Genetic variability in Ethiopian faba bean (Vicia faba L.) accessions

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Abstract: Knowledge on genetic variability in faba bean (Vicia faba L.) is crucial to enhance its production and productivity. However, there has been very limited information on variability of Ethiopian faba bean accessions. Therefore, the present study was conducted to evaluate the phenotypic and genotypic variability, heritability and genetic advance of yield and associated traits in Mecha district during 2019 main cropping season. A total of 81 faba bean accessions were evaluated using 9 × 9 simple lattice design. Data were collected for 14 quantitative and three qualitative traits. The result of analysis of variance showed highly significant (p < 0.01) differences among accessions for all quantitative traits except days to maturity and number of seeds per pod. High phenotypic and genotypic coefficient of variation was observed for hundred-seed weight (24.02 and 20.29), biomass yield (27.25 and 25.35), harvest index (30.06 and 26.67), grain yield (31.32 and 30.77), number of branches per plant (36.81 and 27.52), number of pods per plant (43.66 and 37.600), and for scores for diseases like ascochtya blight (46.17 and 45.64), chocolate spot (50.1 and 47.9), and rust (66.03 and 64.43), indicating the presence of ample variability residing within the accessions; as a result, these traits could be improved through direct selection. High heritability coupled with high genetic advance was observed for hundred-seed weight, harvest index, number of pods per plant, grain yield, biomass yield, and disease-related traits, indicating the importance of genetic variance for the expression of these traits, and these traits could easily be improved through direct selection.

Subjects: Agriculture; Crop Science; Pest Management; Agriculture and Food; Plant Biology

Keywords: coefficient of variance; direct selection; faba bean; genetic advance; heritability; variability

1. Introduction
Faba bean (Vicia faba L.) is one of the earliest domesticated food legumes in the world (Singh et al., 2013) and is one of the most important legume crops, and the crop is believed to be originated and cultivated first in the Near East during early in Neolithic times, 8000 B.C. (Cubero, 1974; Karkkis et al., 2018; Torres et al., 2006). Cubero (1974) also mentioned that Ethiopia is the secondary sources of diversity for the crop.

Currently, the crop is grown under different cropping systems for its importance in human and animal nutrition and for the diverse services it offers for the ecosystem. Faba bean needs a cool season for best growth with moderate amounts of rainfall ranging from 650 to 1000 mm per annum (Gasim & Link, 2007) and considerably tolerate frost but is susceptible to drought and water-logging conditions (Subash & Priya, 2012). Faba bean can also tolerate acidic soils better
than most other legumes (Singh et al., 2010) but grow best in loamy soils (Rajan et al., 2012). Due to its ability to grow over a wide range of climatic and soil conditions and its high nutritional value (Yahia et al., 2012), faba bean had ranked sixth in terms of world production with 4.5 Mt from 2.5 Mha (FAO (Food and Agriculture Organization), 2020). The crop also has a potential to substitute meat due to its high protein content of the seed in many parts of the world where there is demand for non-animal protein sources (Crepon et al., 2010).

Ethiopia was the second major faba bean producer globally with a total production of 1,006,752 metric tons next to China (1,740,945 metric tons; FAO (Food and Agriculture Organization), 2020). These two countries had produced 50% of the total global production. In Ethiopia, the major faba bean-producing regions are Oromia (Wollega, Shoa and Bale zones), Amhara (Gondar, Gojam and Wollo), southern parts of the country (Gamo Gofa), Benishangul-Gumuz and highland parts of Tigray (Central Statistical Agency (CSA), 2017). Ethiopian farmers are also aware of the role of the crop in improving soil health by fixing atmospheric nitrogen and widely use it in rotation with cereals. Faba bean is also a source of cash to the farmers and foreign currency to the country.

Despite its importance and production potential, the productivity of faba bean in Ethiopia is less and is constrained by many different factors including biotic (diseases, weeds and insects), abiotic (drought, water logging and marginal management) and edaphic stresses like soil acidity. The crop is also believed to have high degree of genetic variability for tolerance of different stresses due to its high percentage of out-crossing nature (Polignano & Zeuli, 1985). Therefore, developing tolerant varieties is one of the many options that can be done to address these challenges. To design an appropriate breeding approach and develop such varieties, knowledge on the extent of genetic variability and heritability of traits is crucial. However, information on variability and heritability of traits is limited for Ethiopian faba bean accessions in the study area. Therefore, the present study was conducted to estimate genetic variability, heritability and genetic advance of traits in Ethiopian faba bean accessions.

2. Materials and methods

2.1. Experimental site, materials and design

The experiment was conducted at Bahir Dar University research site in Mecha district of West Gojam zone of Amhara regional state, Ethiopia, in 2019 main cropping season. Mecha is located about 525 km northeast of Addis Ababa and 34 km southwest of Bahir Dar. It is located at a latitude of 10° 30’ N and a longitude of 37°29’ E. The site receives mean annual rainfall of 1572 mm. The mean temperature ranges between 24°C and 27°C, and the altitude is 2009 m.a.s.l.

Totally, 81 faba bean genotypes (78 accessions, 2 improved varieties and 1 local variety) were used in the present study. The 78 accessions were obtained from Ethiopian Biodiversity Institute; the two improved varieties were obtained from Adet Agricultural Research Center; and the local check from local source. The design used was 9 × 9 simple lattice. Each accession was planted in two rows. Spacing between rows and within rows were 40 cm and 10 cm, respectively. The single plot size was 0.8 m × 1 m (0.8 m²). Spacing between blocks was 1 m (Table 1).

2.2. Data collected

Fourteen quantitative and three qualitative data were collected on plant and plot basis. The pre- and post-harvest observations were recorded on five random plants from each plot in each replication for all the traits considered except for days to flowering, days to maturity, biomass yield, grain yield and harvest index which were determined based on plot basis. Data of sampled plants and seeds were taken at the right growth stage of the crop for each trait.

2.3. Quantitative traits

Plant height (cm): It was measured from five randomly taken plants from the ground surface to the tip of the main stem, and the average was used for further analysis.
Pod length (cm): It was measured at harvesting from five randomly taken pods of the five randomly taken plants, and the average was used for further analysis.

Number of pods per plant: It was recorded from all pods borne on the five randomly taken plants and averaged.

Number of seeds per pod: It was recorded from seeds of five randomly taken pods from the five randomly taken plants and averaged to represent the plot.

Number of branches: It was counted and averaged from branches extending from the main stem of the five randomly taken plants.

Disease score: The incidence of disease was scored using 1–9 scale method, where 1 refers to highly resistant and 9 indicates highly susceptible.

The disease data recorded based on scoring scale were converted into percentage severity index (PSI) according to Wheeler (1969). PSI used to convert scale data into percent and for ease of analysis. Percent severity index (PSI%) was calculated using the following formula:

\[
\text{PSI} \% = \frac{\sum \left[ \text{NPC} \times \text{CR} \right]}{\text{NIP} \times \text{MSC}} \times 100
\]

where NPC = number of plants in each class rate,

CR = class rate,

NIP = number of infected plants and

MSC = maximum severity class rate

Days to 50% flowering: These were recorded from the date of sowing to the date of which 50% of the plants on a plot opened their flowers.

Days to 75% maturity: These were recorded from the date of sowing to the stage when 75% of the plants in a plot changed the color of their pods from green to yellow.

Grain yield (g/plot): It was obtained from each plot and was used to estimate grain yield per hectare after cleaned and adjusted to 10% moisture content.

100-seed weight (g/plot): 100-seeds was taken randomly on each plot and weighted to represent this trait.

Biological yield (g/plot): It was recorded from the above ground parts of harvested plants which was sun dried and weighed to get the biological yield per plot in grams.

Harvest Index: It was calculated by dividing grain yield by the biological yield.

\[
\text{Harvest Index (HI)} = \frac{\text{Grain yield (g)}}{\text{Biological yield (g)}} \times 100
\]

2.4. Qualitative traits

Seed size (boldness)—It was classified into three categories based on its 100-seed weight (100/g) as small, medium and bold (1 = small, 2 = medium and 3 = bold).
Seed shape—It was classified into three categories, oblong, semi-spherical and semi-ovals (1 = oblong, 2 = semi spherical and 3 = semi oval) to know the degree of diversity in this trait.

Seed coat colour—It was also classified into light green, pale green and light brown to copper colour (1 = light green, 2 = pale green and 3 = light brown to copper colour).

Then, such qualitative data were converted into percentage by the following formula;

\[
\frac{\text{No of accessions in ascale}}{\text{Total no. of tested accessions}} \times 100
\]

2.5. Data analysis
The data for each trait was subject to analysis of variance (ANOVA) for simple lattice design. ANOVA was done using SAS software version 9.2 (SAS Institute, 2008). Duncan’s Multiple Range Test (DMRT) was used for means separation.

Genotypic variance (\(\sigma^2_g\)), phenotypic variance (\(\sigma^2_p\)), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the formula adopted from Burton and Devane (1953):

Environmental variance (\(\sigma^2_e\)) = MSe. Genotypic variance (\(\sigma^2_g\)) = \(\frac{\text{MSe} - \text{MSe}}{r}\)

Phenotypic variance (\(\sigma^2_p\)) = \(\sigma^2_g + \sigma^2_e\)

where MSe and MSe are the mean square of genotypes and error from the ANOVA, respectively. \(r\) is the number of replications.

Coefficients of variation at phenotypic and genotypic levels were estimated using the following formula:

Genotypic coefficient of variation (GCV) = \(\sqrt{\sigma^2_g / \text{grand mean}} \times 100\).

Phenotypic coefficient of variation (PCV) = \(\sqrt{\sigma^2_p / \text{grand mean}} \times 100\).

2.6. Heritability in the broad sense
Broad sense heritability (\(H^2\)) is the ratio of the genotypic variance (\(\sigma^2_g\)) to the phenotypic variance (\(\sigma^2_p\)) and was computed on genotype mean basis according to Allard (1960) as follows:

\[
H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100
\]

As Johnson et al. (1955) stated, the ranges of heritability were categorized as low = 0–30, medium = 31–60 and high >61.

2.7. Genetic advance
The methods illustrated by Johnson et al. (1955) were used to compute expected genetic advance (GA) and GA as percent of the mean assuming selection of the superior 5% of the genotypes.

\[
GA = K \times \sigma p \times h^2
\]

where \(h^2\) = the heritability ratio, \(\sigma p\) = phenotypic standard deviation and \(K\) = constant (2.06).

GA as % of the mean was calculated by dividing the GA value with the respective grand mean of the trait being evaluated.
3. Results and discussion

Mean squares of the 14 traits from ANOVA are presented in Table 2. Highly significant \( (p < 0.01) \) differences among accessions were observed for all traits except days to maturity and number of seeds per pod. This highly significant difference indicates the existence of variability among accessions for traits studied. The presence of variability in the accessions offers an opportunity in improvement of yield and its contributing traits through selection in faba bean. Similar results were reported by Kenevi et al. (2005) in 160 faba bean accessions. Abdullah (2018) also reported a significant variability among faba bean genotypes.

3.1. Estimation of mean and range

The range and mean of accessions for the 14 traits are shown in Table 3. Grain yield ranged from 1,148 to 5,167 kg ha\(^{-1}\) with a mean value of 2,050 kg ha\(^{-1}\). The highest grain yield was recorded by accession 235433 (5,167 kg ha\(^{-1}\)), while the lowest grain yield was obtained from accession 208085 (1,148 kg ha\(^{-1}\)). This indicates the existence of a wide range of variability among accessions in grain yield. Accessions 235433, 235709, 219089, 25325, 25310 and 25290 were promising for the grain yield improvement of faba bean. The results of the present study are in conformity with findings by Temesgen et al. (2015) who reported the highest yield of 6,649 kg ha\(^{-1}\) at Kulumsa in 2009 and the lowest yield of 1,198 kg ha\(^{-1}\) at Bekoji in 2007. Mitiku and Mekuria (2015) had also reported the highest yield of 4,886.8 kg ha\(^{-1}\) and 4,701.6 kg ha\(^{-1}\) in Agarfa and Sinana trial sites, respectively.

For the phenological trait, days to flowering ranged from 42 to 59 with a mean of 45.56 days. The results indicate the presence of high variability among the accessions for days to flowering. Accordingly, accession 25018 was the late flowering, whereas the local was earliest in flowering. Days to maturity ranged from 109 to 131 with a mean value of 118.20 days. Accession 240497 was the earliest maturing and Doshia was the late maturing. The tested accessions have got good amount of variability with respect to biological yield. Biological yield shows a range of 2,471 to 15,278 kg ha\(^{-1}\) with a mean of 8,310 kg ha\(^{-1}\). The maximum biological yield was recorded from Doshia and minimum from accession 212576. This result indicates that there is ample scope for improvement of this important trait. These results are in the close conformity with the findings of previous researchers (Singh et al., 2017; Veasey et al., 1999). Plant height ranged from 53.6 to 132 cm with a mean of 97.75 cm. The maximum and minimum plant heights were recorded from local and accession 212568, respectively. This indicates the existence of variability among accessions. The minimum and maximum number of branches per plant ranged from 0.6 to 3.8 in accessions 25006 and 255709, respectively.

Number of pods per plant ranged from 3.5 to 39.2, with a mean of 11.70. The maximum number of pods per plant was obtained from accession 235433, while the minimum was from accession 212575. This trait clearly shows that sufficient variability is present in the accessions. Number of seeds per pod ranged from 1 to 3.8, with a mean value of 2.77. Maximum number of seeds per pod was obtained from accession 25274, whereas accession 25018 produced minimum number of seed per pod.

Hundred-seed weight ranged from 24 to 101.2 g; Doshia had the maximum and accession 215748 had the minimum 100-seed weight. Harvest index is an effective indicator of source to sink relation and translocation of photosynthesis. The range of harvest index was 12.27 to 55.13%, with mean value of 25.71. This shows the range of harvest index with a good amount of variability. The results of the present study are in conformity with the earlier findings (Singh et al., 2017; Veasey et al., 1999). Pod length ranged from 2.3 to 6.5 cm, with a mean value of 3.75 cm in accession 25006 and Doshia, respectively. This indicates that the presence of variability among accessions and selection can result in the improvement of pod length of faba bean. Similar results were reported by Singh et al. (2017).

Disease scores for Ascochyta blight, chocolate spot and rust were ranged from 11.11% to 77.78% for each based on percentage severity index (PSI) conversion. Accessions 25274, 25298,
Table 1. List of the 81 faba bean accessions used in the study

| Number | Accession | Collection region | District       | Number | Accession | Collection region | District       |
|--------|-----------|-------------------|----------------|--------|-----------|-------------------|----------------|----------------|
| 1      | 212565    | Amhara            | SyadebrinaWayu | 42     | 235709    | SNPP              | Dirashe Special |
| 2      | 27279     | Amhara            | Machakel       | 43     | 219089    | Oromia            | Amigna          |
| 3      | 25299     | SNPP              | Angacha        | 44     | 25338     | SNPP              | MeskanenaMareko |
| 4      | 243140    | SNPP              | DilaZuria      | 45     | 215748    | Amhara            | DessieZuria     |
| 5      | 212566    | Oromia            | WuchalenaJido  | 46     | 213211    | Oromia            | TiroAfeta       |
| 6      | 25006     | Amhara            | HuletEjEnese   | 47     | 25336     | SNPP              | MeskanenaMareko |
| 7      | 212568    | Amhara            | SyadebrinaWayu | 48     | 226125    | Amhara            | Legambo         |
| 8      | 25018     | Oromia            | WuchalenaJido  | 49     | 240497    | SNPP              | Decha           |
| 9      | 27052     | Oromia            | Kofele         | 50     | 25346     | SNPP              | MeskanenaMareko |
| 10     | 25274     | Oromia            | Becho          | 51     | 25328     | SNPP              | Selti           |
| 11     | 229303    | Amhara            | Ay BetnaTachBet| 52     | 213214    | Oromia            | LimuSeka        |
| 12     | 212567    | Amhara            | SyadebrinaWayu | 53     | 25335     | SNPP              | MeskanenaMareko |
| 13     | 25298     | SNPP              | Angacha        | 54     | 25340     | SNPP              | MeskanenaMareko |
| 14     | 219355    | Oromia            | AdolanaWadera  | 55     | 25339     | SNPP              | MeskanenaMareko |
| 15     | 208085    | Amhara            | WeremoWagetunaMida | 56 | 215129    | Amhara            | MamaMdrinoLalo  |
| 16     | 212811    | Amhara            | Wegera         | 57     | 215128    | Amhara            | MamaMdrinoLalo  |
| 17     | 203105    | Oromia            | Dedesa         | 58     | 228607    | Amhara            | GonchoSsoEnese  |
| 18     | 235955    | Amhara            | Debark         | 59     | 25337     | SNPP              | MeskanenaMareko |
| 19     | 25279     | SNPP              | Cheha          | 60     | 25341     | SNPP              | MeskanenaMareko |
| 20     | 208114    | Amhara            | WeremoWagetunaMida | 61 | 25331     | SNPP              | Selti           |
| 21     | 229310    | Amhara            | WeremoWagetunaMida | 62 | 235433    | Tigray            | KalaTemben     |
| 22     | 212572    | Amhara            | WeremoWagetunaMida | 63 | Tumsa     | ND                | ND             |
| 23     | 25003     | Oromia            | Kuyu           | 64     | 25325     | SNPP              | Selti           |
| 24     | 25323     | SNPP              | Selti          | 65     | 25329     | SNPP              | Selti           |
| 25     | 25022     | Oromia            | Kuyu           | 66     | 25309     | SNPP              | Angacha        |

(Continued)
| Number | Accession | Collection region | District | Number | Accession | Collection region | District |
|--------|-----------|-------------------|----------|--------|-----------|-------------------|----------|
| 26     | 25280     | SNNP              | Cheha    | 67     | 25304     | SNNP              | Angacha  |
| 27     | 235956    | Amhara            | Debark   | 68     | 25330     | SNNP              | Setiti   |
| 28     | 220079    | Tigray            | Adwa     | 69     | 25307     | SNNP              | Angacha  |
| 29     | 212576    | Amhara            | Lay Betina Tach Bet | 70     | 25334     | SNNP              | Setiti   |
| 30     | 212575    | Amhara            | Lay Betina Tach Bet | 71     | 25306     | SNNP              | Angacha  |
| 31     | 25277     | SNNP              | Cheha    | 72     | 25311     | SNNP              | Angacha  |
| 32     | 220076    | Tigray            | Adwa     | 73     | 25332     | SNNP              | Sodo     |
| 33     | 27290     | Oromia            | Jimma Arjo | 74     | 25310     | SNNP              | Angacha  |
| 34     | 25264     | Oromia            | Becho    | 75     | 25333     | SNNP              | Setiti   |
| 35     | 25292     | SNNP              | Limo     | 76     | 25302     | SNNP              | Angacha  |
| 36     | 25270     | Oromia            | Becho    | 77     | 25327     | SNNP              | Setiti   |
| 37     | 212580    | Amhara            | Mamha Midina Lalo | 78     | Dasha     | ND                | ND       |
| 38     | 25017     | Amhara            | Enarj Enawga | 79     | 25303     | SNNP              | Angacha  |
| 39     | 212578    | Amhara            | Geramidirna Keya | 80     | 25301     | SNNP              | Angacha  |
| 40     | 25010     | Oromia            | Gerar Jarso | 81     | Local     | Amhara            | Mecha    |
| 41     | 25290     | SNNP              | Limo     |         |           |                   |          |

ND: no data.
| Traits | Rep (DF = 1) | Accessions (DF = 80) | Rep × Block (16) | Error (DF = 64) | CV (%) | R²  |
|--------|--------------|---------------------|-----------------|-----------------|--------|-----|
| DF     | 0.10ns       | 18.57**             | 3.02**          | 2.21            | 3.30   | 0.92|
| DM     | 43.56ns      | 25.29ns             | 28.53**         | 18.28           | 3.64   | 0.68|
| PH     | 365.70**     | 230.18**            | 212.36**        | 109.68          | 10.75  | 0.77|
| PL     | 2.57**       | 0.53**              | 0.24**          | 0.19            | 11.74  | 0.80|
| NPP    | 1.03ns       | 45.44**             | 7.29**          | 6.74            | 22.36  | 0.89|
| NSP    | 1.81**       | 0.17ns              | 0.09**          | 0.12            | 12.32  | 0.68|
| NBP    | 0.00ns       | 0.61**              | 0.26**          | 0.17            | 24.16  | 0.81|
| BY     | 24966.00**   | 956753.60**         | 817978.00qns    | 691793.00       | 10.23  | 0.95|
| GY     | 31441.00**   | 810072.84**         | 10553.00qns     | 14290.00        | 5.72   | 0.99|
| HSW    | 6.97ns       | 173.27**            | 47.64*          | 28.96           | 12.93  | 0.89|
| HI     | 3.21ns       | 106.81**            | 16.36**         | 12.71           | 14.44  | 0.90|
| AB     | 12.20ns      | 532.02**            | 0.04**          | 6.19            | 7.07   | 0.99|
| CS     | 3.05**       | 547.10**            | 0.33**          | 24.49           | 15.07  | 0.96|
| RT     | 76.22*       | 590.28**            | 0.12**          | 14.48           | 14.30  | 0.98|

**Highly significant (p < 0.01); * significant (p < 0.05); ns : non-significant; CV : coefficient of variation; DF : days to flowering; DM : days to maturity; PH : plant height (cm); PL : pod length; NPP : number of pods per plant; NSP : number of seeds per pod; NBP : number of branches per plant; BY : biomass yield; GY : grain yield; HSW : 100-seed weight; HI : harvest index; AB : ascochyta blight; CS : chocolate spot; RT : rust disease.
Table 3. Minimum, mean and maximum values of 14 traits of 81 faba bean accessions

| Traits                        | Mean | Std. Dev. | Minimum | Acc.  | Maximum | Acc.  |
|-------------------------------|------|-----------|---------|-------|---------|-------|
| Days to flowering             | 45.56| 3.54      | 42      | Local | 59      | 25018 |
| Days to maturity              | 118.20| 5.12      | 109     | 240497| 131     | Dosha |
| Plant height                  | 97.75| 14.64     | 53.6    | 212568| 132     | Local |
| Pod length                    | 3.75 | 0.65      | 2.3     | 25006 | 6.5     | Dosha |
| Number of pods per plant      | 11.70| 5.31      | 3.5     | 212575| 39.2    | 235433|
| Number of seed per pod        | 2.77 | 0.41      | 1       | 25018 | 3.8     | 25274 |
| Number of branches per plant  | 1.70 | 0.62      | 0.6     | 25006 | 3.8     | 235709|
| Biomass yield                 | 8310.00| 2426.00  | 2471    | 212576| 15,278  | Dosha |
| Grain yield                   | 2050.00| 675.77   | 1148    | 208085| 5167    | 235433|
| Hundred-seed weight           | 41.86| 11.06     | 24      | 215748| 101.2   | Dosha |
| Harvest index                 | 25.71| 7.91      | 12.27   | 25006 | 55.13   | 27290 |
| Ascochyta blight              | 35.53| 16.84     | 11.11   | 235433| 77.78   | 215748|
| Chocolate spot                | 33.74| 17.60     | 11.11   | 240497| 77.78   | 215748|
| Rust disease                  | 26.34| 18.11     | 11.11   | 25274 | 77.78   | 212576|

Acc.: accession.

203105, 25279, 25270, 25017, 219089, 240497, 235433, Tumsa, 25304, 25330, 25307, 25311, Dosha and 25301 were resistant to Ascochyta blight disease, but accessions 212568, 219355 and 215748 were susceptible to Ascochyta blight. The responses of accessions 25274, 219089, 240497, 235433, Tumsa, 25311, Dosha, 229303, 25323, 25290, 213211, 25346, 213214, 228607, 25325, 25334, 25306, 25310, 245140, 229310 and Local were resistant to chocolate spot; however, accessions 215748, 212568, 25018, 25340 and 220076 were susceptible. Most of the accessions were categorized under resistant and moderately resistant for rust disease, but accessions 235955, 212576 and 25331 were susceptible. This result is in conformity with previous works (Abo-Hegazy et al., 2012; Asefa & Adare, 2018) who classified faba bean genotypes into different reaction groups.

Qualitative characterization of seed size showed that 37 accessions or 45.68% of the studied accessions were small seeded (Table 4). Medium seed size category had the largest number of accessions which is 39 (48.15%), and five of the accessions or 6.17% out of 81 tested accessions were bold seeded. Considerable amount of variability existed for these traits implies good opportunity to improve the boldness of seeds through selection.

Seed size (1 = small, 2 = medium and 3 = bold); seed shape (1 = oblong, 2 = semi-spherical and 3 = semi-oval); seed coat color (1 = light green, 2 = pale green, 3 = light brown to copper colour).

The result of seed shape characterization showed that 25 accessions (30.86%) were oblong. Semi-spherical and semi-oval seed shapes were seen in 35 (43.21%) and 21 (25.93%) accessions, respectively. Light green seed coat color was observed in 10 accessions. Majority of accessions (39) had pale green seeds and 32 of accessions showed light brown color. Generally, the qualitative
Table 4. Extent of variability in qualitative traits among faba bean accessions

| Traits               | Scale | Number of accessions | Percentage of accessions (%) |
|----------------------|-------|----------------------|------------------------------|
| Seed size            | 1     | 37                   | 45.68                        |
|                      | 2     | 39                   | 48.15                        |
|                      | 3     | 5                    | 6.17                         |
| Seed shape           | 1     | 25                   | 30.86                        |
|                      | 2     | 35                   | 43.21                        |
|                      | 3     | 21                   | 25.93                        |
| Seed coat colour     | 1     | 10                   | 12.35                        |
|                      | 2     | 39                   | 48.15                        |
|                      | 3     | 32                   | 39.51                        |

traits used clearly showed the presence of variability among accessions. This indicates that these traits could be improved by selection. Similar results were reported by Singh et al. (2017).

3.2. Estimates of genetic parameters

3.2.1. Phenotypic and genotypic coefficients of variation

The estimates of genotypic ($\sigma^2_g$) and phenotypic ($\sigma^2_p$) variances, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean were determined for the traits considered and are presented in Table 5.

According to Deshmukh et al. (1986), PCV and GCV values greater than 20% are considered as high, values between 10% and 20% as medium and values less than 10% as low. Accordingly, high PCV was observed for 100-seed weight, biological yield, harvest index, grain yield, number of branches per plant, number of pods per plant, ascochyta blight, chocolate spot and rust disease score. These indicate the existence of wide phenotypic variation among the accessions considered in the present study and the possibility of genetic improvement of those traits through selection. Similar findings were reported by Mulualem et al. (2013) for 100-seed weight, disease resistance, number of pods per plant, grain yield and biological yield. Medium PCV was observed for traits like plant height and pod length, indicating the existence of lesser phenotypic variability among the faba bean accessions for these traits. Similarly, Kumar et al. (2017) have reported medium PCV for plant height and pod length. In the present study, low PCV was observed for days to flowering, which indicate the presence of narrow genetic variation. However, the improvement of this trait could be possible through hybridization or induced mutagenesis followed by selection. Similarly, Dev et al. (2017) reported low PCV for days to flowering in chickpea.

High GCV was observed for traits like number of pods per plant, number of branches per plant, biological yield, grain yield, 100-seed weight, harvest index, ascochyta blight, chocolate spot and rust disease score. These results indicate the existence of considerable genotypic variability among faba bean accessions for these traits and greater influence of genetic factors for the expression of these traits, suggesting the possibility of improving these traits through selection. The result is in conformity with Kumar et al. (2017) who reported high GCV for number of pods per plant, number of branches per plant, and 100-seed weight. Medium GCV was observed for pod length and low GCV for traits like days to flowering and plant height. Kumar et al. (2017) reported medium GCV for pod length. The low GCV estimates observed in the present investigation indicate the presence of narrow genetic variation on the traits and greater influence of environmental factors for the expression of these traits. The result agrees with the findings of Dev et al. (2017) who reported
### Table 5. Estimates of variances, coefficient of variation, heritability and genetic advance of traits

| Traits | $\sigma^2 g$ | $\sigma^2 p$ | GCV (%) | PCV (%) | $H^2$ (%) | GA | GAM (%) |
|--------|--------------|--------------|---------|---------|-----------|----|---------|
| DF     | 8.18         | 10.39        | 6.28    | 7.08    | 78.71     | 5.23| 11.47   |
| PH     | 60.25        | 169.93       | 7.94    | 13.34   | 35.46     | 9.52| 9.74    |
| PL     | 0.17         | 0.36         | 11.02   | 16.00   | 47.48     | 0.59| 15.65   |
| NPP    | 19.35        | 26.09        | 37.60   | 43.66   | 74.16     | 7.80| 66.70   |
| NBP    | 0.22         | 0.39         | 27.52   | 36.81   | 55.89     | 0.72| 42.38   |
| BY     | 4437870.30   | 5,129,663.30 | 25.35   | 27.25   | 86.51     | 4036.43 | 48.57 |
| GY     | 397891.42    | 412,181.42   | 30.77   | 31.32   | 96.53     | 1276.70 | 62.28 |
| HSW    | 72.15        | 101.12       | 20.29   | 24.02   | 71.36     | 14.78| 35.32   |
| HI     | 47.05        | 59.76        | 26.67   | 30.06   | 78.72     | 12.54| 48.76   |
| AB     | 262.91       | 269.11       | 45.64   | 46.17   | 97.70     | 33.08| 93.11   |
| CS     | 261.31       | 285.79       | 47.90   | 50.10   | 91.43     | 32.98| 97.73   |
| RT     | 287.90       | 302.38       | 64.43   | 66.03   | 95.21     | 34.61| 131.43  |

DF: days to flowering; PH: plant height; PL: pod length; NPP: number of pods per plant; NBP: number of branches per plant; BY: biomass yield; GY: grain yield; HSW: 100-seed weight; HI: harvest index; AB: ascochyta blight; CS: chocolate spot; RT: rust disease; GV: genotypic variance; PV: phenotypic variance; GCV: genotypic coefficient of variance; PCV: phenotypic coefficient of variance; $H^2$: broad sense heritability; GA: genetic advance; GAM: genetic advance as percent of mean.
low GCV for plant height in chickpea. Similar findings were reported by Kalia et al. (2003) for days to flowering in faba bean.

Results for all the studied traits revealed a little higher PCV than GCV. Hence, the slight differences indicate minimum environmental influence and consequently greater role of genetic factors on the expression of the traits.

3.3. Broad sense heritability

Broad sense heritability (H²) estimates were generally high for most of the studied traits, which ranged from 35.46% for plant height to 97.70% for ascochyta blight disease score (Table 5). In the present study, high broad sense heritability estimates were found for traits such as 100-seed weight, number of pods per plant, days to flowering, harvest index, biomass yield, chocolate spot, rust disease, grain yield, and ascochyta blight disease score. The result indicates that selection based on phenotypic expression of individual accessions for these traits may be easy due to relatively small contribution of the environment to the phenotype, meaning that most of the variation is genetic rather than environmental. The high H² values of these traits indicate the high possibility of transferring traits from parents to the next progeny. In agreement with these results, high estimates of broad sense heritability were reported for 100-seed weight, grain yield and chocolate spot disease in faba bean genotypes in previous studies (El-BadawyNoha et al., 2012; Fikreselassie & Saboka, 2012; Mulualem et al., 2013).

In the present study, medium heritability estimates were recorded for traits like plant height, pod length and number of branches per plant. These traits may respond moderately for phenotypic selection.

3.4. Genetic advance

According to Johnson et al. (1955), high heritability estimates along with high genetic advance are more helpful in predicting gain under selection than heritability alone. In the present investigation, genetic advance as percent of mean varied from 9.74% for plant height to 131.43% for rust disease score (Table 5). These results indicate that whenever the best 5% of accessions are selected for a given trait, genotypic value of the new population for the traits will be improved from 9.74% to 131.43%. High genetic advance was recorded for number of pods per plant, biomass yield grain yield, harvest index and 100-seed weight, and disease-related traits. These traits also had higher broad sense heritability; consequently, the traits could be improved through direct selection. Panse and Sukhatme (1985) stated that traits with high broad sense heritability and high genetic advance are more influenced by genetic factors. The finding agrees with that of Kalia and Soad (2004) and Solieman and Raghebi (2014) who report high heritability and high genetic advance for number of pods per plant. Similar results were reported by Mulugeta et al. (2018) for number of pods per plant, biomass weight per plot and thousand-seed weight. On the contrary, Abdellatif et al. (2020) reported low estimate of heritability and genetic advance for rust disease reaction.

Medium GAM values were obtained for traits like pod length and days to flowering. On the contrary, the lowest GAM was recorded for plant height. The result indicates that selection of accessions based on this trait might result in low response in new population. In other ways, this would indicate that expression of this trait is governed by non-additive gene effects.

3.5. Conclusion

The ANOVA showed highly significant differences (p < 0.01) among Ethiopian faba bean accessions for days to flowering, plant height (cm), pod length, number of pods per plant, number of branches per plant, biomass yield, grain yield, hundred seed weight, harvest index, ascochyta blight, chocolate spot, and rust disease. High (>20%) genotypic and phenotypic coefficients of variation were also recorded for hundred-seed weight, biomass yield, harvest index, grain yield, number of branches per plant, number of pods per plant, ascochyta blight, chocolate spot and rust disease score, indicating the existence of considerable genetic variation among the faba bean accessions.
Moreover, high heritability coupled with high genetic advance as percent of the mean was observed for hundred-seed weight, harvest index, number of pods per plant, grain yield, biological yield, ascochyta blight, chocolate spot and rust disease, suggesting that the expression of these traits is highly influenced by genetic component of variance and less influenced by the environment. Therefore, these traits could easily be improved through direct selection.

Acknowledgements
First of all, I am highly grateful to The Almighty God who gave me good health, guidance, protection and abundant blessings throughout my studies and because of You; I made this through against all odds. I would like to thank Bahir Dar University, college of Agriculture and environmental sciences for providing me opportunity to study my M.Sc. degree and experimental plot for the field research. I would also like to thank Ethiopian biodiversity institute for the provision of accessions for the study. Particular gratitude and appreciation goes to my father Muchie Hiywotu and my beloved mother Gedam Addis whose crucial decision to invest part of their resource in my education and all my family members for bringing me up with their priceless love, care, for encouraging and supporting me. I also express my heartfelt thanks to my brothers; Tilahun Muchie, Yalaw Muchie, Habtamu Muchie and all my sisters for their financial and moral support specially my brother Tilahun Muchie dreams and determination to educate me until I reached M.Sc. level have come true and he had laid a base for me to reach where I am today. I also express my heartfelt thanks to all my friends for their marvelous support during this research work.

Funding
The authors received no direct funding for this research.

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Disclosure statement
No potential conflict of interest was reported by the authors.

Citation information
Cite this article as: Genetic variability in Ethiopian fava bean (Vicia faba L.) accessions, Andauluem Muchie Hiywotu, Alenu Abate, Fisseha Woreda & Abunu Marefia, Cogent Food & Agriculture (2022), 8: 2132847.

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