	424.30
	SW	2.48	0.55	6.19	2.92	22.22	0.87	3.41
	DSYPP	133.74	249.21	24.77	33.81	186.34	2882.01	6172.66
300GY	LL	1.64	0.38	35.06	16.78	22.90	0.48	13.15
	NRPP	4.99	1.88	18.85	11.56	37.59	4.19	35.34
	RLC	18.64	4.88	10.24	5.24	26.16	21.05	49.93
	NNR	2.01	1.53	25.56	22.25	75.78	2.16	38.98
	DTF	3.45	0.50	25.10	9.56	14.49	0.93	12.55
	PL	0.06	0.11	106.60	150.76	200.00	0.03	11.73
	PH	17.81	33.13	6.14	8.37	185.96	139.80	203.35
	SW	2.20	3.50	18.78	23.68	159.09	5.19	65.71
	DSYPP	31.78	61.15	4.52	6.27	192.45	344.70	276.42
400GY	LL	5.81	1.63	74.18	39.22	27.96	3.92	120.55
	NRPP	14.26	12.13	9.29	8.57	85.01	45.79	112.65

RLC	8.60	0.30	20.22	3.78	3.49	0.88	6.07
NNR	0.58	0.25	54.16	35.71	43.48	0.19	13.54
DTF	6.48	0.85	141.37	51.22	13.13	2.16	120.16
PL	0.11	0.03	213.98	111.75	27.27	0.01	6.42
PH	25.94	29.38	6.27	6.67	113.25	149.60	184.13
SW	3.76	1.13	117.56	64.28	29.90	2.18	132.25
DSYPP	100.42	26.29	4.41	2.26	26.18	263.44	116.00

LL: Leaf length (cm), NRPP: Number of Raceme per plant, RLC: Raceme length (cm), NNR: Number of nodes per raceme, DTF: Days to flowering, PL: Pod length (cm), PH: Plant height (cm), SW: Seed weight (grams) and DSYPP: Dry seed yield per plant

High genetic advance of the mean was observed for the number of racemes per plant 337.93%, 35.34% and 112.65%, plant height (424.30%, 203.35% and 120.16%), dry seed yield per plant 6172.66%, 276.42% and 116.00% in 0gy, 300gy and 400gy respectively. Other traits that recorded high GAM included raceme length 249.46% and 49.93% in 0gy and 300gy. Seed weight 65.71% and 132.25% in 300gy and 400gy, number of nodes per raceme 38.98% in 300gy, leaf length 120.55% and days to flowering 120.16% in 400gy. High heritability with low genetic advance was observed in pod length.

The assessment of variability, expected genetic advances and heritability of agronomic components are significant in crops genetic improvement. Genetic status PCV and GCV in a breeding line is useful for comparing the relative amounts of phenotypic and genotypic variation among traits and to estimate the scope for improvement by selection. The evaluation of genetic estimates in Eldo maridadi and Eldo black I dolichos accessions at M3 showed relatively high phenotypic variance ( $\sigma^2_p$ ) to genotypic variance ( $\sigma^2_g$ ) across the mutation doses. This shows that these characters were under the influence by environment. Phenotype selection alone on the basis of these traits cannot be effective for dolichos improvement. The PCV values were slightly higher than those of GCV by almost half in leaf length, pod length, 100 seed weight, dry seed yield per plant height, number of nodes per raceme and raceme length in 0gy, 300gy and 400gy in both Eldo maridadi and Eldo black I. This effect could be due to the fact that the expression of these traits are highly influenced by environment. Similar findings have also been reported in other studies on soybean [19] and [11] which is in agreement with this present study.

Plant breeders utilize heritability estimates to select accessions based on phenotypic performance and can be used to predict the reliability of a phenotypic value [2]. Effective selection of a particular accession is based therefore, on high heritability of a particular trait of interest such as number of pods per plant. Heritability estimates are classified as low (<30%), medium (30-60%) and high (60% and above) [3]. There was high heritability in 0gy for Eldo maridadi on number of racemes per plant and plant height while for Eldo black I 300gy than 400gy accession it was high in number of raceme per plant, raceme length, number of nodes per raceme, plant height, dry seed yield per plant which indicated that the total variation in these traits are under genetic control and of additive gene action. Selection based on phenotypic levels of these traits in these accessions would be useful in the improvement of these accessions. Similar observations were made on different studies on hyacinthbean [9, 22], mutant soya bean [21]. The low heritability in some traits at 300gy and 400gy (Eldo maridadi), 400gy (Eldo black I) accessions could have been due to some influence of environment and the gene action effect due to mutation.

The estimated percent heritability is not very much useful because it includes the effect of both additive and non-additive gene effects [1]. The genetic advance is therefore a useful

indicator to achieve expected result on the trait of interest after selection. Genetic advance as a percentage of mean is found to give more precise result in comparison to only genetic advance [4]. Genetic advance as percent mean is categorized from low (0-10%), moderate (10-20%) and high ( $\geq 20\%$ ) in the accessions. In the present study based on various traits it indicated mixed variations low to high among the accessions. Eldo maridadi 0gy, 300gy and 400gy accessions had low % GAM except for number of nodes per raceme while Eldo black I recorded high heritability coupled with high genetic advance of the mean in 0gy number of raceme per plant, for raceme length in cm, plant height, dry seed yield per plant, in 300gy number of raceme per plant, raceme length in cm, number of nodes per raceme, plant height, seed weight in grams, and dry seed yield per plant while in 400gy high % GAM was recorded in leaf length, number of racemes per plant, days to flowering plant height, seed weight, dry seed yield per plant. This indicates the lesser influence of environment in expression of these characters in Eldo black 1 genotype and prevalence of additive gene action in their inheritance. Hence, these traits are amenable for simple selection. The existence of variability in heritability and %GAM in the accessions of the two genotypes can be attributed mainly to genotypic differences and response to mutagenic effects. Similar findings have been reported by Khan, S., & Wani, (2006) on yield contributing traits of green gram and mung bean. Following irradiation of seeds material with strong ionizing rays there is formation of genetic distortion and gene shuffling which causes alteration of heritability values.

The percent genetic advance of the mean was low in most of Eldo maridadi which are indicative of non-additive genetic effects in this genotype. Similar results have been reported in other studies by [16] in chick pea mutant accessions in one of the three soya bean genotypes on pod clusters per plant, plant height, number of seeds/pod, 100 seed weight and seed yield/plant [19, 18]. There is restricted scope for the improvement of these characters therefore it is a needful to build a broad germplasm base through collection, introductions or adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously [24].

## CONCLUSION

The high genotypic coefficient of variability and phenotypic coefficient of variability coupled with high heritability and %genetic advance of the mean were observed for characters in Eldo black I compared to Eldo maridadi such as such as plant height, number of racemes per plant, plant height and dry seed yield per plant. This indicated that there was a lesser influence of environment in the expression of these characters which are amenable for selection and also existence of genotypic and uptake of mutational induction differences among the dolichos genotypes. The characters that produced moderate to high heritability and high percent genetic advance of the mean are amenable to simple selection while those that were low are not amenable for selection even with minimizing environmental effect. Hence, other traits can be evaluated or further improvement on genetic variability in the genotypes undertaken.

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