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Multi-Traits Mean Performance and Stability Analysis, And Farmer's Participatory Variety Selection of Common Bean (*Phaseolus vulgaris* L.) Varieties in West Shewa, Ethiopia

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Abstract

Evaluating improved common bean varieties in specific agroecologies is a crucial activity to enhance the production and productivity of the crop. Participatory variety selection plays a vital role in adopting improved crop varieties into a new growing area. The aim of this study was to identify adapted, stable, disease resistant and farmer's preferred varieties. The experiment was conducted at six farmer's fields of two districts for two consecutive cropping seasons (2020 and 20121) in Western Shewa, Ethiopia. Five common bean genotypes were evaluated through a multi-environment trial (MET) carried out in 12 environments (6 locations for 2 years) using a complete randomized block design (RCBD) to select the best genotypes based on the multi-trait mean performance and stability index (MTMPS) and participatory variety selection (PVS). The combined likelihood ratio test (LRT) showed significant differences across environments, genotypes, and GEIs for all tested traits, except for the number of seed per pod (SPP). This finding showed genotypes SER119, and Nasir had satisfactory mean performances and stabilities across all environments. The participatory evaluation revealed that farmers assigned high importance to yield performance and disease resistance for field evaluation and marketability (seed color and size) for quality. In addition, they also ranked some traits, such as earliness and erectness, as important parameters for genotype selection. Accordingly, a SER119 genotype preferred by farmers, followed by Nasir and SER125 genotypes, which indicating excellent harmony between the genotypes selected with the MTPMPS and by farmers during the PVS. These suggest that farmers had deep knowledge to select and make decision of the preferred superior varieties compared to the inferior varieties. Thus, we concluded that farmers' participation in the common bean genotype evaluation is very crucial for future variety adaptation and dissemination process to select the most suitable genotypes for production and adoption in productive areas.

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Keywords

Common bean, Multi-Traits Stability Index (MTSI), Participatory variety selection.

Introduction

Common bean is one of the most important pulse crops grown in many parts of Africa, especially eastern Africa, like Ethiopia, Uganda, and Kenya lead in bean cultivation which contributes significantly to global bean production. Common bean is typically ranked highly in terms of both production and area coverage in the region, particularly in Ethiopia, competing closely with other pulses such as lentils, peas, and chickpeas (1). It is the first most important crop among lowland pulses and second most important food legume next to faba bean

(2). The most suitable bean production areas in Ethiopia are characterized by an altitude range of 1200 to 2200 m a.s.l, and mean maximum temperature of less than 32°C, and well distributed rainfall of 350 to 500 mm throughout the growing season (3, 4).

Common bean is vital for food security, providing a highly nutritious source of protein for millions, and serve as a major source of income for smallholder farmers (5), who grow the crop for both domestic consumption and export. The Association for Strengthening Agricultural Research in Eastern and Central Africa (ASARECA) recognizes research on beans as being of high importance. This is due to, beans are critical for local economies (6), providing income and improving dietary diversity in the region, whether as part of the total farm income or for providing a marketable product at critical times when farmers have nothing else to sell before the other crops are harvested (3). It also serves as an emergency crop in times of crop failure (7). The ability of common bean to grow in a various climates and soils has also made it a vital part of agricultural systems in Ethiopia, particularly for its role in soil improvement through nitrogen fixation, which enhances soil quality for subsequent crops.

Despite its merits and growing demand in the international market there is chronic supply gap in Ethiopia from the production side due to lack of/inappropriate address of improved varieties in the target environments. For instance, the central western part of Ethiopia, like West and south west shew lags behind in its production compared to other regions. The farmers of these areas are using local varieties which mixed with different seed size and color (i.e., large and small seeded of red and white common bean). The farming system in this area is based on old varieties under traditional practice that are low yielder, late maturing and vulnerable to pests so as the crop production is below its potential.

The national lowland pulse breeding program releasing different varieties with various aspect of qualities. But a limitation in dissemination of successful released of new genotypes. Thus, evaluating new common bean genotype for their GEI in agronomic performance, seed quality, stability and economic and/or social benefits is necessary before dissemination.

Several statistical methods have been developed to analyze and discuss multi-environment trials (METs) (8, 9). Among these methods, the additive main effects and multiplicative interaction analysis (AMMI) (10) and genotype-plus-genotype-by-environment (GGE) biplots (11) are widely used, offering accurate estimates and easy interpretation of GGEs through graphical tools. However, these methods have limitations (12), particularly when analyzing the structure of a linear mixed effects model (LMM) (13). This has led to the development of new models such as best linear unbiased prediction (BLUP), improving the predictive accuracy of random effects (14). Another limitation of these analytical tools is that they can only be applied to each trait individually. Thus, the multi-trait stability index (MTSI) was proposed to avoid these issues (12).

The MTSI is a selection index based on factor analysis that utilizes the mean performance and stability of a genotype for multiple trait selection (15). This approach enabled a more comprehensive evaluation of genotypes across multiple traits and environments. The limitation of MTSI is that it utilizes only non-parametric stability methods, such as the weighted average of absolute scores (WAAS) and weighted average of absolute scores from the singular value decomposition of the matrix of BLUPs (WAASB). However, Olivoto (15) developed a variant of the MTSI called the multi-trait mean performance and stability index (MTMPS) to consider other parametric and non-parametric stability methods (besides WAAS and WAASB) in the multivariate-based selection process. The advantage of the MTMPS is that it allows for the simultaneous evaluation of multiple traits, making it a more favorable method of analysis than classical methods. Several studies were used this method, (12, 16-20)

In addition to MTMPS, involvement of farmers' participatory variety selection (PVS) is a vital method to enhance the likelihood of adopting new genotypes. One of the main reasons restricting the adoption of new genotypes, particularly in rural regions, is the failure to understand the farmers' needs and perspectives (21,22).

In this study therefore, a multi environment trials (MET) with PVS was conducted to identifying common bean genotypes which exhibit good performance and stability across multiple environments based on multi-trait analysis, with the objectives of (1) to determine the magnitude of GEI for yield and yield components among common bean genotypes in the West Shewa agro-ecologies, (2) to select superior common bean genotypes that are performing and stable across the targeted environments in multiple traits, and (3) to identify farmers' criteria for evaluating and selecting common bean genotypes, and determine the harmony of MTSI method and PVS for genotype evaluation and selection.

Materials and Methods

Plant materials, site description and experimental design

Four nationally released and one local variety of common bean genotypes were used in this study (Table 1). The trial was implemented by Ambo agricultural research center for two consecutive cropping seasons of 2020 and 2021. Six farmers' fields were identified from two districts (Nono and Toke Kutaye), three experimental sites in each district. These two districts are slightly different in their environmental condition that they apart 104 km from each other and are among the promising common bean-growing areas in the zone.

The farmer's fields were chosen based on their respective potential for bean production with the help of district agricultural extension experts. The detail of experimental condition is described in Table 2. A randomized completed block design (RCBD) with three replications of 1.5 m apart was used to evaluate the agronomic performance. Each plot consists 6 rows of 3m length, with 0.4 m and 0.1 m space between rows and plants, respectively.

Data collection for the field experiments and the farmers' participatory evaluation

The phonological and agronomic data, like days to maturity (DM), plant height (PH), pods per plant (PPP), seeds per pod (SPP), thousand seeds weight (TSW) and grain yield (GY), were recorded for the field experiments. The overall occurred diseases during the experimentation, such as common bacterial blight (CBB), halo blight (HB), angular leaf spot (ALS), and anthracnose (AC) were also scored. A scale of 1–9 was used to record the disease prevalence, where 0 = no incidence and no damage - immunity, 1 = minor (5–15%) - resistant, 3 = moderate (16–30 %) – moderately resistant, 5 = high (31–50 %)- susceptible, 7 = heavy (51-75 %)- highly susceptible and 9 = severe (>75 %)- total lose, with numbers representing intermediate ratings, the modified of (23,24). The genotype selection for field experiments was aimed at selecting genotypes with lower values (negative gains are desired) for maturity date (MD) and disease traits (CBB, HB, ALS AC), and higher values are desired (positive gains) for agronomic parameters (PH, PPP, SPP, TSW, GY).

A group of 15 participants (farmers) were invited per experimental site. The farmers' carried out at crop vegetative growth, maturity stage and after harvested and their evaluation criteria were taken into account to ensure the relevance of variety selection. The seed size, yield, earliness, marketability (attractiveness), and disease resistance were the major farmer's criteria.

Three groups which consist 5 farmers were formed from of the 15 participants and randomly assigned to single block, i.e., each group had the chance to asses only the plots in one block to save the time and reduce the biasness (25). Farmers were then asked to give their preference for each genotype using two options; (a) 1-3 scale or (b) three-card types (red, yellow, green) for the identified traits, where; 1 = red card, for poor performance, 2 = yellow card, for moderate performance and 3 = green card- very good performance. In this study, the yellow card was considered as the genotype was partially (50%) acceptable, whereas green and red cards were used to indicate 'fully acceptable' and 'not acceptable', respectively. The number of cards were sufficiently prepared by considering the number of farmer's traits and invited participants. The selection was conducted by placing a ballot bag in front of each plot for those card users, and they were putted their cards accordingly. Preference evaluation was performed in all environments by 180 total farmers: 90 farmers at the first year and 90 other farmers at the second year. Amongst, 36 women and 54 men, and 30 women and 60 men in the first and second years, respectively.

Data Analysis

Descriptive statistics and variance components analysis

Descriptive parameters such as mean, maximum, minimum, median, coefficient of variation, and standard deviation were computed to provide basic information about variables such as DM, PH, PPP, SPP, TSW, GY, CBB, HB, ALS, and Anth. Each trait was initially analyzed according to the following mixed-effect model (Eq. (1)), that the main effect of the i^{th} genotype (α_i) and the interaction effect of the i^{th} genotype with the j^{th} environment (($(\alpha\tau)_{ij}$ were assumed to random effects; the main effect of the j^{th} environment (τ_j) and the effect of the k^{th} block within the j^{th} environment (γ_{jk}) as fixed effects.

$$Y = Xb + Zu + \varepsilon \qquad (1)$$

where y is an n($=\sum_{j=1}^{e}(gb)$) × 1 vector of the response variable (e.g. grain yield) of the ith genotype in the kth block of the jth environment (i = 1, 2, …,g; j = 1,2, … e); k = 1,2, …. , b); **b** is an (eb) × 1 vector of unknown and unobservable fixed effects of block **b** = ($\mu + Y_{11}, Y_{12}, \ldots, Y_{eb}$)′; **u** is an m(= g+ge)× 1 vector of random effects of genotype u = ($\alpha_1, \alpha_2, \ldots (\alpha\tau)_{11}, (\alpha\tau)_{12}, \ldots, (\alpha\tau)_{ge}$)′; **X** is an n × (eb) design matrix relating y to **b**; Z is an n × m design matrix relating y to u; and ε is an n × 1 vector of random errors ε = ($Y_{111}, Y_{112}, \ldots, Y_{geb}$)′;

The variance components were obtained using the restricted maximum likelihood (REML) and the expectation-maximization algorithm (26). A likelihood ratio test (LRT) was used to determine the significance of random effects using a two-tailed chi-square test with one degree of freedom. The variance components generated from the analysis were used to estimate the broad-sense heritability (H^2) on a genotype mean basis as follows (Eq. (2)) (27):

$$H^2 = \hat{\sigma}_g^2 \Big/ \left[\hat{\sigma}_g^2 + \frac{\hat{\sigma}_{ij}^2}{e} + \frac{\hat{\sigma}_e^2}{eb}\right] \quad (2)$$

Where $\hat{\sigma}_g^2$, $\hat{\sigma}_{ij}^2$ and $\hat{\sigma}_e^2$ are the variances associated with genotypes, GEI, and residuals, respectively; e and b are the number of environments and blocks within environment, respectively.

The selection accuracy (Ac), was estimated using (Eq. (3)):

$$Ac = \sqrt{H^2} \quad (3)$$

All recorded data were subjected to analysis using R software at P<0.05. The significance of random effects in the model is verified with a Likelihood Ratio Tests (LRT).

Mean performance (BLUP and stability (WAASB) analysis for individual variable

The mean performance for each trait of the genotype was computed by Best Linear Unbiased Predictors (BLUPg). In the present study, the genotypes with higher values of mean performance (BLUPs) for yield and yield attributed traits were considered as better, while lower values desired for disease and maturity traits. The stability (WAASB) of each genotype was quantified using the weighted average of absolute scores from the singular value decomposition of the matrix of BLUPs considering linear mixed-effect model (LMM) (28) with random effects for genotype and genotype-by-environment effect. The WAASB is a stability index that considers the genotype with the lowest values of stability across environments as the most stable genotype. The WAASB was estimated as follows (Eq. (4)):

$$WAASB_i = \frac{\sum_{k=1}^{p} |IPCA_{ik} \text{ x } EP_k|}{\sum_{k=1}^{p} EP_k} \quad (4)$$

Where $WAASB_i$ is the weighted average of absolute scores of the i^{th} genotype; IPCAik is the score of the i^{th} genotype in the k^{th} IPCA, and EP_k is the amount of the variance explained by the k^{th} IPCA. The stability of tested genotype across location was determined by the result of WAASBi, i.e., the lowest value of WAASBi is the most stable of genotype, that is, the one that deviates least from the average performance across environments.

The mean performance and stability index (MPSi) was achieved by the WAASBY index. WAASBYi is a superiority index used to select genotypes with high performance and stability. Since, in WAASB index the maximum value for mean performance (e.g., grain yield) is desired and the lowest value for stability (WAASB) is desired, thus the rescaled values were computed according to the following equations (Eq. (5) & (6)) as described by T. Olivoto et al. (2019).

$$rY_i = \frac{100 - 0}{Y_{max} - Y_{min}} \text{ x } (Y_i - Y_{max}) + 100 \quad (5)$$

and

$$rW_i = \frac{0 - 100}{W_{max} - W_{min}} \text{ x } (W_i - W_{max}) + 0 \quad (6)$$

where rYi and rWi are the rescaled values for mean performance of dependent variables and stability of the genotypes (WAASB), respectively, for the i^{th} genotype; Yi and Wi are the values of response variable for mean performance and stability (WAASB), respectively, for i^{th} genotype.

The WAASBY index was calculated based on mixed-effect models (T. Olivoto et al., 2019), as follows (Eq. (7)):

$$WAASBY_i = \frac{(rY_i \times \theta_Y)) + (rW_i \times \theta_S)}{\theta_Y + \theta_S} \quad (7)$$

Where *WAASBYi=MPSi,* is the superiority (simultaneous selection) index for the i^{th} genotype that weights between performance and stability; rY_i and rW_i are the rescaled values (0-100) for mean performance and stability of dependent variable of the i^{th} genotype, respectively; $\boldsymbol{\theta}_Y$ and $\boldsymbol{\theta}_S$ are the weights for mean performance and stability, respectively. Rescaled values are used to make *WAASB* and *Y* directly

Mean performance and stability analysis for multiple traits (MTMPS)

The multi-trait mean performance and stability index (*MTMPS*) is the same approach of multi-traits stability index (MTSI) which computed by considering the WAASBY index as described in (Eq. 7). MTMPS is a selection index computes the multi-trait stability index proposed by T. Olivoto et al., (2019) considering different parametric and non-parametric stability indexes. The WAASBY index was used to select genotypes that combine high performance and stability, which is a superiority index that allows weighting between performance (dependent variables) and stability (WAASB index). The first step is rescaling both performance of response variables (BLUPs) and stability of genotype (WAASB) with value of 0 to 100. The second step is conducting factor analysis (FA) to account for the correlation structure and dimensionality reduction of data, the third step is planning an ideotype based on desired values of traits and finally, compute the distance between each genotype to the planned ideotype (estimate MTMPS of the traits and genotypes (13). The data of this study was prepared as a two-way table with i rows/genotypes and j columns/trait (X_{ij}) to achieve the first step. The rescaled value for the i^{th} genotype and j^{th} traits (rX_{ij}) was calculated according to Eq. (5&6) for mean performance and stability, respectively, for i^{th} row and j^{th} column. After rescaling, exploratory factor analysis was conducted to group the correlated variables into factors and calculate the factorial scores for each genotype, as outlined by Olivoto and Nardino (29). The factor analysis was performed as follows (Eq. (8)):

$$X = \mu + Lf + \varepsilon \quad (8)$$

Where X is a $P \times 1$ vector of rescaled observations; μ is a $P \times 1$ vector of standardized means; L is a $P \times f$ matrix of factorial loadings; f is a $P \times 1$ vector of common factors; and ε is a $P \times 1$ vector of residuals, being p and f, the number of traits and common factors retained, respectively. The eigenvalues and eigenvectors were obtained from the correlation matrix of rescaled two-way-table (rX_{ij}).

The initial loadings were obtained by considering only factors with eigenvalues >1. The *varimax* rotation method (30) was applied to the initial loadings to obtain the final loadings. The scores are calculated as follows (Eq. (9)):

$$F = Z(A^T R^{-1})^T \quad (9)$$

Where F is a $g \times f$ matrix with factorial scores, Z is a $g \times p$ matrix with (rescaled) standardized means, A is a $p \times f$ matrix of canonical loadings, and R is a $p \times p$ correlation matrix between traits. g, f and p represent the number of genotypes, retained factors, and analyzed traits, respectively.

Ideotype is the values gained for response variables after rescaled, i'e., the new maximum or new minimum values after rescaled as described in Eq. (5 and 6). The rescaled value of the mean performance and stability depends on the desired values of the traits, for the desired values (could be higher or lower), the maximum rescaled value would be 100 and the minimum value (0). The scores for I is estimated according to Eq. (9). Based on the rescaled values in *rXij*, the ideotype was defined as the genotype with the best performance and stability for all analyzed traits. This ideotype had the values of 100 for the traits which higher values are desired (e.g., yield and its components) or for lower values are desired (e.g., disease traits), and had 0 values for yield component traits obtained with lower values and disease traits having higher values. Thus, the ideotype can be defined by a 1 x p vector I, where I = 0-100 based on desired sense of selection for analyzed traits. I and p are represented ideotype and number of traits, respectively. The MTMPS and genotype ranking was determined by calculating the Euclidean distance between the score of each genotype and the score of the ideotype using the following equation (Eq. (10)):

$$MTMPS_i = \left[\sum_{j=1}^{f} \left(Y_{ij} - Y_j\right)^2\right]^{0.5} \quad (10)$$

Where $MTMPS_i$ is the multi-trait mean performance and stability index for the i^{th} genotype; Y_{ij} is the score of the

i^{th} genotype in the j^{th} factor ($i = 1, 2, \ldots, g$; $j = 1, 2, \ldots, f$), being g and f the number of genotypes and factors, respectively; and Y_j is the j^{th} score of the ideotype. The genotype with the lowest MTMPS is then closer to the ideotype and therefore presents desired values for all the p traits.

The proportion of the MTMPS index of the i^{th} genotype explained by the j^{th} factor (ω_{ij}) is used to show the strengths and weaknesses of genotypes and is computed as:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f}\sqrt{D_{ij}^2}} \qquad (11)$$

Where D_{ij} is the distance between the i^{th} genotype and the ideotype for the j^{th} factor. Low contributions of a factor indicate that the traits within such a factor are close to the ideotype.

Selection differentials

The selection differential for the mean performance, stability (WAASB), and MPS index was computed for each trait using a selection intensity (SI) of 25%. The selection differential in percentage of population means ($\Delta S\%$) was determined for each trait of genotype as follows (Eq. (12)):

$$\Delta S_i\% = \left(\frac{\Delta X}{X_0}\right)x100 = \left[\frac{X_s - X_0}{X_0}\right]x\,100 \qquad (12)$$

Where ΔS is a selection differential for i^{th} genotype, X_s and X_o are the mean values of the selected genotypes and grand mean (population mean), respectively (10).

Data analysis

All the data was subjected to analysis using the R software 4.4.3 version (31) with ‘metan’ package (version 1.17.0).

Farmers’ preference analysis

The farmers participatory variety selection was conducted by using the farmers’ perception score (PS) and preference index (PI) methods. The PS was calculated from the division of vote differential (ΔV) to the total number of votes (Tv), where the ΔV was defined as positive votes (Pv) minus negative votes (Nv), i.e., (*Pv-Nv*). The preference index (PI) was then conducted to gain the farmer’s selection percentage for each tested variety. The PS and PI were computed separately for each trait and used as the explanatory variable, and the overall performance that the farmers estimated for each variety. Here, the farmer’s evaluation criteria and their preference for a variety allowed us to detect the main factors on which farmers have based themselves to give general appreciation for a variety. The preference score (PS) and preference index (PI) were then computed using the following equations (Eq. 13 and 14), respectively, described by Weltzien and Christinck (32).

$$PS_i = \frac{pv - nv}{Tv}, \quad where\ pv = N_{green} + 0.5 \times N_{yellow},\ nv = N_{red} \qquad (13)$$

$$PI_i\% = \left(\frac{pv}{Tv}\right) \times 100 = \left(\frac{N_{green} + 0.5 \times N_{yellow}}{Tv}\right) \times 100 \qquad (14)$$

Where PS_i and PI_i *(%)* are the farmer’s perception score and selection percentage for i^{th} genotype, respectively, N_{green} is the number of green cards (fully accepted), N_{yellow} is number of yellow cards (partially accepted), N_{red} is the number of red cards (fully rejected), pv is the positive votes (fully + partially accepted), nv is the negative votes (fully rejected), Tv is the total number of votes in the target group.

Results and Discussion

Livelihood Ratio Test (LRT) and Variance Components Analysis (VCA)

The combined data of common bean varieties from the twelve environments were subjected to analysis using linier mixed model (LMM), that genotype (G), and genotype-by-environment interaction (GEI) were considered as random effects, while environments and blocks nested in each environment were considered as fixed effects. The LR test indicated significant effects in both genotype and interaction effects for the traits evaluated except for number of seeds per pod (SPP) (Table 3). The significance level of these traits was high ($P< 0.01$) for genotype effects, where some of them (DM, PH, HB) showed significant ($P< 0.05$) effect in GEI. This indicated that there was good potential for the selection of most of the traits evaluated. Similar findings also reported by (33-35) which found significant variation between common bean varieties for the number of seeds per pod, number of pods per plant, hundred seed weight, days to maturity and grain yield.

As presented in Table 3, a high significant ($p \leq 0.01$) genotype effect for tested traits, indicated that the presence of genetic differences among the evaluated varieties which is crucial for the common bean's future breeding program, to generate new varieties. In addition, the significant effects of the environments and GEI were suggested that the performance of the genotypes is vary depending on the environment in which they grow and that this used to select environmental-friend genotypes.

The broad-sense heritability on a genotype-mean basis (H^2) was very high (≥ 0.96) for all tested variables (Table 3). This heritability was indicated that the genotypic component accounted for high variance in the genotype mean for all traits evaluated. This implied that more than or equal to 96 % of the variation was attributed to genetic factors for the tested traits, indicating good prediction of selection gain for these traits. Similarly, according to T. Olivoto and M. Nardino (27), high values of heritability in traits evaluated suggesting goods prospects of selection gains for those traits.

Agronomic performance of the genotypes across environments

The results in Table 4, showed descriptive analysis (i.e., mean, ranging mean and coefficient variations) for the traits of evaluated common bean varieties in multiple environments. As a result, the mean for days to maturity was 103.9, which ranged from 93 to 119 days and was found highly significantly different (P<0.01) (Table 3). The highest mean for days to maturity (112,22 days) was recorded from local variety indicating late maturity, whereas the lowest days to maturity was observed from SER125 (99.28 days) and SER119 (100.25 days), showing early maturity (Table 5). Plant height resulted in a mean of 49.24 cm, ranging from 30 to 80 cm with comparable coefficient of variation 23.79 % Table 4). Among the tested genotypes, the maximum mean for plant height (69.94 cm) was recorded from Deme variety, while the lowest mean (37.47 cm) was from local variety (Table 5). The longest height for Deme genotype causes as it be lodged and easily affected by different stresses, resulting in poor performance. Regarding the plant height, the selected genotype (SER119) was produced with intermediate height (48.61 cm) which led the genotype as to give rise good agronomic performance.

The mean number of pods per plant was 17.38, ranging from 6 to 36, and it demonstrated higher variability (CV: 40.44 %) (Table 4). In terms of genotypes evaluated, the highest mean for number of pods per plant (26.97) was recorded from variety SER119, followed by Nasir and SER125 varieties with mean of 19.24 and 18.62, respectively (Table 5). The number seeds per pod presented a grand mean of 5.19, varying from 3.8to 6.8, with a slightly lower variability (*CV*: 13.77 %) (Table4). The maximum mean (6.12) for number seeds per pod was recorded from SER119, whereas the lower number of seeds per pod was recorded from Deme and Local variety with mean values of 4.62 and 4.39, respectively (Table 5). The thousand seeds weight (TSW) had a mean of 314.9 gm, ranging from 220 gm to 400 gm, with relatively lower variability (*CV*: 13.43 %) (Table 4). The higher mean for thousand seeds weight was recorded from Deme variety. In some cases, thousand seed weight depended on seed size, in which largest seeded gave higher values of weight, but might be poor in seed yield produced. Likewise, in the present study, the variety Deme was produced with poor in most of traits evaluated but heaviest seed weight (373.32 gm) (Table 5). The highest TSW of Deme variety might probably be because of it relatively large seed sizes. The variety SER119 had the moderate mean value of thousand seed weight (326.27 gm), followed by Nasir (310 gm) and SER125 (300 gm) varieties, while Local variety showed the least mean thousand seeds weight (226 gm) (Table 5). The grand mean of grain yield (GY) was 2572.6 kg/ha, ranging from 898 to 4985 kg/ha, with slightly high variability (CV: 43.33 %) (Table 4). Amongst the varieties evaluated in this study, the maximum mean grain yield was obtained from variety SER119 (3567.19 kg/ha), followed by Nasir (3172.98 kg/ha) and SER125 (3119.36) varieties (Table 5).

The results of the present study indicated that the anthracnose (AC) disease prevalence exhibited a grand mean of 24.22 % with scores ranging from 0 to 55 %, indicating moderately high variability (*CV: 62.81 %*) (Table 4). The maximum mean anthracnose incidence (41.11 %) was recorded from Local variety, followed by Deme variety (32.22 %) that they considered as susceptible varieties, whereas the minimum mean prevalence (12.5 %) of anthracnose was recorded from SER119 (resistant). The varieties Nasir and SER125 were demonstrated as moderately resistant to AC disease with mean prevalence of 21.67 and 18.81 %, respectively

(Table 5). The results in Table 4 also showed the overall mean incidence of angular leaf spot (ALS) was 30.85 % and ranged from 0 to 55 %, with slightly high variability (*CV = 50.23 %*). A variety SER119 was observed as resistant variety with the prevalence percentage of 10.28 % and the varieties SER125 and Nasir were noticed with moderately resistant (22.97 %) and moderately susceptible (31 %), respectively, while Deme variety and farmers' variety were considered as susceptible and highly susceptible to ALS with mean prevalence of 37.08 % and 52.92%, respectively (Table 5). The common bacterial blight (CBB) was resulted with overall mean prevalence of 23.72 which varying from 5 to 50 % and showing relatively low variation (*CV= 42.80 %*). The maximum mean of CBB manifestation (35.85 %) was recorded from local variety, whereas the minimum mean incidence was recorded from Nasir and SER119 with mean values of 15.69 and 18.47 %, respectively, followed by SER125 (20.14 %), indicated moderately resistant varieties. The Halo Bligh (HB) had a mean occurrence of 21.39 % which ranged from 5 to 50 %, with moderately high coefficient variation (48.21 %). The higher mean of HB (33.94 %) was observed from Local variety (moderately susceptible), while the other remain genotypes were demonstrated as moderately resistant to HB disease (Table 5).

Factor analysis

The factorial loadings after varimax rotation (retained factor) could be determined depend on the principal components resulted with Eigenvalue ≥ 1 (12). In the present study, therefore, the first three principal components, which explained 93.2 % of the total variation among the traits, were retained (Eigenvalue ≥ 1) in the factor analysis performed with the mean performance and stability index (MPS) (Table 5). Thus, the ten evaluated traits were grouped into three factors (FA1, FA2 and FA3). The FA1 included the yield and yield component traits GY, PPP, SPP, and most common diseases, like AC, ALS and CBB. The phenological traits (DM, PH), and halo blight disease (HB) were grouped in FA2, whereas FA3 included only TSW (Table 6).

The results of Fig. 1A revealed the genotype ranking based on the MTMPS index considering a selection intensity of 25 %. The MTMPS index of 1.56 shows the cut point (red circle), in which a selected genotype is highlighted in red point. The Nasir genotype was near this circle and could present interesting features, while the Local variety and Deme were far away from the red circle, indicating the poorest varieties in tested traits across evaluated environments. Fig. 1B illustrates the strengths and weaknesses view of the stable genotypes evaluated across the environments, which are accounted for the proportion of each factor to the MTMPS index of the genotypes. Genotype strengths were characterized by lower factor values, whereas weaknesses were determined by higher factor values that tended to cluster toward the center (12). The dashed line represents the theoretical value assuming equal contribution from all factors.

In this study, the selected genotype showed notable strengths, contributing most significantly to the first factor (FA1) which had the smallest contribution to MTMPS for genotype SER119. A smaller contribution of FA1 for genotype SER119 indicated its superior MPS for the traits included in FA1 such as GY, NPP, NSP, AC, ALS and CBB among the evaluated variables. On the other hand, FA1 had the higher contribution to the MTMPS of genotype Deme, suggesting this genotype is poorly performed. The genotypes Nasir and SER125 have strengths related to FA2 (phonological-related traits factor). The smallest contributions of FA2 for Nasir and SER125 (Table 6) suggests that these genotypes have high values of the traits belong to this factor, such as DM, PH, HB and AC, implies that these genotypes have a shorter maturity period, toller in plant height and tolerant/resistant to hallo blight and anthracnose diseases. The genotype Deme had strengths related to FA3 (TSW), considerable MPS for this trait, indicating this genotype has a large seed size. In general, the smaller the proportion explained by a factor (positioned nearer to the outer edge), the closer the traits associated with that factor are to the ideotype. The dashed line represents the theoretical value assuming equal contribution from all factors.

Mean performance, stability, and mean performance and stability (MPS) of the individual traits

The mean performance of the ten traits of five common bean genotypes was analyzed using Best Linear Unbiased Predictors (BLUP) model. In this study, the higher values of mean performance were desired (positive gains) for yield and yield attributed traits, while the lower values were desired for maturity period and disease scores. As a results, the positive gains were observed in the mean performance of PH, PPP, SPP, TSW and GY, whereas negative gains were obtained from DM, AC, ALS, CBB, and HB (Table 7). The population mean performance (Xo) for PPP was 17.38, but the selected genotypes (Xs) was resulted in 26.97, which was 55.2 % higher than the grand mean (Xo). The desired gains for SPP of the selected genotype was 18 % higher than Xo. Similarly, Xs was 38.7 % and 3.6 % higher than Xo for GY and TSW, respectively. Although the higher value was desired for plant height, the data was resulted with negative SD%, i.e., Xo is higher than Xs, resulting in not success (0). In terms of disease prevalence, the mean performance of all identified disease traits was negative gains (-SD%), indicating lower values of Xs than Xo, implies desired gains for the selected genotype (Table 7).

The stability (WAASB) of the traits of selected genotype evaluated in 12 environments revealed that only three variables such as DM, TSW and GY were observed with desired gains. Contrary to BLUP, in stability (WAASB) analysis the lower value in Xs, (i.e., Xs < Xo) was considered as desired gains and the selected genotype with negative SD% for the traits was noticed as stable across environments in those traits. The result in Table 8 therefore shown as a negative SD% was observed for the WAASB index for DM, TSW, and GY, in which Xs was -2.53 %, 62.7 % and 18.3 % lower than Xo for these traits, respectively, resulting in the selected genotype was stable across evaluated environments only in DM, TSW, and GY traits.

In addition, considering both the mean performance and stability/MPS (WAASBY) of the selected genotype, a positive SD% was observed for the PPP, SPP, and GY. This indicated that the selected genotype (SER119) was superior in these traits both in mean performance and stability across environments with strong selection gain percentage, 70.4 %, 61 %, and 65.8 % for PPP, SPP and GY, respectively (Table 7).

Traits Correlations

Correlation analysis was conducted for all evaluated traits and the significancy of their strength and direction was measured by correlation coefficient. As shown in Fig.1, all yield and yield component traits were significantly positively correlated with each other, but they were significantly ($P< 0.01$) negatively correlated with all the traits of diseases evaluated. Highly significant positive correlations were observed between grain yield (GY) and PPP (0.79***), SPP (0.57***) and TSW (0.29**), but non-significant positive relationship with PH ($r =0.08$). The number of pods per plant (PPP) was also significantly ($p < 0.01$) positively correlated with SPP ($r = 0.64$), TSW ($r = 0.29$), and PH ($r = 0.23$). The relationship between SPP and TSW was non-significant and negative ($r = -0.02$), but non-significant positive correlation with PH ($r = 0.03$), indicating that these traits had no important effect on the number of seeds per pod. TSW showed a positive high significant ($p < 0.001$) correlation with PH ($r = 0.77$). Similar associations have been reported by Kwabena D et al., (36) in common bean and Yahaya et al., (37) in sweet potatoes.

However, the associations of all agronomic traits, (such as GY, PPP, SPP, TSW and PH) with all disease traits (AC, ALS, HB and CBB) was showed significant and negative but varied in their correlation strengths. The negative and high significant correlations between yield components and diseases traits suggested that these traits may be grouped as a opposite factor, indicated that genotypes with reduced diseases damage habitually showed better yield and yield attribute. This confirms that these pests reduce the productivity of the crop in general and remains a major problem in common bean production. These correlations highlight the key traits affecting grain yield and underscores the necessity for a comprehensive approach to genotype selection using multi-trait indices that account for performance and stability across different environments. In addition, all of the evaluated disease traits exhibited significant positive connections with each other, except for anthracnose (AC) with halo blight (HB), indicating the occurrence of one of these diseases may facilitate for the prevalence of the others, suggesting that controlling the one disease infestation could enhance the control for another diseases.

Environmental favorability for the evaluated traits of common bean genotypes

In this study, the yield and yield attributed traits of five common bean genotypes and important diseases were evaluated in six locations over two consecutive years. The LRT indicated highly significant environmental effect ($P<0.01$) for all evaluated traits except for SPP (Table 3). Significant variations observed across different locations noticed the existence of significant differences in environmental conditions across these locations for each trait evaluated. The locations in Nono district, such as (Nono Kondala, Nono Hallo and Imboro), showed superior performance than Toke Kutaye district in the traits of DM, PH, PPP, TSW and GY (Table 8). In contrast, the Toke Kutaye district demonstrated low in diseases prevalence, indicating that the environments in this district were comparatively not suitable for the diseases evaluated. In addition to genetic variation, the differences in phenotypic performance of each genotype in individual locations, is due to variation among environments, such as the unequal amount of rainfall, different temperature and soil type. Gasura et al., (38) noted that environmental factors, such as soil characteristics, rainfall, and temperature, lead to significant genotype and environmental interactions. The current significant disparity across locations for most plant characteristics is also consistent with the findings of (34, 39). Accordingly, the combined analysis result showed that the environments of Nono district were favorable for common bean production than Toke kutaye district.

The interaction effects of the genotype-by-location was also revealed significant in yield and yield components and in diseases identified, while the replicate-by-environment (REP/ENV) effect was significant for all traits except DM, CBB and ALS. (Table 3). This interaction effect implies that in addition to genetic makeup, the performance of the traits was influenced by environmental variability, resulting in inconsistency of genotypes performance across the locations for such traits. Similar result reported by Dembele and Ashenafi (39) that found substantial variation in yield component for the treatment by location interaction. In the present study therefore, one mega-environment (Nono district) showed as the top-performing environment for the most agronomic traits, whereas the second mega-environment (Toke Kutaye district) showed the best performance in terms of evaluated diseases such as AC, ALS, CBB, and HB. The Nono Hallo and Nono Kondala were noticed as best locations in the performance of the selected genotype SER119 for the traits of PH, PPP, TSW, and GY, while the agronomic performance of this genotype was relatively poor in the Birbirsa, Imela Dawe and Nega File locations but performed particularly well in the AC, ALS, CBB, and HB. The maximum GY was observed in Nono Kondale with overall mean of 3376.71Kg ha^{-1}, followed by Nono Hallo (3184.91 kg ha^{-1}, whereas the lower grand mean 1808.86 kg ha^{-1} was observed in Imela Dawe location (Table 8).

In general, the result of current study indicated that no single variety is found that showed generally superior performance in all tested traits across all locations. However, the selected genotype SER119 was produced superior in all most all traits than the other genotypes in both mega-environments. Contrary, the farmers variety was observed with inferior (poor performance) in all traits evaluated across all locations, while the other remain genotypes were observed superior in not more than two traits (Supplementary Table 1).

MTMPS index and selection of superior genotype/s

The multi traits mean performance and stability (MTMPS) index is understanding as valuable methods of genotype selection, which provide the genotypes with considerable performance and stable across evaluated environments. In the present investigation, the efficiency of the MTMPS index method in selecting superior common bean genotypes was evident. For instance, the selected genotypes exhibited positive SD for BLUBs in most agronomic traits (PH, NPP, NSP, TSW, GY) and negative SD in the identified diseases (AC, ALS, CBB and HB), indicating desired gains in the mean performance of those traits.

A negative SD for BLUPs in disease traits is desirable, as it aligns with the objective of reducing the disease reaction in the selected genotypes. The negative SD observed for stability index in analyzed traits showed the greater small value of WAASB, which further demonstrated the selected genotype offered greater genotypic stability than the original population. These performance and stability across diverse environments confirm the potential of this genotype for broader adoption and more consistent performance, because, in MTMPS index, the adaptability was determined by the superiority of genotype in desired value for multi-trait mean performance whereas stability was determined by their consistence across environments.

A genotype with lower MTMPS values suggested a higher level of MPS for the multiple traits assessed during the study. In the present study, therefore, one of the five common bean genotypes was identified as superior genotype based on the desired mean performance and stability obtained from the most of traits evaluated in 12 environments at an SI of 25 %. A selected genotype was SER119 with MTMPS of 1.56 (Table 9).

The second lower MTMPS was recorded from Nasir variety, whereas the SER125, Deme and Local variety were recorded with 3.02, 3.17 and 4.12 of MTMPS scores, respectively. Similarly, several studies have utilized multi-trait-based genotype selection indices, such as the MTSI in sweet potato (16,40-42) and maize (43); MTMPS in maize (44); the MGIDI in maize (45) and yam (46), to select superior genotypes.

Fig.1 (A) genotype ranking based on the MTMPS index, selected genotypes are highlighted in red; (B) strengths and weaknesses view of the stable genotypes identified across the different environments.

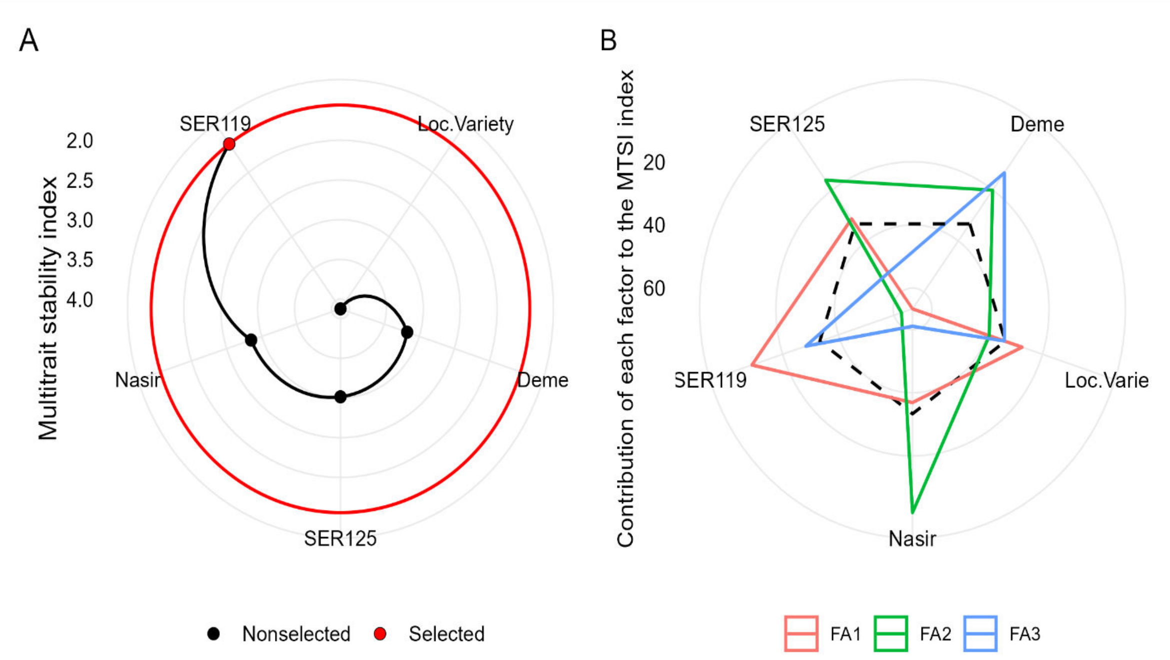

Fig.2 Correlation coefficient of the traits evaluated in different environments; (*PPP: pods per plant, SPP: seeds per pod, TSW: thousand seeds weight, PH: plant height, GY: grain yield, AC: anthracnose; ALS: angular leaf spot; HB: halo blight; CBB: common bacterial blight; *, **, *** and ns, represent significance at 0.05, 0.01, 0.001 and non-significant, respectively*)

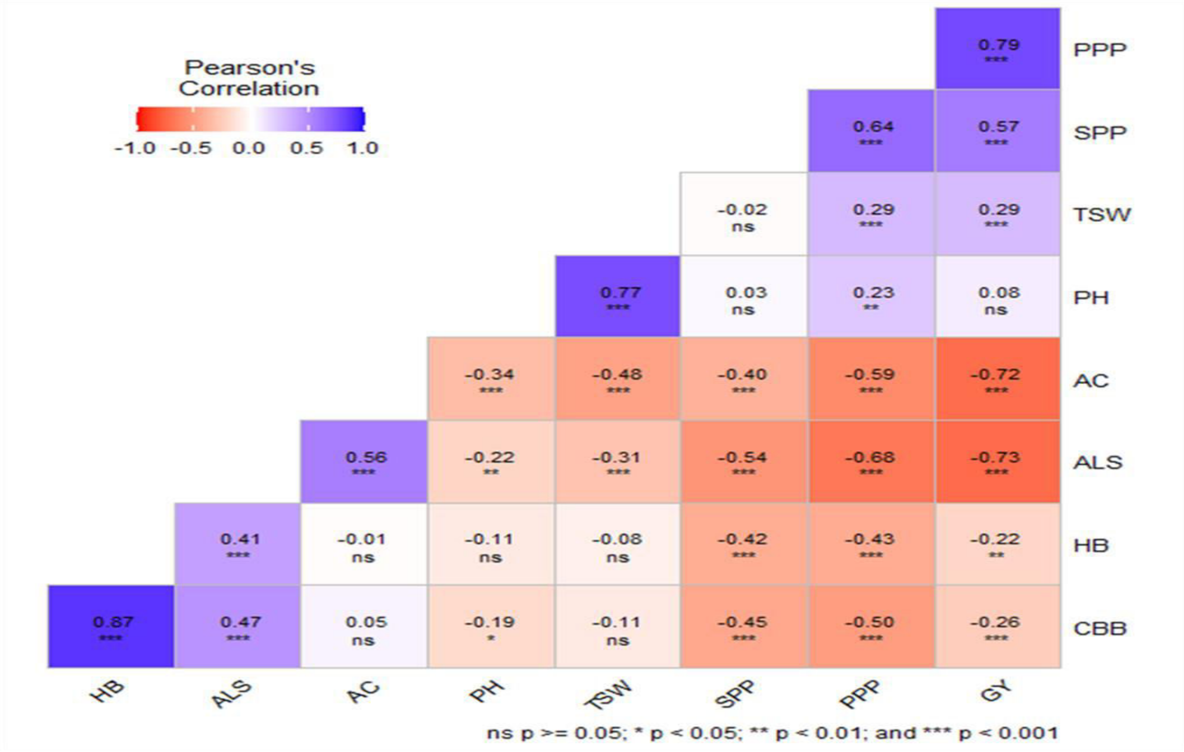

Fig.3 Diseases' prevalence view in 12 environments

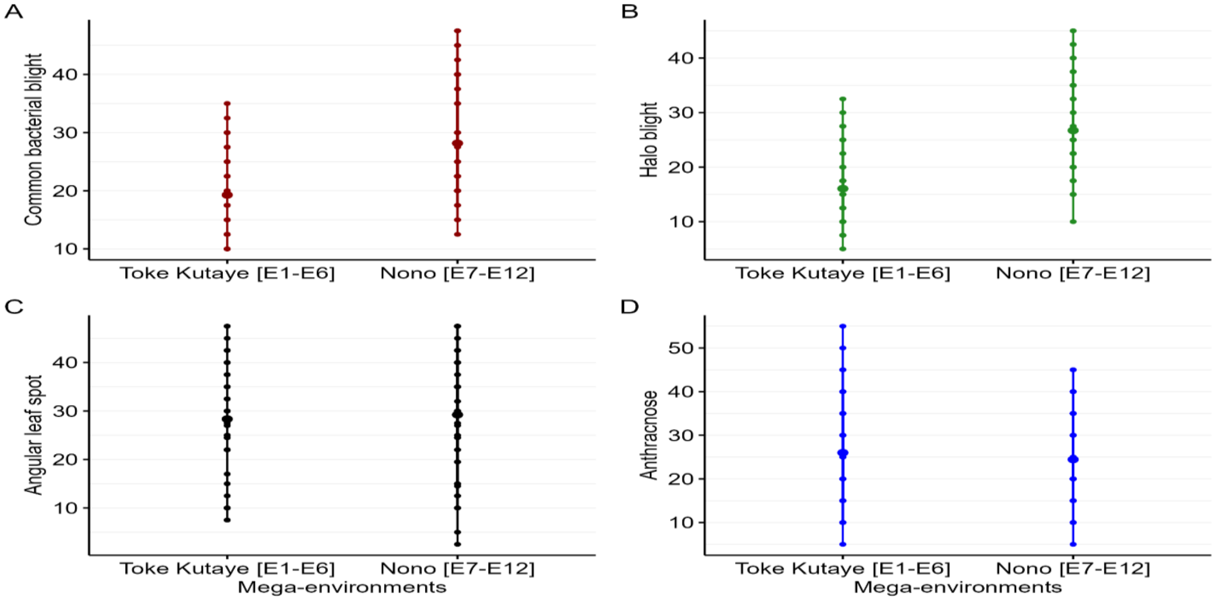

Fig.4 Response of genotypes to diseases evaluated across 12 environments

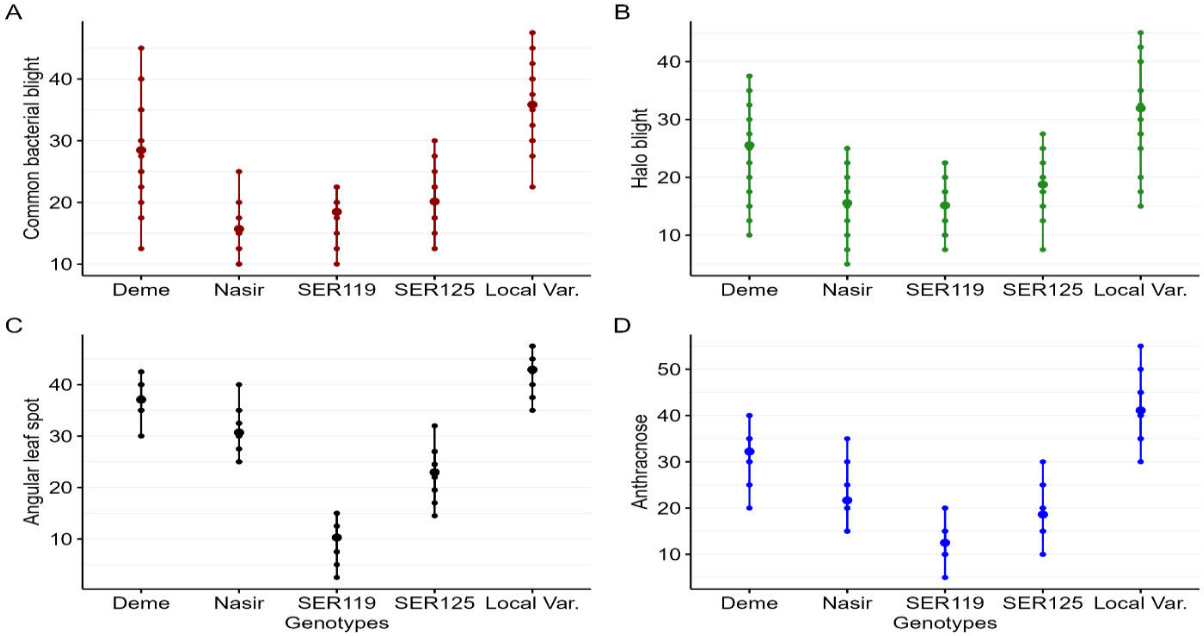

Table.1 List of common bean varieties

S/N	Varieties	Year of release (G.C)	CENTER
1	SER119	2014	MARC
2	SER125	2014	MARC
3	DEME	2008	MARC
4	NASIR	2003	MARC
5	Local variety	-	-

Table.2 Description of the experimental locations; Sources: using GPS tool and © 2024 Google-Map Data.

Districts	Specific Location	Latitude	Longitude	Altitude (m.a.s.l)	Avg.Temp. (°C)	Rainfall (mm)
Nono	Imboro	8.9302	37.9282	2496	21	800-1300
	Nano Kondala	8.6875	37.9001	2638	20	100-1390
	Nano Halo	8.6988	37.9012	2642	20	100-1400
Toke kutaye	Birbirsa	8.9715	37.8610	2200	21	650-1000
	Imala Dawe	9.0156	38.1056	2300	20	700-1200
	Nega File	9.1324	38.1085	2360	19	750-1300

Table.3 Likelihood ratio test (LRT) for genotype, environment, replicate, genotype × environment interaction effect, and heritability regarding ten traits evaluated in five common bean genotypes in 12 evaluation environments, and across years 2020 and 2021.

Traits	Source of variations				H^2
	Gen	Env	Rep (Env)	Gen:Env	
Days to maturity (DM)	68.79**	139.36**	3.63ns	0.03*	0.99
Plant height (PH)	84.17**	139.10**	0.06*	10.42*	0.99
Number of pods per plant (PPP)	59.37**	51.11**	8.09**	20.41**	0.99
Number of seeds per pod (SSP)	42.21**	0.09ns	9.27*	0.11ns	0.98
Thousand seeds weight (TSW)	50.97**	1387.5**	5.51*	182.2**	0.99
Grain yield (GY)	39.18**	740644**	105.4**	69944**	0.98
Common bacterial blight (CBB)	41.12**	267.03**	2.9ns	54.86**	0.97
Hallo blight (HB)	31.21**	518.81**	7.81**	58.8*	0.96
Angular leaf spot (ALS)	65.72**	103.78**	0.56ns	60.97**	0.99
Anthracnose (AC)	61.46**	98.93**	13.15**	79.72**	0.99

Gen: Genotypes, Env: Environments, Rep: replicates nested in environments, Gen:Env: Genotype-by-environment interaction, H^2= heritability, *, ** and ns are significant at P<0.05, P< 0.01 and non-significant, respectively.

Table.4 Descriptive analysis of phenological, yield and yield component, and common disease prevalence (%) in five common baan genotypes across the 12 environments.

Traits	Grand Mean	Maximum	Median	Minimum	Standard deviation	CV (%)
DM	103.9	119.0	103.5	93	6.19	5.96
PH	49.24	80	46.0	30	11.71	23.79
PPP	17.38	36	16.5	6	7.03	40.44
SPP	5.19	6.8	5.05	3.8	0.71	13.77
TSW	314.9	400	316.5	220	42.3	13.43
GY	2572.6	4985	2359.3	898	1114.6	43.33
AC	24.22	55	25.0	0	12.79	52.81
ALS	30.85	55	30	0	12.45	50.23
CBB	23.72	50	20	5	10.15	42.80
HB	21.39	50	20	5	10.10	48.21

DM: days to maturity, PH: plant height, PPP: pods per plant, SPP: seeds per pod, TSW: thousand seeds weight, GY: grain yield, AC: anthracnose, ALS: angular leaf spot, CBB: common bacterial blight, HB: halo blight

Table.5 Principal Component Analysis (PCA)

PC	**Eigenvalues**	**Variance (%)**	**Cum. variance (%)**
PC1	6.50	64.58	64.58
PC2	1.70	17.18	81.8
PC3	1.20	11.5	93.2
PC4	0.68	6.77	100
PC5	0.00	0.00	100
PC6	0.00	0.00	100
PC7	0.00	0.00	100
PC8	0.00	0.00	100
PC9	0.00	0.00	100
PC10	0.00	0.00	100

Table.6 Factorial loadings after varimax rotation in factor analysis

VAR	**FA1**	**FA2**	**FA3**	**Communality**
PPP	**-0.89**	-0.44	-0.11	0.99
SPP	**-0.84**	-0.39	-0.15	0.88
GY	**-0.72**	-0.67	0.05	0.97
ALS	**-0.99**	0.05	0.09	1.00
CBB	**-0.63**	-0.59	-0.5	0.99
DM	-0.34	**-0.91**	0.14	0.96
HB	-0.46	**-0.81**	-0.08	0.87
PH	0.06	**-0.93**	0.04	0.87
AC	-0.34	**-0.82**	0.05	0.80
TSW	0.02	-0.15	**-0.99**	0.99
Mean of communality				0.93

DM: days to maturity, PH: plant height, PPP: pods per plant, SPP: seeds per pod, TSW: thousand seeds weight, GY: grain yield, AC: anthracnose, ALS: angular leaf spot, CBB: common bacterial blight, HB: halo blight and FA: factor analysis.

Table.7 Selection gains for mean performance (BLUPs), stability (WAASB), mean performance and stability (WAASBY) for the tested traits of five Common bean genotypes evaluated in six locations and two years (12 environments).

		Mean Performance (BLUPs)				**Stability (WAASB)**				**MPS (WAASBY)**			
Traits	Factors	Xo	Xs	SD%	Success	Xo	Xs	SD%	Success	Xo	Xs	SD%	Success
NPP	FA 1	17.38	26.97	55.2	100	0.69	0.62	-10.2	100	49.94	85.1	70.4	100
NSP	FA 1	5.19	6.12	18.0	100	0.24	0.27	15.4	0	43.65	70.3	61.0	100
GY	FA 1	2573	3567	38.7	100	15.92	13.0	-18.3	100	60.31	100	65.8	100
CBB	FA 1	23.72	18.47	-22.1	100	0.88	0.96	9.1	0	60.46	68.2	12.7	0
ALS	FA 1	28.79	10.28	-64.3	100	0.41	0.45	9.84	0	50.97	44.6	-12.0	100
AC	FA 1	25.22	12.50	-50.4	100	0.86	0.75	-12.8	100	65.00	55.0	-15.4	100
DM	FA 2	103.9	100.3	-3.5	100	0.38	0.37	-2.53	100	61.49	76.7	24.8	0
PH	FA 2	49.24	48.61	-1.3	0	0.23	0.25	10.5	0	33.66	27.6	-18.0	0
HB	FA 2	21.39	15.14	-29.2	100	0.96	1.03	7.85	0	45.15	60.1	33.2	0
TSW	FA 3	314.9	326.3	3.6	100	1.56	0.58	-62.7	100	44.32	71.8	61.96	100

DM: days to maturity, PH: plant height, PPP: pods per plant, SPP: seeds per pod, TSW: thousand seeds weight, GY: grain yield, AC: anthracnose, ALS: angular leaf spot, CBB: common bacterial blight, HB: halo blight

Table.8 Overall means of genotypes and environments in traits evaluated across 6 location and 2 years

Genotypes	DM	PH	NPP	NSP	TSW	GY	AC	ALS	CBB	HB
SER119	100.25	48.61	26.97	6.12	326.27	3567.19	12.5	10.28	18.47	15.14
Nasir	102.69	45.09	19.24	5.43	310.62	3172.98	21.67	31.00	15.69	15.56
SER125	99.28	45.11	18.62	5.38	300.13	3119.36	18.61	22.97	20.14	18.75
Deme	105.22	69.94	12.29	4.62	375.32	1622.35	32.22	37.08	28.47	25.56
Local Var	112.22	37.47	9.79	4.39	262.36	1381.12	41.11	52.92	35.83	33.94
Environments										
Birbirsa	106.67	47.08	15.19	5.24	307.5	2350.56	23.83	27.9	20.17	16
Imbro	103.73	47.14	16.73	5.1	316.02	2699.83	20.33	30.9	25.67	23.67
Imela Dawe	106.9	47.54	14.83	5.21	310.96	1808.86	23.83	29.57	18.83	14.17
Nega File	108.5	47.43	15.66	5.28	298.14	2014.75	21.33	27.57	18.83	18
Nano Hallo	99.5	52.45	22.29	5.13	323.51	3184.91	29	29.57	29	28.67
Nano kondala	98.3	53.81	19.6	5.16	333.50	3376.71	24	27.23	29.83	27.83

DM: days to maturity, PH: plant height, PPP: pods per plant, SPP: seeds per pod, TSW: thousand seeds weight, GY: grain yield, AC: anthracnose, ALS: angular leaf spot, CBB: common bacterial blight, HB: halo blight.

Table.9 Scores for genotypes and ideotype distance (ID) estimated in the three factors, multi traits stability index for genotypes with relative contribution of each factor to the MTMPS.

	Genotypes and Ideotype (ID) scores			**MTMPS**	**Factors contribution to MTMPS**		
Genotypes	FA1	FA2	FA3		FA1	FA2	FA3
SER119	-2.9	-1.01	2.27	**1.56**	**9.01**	62.65	28.35
Nasir	-1.63	-2.34	0.46	2.85	36.9	**2.025**	61.08
SER125	-1.61	-1.64	0.4	3.02	31.3	**16.19**	52.5
Deme	-0.12	-1.52	2.31	3.17	66.6	20.12	**13.28**
Local Var.	-1.18	0.34	0.52	4.12	27.29	39.06	33.65
ID	-3.11	-2.42	2.9	**-**	**-**	**-**	**-**

Table.10 Mean of Farmers' preference score, preference index (selection percentage) and preferential ranking of common bean varieties

Genotypes	N_{green}	N_{yellow}	N_{red}	Total	PS	PI (%)	Rank
SER119	145	30	5	180	0.86	88.9	1
Nasir	113	44	23	180	0.62	75	2
SER125	96	50	34	180	0.48	67.2	3
Deme	51	26	103	180	-0.22	35.6	4
Local Var.	0	20	160	180	-0.83	5.6	5

N_{green}, N_{yellow} and N_{red} are number of green, yellow and red cards, respectively, PS= Preference score and PI= Preference index

Supplementary Table.1 Mean of genotype by mega-environment interaction for traits evaluated over two years in six locations

Gen	Env	DM	PH	NPP	NSP	TSW	GY	AC	ALS	CBB	HB
SER119	Nono	96.67	51.47	29.99	6.14	335.11	4254.48	13.33	10.28	21.11	18.61
Nasir	Nono	99.22	46.78	21.39	5.40	317.97	3891.67	21.67	31.94	18.61	20.83
SER125	Nono	95.78	46.39	21.31	5.25	317.15	3819.40	17.78	22.83	23.33	21.94
Deme	Nono	101.61	72.61	13.96	4.41	381.45	1905.84	31.11	37.78	35.56	33.01
Local Variety	Nono	109.28	38.41	11.10	4.46	270.06	1564.37	38.33	43.33	42.22	39.17
Mean		100.51	51.13	19.55	5.13	324.35	3087.15	24.44	29.23	28.17	26.71
SER119	Toke Kutaye	103.83	45.74	23.96	6.1	317.44	2879.91	11.67	10.28	15.83	11.67
Nasir	Toke Kutaye	106.17	43.40	17.10	5.47	303.28	2454.29	21.67	29.44	12.78	10.28
SER125	Toke Kutaye	102.78	43.82	15.93	5.50	283.10	2419.33	19.44	23.11	16.94	15.56
Deme	Toke Kutaye	108.83	67.27	10.63	4.83	369.19	1338.87	33.33	36.39	21.39	18.06
Local Variety	Toke Kutaye	115.17	36.53	8.51	4.32	254.67	1197.88	43.89	42.50	29.45	24.72
Mean		107.36	47.35	15.23	5.24	305.54	2058.06	26.00	28.34	19.28	16.06

Supplementary Table.2 Information feature of farmers participated in PVS over two cropping seasons.

Year	Farmers participated in PVS (Different farmers/season)								Educated & illiterate percentage of the participants				
	Male				Female				Total Educated	Total Illiterate	Grand Total	Educated %	Illiterate %
	Educated	Illiterate	Total		Educated	Illiterate	Total						
2020	39	17	56		16	18	34		55	35	90	61.1	38.9
2021	42	19	61		15	14	29		57	33	90	63.3	36.7
Total	84	36	117		31	32	63		112	68	180	62.2	37.8

Supplementary Table.3 Participants' percentage and average area of production per mega-environment

Year	Participants (different farmers/year)				Percentage			Average area of production (ha/farmers)		
	Male (M)	Female (F)	Total		M%	F%		Nono district	Toke kutaye	Mean
2020	56	34	90		62.2	37.8		6.2	2.4	4.3
2021	61	29	90		67.8	32.2		6.4	2.6	4.5
Total	117	63	180		65	35		-	-	-
Mean	-	-	-					6.2	2.5	4.4

The contribution of each factor to the MTMPS index revealed that lower contribution of FA1 (9 %) to MTMPS for selected genotype (SER119), indicated the traits grouped in this factor are closer to the ideotype, whereas higher contribution of FA2 to MTMPS (62.6 % of the distance from the selected genotype to the ideotype), and about 28.4 % of MTMPS indices were attributed to FA3 (Table 9). For the second interest genotype (Nasir), the MTMPS indices were attributed to FA3 (61 %) and FA1 (36.9 %), but FA2 contributed the least to the MTMPS index (2 %, shewed best performed in the traits linked to this factor). Regarding the third ranked genotype (SER125), comparatively lower FA2 values was contributed to MTMPS (16.2 %) and this genotype is good in the traits associated with this factor (FA2). The fourth ranked genotype (Deme) was resulted good with the traits clustered in FA3, as relatively lower contribution of FA3 to MTMPS (13.3 %) for this genotype. But, since the FA3 included only one trait (TSW) in high value, this genotype was considered as poor performance. However, the last ranked variety was resulted in poor performance by all traits evaluated, in which the contribution of all the three factors to MTMPS was relatively high for this variety.

The strengths and weaknesses view of the stable genotypes also identified across the different environments, shown as the proportion of each factor on the computed MTMPS index; the smaller the proportion explained by a factor (positioned nearer to the outer edge), the closer the traits associated with that factor are to the ideotype. The higher contribution of FA to the MTMPS of genotype indicated its weak performance for FA1-related traits. However, smaller contributions of FA to MTMPS of the genotype suggested that genotype had the best MPS for traits linked to that FA. The genotype SER119 had lower MPS values for traits such as DM, PH and HB, as evidenced by its higher contribution to the MTMPS index from FA2 than from FA1. This indicated that this genotype is closer to the FA1 ideotype, which included most important traits (PPP, SPP, GY, CBB, ALS and AC). In contrast, Nasir had lower contribution to the MTMPS index from FA2, suggested that it is closer to the ideotypes concerning DM, PH and HB.

Farmer’s participatory selection of common bean genotypes evaluated across environments

In this PVS about 180 farmers were participated in genotype evaluations over two years in the six locations. Amongst, about 25 % of the participants were women, whereas 75 % were male farmers. Of the total participants, about 35 % were uneducated, where half of the female participants are illiterate (Supplementary Table 3). The income of all participants was depended on agricultural practice and the average landholding was 4.3 ha per farmer. The smallest fields were observed in Tuke Kutaye district with the average area under production was 2.4 ha (Supplementary Table 2), where the average area dedicated to common bean production is 0.16 ha. However, large field under production with average area under production 6.2 ha was observed in Nono district, where the common bean production is sharing 0.5 ha.

Although the attended farmers were listed various traits during evaluation, there were a few traits, such as yield, disease reaction, earliness, marketability/attractiveness and suitability to diet were prioritized and focused to select the superior varieties. Previous study by Asfaw *et al*, (47) work on common beans reported similar findings of farmers using a combination of a few traits when evaluating new varieties. Furthermore, yield, disease reaction and attractiveness of seed color and size were the most relevant factors affecting farmers’ choices throughout the assessment.

The overall perception scores and preference index were computed for each important trait to determine the superior genotypes which deliberately met the participants’ preferences. The summary result therefore revealed that a variety “SER119” was observed with higher farmer’s perception score (0.86) which indices to score 88.9 % of PI, indicating the most desirable genotype than the others in most parameters (Table 10). The variety Nasir was also well-appreciated for its dietary tastes and good tolerance to pests and diseases received satisfactory PS of 0.62 and preference index of 75 %, while SER125 for its earliness which received PI score of 67.2 %; while Deme and Local variety were produced with low farmers’ perception score and negatively preferred by farmers with 35.6 % and 5.6% of selection percentage.

Farmer’s variety evaluation and selection in this study had slightly diverse perception among participant to accept and reject the tested common bean varieties. The diversity of farmers’ perception during selection is an indication of the complexity of users’ preference, which directly and indirectly helps as strainer of real variety with desired traits. Asrat (48) also reported that, when there is more diversity in selection criteria, there is better chance of maintaining on farm diversity since positive traits are seldom found on single variety. Since the variety vote was made both for traits evaluated at field and after trashing, any information of each variety during field evaluation is strictly secured to avoid a bias. Most of the farmers however had select the variety which they voted at field, whereas few of them inversely surprised by the traits of varieties after trashing, this implies that the accessibility of varieties with different suites of traits allows farmers to satisfy their multiple needs is very rare (49). The number of positive vote and selection percentage were the major decisive criteria in retaining and rejecting the variety. Therefore, although, it is impossible to find single variety that fulfills all the characteristics farmers want (50), the result from farmers' preference index analysis revealed "SER119" has got maximum PI score, resulting in higher positive selection in traits evaluated.

In general, involving farmers in common bean variety evaluation can improve variety selection as the farmers are capable of identifying superior varieties that meet their specific requirements within relatively short period and increase the chance of adoption of new varieties by other farmers in a community. Accordingly, SER119 was preferred by majority of farmers for most traits, whereas Nasir was second preferred variety particularly for three criteria (Attractiveness, suitably of diet, and disease tolerance), while SER125 was preferred specifically for earliness. These findings were comparable to the genotype ranking produced using the statistical approach (MTMPS), which considered both the average performance and stability of the genotypes assessed.

Diseases prevalences across evaluated environments and response of genotypes

This study highlights the importance of genotypic performance and stability when selecting common bean genotypes. Thus, data on disease prevalence and intensity, yield and yield components were recorded and analyzed with integration of genotypic stability to enhance the reliability of selection recommendations. This approach is essential for enhancing disease tolerance in the common bean varieties, because the strong environmental influence complicates the selection of genotypes tolerant or resistant to diseases with good stability.

The bacterial diseases (common bacterial blight and halo blight), and fungal diseases (Angular leaf spot and Anthracnose) were the major diseases identified during the study. The prevalence of these diseases was slightly different across evaluated environments; but there was little or/ no variation among similar agro-ecologies. The results in Fig. 3 therefore revealed that the overall mean of each disease occurrence across environments, which described in mega-environments, this is because the condition of each environment in single mega-environment is closely related. The projection of points on the vertical line are indicating the ranges of each disease occurrence in each mega-environment, and the bold point is represented the mean disease occurrence in that mega-environment. As a result, in the first mega-environment (Toke Kutaye district) the common bacterial blight (CBB) was recorded with average score of 19 %, represented by bold point and ranging from 10 to 35 % (Fig. 3A), whereas it was recorded with grand mean of 27 % and mean ranged from 12 to 48% in the second mega-environment (Nono district). This indicated that the Nono district had favorable condition for CBB than Toke Kutaye. Halo blight (HB) was highly observed in Nono district with overall mean value approximately 26 % and mean ranged from 10-45 % of occurrence, whereas the lower HB was occurred in Toke Kutaye district which recorded with grand mean of 16 %, ranging from 5-33 % in this agroecology (Fig. 3B). In contrary to CBB and HB, the anthracnose (AC) disease was highly scored in Toke kutaye district than Nono district (Fig. 3D), implies that Toke Kutaye is more suitable for anthracnose diseases. However, the result of this finding demonstrated that the angular leaf spot (ALS) was the one which widely occurred across tested environment than the other diseases evaluated (Fig. 3C).

In terms of disease reaction, the varieties' responses to evaluated diseases showed significant variation. Nasir and SER119 were considered as less susceptible to Common bacterial blight and Halo blight, in which lower mean severity of CBB (≤ 25 %) and HB (≤ 30 %) were recorded from these genotypes. The overall mean 15 % and 18 % of CBB was recorded from Nasir and SER119, respectively, while 15 % in HB for both genotypes (Fig. 4 (A and B)). The highest mean severity of CBB and HB were recorded from Local variety and Deme, ranging approximately from 22-47% and 12-45 % of CBB for Local variety and Deme, respectively, and ranging approximately from 15-45 % and 10-43 % of HB for Local variety and Deme, respectively (Fig. 4A). This concluded that these varieties were categorized as susceptible to CBB and HB, while SER125 genotype was noticed as intermediate. Figure 4 (C and D) shown as the genotype SER119 was resistant to Angular leaf spot (ALS) and Anthracnose (AC) diseases, with mean severity ≤ 15 % recorded from this variety for both diseases. The response of SER125 variety to ALS and

AC was highlighted that less susceptible, while Nasir variety was intermediate to AC, but susceptible to ALS. In general, a Nasir variety was observed as moderately resistant to bacterial disease (CBB and HB) but the SER119 was noticed as moderately resistant genotype to all most all of the diseases evaluated.

In conclusion, in this study, multi environment trials (MET) and farmers' participatory evaluation were used to evaluate common bean genotypes in six locations over two years (12 environments) in West Shewa, Ethiopia to identify genotypes suitable for field production which also met farmers' expectations. Using LMM considering genotypic random effect and MTMPS model were used in the study, in which the genotypic stability index, WAASB, and simultaneous selection index, WAASBY realized the stability and both performance and stability of the superior genotype in multiple traits across multi environments.

As a results, one superior genotype (SER119) was identified as having excellent performance and stability for most traits studied. More importantly, this genotype was selected by farmers as a best among the evaluated genotypes in terms of both yield and quality. Involving famers in research, specially, in crop evaluation is important for variety development as the famers are capable to identifying important traits and increase the chance of adoption of new varieties Therefore, we recommend that the dissemination of this genotype in similar agroecological zone of Ethiopia can improve common bean production and productivity in the country.

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Data Availability

Data will be made available upon reasonable request.

Conflicts of Interest

The author declare no conflicts of interest.

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