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EVALUATION OF ADVANCED COMMON BEAN (*PHASEOLUS VULGARIS* L.) BREEDING LINES FOR MULTIPLE DISEASE RESISTANCE AND YIELD IN WESTERN KENYA

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ABSTRACT

Common bean (*Phaseolus vulgaris* L.) is one of the most important legume crops in the world, grown for economical and nutritional value. However, its productivity is constrained by diseases such as angular leaf spot, anthracnose, common bacterial blight, halo blight and bean scab. Under favourable conditions, yield losses of between 50 -100 percent have been reported in susceptible cultivars. Identifying and using resistant common bean genotypes with broad resistance is the best economical and sustainable option to reduce the impact of such diseases. So far, no cultivars have been identified with desirable agronomic traits possessing multiple disease resistance (MDR) to these diseases for adoption by dry bean farmers in western Kenya. Field experiments were carried out to evaluate thirty-six advanced dry bean breeding lines for their resistance to major diseases and agronomic performances. The experiment was laid using 6 x 6 lattice design replicated 3 times during the long rain cropping season of 2020. Data on disease severity and agronomic traits were recorded and subjected to analysis using SAS statistical software. Major diseases observed in the field included Angular leafspot, anthracnose, bean scab, common bacterial blight and halo blight. Analysis of variance indicated significant ($p < 0.05$) variations existed among the genotypes for yield and disease resilience. Nine genotypes (CAL 110, CAL 97, RWR 2245, CAL 232A, CAL 51, CAL 70, CAL 94A, CAL 273 and CAL 257) were identified to possess anthracnose, ALS, CBB, halo blight and scab resistance. Among these, genotypes CAL 70, CAL 110, CAL 51, CAL 232A, RWR 2245 and CAL 257 executed well for grain yield. The identified genotypes possessing multiple disease resistance and with good yield potential stand out as potential candidates for release to farmers in the target area and other similar agro-ecologies in Kenya even though further evaluations on farmers' fields are recommended.

Key words: *Phaseolus vulgaris* L., elite germplasm, disease resilience, agronomic performance, yield

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is an important legume grown worldwide for its economic, social importance and high nutritional value [1]. However, diseases remain a major biotic constraint limiting its production. In Kenya, diseases such as anthracnose, angular leaf spot (ALS), common bacterial blight (CBB), halo blight and scab are prevalent across all bean growing regions [2]. Under favourable environmental conditions, yield losses attributed to these diseases range from 50% – 100% in susceptible cultivars [3]. The impact is severe when multiple diseases co-occur within the same field or on individual plants, resulting in total crop failure [4]. This challenge is especially critical in western Kenya, where environmental conditions favour pathogen proliferation, resulting in high disease pressure causing substantial yield losses [5]. Moreover, dry bean production in the region is predominantly practiced under low-input systems by resource-constrained farmers [6]. The widespread use of farm-saved seed, continuous cropping, and poor field sanitation contribute to inoculum build-up, thereby increasing the vulnerability of bean crop to diseases. The lack of access to alternative disease management strategies further exacerbates this situation [7].

Presently, in most farming systems, diseases are managed through chemicals and cultural practices such as crop rotation and cultivar mixtures [8]. However, these control measures cannot be fully practiced due to land shortage and high cost of chemicals that poor resource endowed farmers cannot afford [9]. Thus, development and use of resistant cultivars presents a viable alternative that is least expensive and easy for farmers to adopt Mundt [10], because resistance is already embedded in the seed farmers' plant. The use of multiple disease resistance (MDR) cultivars possessing desirable agronomic traits are well-suited to smallholder farming systems, like those in western Kenya. The MDR offers the plant ability to resist two or more diseases simultaneously, beyond single-disease resistance. Resistance to multiple diseases results from several mechanisms; pleiotropic genes, where a single gene influence plant's resistance to multiple diseases; cluster resistant genes (R genes) that confer resistance to various diseases or insect pests and linked genes that are closely spaced on chromosome, each conferring resistance to a different disease. Resistance to multiple diseases is a highly valuable trait in plant breeding programs that aim to develop varieties resistant to a wide range of diseases to reduce crop losses and increase productivity [4].

Evaluation of common bean genotypes under natural infection for two or more diseases to identify elite genotypes is important because this counteracts with the newly evolving pathogen races to reinforce established resistance in existing cultivars [11,12]. Most of the varieties cultivated in the Western Kenya have not exhibited enough resilience to multiple diseases, posing a significant challenge to



sustainable dry bean production. Consequently, there is a need to identify common bean genotypes that combine high yield potential with broad resistance. With this in mind, the current study assessed advanced common bean breeding lines for resistance to major diseases under natural conditions and evaluated their agronomic performance.

MATERIALS AND METHODS

Plant genetic materials

Genetic materials for the study comprised of thirty-one advanced dry bean lines of Calima genetic background obtained from KALRO - Kakamega legume breeding programme and five check varieties. The lines were developed for root rot resistance by crossing GLP 2 (a commercial variety susceptible to bean root rot) to resistance donors (MLB-49-89, RWR 719, SCAM-CM 80/15, AND 1062 and AND 155) although some of the parents' showed resistance to some diseases [6]. They are of preferred market-classes (seed color and seed size) which give them an advantage for release and high adoption rate by farmers. The checks comprised of GLP 2 and KK 8; market-class varieties that have been in commercial production and popular with farmers in the region while G2333, MCM 2001 and VAX 3 are known resistance donors for anthracnose, BCMV/BCMNV and CBB, respectively. (Table 1, Figure 1).



Figure 1: Colour of some genotypes under evaluation

The study was conducted at the Kenya Agricultural & Livestock Research Organization (KALRO – Kakamega), located (00°, 17' N and 34°, 47' E) with an elevation of 1585 m above sea level [13]. The station falls in a bimodal climate region

with an average annual rainfall of 1200 mm and average annual temperature of 21 to 27°C [6]. The long rain season is March - June and while the short rain season is August - November [13]. The site is one of the major common bean production areas in the region. However, it experiences warm and humid weather conditions conducive to the development of bean pathogens and thus, a disease hotspot for bean germplasm screening [14].

Experimental design and crop management

The experiment was set up on KALRO Kakamega farm during the long rain season of 2020 (April – July). Trials were laid in a 6 x 6 lattice design with three replications. The plots consisted of 12 plants sown in a 1 m row spaced 0.2 m within rows and 0.5m between rows. The seeds were planted in four rows per plot and 12 plants were maintained per row. Di-ammonium phosphate was applied at a rate of 50 Kg ha⁻¹ at planting. Weeding was carried out three times: two weeks after seedling emergence, before flowering and after podding [6]. The plants were subjected to natural disease infection and development.

Disease severity assessment and data analysis

The genotypes were evaluated for disease severity at the vegetative, flowering (R6) and podding (R8) growth stages. Disease identification was based on characteristic symptoms developed on the plants. Disease severity was scored using the standard system for evaluation of bean germplasm [15]. Final disease scores were used to classify the genotypes into three categories: resistant (scores 1–3), intermediate (scores 4–6), and susceptible (scores 7–9).

Agronomic Data

Six plants were randomly selected from two central rows of each plot to determine yield and yield components. The number of pods per plant was recorded by counting all the pods on selected plants while number of seeds per pod was determined by counting seeds from ten randomly sampled pods taken from the six randomly selected plants. Grain yield was estimated from the harvest of two central rows. Seed weight was determined using a random sample of 100 seeds and extrapolated to yield (t ha⁻¹) at 12.5% moisture content using the formula below [16].

$$\text{Grain yield (Kg/ha)} = \frac{\text{Plot yield (kilograms X 1000)}}{\text{Plot size in meters (M}^2\text{)}}$$



Statistical analysis

Data on disease severity, growth, yield and yield parameters were subjected to analysis of variance (ANOVA) of SAS GLM procedure and means separated using Duncan's Multiple Range Test (DMRT) at 5% probability level [17].

RESULTS AND DISCUSSION

Sustainable dry bean production in Kenya is dependent on availability of cultivars possessing MDR with desirable farmer and market-preferred traits. In this study, selection focused on multiple disease resistance beside agronomic traits. The major diseases observed in the field were ALS, BCMV, BCMNV, CBB, anthracnose and scab (Figure 2).

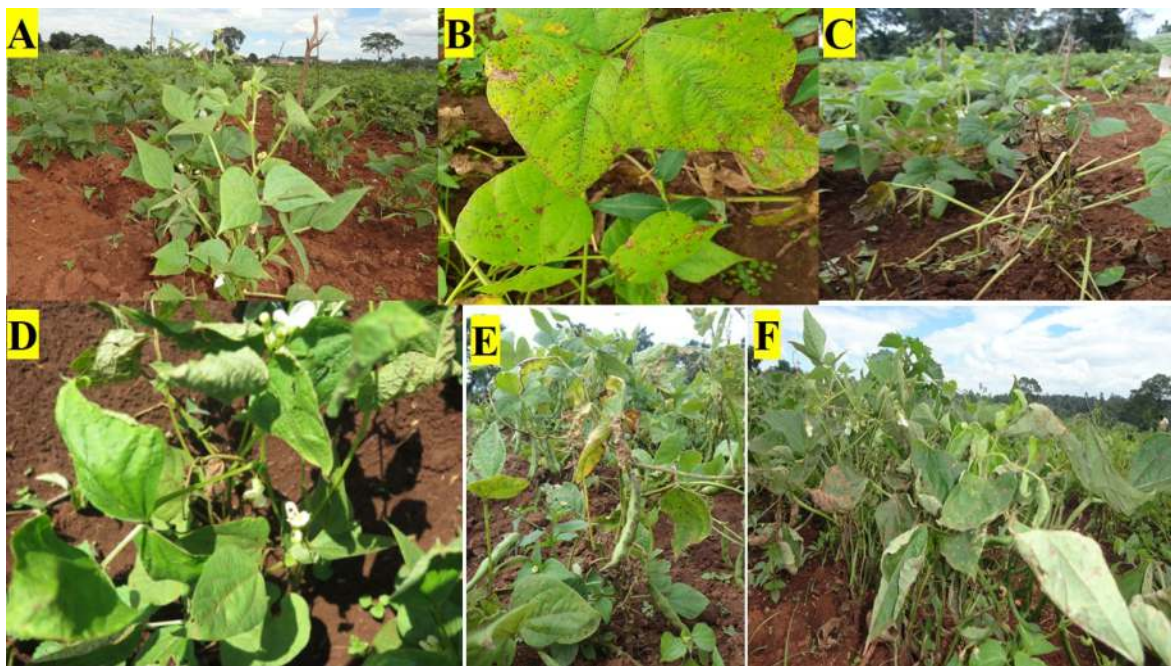


Figure 2: Reaction of the breeding lines to various diseases under field conditions. A -No disease, B- ALS and CBB, C- BCMNV, D & E - anthracnose and F - Scab

These diseases have also been documented previously in western region and Kenya at large, confirming their economic importance [2,3,5,6]. They have also been reported in neighboring countries like Uganda [18], Ethiopia [19], Rwanda [20] and Tanzania [21] causing severe losses. As observed in our study, there were multiple coinfections of pathogens on the plants. This agrees with earlier findings that diseases appear in complexes of two or more and rarely singly in the field [4,12]. This is clear evidence that bean breeding for disease resistance should target multiple pathogens for durable resistance.

Majority of genotypes exhibited resistance to most diseases, although few lines were susceptible to one or more pathogens (Table 2). All the genotypes were resistant to halo blight, whereas only CAL 257 was susceptible to ALS. Regarding CBB and anthracnose, six and three lines were susceptible respectively and ten genotypes showed scab resistance (Figure 3). The observed phenotypic resistance suggests presence of underlying genetic resistance inherited from the parents. These lines, derived from GLP2; a widely cultivated commercial variety for over two decades and popular with farmers [22], that contributed to the observed resistance resulting from prolonged exposure to selection pressure. It was used a check variety, and it showed resistance to CBB, anthracnose and halo blight. Results of this study confirm observation that earlier generations of these lines were resistant to some diseases [6].

However, some lines were susceptible to anthracnose, ALS, CBB and bean scab. The observed susceptibility could be attributed to breakdown of host resistance by pathogens [8]. Because of the inherent evolutionary variability of pathogens over time, new strains develop that overcome previous incorporated resistance [19]. Furthermore, the observed susceptibility in some genotypes could be explained by the fact that resistance alleles may not have been fixed during the breeding process, due to genetic recombination rendering them susceptible [23].

Use of certified seed sourced from KALRO also contributed to the observed resistance given that these diseases are seed-borne. Use of farm-saved seed has been reported as a major source of inoculum for seed-borne diseases in common bean [24]. Since most bean farmers in the region are small scale producers who rely on farm-saved seeds or obtain seed from informal sources that are usually infected, leading to spread of seed-borne pathogens such as anthracnose, angular leaf spot, common bacterial blight and various virus complexes Dube *et al.* [25]. These findings highlight the importance of using certified seed among bean farmers to minimize inoculums levels in the field.



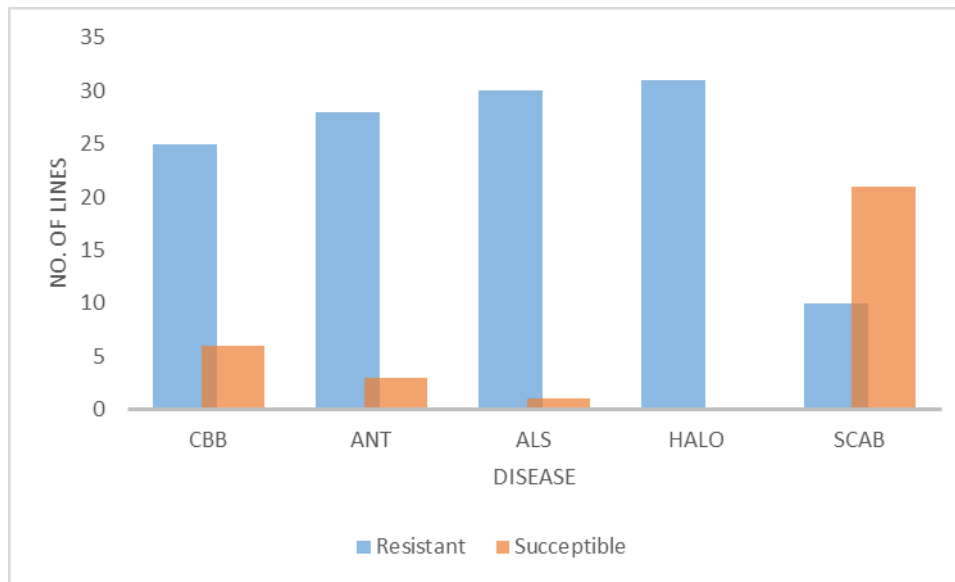


Figure 3: Number of resistant / susceptible genotypes per constraint

Scab is an emerging disease in western Kenya of great economic significance, yet it has not been considered in previous breeding programmes [26]. Hence, there has been an inoculum build-up overtime resulting in high scab pressure. It is not surprising that most genotypes succumbed to this disease. However, the identification of scab resistance in three genotypes (CAL 110, RWR 2245, CAL 232A) presents a valuable opportunity for incorporating this trait into future bean breeding programmes.

Significant variations ($p < 0.05$) for days to 50% flowering, physiological maturity, plant height, number of pods per plant (NPP), number of seeds per pod (NSP), hundred seed weight (HSW) and grain yield were observed across genotypes (Table 3). A difference of 6.0 and 12.0 days was observed between the longest and shortest days to flowering and maturity, respectively. Similar variations in days to flowering and physiological maturity in common bean genotypes have been reported by Yohannes *et al.* [27]. Genotypes CAL 51, CAL 108A, RWR 2245 and CAL 232B flowered early and would be ideal for cultivation by farmers who prefer early maturing varieties during the short rainy season, hence play an important role in sustainable dry bean production as they would motivate farmers to bring more land under bean cultivation. On the other hand, CAL 194, CAL 97A, CAL 251, CAL 94A, CAL 232A, CAL 66A and CAL 302A took longer to flower, implying they mature late. This is not interesting because late maturing genotypes are less preferred by farmers due to their reduced adaptability to harsh climatic conditions. Moreover, delayed flowering has been associated with a reduction in the number of seeds per pod, seed weight and overall yield [28].

Significant differences were obtained for plant height, number of seed per pod, pod length, 100-seed weight and yield (Table 4). The number of pods per plant is a yield component with the largest influence on bean yield as it includes other yield related traits like number of seeds per pod and hundred seed weight. Our findings reveal that genotypes (G2333, CAL 180A and CAL 77A) had high number of pods per plant while the highest number of seeds per pod was observed in G2333, CAL 177A and CAL 165A. These genotypes had indeterminate growth habits and did not give high grain yields. These findings agree with previous reported results [29]. Contrastingly, Wortmann *et al.* [30] reported that common beans with climbing growth habits were high yielding, hence ideal for small-scale farmers with small sizes of land. However, climbing genotypes are labor-intensive as they require staking and may not be ideal for mixed cropping [31]. Hence, bush types are preferred because they do not require support and are early maturing convenient for commercial production [32].

Significant variation in 100-seed weight and grain yield was observed among the evaluated genotypes. The highest 100-seed weight was recorded in CAL 110 (46.7g) followed by RWR 2245 (45.3g) and CAL 232A (45.2g); that also produced the highest yields (Table 5). Similar variations in yield and seed weight among bean cultivars have been reported by Motlatsi *et al.* [33]. Yield is a complex polygenic trait governed by multiple genes and is highly influenced by environmental factors, making its selection less effective. However, direct selection for heritable traits that exhibit strong correlations with yield can result in greater genetic gains in breeding programs [34].

Correlation coefficient

Among the yield components: Number of pods per plant and 100 seed weight showed a strong positive relationship with yield while pod length and number of seeds per pod had a low positive correlation with yield (Table 5). On contrary, Alemu *et al.* [35] observed negative relationship between yield and number of pods per plant and postulated that this may be caused by negative indirect effects of this trait on number of grains per pod and per plant and on 100-grain weight. Grain yield is a polygenic trait that is influenced by yield components such as pods per plant, seeds per pod and seed weight [36]. In the present study, a significant positive but weak relationship between grain yield and pod length (0.11) and seeds per pod (0.33) are important yield determinants, so selection could be done focusing on these traits to improve grain yield. There were strong positive correlations between yield and number of pods per plant (0.85) and 100 seed weight (0.80). Similar findings have been reported [37,38]. This finding showed that if pod length, number of pods per plant and 100 seed weight were improved, a significant grain yield response would be expected. On the contrary, grain yield also showed negative relationship with days to flowering, maturity and plant height. Similar negative correlation between



seed weight and the number of pods per plant, number of seeds per plant and days to maturity in beans have been reported by Okii *et al.* [32] and Loko *et al.* [39].

Genotypes CAL 51, CAL 70, CAL 110, CAL 232A, CAL 257 and RWR 2245 had a yield advantage over KK8, a commercial check. (Table 6). Fortunately, these genotypes were also resistant to most diseases. Since diseases cause yield loss in common beans [Kimani *et al.* 3], we hypothesize that disease tolerance in these genotypes gave compensatory growth that contributed to higher yields. Ribeiro *et al.* [37] reported that even in resistant cultivars, pathogens reduce yield, although it is not as drastic as in susceptible cultivars, and this makes crop yield levels viable even though the pathogen is widespread in common bean production regions. On contrast, five genotypes (CAL 70, CAL 135, CAL 165, CAL 192 and CAL 235) exhibited significantly reduced ($p < 0.05$) yields and heightened susceptibility to CBB, anthracnose, halo blight and scab. However, Nkalubo [40], reported that yields varied significantly among different accessions but not between resistant classes. These discrepancies may arise because yield is a complex trait influenced by multiple physiological and environmental factors [36].

Our study identified six genotypes (CAL 51, CAL 110, RWR 2245, CAL 232A, CAL 70, and CAL 257) with superior yield advantage (Figure 4, table 6). These high-performing genotypes are candidates for release in the study region and other agro-ecological zones with similar constraints after conducting multi-location trials under farmer-managed conditions to confirm their resistance and adaptability.

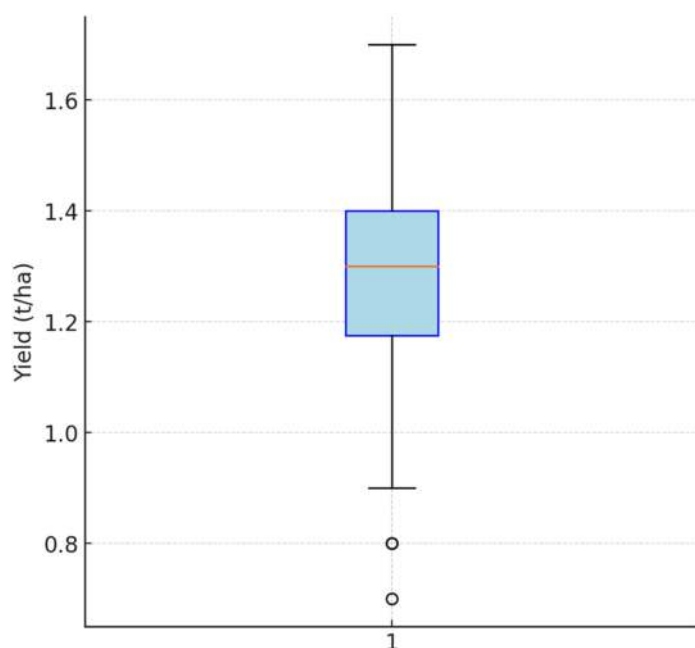


Figure 4: A box plot on yield

CONCLUSION AND RECOMMENDATIONS FOR DEVELOPMENT

Nine genotypes (CAL 110, CAL 97, RWR 2245, CAL 232A, CAL 51, CAL 70, CAL 94A, CAL 273 and CAL 257) exhibited ALS, CBB, anthracnose, halo blight and scab resistance. Among these, CAL 110, CAL 51, CAL 70, CAL 232A, RWR 2245 and CAL 257 displayed superior yield performance. These genotypes are promising candidates for varietal release and as donors in breeding programs to improve resistance to multiple diseases in common bean. Further genetic and molecular studies are warranted to determine the number, nature, and inheritance patterns of resistance genes present in these genotypes.

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Conflict of interest

The authors affirm that there are no conflicts of interest regarding the publication of this paper.



Table 1: Characteristics of advanced lines evaluated under field conditions at KALRO – Kakamega

Genotype	Growth habit	Days to maturity	Seed size	Seed colour
Cal 257	II	84	Medium	Red Calima
Cal 254	I	83	Small	Red Calima
Cal 110	II	84	Medium	Red Calima
Cal 143A	I	82	Large	Red Calima
Cal 194	I	83	Medium	Red Mottled
Cal 135	II	86	Medium	Red Calima
Cal 51	I	80	Medium	Red Calima
Cal 180A	I	79	Medium	Red Calima
Cal 207	II	84	Medium	Red Calima
Cal 203	II	83	Small	Red Calima
Cal 97A	II	80	Medium	Red Calima
Cal 304A	II	84	Medium	Red Calima
Cal 70	I	90	Small	Red Calima
Cal 251	I	84	Small	Red Calima
Cal 192	I	84	Medium	Red Calima
RWR 2245	I	83	Large	Red Calima
Cal 232B	I	81	Medium	Red Calima
Cal 165A	I	84	Large	Red Calima
Cal 270	I	83	Medium	Red Calima
Cal 177B	I	80	Medium	Red Calima
Cal 176B	I	84	Medium	Red Calima
Cal 77A	II	84	Large	Red Calima
Cal 235	II	82	Large	Red Calima
Cal 94A	I	84	Medium	Red Calima
Cal 101B	II	82	Large	Red Calima
Cal 232A	I	86	Small	Red Calima
Cal 66A	II	80	Small	Red Calima
Cal 195B	I	81	Medium	Red Calima



Cal 181	I	83	Medium	Red Calima
Cal 273	I	84	Medium	Red Calima
Cal 302A	I	84	Small	Red Calima
Checks				
GLP 2	I	82	Large	Red Mottled
G2333	IV	85	Small	Red
KK 8	I	82	Medium	Red Mottled
MCM 2001	III	78	Small	Red
VAX 3	II	75	Small	Red

Source: KALRO (2019)

Table 2: Mean disease severity scores for major field diseases among common bean lines evaluated at KALRO Kakamega

LINE	CBB	ANTH	ALS	HALO	SCAB
CAL257	2.7	2.7	3.3	2.3	3.0
CAL254	2.7	3.3	2.3	2.7	3.7
CAL110	2.0	2.0	2.0	2.3	2.3
CAL143A	2.0	2.3	2.3	2.0	2.7
CAL194	3.7	3.7	2.0	2.7	3.7
CAL135	3.3	2.3	2.0	2.7	3.3
CAL51	2.3	2.7	2.0	2.3	3.0
CAL180A	2.7	3.0	2.0	2.7	3.3
CAL207	3.0	3.0	2.3	2.7	3.3
CAL203	2.7	2.3	2.7	2.7	3.7
CAL97A	2.0	2.3	2.7	2.7	3.7
CAL304A	2.3	3.3	2.3	2.3	3.7
CAL70	3.3	2.7	2.7	2.7	2.3
CAL251	2.7	2.3	2.0	2.7	3.7
CAL192	4.7	2.7	2.7	2.7	4.0
RWR2245	2.0	2.0	2.0	2.0	3.0
CAL232B	3.3	3.0	2.3	3.0	3.3



CAL165A	3.7	3.0	2.3	3.3	4.0
CAL270	2.7	2.3	2.0	2.7	4.0
CAL177B	2.3	2.7	2.3	2.3	3.3
CAL176B	2.3	2.7	2.3	2.3	3.7
CAL77A	2.0	2.3	2.0	2.3	3.3
CAL235	2.3	3.3	2.0	2.3	4.0
CAL94A	2.7	2.7	2.3	3.0	3.0
CAL101B	2.0	2.3	2.3	3.0	3.7
CAL232A	2.0	2.0	2.0	2.0	2.0
CAL66A	2.3	2.0	2.3	2.7	3.3
CAL195B	2.0	2.7	2.3	2.0	3.7
CAL181	2.3	3.0	2.7	2.3	3.7
CAL273	2.0	2.7	2.0	2.3	2.7
CAL302A	2.7	2.7	2.7	2.0	3.7
Checks					
GLP2	3.0	2.0	3.7	2.0	3.7
KK8	3.0	2.7	2.0	2.3	3.3
VAX3	2.0	3.3	2.3	3.0	3.3
G2333	3.7	2.0	3.0	3.3	4.0
MCM2001	2.3	3.7	2.3	3.3	3.3
Mean	2.5	2.7	2.3	2.5	3.4
CV	17.9	23.0	19.3	24.0	16.3

Significantly different at ($P \leq 0.05$). CBB= common bacterial blight; ANTH= anthracnose; ALS= angular leafspot; HALO= halo blight



Table 3: Variability parameters for agronomic traits, seed yield and yield components among bean genotypes grown at KALRO Kakamega

Trait	Mean	Range	Min	Max	Variance	SE	CV %
Days to flowering	39.3	6.0	37.0	43.0	2.4	0.3	2.1
Days to maturity	81.5	12.0	77.0	89.0	4.0	0.3	1.3
Plant height (cm)	56.3	83.0	17.0	100.0	196.90	2.3	29.0
Pods / plant (No.)	10.7	26.0	3.0	29.0	24.44	0.8	18.9
Pod length (cm)	13.9	17.0	4.0	21.0	12.36	0.6	41.2
Seeds / pod (No.)	4.1	4.0	2.0	6.0	0.45	0.1	21.7
100-seed weight (g)	38.6	19.9	26.8	46.7	18.07	0.7	11.0
Yield (t/ha)	1.6	2.5	0.7	3.2	0.075	0.1	26.1

Table 4: Mean values for agronomic traits of common bean genotypes and checks evaluated at KALRO Kakamega

Genotype	DF (days)	DM (days)	PH (cm)	Pod/plant (No)	Pod length (cm)	Seeds/pod (No.)	100-seed weight (g)	Yield (t/ha)
CAL 257	38.7 ^{efgh}	82.0 ^{efgh}	51.7 ^{abcdef}	10.3 ^{bcd}	10.0 ^{bcde}	4.3 ^{abcde}	38.7 ^{bcde}	1.5 ^{bc}
CAL 254	38.3 ^{ghi}	82.3 ^{defg}	69.3 ^{abcd}	14.7 ^{abcd}	9.7 ^{bcde}	4.3 ^{abcde}	37.3 ^{bcde}	1.3 ^{bcde}
CAL 110	39.0 ^{efgh}	82.0 ^{efgh}	64.7 ^{abcde}	15.3 ^{abcd}	9.7 ^{bcde}	5.0 ^{abcd}	46.7 ^a	1.7 ^{ab}
CAL 143A	37.6 ^{hi}	81.3 ^{efghij}	56.0 ^{abcdef}	15.0 ^{abcd}	10.7 ^{abcde}	4.3 ^{abcde}	33.9 ^{defg}	1.4 ^{bcd}
CAL 194	41.7 ^{ab}	82.0 ^{defgh}	68.3 ^{abcde}	10.3 ^{bcd}	11.0 ^{abcde}	3.7 ^{bcde}	39.3 ^{abcd}	1.4 ^{bcd}
CAL 135	39.7 ^{defg}	84.0 ^{bcd}	74.3 ^{abc}	7.7 ^d	9.3 ^{bcde}	3.7 ^{bcde}	41.1 ^{abcd}	1.2 ^{cdefg}
CAL 51	37.6 ^{hi}	79.3 ^{ijk}	43.7 ^{bcdef}	12.3 ^{bcd}	9.0 ^{cde}	3.3 ^{cde}	40.6 ^{abcd}	1.7 ^a
CAL 180A	37.0 ⁱ	78.0 ^{kl}	52.0 ^{abcdef}	21.3 ^{ab}	12.3 ^{abc}	4.7 ^{abcd}	35.7 ^{cdef}	1.1 ^{cdefg}
CAL 207	39.3 ^{efgh}	81.3 ^{efghij}	59.0 ^{abcdef}	7.7 ^d	10.7 ^{abcde}	3.7 ^{bcde}	38.0 ^{bcde}	1.3 ^{bcdef}
CAL 203	40.3 ^{bcde}	82.0 ^{defgh}	51.0 ^{abcdef}	10.3 ^{bcd}	10.7 ^{abcde}	4.7 ^{abcd}	42.3 ^{abcd}	1.3 ^{cdef}
CAL 97A	41.7 ^{ab}	79.3 ^{ijk}	44.3 ^{bcdef}	12.3 ^{bcd}	9.7 ^{bcde}	3.7 ^{bcde}	42.1 ^{abcd}	1.2 ^{cdefg}
CAL 304A	39.0 ^{efgh}	82.7 ^{def}	67.3 ^{abcde}	11.3 ^{bcd}	11.7 ^{abcd}	4.0 ^{bcde}	41.0 ^{abcd}	1.3 ^{cdef}
CAL 70	40.3 ^{bcde}	88.3 ^a	76.0 ^{ab}	16.3 ^{abcd}	9.7 ^{bcde}	3.7 ^{bcde}	42.6 ^{abc}	1.5 ^{bc}
CAL 251	41.0 ^{abcd}	82.7 ^{def}	75.3 ^{abc}	17.3 ^{abcd}	11.3 ^{abcd}	4.7 ^{abcd}	37.8 ^{bcde}	1.4 ^{bcd}
CAL 192	38.0 ^{hi}	83.0 ^{cde}	63.7 ^{abcdef}	13.7 ^{abcd}	12.0 ^{abcd}	4.0 ^{bcde}	37.8 ^{bcde}	1.4 ^{bcd}
RWR 2245	37.6 ^{hi}	81.0 ^{efghij}	43.3 ^{bcdef}	17.0 ^{abcd}	10.7 ^{abcde}	4.7 ^{abcd}	45.3 ^{ab}	1.7 ^a



CAL 232B	37.7 ^{hi}	79.3 ^{jk}	37.7 ^{def}	10.0 ^{bcd}	12.3 ^{abc}	3.3 ^{cde}	38.6 ^{abcde}	1.4 ^{bcd}
CAL 165A	40.0 ^{cdef}	82.7 ^{def}	75.7 ^{abc}	14.7 ^{abcd}	12.0 ^{abcd}	5.0 ^{abc}	40.0 ^{abcd}	1.0 ^{defg}
CAL 270	39.3 ^{efgh}	79.7 ^{ijk}	42.7 ^{cdef}	9.7 ^{cd}	10.7 ^{abcde}	3.7 ^{bcd}	38.6 ^{abcde}	1.2 ^{cdefg}
CAL 177B	37.7 ^{hi}	85.3 ^b	50.7 ^{abcdef}	15.0 ^{abcd}	9.7 ^{bcde}	5.3 ^{ab}	42.5 ^{abc}	1.2 ^{cdefg}
CAL 176B	38.3 ^{ghi}	82.3 ^{defg}	50.0 ^{abcdef}	13.3 ^{bcd}	10.3 ^{bcde}	3.7 ^{bcde}	35.8 ^{cdef}	1.4 ^{bcd}
CAL 77A	38.0 ^{hi}	81.3 ^{efghij}	60.3 ^{abcdef}	21.0 ^{abc}	14.7 ^a	4.3 ^{abcde}	42.2 ^{abcd}	1.4 ^{cd}
CAL 235	38.0 ^{hi}	80.0 ^{hijk}	62.3 ^{abcdef}	15.3 ^{abcd}	11.3 ^{abcd}	4.7 ^{abcd}	37.2 ^{bcde}	1.2 ^{cdefg}
CAL 94A	41.3 ^{abc}	81.3 ^{efghij}	63.3 ^{abcdef}	11.7 ^{bcd}	9.7 ^{bcde}	4.3 ^{abcde}	39.8 ^{abcd}	0.9 ^{gf}
CAL 101B	38.7 ^{fgh}	80.7 ^{efghij}	60.7 ^{abcdef}	10.7 ^{bcd}	11.0 ^{abcde}	4.3 ^{abcde}	36.2 ^{cdef}	1.4 ^{cd}
CAL 232A	41.3 ^{abc}	81.0 ^{efghij}	71.7 ^{abc}	18.7 ^{abcd}	9.0 ^{cde}	4.7 ^{abcd}	45.2 ^{ab}	1.6 ^{ab}
CAL 66A	41.7 ^{ab}	80.0 ^{hijk}	57.0 ^{abcdef}	17.7 ^{abcd}	8.0 ^{de}	3.0 ^{de}	36.2 ^{cdef}	1.0 ^{defg}
CAL 195B	37.7 ^{hi}	80.3 ^{efghij}	36.0 ^{ef}	12.3 ^{bcd}	11.0 ^{abcde}	3.3 ^{cde}	38.2 ^{bcde}	1.2 ^{cdefg}
CAL 181	38.7 ^{fgh}	81.6 ^{efghi}	77.7 ^a	13.7 ^{abcd}	10.0 ^{bcde}	4.7 ^{abcd}	36.0 ^{cdef}	1.1 ^{defg}
CAL 273	38.3	82.0 ^{defgh}	63.3 ^{abcdef}	14.3 ^{abcd}	11.3 ^{abcd}	4.7 ^{abcd}	35.0 ^{cdef}	1.4 ^{cd}
CAL 302A	41.3 ^{abc}	81.0 ^{efghij}	35.7 ^{ef}	14.0 ^{abcd}	7.0 ^e	2.7 ^e	42.3 ^{abcd}	0.7 ^g
GLP 2	37.0 ⁱ	77.3 ^l	31.3 ^f	12.0 ^{bcd}	12.7 ^{abc}	4.0 ^{bcde}	38.6 ^{abcde}	1.2 ^{cdefg}
KK 8	39.0 ^{efgh}	81.0 ^{efghij}	38.7 ^{def}	9.7 ^{cd}	11.0 ^{abcde}	3.7 ^{bcde}	41.5 ^{abcd}	1.5 ^{bc}
VAX 3	40.0 ^{cdef}	82.0 ^{defgh}	38.0 ^{def}	16.7 ^{abcd}	11.0 ^{abcde}	4.0 ^{bcde}	30.3 ^{efg}	0.8 ^{gf}
G2333	41.3 ^{abc}	84.7 ^{bc}	79.7 ^a	25.0 ^a	13.3 ^{ab}	6.0 ^a	26.8 ^g	1.1 ^{defg}



MCM2001	42.3 ^a	80.0 ^{hijk}	36.0 ^{ef}	12.0 ^{bcd}	11.0 ^{abcd}	4.0 ^{bcd}	28.5 ^{fg}	0.8 ^{fg}
Overall Mean	39.3	81.5	56.3	10.7	13.9	4.2	38.6	1.3
CV	2.1	1.3	29.0	18.9	41.2	21.7	11.0	26.1
LSD _{0.05}	0.7	1.2	267.5	4.1	32.7	0.8	0.7	0.2



Table 5: Correlation coefficient for agronomic traits of common bean lines evaluated at KALRO Kakamega

Correlation	DF	DM	PH	Pods/plant	Pod length	Seeds/pod	100 seed wgt	Yield
DF	1							
DM	0.43	1						
PH	0.10 [*]	-0.14	1					
Pods/plant	-0.26	-0.22	0.08	1				
Pod length	-0.19	-0.11	0.08	0.28	1			
Seed/pod	0.12	-0.03	0.32	0.33	0.08	1		
100 seed weight	-0.22	0.04	-0.04	0.74 [*]	0.10	0.42	1	
Yield	-0.28	-0.03	-0.09	0.85 [*]	0.11	0.33	0.80 [*]	1

^{*}Significant at 5% probability level, DF = Days to flowering, DM =Days to maturity, PH= Plant height

Table 6: Yield advantage of best performing genotypes over commercial check (KK8)

Genotype	Yield (t/ha)	Yield advantage %	Rank	Remark
CAL 110	1.7	21.4	1	
CAL 51	1.7	21.4	1	
RWR 2245	1.7	21.4	1	
CAL 232A	1.6	14.3	4	
CAL 70	1.5	7.1	5	
CAL 257	1.5	7.1	5	
KK8	1.4	*		*Not meaningful

REFERENCES

1. **Givanildo RS, Marcos ARG, Gonçalves-Vidigal MC, Serafim ME, Romano LR, Neves LG and ASG Thiago** Common bean line selection for drought resistance. *Bean Improvement Cooperative*, 2020; **63**.
2. **Leitich KR, Omayio DO, Mukoye B, Mangeni CB, Wosula WD, Arinaitwe W, Otsyula MR, Were KH and MM Abang** Pathogenic Variability of Angular Leaf Spot Disease of Common Bean in Western Kenya. *International Journal of Applied Agricultural Sciences*, 2016; **2(6)**: 92-98.
3. **Kimani MP, Njau S, Mulanya M and DR Narla** Breeding runner bean for short-day adaptation, grain yield, and disease resistance in Eastern Africa. *Food Energy Security*, 2019; 1-12.
4. **Degu T, Yarega W and T Gudisa** Status of Common Bean (*Phaseolus vulgaris* L.) Diseases in Metekel Zone, Northwest Ethiopia. *Journal Plant Pathology Microbiology*, 2020; **11(5)**: 494. <https://doi.org/10.35248/2157-7471.20.11.494>
5. **Masheti OY** Performance of bean genotypes under disease pressure in different environments and planting dates in western Kenya. (A Master's of Science dissertation, University of Nairobi), 2019.
6. **Kenya Agricultural and Livestock Research Institute, Kakamega.** Annual Report, 2017.
7. **One Acre Fund.** Improved Bean Seed, 2015 full scale report. 2015.
8. **Ddamulira G, Mukankusi C, Ochwo-Ssemakula M, Edema R, Sseruwagi P and P Gepts** Gene Pyramiding Improved Resistance to Angular Leaf Spot in Common Bean. *American Journal of Experimental Agriculture*. 2015;**9(2)**: 1-12.
9. **Khan M and CA Damalas** Farmers' knowledge about common pests and pesticide safety in conventional cotton production in Pakistan. *Crop. Protection*, 2015; **77**: 45–51.
10. **Mundt C** Durable Resistance: A Key to Sustainable Management of Pathogens and Pests Infection, Genetics and Evolution, 2014; **27**:446-455.



11. **Fininsa C and T Tefera** Multiple disease resistance in common bean genotypes and their agronomic performance in Eastern Ethiopia. *International Journal of Pest Management*, 2006; **52(4)**: 291 – 296.
12. **Girma F, Fininsa C, Terefe H and B Amsalu** Evaluation of common bean (*Phaseolus vulgaris*) genotypes for resistance to common bacterial blight and angular leaf spot diseases, and agronomic performances. *Heliyon*. 2022; **8**.
13. **Jaetzold R, Schmidt H, Hornetz B and C Shisanya** Farm Management Handbook of Kenya. VOL. II– Natural Conditions and Farm Management Information –2nd Edition. Ministry of Agriculture, Kenya and the German Agency for Technical Cooperation (GTZ), Nairobi, Kenya, 2009; **2**:1-573.
14. **Kimno SK, Kiplagat OK, Arunga EE and E Chepkoech** Evaluation of Selected French Bean (*Phaseolus vulgaris* L.) Genotypes for Resistance to Angular Leaf Spot (*Pseudocercospora griseola*) in Western Kenya. *American Journal of Experimental Agriculture*, 2016; **13(4)**: 1-6. Article no. AJEA.26874 ISSN: 2231-0606.
15. **Van Schoonhoven A and MA Pastor-Corrales** Standard system for the evaluation of bean germplasm, Calli: CIAT, 1987.
16. **FAO**. United Nations Food and Agricultural Organization. Farming Systems Approach Development and Appropriate Technology Generation. FAO, 1995.
17. **SAS Institute Inc**. SAS statistical computer software Version 9.4, 2019 <https://support.sas.com/documentation/onlinedoc/stat>
18. **Mukankusi C, Raatz B, Nkalubo S, Berhanu F, Binagwa P, Kilango M, Magdalena W, Katungi E, Chirwa R and S Beebe** Genomics, genetics and breeding of common bean in Africa: A review of tropical legume project. *Plant Breeding*. 2019; **138**:401–414.
19. **Gabrekiristos E and M Wondimu** Emerging and Reemerging Diseases of Common Bean (*Phaseolus vulgaris* L.) in Major Production Areas: In the Case of Ethiopia. *Journal Plant Pathology Microbiology*. 2022; **13**: 619.
20. **Mukamuhirwa F, Bizimana JP and L Kankundiye** Yield and Agronomic Performance of Selected Bean Varieties against Major Bean Diseases in Rwanda. *Advances Crop Science Technology*, 2022; **10**:534.



21. **Mvile B** Genotype x environment interaction of common bean (*Phaseolus vulgaris* L.) genotypes on reaction to four bean diseases (Doctoral dissertation, Sokoine University of Agriculture). 2015.
22. **Kenya Agricultural and Livestock Research Institute-Kakamega**. Annual Report, 2015.
23. **Jiang GL** Plant Marker-Assisted Breeding and Conventional Breeding: Challenges and Perspectives. *Advances Crop Science Technology*, 2013; **1**: e106. <https://doi.org/10.4172/acst.1000e106>
24. **Karanja DR, Kavoi J, Sperling L, Rubyigo J and J Ogecha** Promotion of improved beans varieties in Nyanza, Western and Central Rift Valley in Kenya. 12th KARI Scientific Conference Proceedings held on 8-12th Nov. 2010. Nairobi, Kenya.
25. **Dube E, Sibiya J and M Fanadzo** Early planting and hand sorting effectively controls seed-borne fungi in Farm-retained bean seed. *African Journal of Science*, 2014; **110**:36-42.
26. **Masheti Y, Muthomi WJ, Muiru MW, Arunga EE and P Gepts** Inoculum sources and management of bean scab caused by *Elsinoë phaseoli*. *Journal of Phytopathology*. 2024;**172**: e13355. <https://doi.org/10.1111/jph.13355>
27. **Yohannes S, Loha G and MK Gesses** Performance Evaluation of Common Bean (*Phaseolus vulgaris* L.) Genotypes for Yield and Related Traits at Areka, Southern Ethiopia. *Advances in Agriculture*, 2020, <https://doi.org/10.1155/2020/1497530>
28. **Batumike NR** Resistance of Common Bean Genotypes to Foliar Fungal and bacterial Diseases. (A Master's of Science dissertation, University of Nairobi), 2018.
29. **Mitiku M and T Mesera** Performance evaluation of common bean (*Phaseolus vulgaris* (L.)) varieties at Benatsemay Woreda of South Omo Zone, SNNPR, Ethiopia. *International Journal Agriculture Biosciences*, 2017, **6(6)**: 277-280.
30. **Wortmann SC, Kirkby RA, Eledu CA and JD Allen** Atlas of Common Bean (*Phaseolus vulgaris* (L.) production in Africa. Cali, Colombia: Centro Internacional de Agricultura Tropical, 1998.



31. **Wahome W, Githiri M, Kinyanjui KP, Toili EMM and G Angeno** Screening for yield-related agronomic traits in a panel of locally conserved common bean (*Phaseolus vulgaris* L.) accessions. *Journal of Plant Breeding and Crop Science*, 2023; Vol. **15(1)**: pp. 14-31.
32. **Okii DP, Tukamuhabwa JK, Namayanja A, Paparu P, Ugen M and P Gepts** The Genetic Diversity and Population Structure of Common Bean (*Phaseolus vulgaris* L.) Germplasm in Uganda. *African Journal of Biotechnology*, 2014; **13(29)**: 2935–2949.
33. **Motlatsi EM, Refiloe P and S Lesole** Variability in yield and yield components among common bean (*Phaseolus Vulgaris* L.) genotypes. *Global Journal of Agricultural Research*. 2016; **4(5)**: pp.1-9.
34. **Guimarães MC, Stone LF, Melo LC, Melo MF, Silva JAV, Sousa RS and RP Moraes** Morphological traits and yield in common bean. *Jaboticabal* 2021; **49(1)**: 27-35.
35. **Alemu Y, Alamirew S and L Dessalegn** Correlation and Path Analysis of Green Pod Yield and its Components in Snap Bean (*Phaseolus Vulgaris* L.) Genotypes. *International Journal of Research in Agriculture and Forestry*, 2017; **4(1)**: 30-36.
36. **Welde K** Yield Performance Evaluation of Common Bean (*Phaseolus vulgaris* L.) Varieties Under Rain Fed in Western Ethiopia. *American Journal of Plant Biology*, 2022; **7(1)**: 60-64.
37. **Ribeiro T, Rovaris SRS, Esteves JAF, Carbonell SAM and AF Chiorato** Selection of common bean lines obtained by the genealogical and bulk methods for disease resistance and agronomic traits. *Chilean Journal of Agricultural Research*, 2019; **79(3)**: 456-463.
38. **Anunda NH, Nyaboga NE and ON Amugune** Evaluation of genetic variability, heritability, genetic advance and correlation for agronomic and yield components in common bean landraces from South western Kenya. *Journal of Plant Breeding and Crop Science*, 2019; **11(5)**: 144-157.
39. **Loko LEY, Orobiyi A, Adjatin A, Akpo J, Toffa J, Djedatin G and A Dans** Morphological characterization of common bean (*Phaseolus vulgaris* L.) landraces of Central region of Benin Republic. *Journal of Plant Breeding and Crop Science*, 2018; **10(11)**: 304-318.



40. **Nkalubo S** Study of Anthracnose (*Colletotrichum lindemuthianum*) Resistance and its Inheritance in Ugandan Dry Bean Germplasm. (A Doctoral dissertation, University of Kwazulu-Natal, Pietermaritzburg), 2006.