Yield performance and agronomic character association in soybean genotypes

RT Hapsari, MM Adie and A Krisnawati

Indonesian Legume and Tuber Crops Research Institute (ILETRI), JL. Raya Kendalpayak Km 8 Malang, East Java, Indonesia

Email: ratri.3hapsari@gmail.com

Abstract. The aim of this research was to evaluate the performance of yield and yield components of soybean genotypes, as well as the relationship pattern among characters that affect the seed yield. The research material consists of 145 F5 lines and five check cultivars, which were evaluated for their yield and yield components in Malang and Probolinggo, using a randomized block design with two replicates. The combined analysis of variance for yield and yield component showed a significant interaction effect between location and genotype for the number of branches, the number of empty pods, 100 seed weight, and seed yield. The performance of yield and yield components of soybean genotypes tested in Malang showed earlier maturity, taller plants, larger seed size, and higher seed yields when compared to research conducted in Probolinggo. In the selection for the best genotypes, ten genotypes were chosen for their large seed size criteria, while two genotypes were chosen for their relatively medium maturity (81 days) in the location of Malang. In Probolinggo, of the ten genotypes, three genotypes with medium maturity, and three genotypes with medium seed size. The selected genotypes will proceed to the stage of the advanced yield trial. The association study revealed that soybean yield has a positive correlation with plant height, number of nodes, number of branches, number of filled pods, days to flowering, and days to maturity. Those yield components could be used as selection criteria in the breeding program to obtain high-yielding soybean cultivars.

1. Introduction
Soybean is the third most important food crop commodity in Indonesia after rice and maize. Soybean demand in Indonesia is rising, necessitating new approaches to increasing productivity per unit area. Variety is one of the technological innovations that are considered to have a significant impact on increasing productivity per unit area [1]. As a result, in order to generate high-yielding soybean genotypes, it is needed to examine the determinants and interrelationships among agronomic traits.

Seed yield, as a complex trait, is the result of the expression of the association of several plant growth components. Selection for seed yield should take into account related characters [2]. According to various research findings, soybean yield is also related to the interaction between genotype and environment [3,4]. Several traits, including the number of root nodules, the weight of 100 seeds, the weight of biomass, the number of pods, and the plant height, were reported to be considered as determinants of soybean yield in Ethiopia [5]. Another study reported that plant height, number of pods/inflorescences, and 100 seed weight were all characteristics that can be used as practically selection criteria [6]. The number of pods, weight of 100 seeds, and 50% days to flowering were reported to have
a direct impact on soybean yield, hence these two characteristics can be considered as selection criteria in soybean [7]. In chickpea, grain yield showed a significant positive association with plant height, branches number, and one hundred seed weight, but it has a significant negative correlation with days to flowering and maturity [8]. The high significant and positive correlation of oil yield per plant with 1000 seed weight suggested that heavy seed weight might have higher oil content in the *Linum usitatissimum* L. [9].

A study in Indonesian soybean showed that plant height has the potential to be used as a selection criterion for soybean due to its character as a determinant of high yield [10]. Another study also stated that soybean with high yield potential has relatively tall plants, a large number of pods, and a high harvest index [11]. In addition to the character of plant height, it is necessary to consider the number of fertile nodes as a determinant of high yield in soybean [12]. The varied findings revealed that seed yield and its yield determinants are complex traits that interact with one another, as well as the importance of the environment.

Understanding the relationship between yield and yield components is important for using it as an indicator of indirect selection on seed yield as well as yield improvement through the characters that have the greatest impact on grain yield. The association among yield concurrently with its component parameters provides the basis for the effective selection in breeding schemes, than the selection that is merely based on yield [13]. In soybean, grain yield, as in other crops, is a complex character, quantitative in nature, and an integrated function of a number of component traits. Therefore, selection for yield per se may not be much rewarding unless other yield attributing traits are taken into consideration [14].

The aim of this research was to evaluate the performance of yield and yield components of 150 soybean genotypes, as well as the relationship pattern among characters that affect the seed yield.

2. Materials and method

2.1. Research material and study location

The research material consists of 150 soybean genotypes which consisted of 145 F5 lines derived from crossing combination, and five check cultivars (Grobogan, Burangrang, Anjasmor, Dega 1, and Argomulyo). The research was conducted in two locations, i.e., Malang (located at 8° 2′ 56.4″ South Latitude, 112° 37′ 30″ East Longitude, 445 m a.s.l, climate type of C2 Oldeman system, 90% of relative humidity, and soil type of Entisol) and Probolinggo (located at 7° 48′ 7.2″ South Latitude, 113° 9′ 32.4″ East Longitude, 10 m a.s.l, climate type of E1 Oldeman system, 77% of relative humidity, and soil type of Alfisol).

2.2. Field research

In each location, a randomized block design was applied, with two replicates. Each genotype was planted in a plot size of 1.2 × 4.5 m, plant spacing of 40 cm × 15 cm, two plants per hill. Plants were fertilized by 250 kg Phonska/ha + 100 kg SP 36/ha and 1 t/ha organic fertilizer, which applied entirely at the time of planting. The pests, diseases, and weeds were optimally controlled.

2.3. Data observation

The evaluation for shattering resistance of soybean advanced lines using the oven-dry method [19] was Data were observed on each location, consisted of days to flowering, days to maturity, plant height, number of branches/plant, number of nodes/plant, number of filled pods/plant, number of empty pods per plant, 100 seed weight (g), and seed yield (t/ha).

2.4. Data analysis

A combined analysis of variance was performed for all observed data, using SAS software version 9.1.3 [15]. The relationship among agronomic traits was investigated using the genotype by trait biplot [16] using the RStudio program [17].
3. Results and Discussion

3.1. Combined analysis of variance
The combined analysis of variance for yield and yield component showed a significant interaction effect between location and genotype for the number of branches, the number of empty pods, 100 seed weight, and seed yield (Table 1). Genotype had a significant effect on all observed characters. The location also showed a significant effect for almost all characters, except days to flowering and the number of nodes. The significant interaction of G × E indicates that there was the suitability of adaptation for each genotype. The significant effect of genotype showed the variations in the genetic potential of all tested genotypes.

Table 1. Combined analysis of variance for yield and yield components of 150 soybean genotypes

| Character                        | Replication/E | Location (E) | Genotype (G) | G × E   |
|---------------------------------|---------------|--------------|--------------|---------|
| Days to flowering (day)         | 62.6283**     | 1.0416 ns    | 18.0419**    | 0.0685 ns |
| Days to maturity (day)          | 129.4083**    | 63.3750**    | 34.8252**    | 1.9186 ns |
| Plant height (cm)               | 990.5541**    | 7652.9387**  | 124.1179**   | 62.1884 ns |
| Number of branches/plant        | 1.5521 ns     | 37.0265**    | 1.5058**     | 0.7154*  |
| Number of nodes/plant           | 2.6216 ns     | 2.0886 ns    | 4.5989**     | 0.5834 ns |
| Number of filled pod/plant      | 142.0363 ns   | 1145.401**   | 332.4335**   | 99.2780 ns |
| Number of empty pod/plant       | 2.3256 ns     | 66.8000**    | 2.7521**     | 1.9240*  |
| 100 seed weight (g)             | 14.5494**     | 273.0241**   | 8.1248**     | 2.4584** |
| Seed yield (t/ha)               | 14.3556**     | 1.3954**     | 0.6734**     | 0.4213*  |

** = significant at 1% probability level (p < 0.01), * = significant at 5% probability level (p < 0.05), ns = not significant

3.2. Agronomic performance
The performance of yield and yield components of soybean genotypes tested in Malang showed earlier maturity, taller plants, larger seed size, and higher seed yields when compared to research conducted in Probolinggo (Figure 1). The performance of the main agronomic characters in Malang, i.e, the days to maturity ranged from 73 – 84 days (an average of 77 days), the seed size ranged from 13.07 to 22.65 g/100 seeds (an average of 16.60 g/100 seeds), and the range of seed yield was 0.91 - 3.08 t/ha (an average of 2.31 t/ha) (Table 2). Accordingly, the tested genotypes tend to have early maturity, a large seed size, and some produced high yields. Meanwhile, in Probolinggo, the days to maturity ranged from 73-89 days with an average of 73 days, the seed size ranged from 11.59 – 21.23 g/100 seeds (an average of 15.25 g/100 seeds), and the range of seed yield was 0.23 – 4.66 t/ha with an average of 1.35 t/ha (Table 2). Excessive rainfall at the start of the growth period impeded the growth of the genotypes evaluated, resulting in decreased yield and yield component in Probolinggo. This suggest that the poor performance is caused by environmental factors rather than genetic factors.
Figure 1. Yield and yield components of soybean genotypes tested in Malang and Probolinggo: (a) days to flowering, (b) days to maturity, (c) plant height, (d) number of branches/plant, (e) number of nodes/plant, (f) number of filled pods/plant, (g) number of empty pods/plant, (h) 100 seed weight, (i) seed yield.

Table 2. The agronomic performance of 150 soybean genotypes in Malang and Probolinggo

| Character                        | Malang                  | Probolinggo             | Mean of 2 locations |
|---------------------------------|-------------------------|-------------------------|---------------------|
|                                 | Min | Max | Mean | Min | Max | Mean | Min | Max | Mean | Min | Max | Mean |
| Days to flowering (day)         | 29  | 39  | 33   | 29  | 39  | 33   | 29  | 39  | 33   |
| Days to maturity (day)          | 73  | 84  | 77   | 73  | 89  | 78   | 73  | 86  | 77   |
| Plant height (cm)               | 33.70 | 74.00 | 55.45 | 33.40 | 67.80 | 48.31 | 36.65 | 64.85 | 51.88 |
| Number of branches/plant        | 0.70 | 5.30 | 2.08 | 0.50 | 3.90 | 2.38 | 1.20 | 3.80 | 2.63 |
| Number of nodes/plant           | 7.50 | 15.50 | 10.19 | 7.50 | 14.30 | 10.07 | 7.50 | 14.90 | 10.13 |
| Number of filled pod/plant      | 22.70 | 81.80 | 39.89 | 22.00 | 83.30 | 42.65 | 26.70 | 75.10 | 41.27 |
| Number of empty pod/plant       | 0.10 | 8.70 | 1.39 | 0.20 | 5.40 | 2.05 | 0.30 | 6.75 | 1.72 |
| 100 seed weight (g)             | 13.07 | 22.65 | 16.60 | 11.59 | 21.23 | 15.25 | 13.04 | 21.94 | 15.92 |
| Seed yield (t/ha)               | 0.91 | 3.08 | 2.31 | 0.23 | 4.66 | 1.35 | 0.97 | 3.55 | 1.83 |

3.3. Selection for the best genotype

Table 3. Performance of the 10 best lines based on seed yield in Malang and Probolinggo

| Geno code | Malang | Probolinggo | Mean of two locations |
|-----------|--------|-------------|-----------------------|
|           | Yield  | DTM (day)   | B100 (g)              | Geno code | Yield  | DTM (day) | B100 (g) |
|           | t/ha   |            |                       | G code    | t/ha   |            | G code    |
| G 68      | 3.08   | 75          | 16.92                 | G 4       | 4.66   | 76          | 17.35     | G 4       | 3.55   | 76          | 16.85     |
| G 92      | 3.05   | 79          | 16.48                 | G 99      | 3.59   | 77          | 15.69     | G 9       | 2.90   | 77          | 15.92     |
| G 39      | 3.03   | 80          | 18.76                 | G 51      | 2.89   | 79          | 14.29     | G 47      | 2.74   | 74          | 15.17     |
| G 10      | 3.02   | 81          | 19.61                 | G 47      | 2.61   | 74          | 15.53     | G 10      | 2.68   | 82          | 17.77     |
| G 21      | 2.98   | 73          | 17.20                 | G 97      | 2.46   | 78          | 13.67     | G 1       | 2.68   | 79          | 16.73     |
| G 4       | 2.95   | 80          | 16.61                 | G 102     | 2.43   | 79          | 12.65     | G 7       | 2.63   | 78          | 15.31     |
| G 22      | 2.93   | 81          | 14.48                 | G 143     | 2.40   | 82          | 13.46     | G 28      | 2.56   | 83          | 15.66     |
| G 86      | 2.93   | 80          | 17.17                 | G 128     | 2.35   | 85          | 15.28     | G 6       | 2.54   | 81          | 16.02     |
| G 28      | 2.91   | 76          | 15.84                 | G 110     | 2.34   | 83          | 15.92     | G 43      | 2.51   | 81          | 14.07     |
| G 26      | 2.89   | 75          | 17.16                 | G 63      | 2.17   | 78          | 15.31     | G 8       | 2.49   | 76          | 16.61     |
| Mean      | 2.97   | 78          | 17.02                 | Mean      | 2.79   | 79          | 14.91     | Mean      | 2.73   | 78          | 16.01     |

Geno code = genotype code, DTM = days to maturity, B100 = 100 seed weight
The best soybean genotypes based on seed yield characters at each location and also the 10 best genotypes based on the average of the two locations are presented in Table 3. In the location of Malang, the 10 selected genotypes have an average yield of 2.97 t/ha with days to maturity of 78 days, and the seed size was 17.02 g/100 seeds. In the location of Probolinggo, the 10 selected genotypes have an average yield of 2.79 t/ha with days to maturity of 79 days, and the seed size was 14.91 g/100 seeds (Table 3). The better plant growth in Malang resulted in higher seed yield and larger seed size, whereas the days to maturity among the selected lines in the two locations were remarkably similar.

The purpose of this study is to find soybean genotypes with high yield, early maturity, and large seed size. In Malang, ten genotypes were chosen for their large seed size criteria, while two genotypes were chosen for their relatively medium maturity (81 days). In Probolinggo, of the ten genotypes, three genotypes with medium maturity, and three genotypes with medium seed size. The selected genotypes will proceed to the stage of the advanced yield trial.

3.4. Association among characters

The association among agronomic characters was identified using the GT biplot graph. Based on Figure 2, soybean yield (YLD) showed a positive correlation with plant height (PHG), number of nodes (NON), number of branches (NOB), number of filled pods (NFP), days to flowering (DTF), and days to maturity (DTM). This means that a higher value of those agronomic characters will result in a higher seed yield. A similar result was obtained by Karyawati and Puspitaningrum [18]. A previous study found a positive and significant correlation between seed yield with the number of pods per plant, seeds per pod, 100 seed weight, both at genotypic and phenotypic levels [19].

![Figure 2. Association among agronomic characters using GT biplot](image)

In this study, the association study showed that a higher plant caused a high number of nodes, number of branches, and number of filled pods, as showed by a positive correlation among them. Thus, a higher number of the filled pods will contribute to the increase of the seed yield. In terms of plant age, longer days to flowering and maturity will increase the seed yield. Another study also obtained a similar result [20]. Meanwhile, seed size and the number of empty pods were negatively correlated with seed yield. A larger seed size resulted in a lower yield, and a high number of empty pods contributed to the lower yield. The information in the yield components that showed a positive correlation with seed yield can be used as the selection criteria in a soybean breeding program to obtain high-yielding cultivars.
4. Conclusion

The performance of yield and yield components of soybean genotypes differ among locations. Genotypes planted in Malang showed earlier maturity, taller plants, larger seed size, and higher seed yields when compared to research conducted in Probolinggo. The association study revealed that soybean yield has a positive correlation with plant height, number of nodes, number of branches, number of filled pods, days to flowering, and days to maturity. Those yield components could be used as selection criteria in the breeding program to obtain high-yielding soybean cultivars.

Acknowledgment

This research was funded by the Indonesian Agency for Agricultural Research and Development (IAARD).

References

[1] Emerick K, de Janvry A, Sadoulet E, Dar MH 2016 Technological Innovations, Downside Risk, and the Modernization of Agriculture  *Am. Econ. Rev.* **106**(6) 1537-1561.
[2] Toledo JFF, de Arias CAA, Oliveira MF, de Triller C, and Miranda Z de FS 2000 Genetical and environmental analyses of yield in six biparental soybean crosses.  *Pesq. agropec. bras.* Brasilia **35** 1783-1796.
[3] Matei G, Benin G, Woyann LG, Dalló SC, Milioli AS, Zdziarski AD 2017 Agronomic performance of modern soybean cultivars in multi-environment trials  *Pesq. agropec. bras.*, Brasília **52**(7) 500-511.
[4] Li M, Liu Y, Wang C, Yang X, Li D, Zhang X, Xu C, Zhang Y, Li W and Zhao L 2020 Identification of traits contributing to high and stable yields in different soybean varieties across three Chinese latitudes  *Front. Plant Sci.* **10** 1642.
[5] Enideg B, Alamerew S, Tesfaye A, Barnabas J 2016 Correlation and path analysis for yield and yield related components in soybean (*Glycine max* L.) genotypes  *IJSAR* **3**(12) 105-112.
[6] Bhor TJ, Chimote VP, Deshmukh MP 2014 Genetic analysis of yield and yield components in soybean (*Glycine max* (L.) Merrill)  *Indian J. Agric. Res.* **48**(6) 446-452.
[7] Chavan BH, Dahat DV, Rajput HJ, Deshmukh MP, Diwane SL 2016 Correlation and path analysis in soybean  *Intl. Res. J. Multidiscip. Stud.* **2**(9) 2454-2499.
[8] Alemu B, Lule D, Tesfaye K, Haileselassie T 2018 Interrelationships of quantitative traits and genetic variability of *Desi* type chickpea genotypes as revealed by agro-morphology and inter simple sequence repeat markers  *Afr J of Biotech.* **17**(21) 685-693.
[9] Belsariya N, Mehta N 2020 Interrelationship analysis among morphological and seed yielding characters in yellow seeded genotypes of linseed (*Linum usitatissimum* L.)  *Int. J. Curr. Microbiol. App. Sci.* **9**(7) 2860-2867.
[10] Krisnawati A, Adie MM 2016 Relationship between morphological component with seed yield characters of soybean  *Buletin Palawija* **49**(2) 49-54.
[11] Hakim L 2011 Correlation among characters and path analyses between agronomic traits with grain yield on soybean (*Glycine max* (L.) Merrill)  *Berita Biologi* **10**(6) 709-720.
[12] Sulistyo A, Sari KP, Purwantoro 2018 *IOP Conf. Ser.: Earth Environ. Sci.* **102** 012034.
[13] Kumar P, Shukla RS 2002 Genetic analysis for yield and its attributed traits in bread wheat under various situations  *Jawaharlal NehruKrishi Vishwa Vidyalaya Res. J.* **36** 95-97.
[14] Amogne A, Atnaf M, Bantayehu M 2020 Association of traits in soybean (*Glycine max* (L.) Merrill) genotypes in Northwestern Ethiopia  *IJSES* **4**(10) 8-14.
[15] SAS Institute Inc. 2007 *SAS/STAT® 9.1.3 User’s Guide*. Cary, NC: SAS Institute Inc.
[16] Yan W, Rajcan I 2002 Biplot analysis of test sites and trait relations of soybean in Ontario Crop Sci. **42** 11-20.
[17] RStudio Team 2020 R: A language and environment for statistical computing R Foundation for Statistical Computing, Vienna, Austria.
[18] Karyawati AS, Puspitaningrum ESV 2021 Correlation and path analysis for agronomic traits
contributing to yield in 30 genotypes of soybean Biodiversitas 22 1146-1151.

[19] Shree Y, Ram S, Bhushan S, Verma N, Ahmad E, Kumar S 2018 Correlation between yield and yield attributing traits in soybean (Glycine max (L.) Merrill). J. Pharmacogn. Phytochem 1 298-301.

[20] Abugalieva S, Didorenko S, Anuarbek S, Volkova L, Gerasimova Y, Sidorik I, et al. 2016 Assessment of soybean flowering and seed maturation time in different latitude regions of Kazakhstan PLoS ONE 11(12) e0166894.