Genotype x environment interaction and yield stability analysis of mung bean (Vigna radiata (L.) Wilczek) genotypes in Northern Ethiopia

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Abstract: The experiment was conducted from 2009–2011 cropping seasons. Six mung bean genotypes viz. SML-668, Black bean, Bored, Local Gofa, SML-32 and Local 2-Sheraro were evaluated to early maturing and high yielding genotypes and the design was RCBD with three replications. The combined analysis of variance reviled that there was highly significant variation (p < 0.01) of grain yield among the genotypes, environments and genotype by environment interaction. The genotypic, environmental and the genotype x environment interaction (GIE) accounted about 30.47%, 45.01% and 11.59% of the total variation. The average grain yield of the genotypes was 2008.17 kg/ha. The highest and the lowest mean yield was obtained from SML-668 (2536.47 kg/ha) and SML-32 (1773.59 kg/ha) respectively. The AMMI bi-plot also depicted that, SML-668 and SML-32 were the high yielding and low yielding genotype, respectively. Similar to the AMMI bi-plot, the GGE bi-plot also confirmed that SML-668 was the winning genotype in most of the environments; whereas, SML-32 and local 2-sheraro, were the low yielding genotypes in some or all of the environments. E1, E2 and E6 are discriminating environments and declared as the most representative than E3, E4 and E5. Generally, SML-668 was the ideal genotype with higher mean yield and relatively good stability; Local-2 Sheraro was the moderately good yielding genotype and the most unstable genotype; Whereas, SML-32 was the poorly yielding and unstable genotype.

ABOUT THE AUTHOR
The research group is engaged on lowland legume and oil crops research. The team is mainly working on evaluation and development of early maturing and high yielding mung bean varieties for the moisture stress areas in Northern Ethiopia. The team is interested in mung bean germplasms collection and characterization, study of biotic and abiotic stresses in mung bean production, and finally enhancing mung bean productivity and quality in the mung bean growing areas.

PUBLIC INTEREST STATEMENT
In Ethiopia, legume crops are the second most important next to cereals in area coverage and production. Mung bean, a warm season legume crop, is grown mainly for its edible seeds. In Ethiopia, farmers in some moisture stress areas of Southern Ethiopia, Amhara, Tigray and in some parts of Oromya have been producing mung bean to supplement their protein needs and also to harvest reasonable yield during cropping seasons of insufficient rainfall. This study was conducted so as to identify early maturing and high yielding mung bean varieties and the finding of this study showed a variety named SML-668 with higher mean yield and relatively good stability is the ideal variety for the moisture stress areas. Hence, having such early maturing varieties which can tolerate climate variability are important for farmers in the dry land areas.
1. Introduction

Mung bean (Vigna radiata (L.) Wilczek), which is also known as Green gram, mung and moong in India, mungo in the Philippines (Morton, Smith, & Poehlman, 1982b) “masha” in Amharic, “katsal ater, Zerei Kahasay or Zerei keshi Shishay” in Tigrigna, is an important pulse and protein-rich crop. Mung bean which is classified in the Order Leguminosae, Family Papilionoideae (Padulosi & Ng, 1997), is native to the India-Burma area of Southeast Asia (Vavilov, 1951). India is the largest mung bean producer which accounts 54% of the world mung bean production and 65% of the world acreage. In Ethiopia, farmers in some moisture stress areas of Southern Ethiopia (Gofa, Konso, South Omo Zone and Konta) (Asfaw, Gurum, Alemayehu, & Rezene, 2012) in Amhara (shewarobit), Tigray (North Western and Western Zone) and in some parts of Oromya have been producing mung bean to supplement their protein needs and also to have a yield during cropping seasons of insufficient rainfall.

Mung bean is grown mainly in semi-arid to sub-humid lowland tropics and subtropics with 600 to 900 mm annual rainfall and not exceeding 2,000 meter elevation. It is a warm season crop, and will grow within a mean temperature range of about 20°C to 40°C and it is sensitive to low temperatures and is killed by frost (Morton, Smith, & Poehlman, 1982a). Mung bean is an annual, semi-erect to erect or sometimes twining herb, 25 to 116 cm tall (Waniale, Wanyera, & Talwana, 2014), can mature in 50–60 days and produce up to 2457 kg/ha (Gebrelibanos & Fiseha, 2018).

Mung bean is a leguminous species, grown principally for its edible seeds. Mung bean seeds are eaten as boiled beans, roasted beans, soup or mung bean pancake, as sauce and mung bean flour also mixed with different cereals to make different local breads. The nutritive value of mung bean lies in its high and easily digestible protein, and contains approximately 25–28% protein, 1.0% oil, 3.5–4.5% fiber, 4.5–5.5% ash and 62–65% carbohydrates on dry weight basis (Somta, Sommanas, & Srinives, 2009). Mung bean contains 504 mg g⁻¹ lysine content (Saini, Singh, Hussain, & Sikka, 2010) and this essential amino acid makes it a good supplement for most cereal-based diets since, they lack this essential amino acid (Baskaran & Bordawekar, 2009). In addition, the forage remaining from mung bean after the pods are picked and threshed is highly important and preferable for animal feed. Apart from these, the ability to fix nitrogen and addition of organic matter to the soil are important factors in maintaining soil fertility (Delfin, Paterno, TORRESº, & Santos, 2008; Senanayake, Knievel, & Stevens, 1987; Zapata, Danso, Hardarson, & Fried, 1987). According to the study from (Hayat & ALI, 2010) N2-fixation under normal soil fertility condition by mung bean yielded 47 kg ha⁻¹ Nitrogen.

The ultimate objective of most plant breeders is improving quality and/or quantity of their crops with better adaptability and stability in different growing environments. An ideal variety always combines high yield with the stability of performance (Eberhart & Russell, 1966) although it is difficult to find such high yielding and stable variety over a wide range of variable environments. In such widely variable environments, the occurrence of significant genotype x environment interaction (GEI) is largely possible. Such occurrence of significant GEI in plant breeding is both an opportunity and a challenge for plant breeders (Baraki, Tsehaye, & Abay, 2014). The process of identification of stable and high yielding genotype under different growing environments like the mung bean growing areas of western and North Western Tigray is difficult because of the occurrence of GEI. Therefore, an in-depth knowledge of the degree and pattern of GEI is important for plant breeders to minimize the cost of genotype evaluation by eliminating unnecessary spatial and temporal replication of yield trials (Basford & Cooper, 1998). As a result, it is indispensably...
important to undertake experiments over years and locations to identify stable and high yielding mung bean variety.

2. Materials and methods

2.1. Experimental material and method

The experiment was conducted in Western Tigray, Northern Ethiopia, under rainfed condition from 2009–2011 cropping seasons in Humera and Dansha areas having a total of six environments. Where; E1, E2, E3 are 2009, 2010, 2011 growing seasons, respectively, in Humera; E4, E5, E6 are 2009, 2010, 2011 growing seasons, respectively, in Dansha. Edaphic and climatic description of the study areas is listed in Table 1. Six mung bean genotypes viz. SML–668, Black bean, Bored, Local Gofa, SML–32 and Local 2-Sheraro (local check) were planted in RCBD design with three replications. Each genotype was randomly assigned and sown in a plot area of 2.1 m by 5 m with 1 m and 1.5 m buffer zone between plots and blocks, respectively, keeping inter and intra row spacing of 30 cm and 10 cm, respectively. Each experimental plot received all management practices equally and properly as per the recommendations for the crop.

2.2. Statistical analysis

Homogeneity of residual variances was tested prior to a combined analysis over locations in each year as well as over locations and years (for the combined data) using Bartlet’s test (Steel & Torrie, 1980). Accordingly, the data collected were homogenous and all data showed normal distribution.

A combined analysis of variance was performed from the mean data of all environments to detect the presence of GEI and to partition the variation due to genotype, environment and genotype x environment interaction. Moreover, a mean comparison using Duncan’s Multiple Range Test (DMRT) was performed to explain the significant differences among means of the genotypes. GenStat 18th edition (Payne, Murray, Harding, Baird, & Soutar, 2009) statistical software was used to analyze the combined mean of the different agronomic traits of the mung bean genotypes. The model employed in the analysis was; 

\[ Y_{ijk} = \mu + G_i + E_j + B_k + GE_{ij} + \varepsilon_{ijk} \]

where: \( \mu \) is the overall mean; \( Y_{ijk} \) is the observed mean of the \( i \)th genotype (\( G_i \)) in the \( j \)th environment (\( E_j \)), in the \( k \)th block (\( B_k \)); \( G_i \) is effect of the \( i \)th genotype; \( E_j \) is effect of the \( j \)th environment; \( B_k \) is block effect of the \( i \)th genotype in the \( j \)th environment; \( GE_{ij} \) is the interaction effects of the \( i \)th genotype and the \( j \)th environment; and \( \varepsilon_{ijk} \) is the error term.

| Table 1. Geographic, agro-climatic and edaphic description of the study areas |
|-----------------|-----------------|-----------------|
| Location        | Humera          | Dansha          |
| Latitude (°N)   | 14°16’          | 13°34’          |
| Longitude (°E)  | 36°39’          | 36°40’          |
| Altitude (masl) | 619             | 706             |
| Annual Rain Fall (mm) | 536     | 824             |
| Min—Max Temp (°c) | 22–37.4       | 28.7(mean)      |
| Soil Characteristics | Clay (%)  | 35.66           |
|                  | Silt (%)       | 25.66           |
|                  | Sand (%)       | 38.66           |
|                  | Total-N (%)    | 0.066           |
|                  | pHwater(1:2.5) | 8.15            |
|                  | ECwater (1:2.5)| 0.11            |
A bi-plot showing the genotype and environmental means against Interaction Principal component analysis one (IPCA1) (AMMI1 bi-plot), and GGE bi-plot was also performed using AMMI model using GenStat 18th edition (Payne et al., 2009).

3. Result and discussion

3.1. Combined analysis of variance

The combined analysis of variance for mung bean genotypes evaluated in six environments is depicted in Table 2. There was highly significant variation (p < 0.01) of grain yield among the genotypes, environments (year, location, year x location) and genotype by environment interaction (Genotype x Year, Genotype x Location and Genotype x Year x Location) (Table 2). These significant variations of the main effects and their interactions indicated that the ranking of the genotypes were changing from environment to environment confirming the absence of stable genotype over all environments and the existence of significant genotype by environment interaction in this experiment. Asfaw et al. (2012) also reported significant GEI in grain yield of mung bean genotypes evaluated in different environments.

3.2. Grain yield of mung bean genotypes in different environments

Due to the existence of significant GEI, the grain yield of the genotypes varies from environment to environment in the growing environments (Table 2 and Figure 1). The average grain yield of mung bean genotypes evaluated in two locations and 3 years (a total of six environments) was 2008.17 kg/ha

| Source of Variation       | DF | SS        | MS      |
|---------------------------|----|-----------|---------|
| Replication               | 2  | 25,313    | 12,656  |
| Genotype                  | 5  | 6,667,371 | 1,333,474** |
| Location                  | 1  | 1,729,916 | 1,729,916** |
| Year                      | 2  | 599,473   | 299,736** |
| Genotype * Location       | 5  | 359,766   | 71,953** |
| Genotype * Year           | 10 | 1,170,420 | 117,042** |
| Location * Year           | 2  | 7,519,832 | 3,759,916** |
| Genotype *Location * Year | 10 | 1,006,684 | 100,668,888** |
| Residual                  | 70 | 2,803,770 | 40,054  |
| Total                     | 107| 21,882,544|         |

Table 2. Combined analysis of variance for grain yield of mung bean genotypes

Figure 1. Cross over performance of the mung bean genotypes across the growing environments.
| Genotype       | Location | Humera          | Dansha          | Average Yield (kg/ha) |
|---------------|----------|-----------------|-----------------|-----------------------|
|               | Year     | 2009 E1 | 2010 E2 | 2011 E3 | 2009 E4 | 2010 E5 | 2011 E6 |           |
| Black bean    | 1945.45  | 2518.54  | 1770.73  | 2139.16 | 1357.57 | 2207.66 | 1989.85 |           |
| Bored         | 1766.59  | 2323.7   | 2019.31  | 1783.74 | 1564.37 | 1624.08 | 1846.97 |           |
| Local 2-Sheraro | 1748.33   | 2202.96  | 2142.35  | 1837.89 | 1623.96 | 2399.63 | 1992.52 |           |
| Local Gofa    | 1706.47  | 2543.63  | 1825.16  | 1928.51 | 1422.09 | 2031.79 | 1909.61 |           |
| SML-32        | 1621.62  | 2473.91  | 1582.44  | 1666.78 | 1545.68 | 1751.11 | 1773.59 |           |
| SML-668       | 2331.88  | 3378.51  | 2523.53  | 2371.61 | 1932.68 | 2680.61 | 2536.47 |           |
| Environment Mean | 1853.39  | 2573.54  | 1977.25  | 1954.62 | 1574.39 | 2115.81 | 2008.17 |           |
| Location Mean | 2134.73  |           |           | 1881.61 |           |           |           | 2008.17  |
The highest mean yield was obtained from SML-668 (2536.47 kg/ha) followed by Local 2-Sheraro (1992.52 kg/ha) and the lowest mean yield was obtained from SML-32 (1773.59 kg/ha) and this variation might be due to the genetic potential of the genotypes. Regarding the mean of the genotypes across the environments, the highest grain yield (3378.51 kg/ha) was obtained from SML-668 in E2 (grown in Humera in 2010 growing season) and the lowest grain yield (1357.57 kg/ha) was recorded from Black bean in E5 (grown in Dansha in 2010 growing season) (Table 3). Regarding to the growing locations Humera was comparatively the better mung bean growing area, with an average grain yield of 2134.73 kg/ha, than Dansha, with average grain yield of 1881.61 kg/ha, in the three growing seasons. This might be due to the reason that Humera received lower rainfall in the growing seasons which is favorable for mung bean production and the average highest rainfall in Dansha adversely affected the mung bean production (Table 1). The highest and late rainfall in this growing location (Dansha) enforced the pods to shatter prior to harvesting and discolored the harvested mung bean pods.

3.3. AMMI model analysis

When genotypes are tested in multi-location yield trials, a cross over GEI most often occurs (Ceccarelli, Grando, & Booth, 1996). The genotypes (G), environments (E) and the genotype × environment interaction (GEI) were significant (P ≤ 0.01) for mung bean grain yield. Hence, the variation of the mung bean mean grain yield was affected by the abovementioned factors and the variation was due to the inherent variability of the genotypes (30.47%), due to the environments on which the genotypes grown (45.01%) and the interaction (GEI) (11.59%) (Table 4). This significant genotype × environment interaction effects indicates that genotypes responded differently to the variation in environmental conditions of locations which indicated the necessity of testing mung bean varieties at multiple locations. Asfaw et al. (2012), Hussain & Fatima (2011) and Waniale et al. (2014) and also reported similar findings in mung bean that there was a significant variation in the genotypes, environments and the GEI for grain yield. The AMMI model also extracted a total of four IPCAs with two significant IPCAs contributing with 40.93% and 35.01% of the first IPCA and second IPCAs, respectively.

To easily visualize the performance and the stability of the genotypes and the environments AMMI1 bi-plot is depicted in Table 4. Both the Genotypes and environments become unstable as they become far away from the abscissa (with greater magnitude of IPCA1) and they become stable as they become closest to the abscissa (with smaller magnitude of IPCA1). Similarly, both the Genotypes and environments become high yielding as they become far away to the right side of the ordinate and they become low yielding as they become far away to the left side of the ordinate (Yan & Tinker, 2006). Accordingly,
SML-668, which located far away to the right side of the ordinate, was the high yielding genotype. On the other hand, SML-32, which located far away to the left side of the ordinate, was the low yielding genotype (Figure 2 and Table 3). Regarding to the stability Local 2-Sheraro which has greater IPCA1 is the most unstable genotype and Bored which had lower IPCA1 is the most stable genotype among the evaluated mung bean genotypes.

3.4. GGE bi-plot analysis

3.4.1. Which-won-where view of the GGE bi-plot?
The which-wins-where view of the GGE bi-plot (Yan, Hunt, Sheng, & Szlavnics, 2000) is best for what pattern of multi-environment trial data is important for studying the possible existence of different mega-environments in growing environments (Gauch & Zobel, 1997). The polygon view of a GGE bi-plot explicitly displays the which-wins-where pattern, and hence is a brief summary of the GEI pattern of a multi-environment trial data set (Figure 3). Hence, this GGE bi-plot is depicted to effectively identify the GEI pattern of the data to clearly show which genotype won in which environments. In the GGE bi-plot, there are three sectors on which at least one genotype is fall down on. Out of the three sectors, there is only one sector on which six of the different environments fall down. The genotypes in the vertex of the GGE bi-plot are the best genotypes in the respective environments or the worst genotypes in some or all of the environments (Yan & Tinker, 2006). Accordingly, SML-668, on which all of the environments fall down, is the winning genotype in most of the environments; whereas, SML-32 and local 2-sheraro which fall down in the sectors without any environments, were the low yielding genotypes in some or all of the environments.

3.4.2. Evaluation/association of test environments
It is possible to portray the relationship between the genotypes and environments for grain yield graphically. Yan (2001) proposed a GGE bi-plot that allows visual examination of the GEI pattern of multi-environment trial data. The similarity between two environments as well as genotypes is determined by both the length of their vectors and the cosine of the angle between them and the representativeness and discrimination of the environments is length of the vectors and the angle from the abscissa (Yan & Tinker, 2006). The existence of close associations among test environments suggests that similar information regarding the genotypes could be obtained from fewer test environments, and hence the probability to reduce testing cost. If two given test environments are closely correlated consistently across years,
one of them can be throwing down without loss of abundant information about the genotypes (Yan, Kang, Ma, Woods, & Cornelius, 2007).

Furthermore, the presence of wide obtuse angles (i.e., strong negative correlations) among test environments is an indication of strong crossover GE and on the other hand, the existence of acute angles (i.e., strong positive correlations) among test environments is an indication of no crossover GE. Accordingly, both of the environments, with an acute angle among each other are highly correlated. However, E1, E4 and E5 with a very narrow angle among each other are highly and positively correlated while, E3 and E6 were also highly correlated to each other.

3.4.3. Similarity of the genotypes in the testing environments

The GGE bi-plot in Figure 5 is similar to Figure 4, except that it is genotype-metric preserving (SVP = 1) and hence, it is correct for comparing genotypes. The distance between two genotypes measures the overall similarity or dissimilarity between them. This similarity can be in terms of grain yield or stability. Furthermore, genotypes with shorter vector length from the bi-plot origin have a small contribution to both G and GE and in contrary to this genotypes far away from the bi-plot origin have large contributions to the GEI. Accordingly, SML-32, Bored, Local Gofa and Black bean were highly associated among each other, and these genotypes were consistently low yielding genotypes. Whereas, SML-668 with highest mean grain yield and longer vector length, was not correlated with the other genotypes.

3.5. Discriminating and representativeness of the test environments

Figure 6 (the average tester coordination for tester evaluation) depicts similar bi-plot as Figure 4 (relationship among testers) except that an “Average-Environment Axis” (AEA) (Yan, Cornelius, Crossa, & Hunt, 2001). The average environment (represented by the small circle at the end of the arrow) has the average coordinates of all testing environments, and the AEA is the line that passes through the bi-plot origin and the average environment Regarding the
The discrimination ability of the testing environments both environments on the same concentric circle indicating their vector length is almost similar. Hence, both of the environments have the similar discriminating ability and a similar possibility to generate information on the genotypes.
A test environment which has a smaller angle with the AEA is highly representative of other test environments (Frutos, Galindo, & Leiva, 2014) and a test environment which has a long vector length is considered as discriminating environment (Yan, 2002) and (Yan et al., 2007).

Figure 6. The discriminating vs. representativeness view of the GGE bi-plot to visualize the discriminating ability and representativeness of the test.

Figure 7. The average-environment coordination (AEC) view to evaluate genotypes relative to an ideal genotype.
Accordingly, environments E1, E2 and E5 having smaller angle with the AEA are declared as the most representative than E3, E4 and E5 which are with a relatively higher degree with the AEA. Furthermore, environments E1, E2 and E5 are also with longer vector length and are considered as good test environments for selecting widely adapted genotypes. Asfaw et al. (2012) also used the discriminating versus representativeness view of the GGE bi-plot to evaluate the testing environments for mung bean.

3.5.1. Evaluation of the genotypes in relation to the ideal genotype
SML-668 is the ideal genotype with a higher mean yield and relatively good stability (Figure 7). Black bean is also the genotype with relatively higher yield and stable while SML-32 is the poorly yielding genotype which is too far from the ideal genotype and also not stable. Local-2 Sheraro was the moderately good yielding genotype and the most unstable genotype since it is with longer vector length from the AEA. Asfaw et al. (2012) also used the GGE bi-plot of the mean and stability to evaluate the performance and stability of mung bean genotypes against the ideal genotypes.

3.6. Performance of the genotypes in the testing environments
The performance of a genotype in a given environment is better than average if the angle between its vector and the environment’s vector is <90°; and it is lower than average if the angle is >90°; and it is similar to the average if the angle is near to 90° (Yan & Tinker, 2006). Hence, SML-668 with an acute angle with all of the environments is with the mean of above average mean of the genotypes (Figure 8). Local 2 Sheraro with lower than 90° is also with a higher mean than the average mean of the genotypes. Whereas, Black Bean, Local Gofa, Bored and SML-32 with an obtuse angle with all of the environments are with lower than the average yield in most of the environments. Alam, Somta, Jompuk, Chatwachirawong, and Srinives (2014) also used the GGE bi-plot of performance of each genotypes in each environments to evaluate the performance of mung bean genotypes in different growing locations.
4. Conclusion and recommendation

The genotypes (G) (30.47%), environments (E) (45.01%) and the genotype × environment interaction (G × E) (11.59%) were significant (P ≤ 0.01) for mung bean grain yield confirming there was a cross over interaction in this study. The highest mean yield was obtained from SML-668 (2536.47 kg/ha) while the lowest mean yield was obtained from SML-32 (1773.59 kg/ha). According to AMMI2 bi-plot, SML-668, was the high yielding genotype while, SML-32 was the low yielding genotype. Furthermore, according to the which-won-where view of the GGE bi-plot, SML-668 was the winning genotype in most of the environments; whereas, SML-32 and local 2-sheraro were the low yielding genotypes in some or all of the environments.

Generally, SML-668 with an acute angle with all of the environments is with the mean of above average mean of the genotypes while, SML-32 with an obtuse angle with all of the environments was with lower than the average yield in all of the environments.

Finally, SML-668 was the ideal genotype with higher mean yield and relatively good stability and Local 2-Shareraro was the moderately good yielding genotype and the most unstable genotype. Whereas, SML-32 was the poorly yielding and unstable genotype.

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Competing Interests

The authors declare that they have no competing of interests.

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