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GENETIC VARIABILITY AND ASSOCIATION OF TRAITS IN SOYBEAN (Glycine max (L.) MERRILL) GENOTYPES IN WEST GONDAR, NORTHWESTERN ETHIOPIA

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BAHIR DAR UNIVERSITY

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GRADUATE PROGRAM IN PLANT BREEDING

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MSc. Thesis

By

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November 2021

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SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE (MSc.) IN PLANT BREEDING

Major Supervisor: Mulugeta Atnaf (PhD)

Co-Supervisor: Alemu Abate (PhD)

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THESIS APPROVAL SHEET

As a member of the Board of Examiners of the Master of Science (MSc.) thesis open defense examination. We have read and evaluated this thesis prepared by **Mr. Gobezie Chakelie Besete,** entitled with "**Genetic Variability and Association of Traits in Soybean (***Glycine max* **(L.) MERRILL) Genotypes in West Gondar, Northwestern Ethiopia**". We hereby certify that the thesis is accepted for fulfilling the requirements for the award of the degree of Master of Science **(MSc.) in Plant Breeding.**

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DECLARATION

This is to certify that this thesis entitled with "**Genetic Variability and Association of Traits in Soybean** (*Glycine max* **(L.) MERRILL**) **Genotypes in West Gondar, Northwestern Ethiopia**" submitted in partial fulfillment of the requirements for the award of the degree of Master of Science in Plant breeding to the Graduate Program of College of Agriculture and Environmental Sciences, Bahir Dar University by Mr. **Gobezie Chakelie Besete** (ID. No. BDU1207124PR) is an authentic work carried out by him under our guidance. The matter embodied in this thesis work has not been submitted earlier for award of any degree or diploma to the best of our knowledge and belief.

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DEDICATION

This piece of work is dedicated to my family for nursing me with affection and for their deep-hearted partnership in the success of my life.

LIST OF ABBREVIATIONS AND ACRONYMS

ANOVA   Analysis of Variance

ARARI   Amhara Regional Agricultural Research Institute

CSA   Central Statistics Agency

D^2 Genetic Distance

FAO   Food and Agricultural Organization

GA   Genetic Advance

GARC   Gondar Agricultural Research Center

GCV   Genotypic Coefficient of Variation

H^2 Broad sense heritability

IBPGR   International Board for Plant Genetic Resources

IITA   International Institute of Tropical Agriculture

JARC   Jimma Agricultural Research Center

NMA   National Meteorology Agency

PARC   Pawe Agricultural Research Center

PCA   Principal Component Analysis

PCV   Phenotypic Coefficient of Variation

RAPD   Random Amplified Polymorphic DNA

RV   Released Variety

SAS   Statistical Analysis System

THSD   Tukey`s Honestly Significant Difference

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By

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ABSTRACT

Soybean (Glycine max (L.) Merr.) is an economically important crop worldwide including Ethiopia. In Ethiopia, considerable genetic materials are available. However, research on soybean genetic variability and association of traits in the study area was limited. Hence, a field experiment was conducted to estimate genetic variability and trait associations of 81 soybean genotypes at Metema and West Armachiho, West Gondar, Ethiopia. The trial was laid out in a 9 x 9 simple lattice design in 2020 main cropping season. Data were taken on both quantitative and qualitative traits. Data analyses were done using SAS, Minitab, and Past Software for analysis of variance, cluster, path, and principal component analyses. Combined analysis of variance revealed highly significant (p<0.01) differences among genotypes for the studied traits, implying existence of variability. Genotype x location interactions were also significant (p<0.05) for most of the traits. Estimated Shannon diversity index indicates polymorphic variation for most of the traits. The phenotypic coefficient of variation ranged from 4.63%-37.76% for protein content and seed yield, while the genotypic coefficient of variation varied from 1.24% -34.58% for pod length and seed yield, respectively. Broad sense heritability values ranged from 4.03% for pod length to 94.84% for days to 50% flowering. Genetic advance as percent of mean was varied from 0.51%-65.22% for pod length and seed yield, respectively. High heritability coupled with high genetic advance was observed for number of pods per plant, and seed yield indicating possibility for improving these traits through selection. Seed yield exhibited positive and significant correlations with most studied both at phenotypic and genotypic levels. Path coefficient analysis indicated days to maturity and harvest index showed highest phenotypic and genotypic positive direct effects, respectively on seed yield. The cluster analysis grouped the 81 genotypes into six clusters based on quantitative traits, and cluster I was found to be the largest (63% of genotypes) cluster. The highest inter-cluster distance was noted between cluster II and VI (D^2=154.64), which would indicate, genotypes of these clusters are divergent and can be exploited in breeding for hybridization program. Principal component analysis revealed that 77.98% of the total variation among genotypes was explained by the first four components. Generally, the present study indicated existence of reasonable variability among genotypes, and this variability shall be exploited for future soybean improvement program.

Keywords: Cluster, Correlation, Direct effect, Genetic Advance, Heritability, Traits

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Chapter 1. INTRODUCTION

1.1. Background and Justification

Soybean (*Glycine max* (L.) Merrill) is a self-pollinated (2n=4x=40) but natural cross-pollination has also been observed with a rate of 0.03–1.14% in cultivated species (Chiang and Kiang, 1987). It belongs to the family *Leguminosae*, subfamily *Papilionoideae,* tribe *Phaseolae*, and genus *Glycine*. It is reported to be domesticated in Asia, probably in northeastern China (Singh and Hymowitz, 1999).

Soybean well-grows in tropical, subtropical, and temperate regions. It has a wide range of agro-ecological adaptation and is most widely cultivated in rain-fed agriculture (Fageria *et al.*, 2006). Soybean requires 350 - 750 mm rainfall and is well distributed throughout the growth cycle (Ngeze, 1993). It performs well in fertile sandy loam soils with 5.5 - 7.0 pH ranges (Singh, 2010).

Soybean, could be considered as an ideal food for the people of third-world countries as it contains quality proteins and a reasonable quantity of oil as a source of energy (Kumar *et al*., 2018a). This crop is comparatively the cheapest source of protein (Okolie and Ehiemere, 2009). Soybean seeds contain 40-42% protein, 18-20% oil, 11% soluble carbohydrates, and dry matter (Devi *et al*., 2012). Due to its multiple usage soybean is aptly also called the 'golden bean' of the 20th century (Jain *et al*., 2018).

Nowadays, the world production of soybean is greater than any other oilseed crop (Shea *et al*., 2020). Moreover, the share of soybean in global oilseed production is about 61%, and over the last decade, its production has increased averagely 5% per year (Pratap *et al*., 2016; Shea *et al*., 2020). It is a major crop in the United States, Brazil, China, and Argentina (Bilyeu *et al*., 2016). In Africa, it has a recent story; during the second half of the 20th century and it is believed to be introduced to Ethiopia in the 1950s (Mekonnen Hailu and Kaleb Kelemu, 2014). According to FAO (2019), soybean production is estimated to be about 3.09 and 0.126 million tons with a productivity of 1.25 and 2.30 tons per hectare in Africa and Ethiopia, respectively.

In the agricultural production system with the context of crop improvement, the presence of genetic variability is so important as source of genes for breeding programs, developing new cultivars, and farming systems, diversification of production, and new quality products (Jing *et al*., 2010). Knowledge of genetic diversity within a crop and association among the yield contributing traits is vital for the success of a breeding program and maximizes the exploration of germplasm resources (Rahman *et al*., 2011). Estimating the level of genetic variability is vital for further trait discovery, intercrossing design, economic trait detection, and good parental lines establishment (Islam *et al.*, 2016).

As soybean is genetically diverse and grown in wide agro-ecological environments, thus, variation in the genetic constitution will exist among the genotypes (Molua, 2009; Pratap *et al*., 2016). This indicates the potentials for utilizing such variability in soybean crop improvement programs. Globally, yield and yield contributing traits are the most focused traits for soybean improvement. Improvement of a crop is widely reliant on the nature and magnitude of available genetic variability (Reni and Rao, 2013). Therefore, knowledge of genetic parameters (like genotypic and phenotypic coefficient of variation, heritability, and genetic advance) is important for crop improvement programs, providing useful information for selection (Aditya *et al*., 2011). Thus, characterizing the genetic background of soybean and estimating breeding values could be done before designing improvement program (Arshyad *et al*., 2009).

1.2. Statement of the Problem

In Ethiopia, soybean is an introduced crop and had a higher expansion of the cultivated area in recent years, with a production of 0.126 million tons of harvest with average productivity of 2.30 ton per hectare in 2019 (FAO, 2019). However, the national average yield is significantly low compared with its potential and yields obtained in other soybean-producing countries like America (3.1 ton ha^{-1}), Serbia (3.16 ton ha[1]), Greece (3.11 ton ha^{-1}), and Croatia (3.11 ton ha^{-1}) (Terzic *et al*., 2018; FAO, 2018). It is noted that the soybean crop yield potential reaches up to 8.00-ton ha^{-1} (Specht *et al*., 1999). This indicates the existing of variations in soybean germplasm resources which could be exploited in the future soybean breeding programs.

In Central - and West Gondar lowland areas, the crop is introduced recently as a breakthrough crop due to its diverse importance. Along with this, the product of soybean become significantly demanded due to population increment, expansion of agro-processor, crop diversification in relation with fertility. However, the productivity and production are still low mainly associated with low yielding cultivars. As a result, to sustain and satisfy such requirements, soybean breeding becomes highly important for the creation of high-yielding cultivars through the exploitation of existing genetic variation for yield and its components. In Ethiopia, considerable genetic materials are available in the soybean improvement program (Mesfin Hailemariam and Abush Tesfaye, 2018) However, information regarding the magnitude of variation among different genotypes for various traits is limited to produce high-yielding and quality lines for release as cultivars to the farming community. Moreover, quantitative traits are also significantly influenced by environmental factors (Bernardo, 2010) hence genotypes respond differently in different locations for desirable quantitative and quality related traits.

Furthermore, this crop is cultivated in Central and West Gondar areas without investigating the variability of genotypes in the area. As a result, there is no information on the potential variability of soybean genotypes. Therefore, genetic variability study is required to identify genetic variability among soybean genotypes for economic traits as potential selection criteria in a breeding program. The study helps to exploit the immense potentials of the available tested genotypes.

1.3. Objectives of the Study

1.3.1. General objective

- To facilitate exploitation of soybean genotypes in the future breeding program

1.3.2. Specific objectives

- ✓ To examine genetic variability among genotypes;
- ✓ To determine associations among yield and yield-related traits;
- ✓ To cluster genotypes into similarity groups;
- ✓ To suggest promising genotypes for future soybean breeding programs.

Chapter 2. LITERATURE REVIEW

2.1. Origin and Distribution of Soybean

Soybean (*Glycine max* (L.) Merrill) is an old, cultivated crop native to North Eastern China (Hymowitz, 1970). Ngeze (1993) also suggested that soybean is native to Eastern Asia, mainly China, Japan, and Korea, from where it was distributed to America and Europe, and the remaining world in the 18th century. To strength this, the recent findings of Lersten and Carlson (2004) indicated soybean was domesticated around 5000 years ago from *Glycine soja,* its wild progenitor that is found all over East Asia, such as half of China, Korea, Japan, and some part of Russia.

Since its domestication, the *Glycine* is distributed in the Old World and became an established component of world agriculture (Hymowitz, 2008). In Africa, soybean was first introduced in the early 19th century (Ngeze, 1993) and is currently wide spread largely across the continent (Hymowitz, 2008). Evidence indicated that it might have been introduced at an earlier date back in Eastern Africa since that region had a long trade relationship with the Chinese (Shurtleff and Aoyagi, 2016). A similar report stated that soybean has been under cultivation in African particularly in 1907 in Tanzania and 1909 in Malawi. According to Shurtleff and Aoyagi (2009), soybean was introduced to Ethiopia since the year 1950.

2.2. Botanical Description

Soybean (*Glycine max* (L.) Merrill) is a self-pollinated legume crop and it belongs to the botanical family *Fabaceae (Leguminosae)* and subfamily *Papilionideae*, tribe *Phaseolae*, and genus *Glycine* (Shurtleff and Aoyagi, 2009). Taxonomically, the genus *Glycine* is divided into two subgenera, *Glycine* Willd. (perennial) and Soja (Moench) F.J. Herm (annual). Subgenus Soja again includes two species which economically are very important cultivated soybean (*Glycine max* (L.) Merrill), and its wild annual progenitor, *Glycine* soja Sieb. and Zucc. (Ratnaparkhe *et al*., 2011).

Both the cultivated *Glycine max* and wild type *Glycine Soja* consists of 40 chromosomes (2n=2x=40) and are self-fertile species with less than 1% out-crossing (Norman *et al*., 1995; Shurtleff and Aoyagi, 2016). *Glycine* is a genus name that was originally introduced by Linnaeus in the first edition of his Genera Plantarum (Linnaeus, 1957). Currently, the combination *Glycine max* (L.) Merrill. was proposed by Merrill in 1917 and has since become the valid name for this useful plant (Merrill, 1917).

The typical cultivated soybean morphology displays a bush-type growth habit with a stout primary stem and sparse branches, bearing various seeds with variable seed coat colors (Ratnaparkhe *et al.*, 2011). It is erect and has prostrate growth and grows up to two meters high. The primary leaves are unifoliate, opposite, and ovate, the secondary leaves are trifoliolate and alternate, and compound leaves with four or more leaflets are occasionally present (Carlson and Lersten, 2004). The flowers are borne in the axillary racemes on peduncles at the nodes, and normally large number of flowers have emerged, but only about two-thirds to three-quarters can effectively produce pods. The developed pods consist of one up to five seeds (Rienke and Joke, 2005).

The root system can be considered as a vegetative morphology which is made up of the main root and secondary roots (Muller, 1981). The development of the root system starts at the soybean seed becomes germinate and reaches the plant's physiological maturity (Muller, 1981). The axillary root can reach a depth of 150 cm, while the secondary measures up to 180 cm (Mitchell and Russell, 1971). The growth habits of the soybean crop variety can be determinate, semi-determinate, and indeterminate (Pratap *et al.*, 2016). The determinate types grow shorter and produce fewer leaves, but produce comparatively more pods, while the indeterminate types grow taller, produce more leaves and more pods right from the stem to shoot (Ngeze, 1993; Pratap *et al*., 2016).

2.3. Ecological Requirements

Soybean is a short-day plant and hence flowers more quickly under short days (Criswell and Hume, 1972; Rienke and Joke, 2005). According to Shibles *et al*. (1975) for flowering, the critical day length ranges from nearly 13 hours for genotypes adapted to tropic areas to 24 hours for photoperiod-insensitive genotypes grown at other latitudinal areas. Consequently, photoperiodism and temperature response is key in determining

areas of cultivar adaptation. The growth duration of the world soybean ranged from 75-200 days, while in tropical areas, the growth duration of adapted genotypes is commonly 90-110 days, and up to 140 days for the late maturing ones (Liu *et al*., 2017). Short growth duration is primarily might be related with sensitivity to the day length. Such a situation affects the extent of vegetative growth, flower induction and pollen viability, and flowering duration, pod filling, and maturity characteristics (Norman *et al*., 1995). Most of the crop legumes for growth and development require a temperature between 17.5 ℃ and 27.5 ℃, optimum being 22 ℃ and the maximum about 40 ℃. The seeds grow well between 15 ℃ and 40 ℃ temperatures, but the optimum is about 30 ℃ (Rienke and Joke, 2005).

Soybean requires an optimum rainfall amount in between 350 and 750 mm and is well distributed throughout the growth cycle (Ngeze, 1993). Rienke and Joke (2005) reported that two periods being critical for soybean moisture demands (sowing to germination and flowering to pod filling periods). The soil moisture should be between 50 and 85% during seed germination. Soybean withstands various soil types but mostly favors warm, moist, and well-drained fertile loamy soils, which supply adequate nutrients (Hans *et al*., 1997). According to Ngeze (1993) and Singh (2010), soybean performs well in soils with a pH range of 5.5 - 7.0, and it can tolerate acidic soils than other legumes but does not grow well in waterlogged, alkaline, and saline soil areas. Rienke and Joke (2005) also reported that this crop produces high yields in loamy textured soil and that if the seeds can germinate, they grow better in clayey soils.

2.4. Production and Importance

Soybean (*Glycine max* (L.) Merrill.) is aptly called "golden bean" or "miracle crop" of the 20th century and is one of the most valuable oilseed crops in the globe (Chung and Singh, 2008). It is the foremost important vegetable and oilseed crop having a greater production contribution worldwide (Chung and Singh, 2008). Production of soybeans is rising and is expected to stay to increase as demand for soybean oil for both human consumption and biodiesel and high-protein meal for animal feed increases in the world. Particularly, the soybean oil is considered as healthiest vegetable oil (Wilson, 2016).

In general, a soybean seed has high nutritional value and is rich in proteins and oil with an average of 40% protein and 20% oil, respectively (Arefrad *et al*., 2012). However, products of soybean are lacking in the sulfur-containing amino acids such as methionine and cysteine, and currently, the breeders concern goes to enhance their concentrations (Panthee *et al*., 2006; Krishnan and Jez, 2018). Beyond the nutritional values, soybean is also used as a nitrogen-fixing crop globally for the restoration and maintenance of soil fertility in a sustainable way and consequently contributes much to the improvement of crop yields (Smaling *et al*., 2008). Herridge *et al*. (2008) reported that soybean require more nitrogen, and it is estimated that biological nitrogen fixation can cover 60 to 70% of the nitrogen requirements of the plant.

Global soybean production is estimated at about 336.71 million tons with a productivity of 2.77 tons (FAO, 2019). According to FAO (2019), soybean production is estimated at about 3.09 and 0.126 million tons with the productivity of 1.25 and 2.30 tons per hectare in Africa and Ethiopia, respectively. Production and area cultivated under soybean in Ethiopia have an increasing trend from 2014 to 2020 (Figure 2.1). Major soybean-producing countries are USA, Brazil, Argentina, China, and India which accounts for nearly 87.7% of production worldwide (Bilyeu *et al*., 2016).
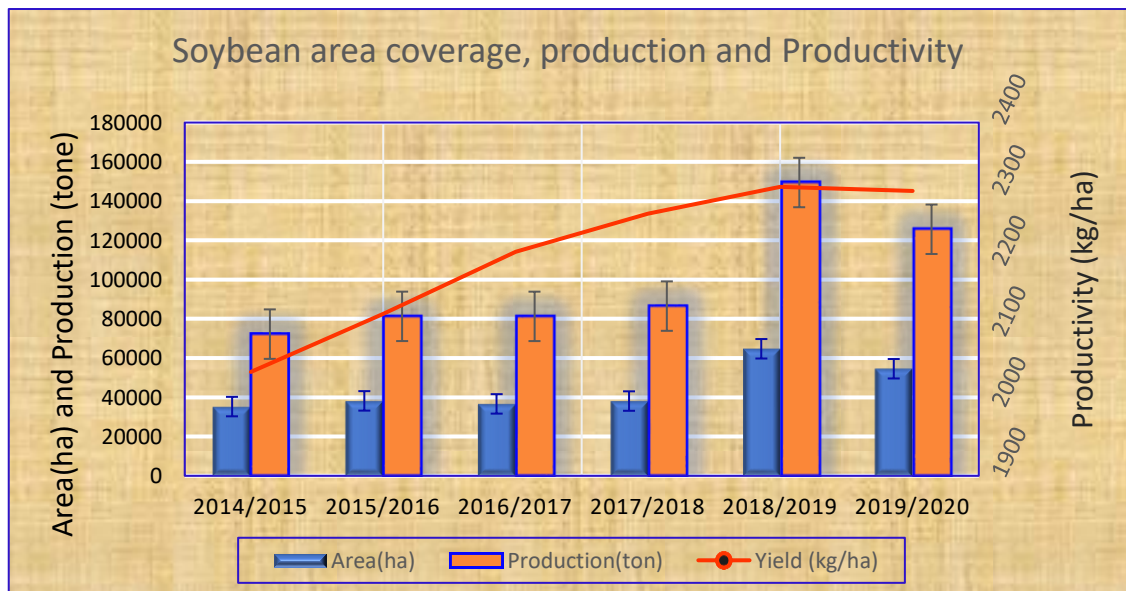
Figure 2.1. Soybean production, and productivity trend in Ethiopia (CSA, 2014 - 2020)

2.5. Genetic Diversity and Variability of Soybean

Plant genetic resources and the genetic diversity present in a particular crop species offer assurance for future genetic progress and insurance to unpredicted threats to agricultural production (Upadhyaya *et al.*, 2008). Traditionally, the evaluation of genetic diversity in soybean has been based on variation detections of morphological and agronomic traits or pedigree information (Ghaffari *et al.*, 2014) which has provided valuable information for germplasm evaluation. Phenotypic diversity in soybean is extensive and is under the genetic control of qualitative and quantitative traits (Oliveira *et al.*, 2017).

Soybeans, has the subgenus *Soja* and 22 perennial species within the subgenus *Glycine*. These species are considered as genetic resources for breeding purposes of the soybean crop (Hymowitz, 2004; Oliveira *et al.*, 2017). As reviewed by Oliveira *et al.* (2017) the collected data and updated by the International Plant Genetic Resources Institute (IPGRI), indicated that more than 170,000 accessions of *Glycine max* are maintained by around 160 institutions in about 70 countries in the world.

Genetic diversity investigation of plants provides a key role for developing high-yielding varieties and improvements in other relevant traits in the plant breeding strategies. The screening and selection for crop improvement would be based more likely on the availability of promising genotypes, which depends on the availability of diversity (Gemechu Keneni *et al.*, 2012). Genetic variability is essential for any breeding program, which offers an opportunity to a breeder for the selection of high-yielding and desirable genotypes. Understanding the magnitude of existing variability, proper characterization of key physiological traits and their relationships with yield and yield components would be very helpful in the development of efficient and highly productive genotypes (Aditya *et al.*, 2011).

Tadesse Ghiday *et al.* (2017) reported that the estimates of genotypic coefficient of variation were high for the number of seeds per pod, seed yield per plant, number of pods per plant, seed filling period, number of branches, and plant height. Bisht *et al.* (2018) and Diriba Beyene and Negash Geleta (2021) also found significant genotypic and phenotypic variations of most quantitative traits of 22 and 100 soybean genotypes. Moreover, several authors studied and reported the existence of a wide range of genetic variability and

diversity on different yield and yield-related traits of soybean. Dubey *et al*. (2018a) and Mishram *et al*. (2018) examined soybean genotypes and reported, the presence of sufficient genetic variation and diversity based on the quantitative traits data.

2.6. Heritability

Warner (1952) gives a detailed method for estimation of heritability in crop plants. Robinson *et al*. (1949) classified heritability as low (0-30%), moderate (30-60%), and high (60% and above). Genetic parameters such as heritability and genetic advance are key parameters for measuring genetic variability (Aditya *et al*., 2011). Several authors such as Baraskar *et al*. (2014), Malek *et al*. (2014), and Ali *et al*. (2016) reported high heritability for traits viz., days to 50% flowering, plant height, number branches per plant, number of pods per plant, harvest index, seed yield and medium heritability for oil content in soybean genotypes. Such a result suggested that selection based on phenotypic levels would be useful for the improvement of these traits. High heritability estimates were also recorded for days to 50% flowering, seed filling period, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seed per pod, seed yield, hundred seed weight and harvest index (Tadesse Ghiday *et al.*, 2017).

Jain *et al*. (2018) found moderate heritability for most economical traits of soybean genotypes. Sood and Sood (2001) examined soybean genotypes and found high heritability for most of the evaluated seed and seed-related traits, while the number of branches per plant, and the number of seeds per pod exhibited low heritability. Reni and Rao (2013) also observed high heritability for the most common soybean traits including seed yield. It indicated these traits seem more influenced due to a genetic base with lesser effects from the environment and the high heritability also suggests a greater scope for selection to improve these traits. High heritability for number of pods per plant, hundred seed weight and seed yield, medium value for days to maturity, pod length, and low heritability for the number of seeds per pod and harvest index was reported by Yechalew Sileshi (2019). Traits having high heritability are easy to improve through selection.

In general, different research findings observed different values of heritably for different soybean genotypes with mostly economical traits. Among these, Shilpashree *et al*. (2021) experimented for the estimation of heritability in different soybean accessions of diverse

genetic backgrounds and found that high heritability for days to 50% flowering, for days to maturity, for plant height, for the number of pods plant^{-1}, for pod length, and for protein contents. Aditya *et al*. (2011) had also reported high heritability for plant height, number of pods per plant, hundred seed weight, and seed yield. Generally, the implication of heritability in broad sense is that according to Robinson *et al*. (1949), if the heritability of a trait is high, say 60% or more, selection for such traits could be fairly easy-going. This might be due to, a close correspondence between the genotype and the phenotype due to the relatively small contribution of the environment to the phenotype. However, for traits with low heritability, say less than 30%, selection may be considered difficult or virtually impractical due to the masking effect of the environment.

2.7. Genetic Advance as Percent of Mean

Genetic advance indicates the estimate of the expected gain for a particular character through selection (Burton and Devane, 1953). High heritability along with high genetic advance in a particular character is a key issue for expecting the resultant effect for selecting individuals. This is due to providing the estimation of expected gain for a particular character (Burton, 1952; Johnson *et al*., 1955). The magnitudes of genetic advance were classified as high (> 20%), medium (10-20%), and low (<10%) (Johnson *et al.,* 1955). Tadesse Ghiday *et al*. (2017) reported that number of pods per plant, number of seeds per pod, plant height, hundred seed weight, seed yield, and seed filling period showed high broad sense heritability accompanied by high genetic advance, while days to 50% flowering, days to maturity and harvest index low genetic advance. High heritability along with high genetic advance as percent of the mean for plant height, number of branches per plant, number of pods per plant, and seed yield also revealed by the studies of Gohil *et al*. (2007). High heritability along with high genetic advance as percent of mean suggests that selection can be effective for these traits based on phenotypic expression. In other reports, high heritability, and low genetic advance for days to 50% flowering, days to maturity, number of seeds per pod, protein- and oil content have been found by Baraskar *et al*. (2014) which is may due to lack of genetic variability for these traits. Such, a condition favors improvement through recombination breeding and recurrent selection because improvement of these traits through simple selection may be difficult.

According to the classification, Baraskar *et al.* (2014) found high genetic advances for plant height, seed yield, number of branches per plant, and number of pods per plant; moderate for harvest index and low for days to maturity, pod length, number of seeds per pod, hundred seed weight, oil-and protein content. The genetic advance considered as high magnitude, it is important in identifying the appropriate traits and allowing the breeder to draw a selection on such traits. Baraskar *et al.* (2014) also found high heritability coupled with high genetic advance for plant height, seed yield, and the number of pods per plant indicating selection can be successful for these traits based on phenotypic performances.

Genetic advance and genetic advance as percent of mean provide helpful information on the expected gain in a specific trait due to selection. Ali *et al.* (2016) observed high genetic advances for number of pods per plant, and seed yield, low genetic advance for days to maturity, pod length, hundred seed weight, and oil content. However, these authors found high genetic advance as percent of mean for plant height, number of pods per plant, hundred seed weight, and seed yield, while low values for days to maturity, and pod length. High genetic advance as percent of mean coupled with either medium or low value of genetic advance suggests this trait can be improved through selection (Ali *et al.*, 2016). Similarly, Jain *et al.* (2018) reported high genetic advance coupled with high genetic advance as percent of mean for traits days to maturity, plant height, number of pods per plant, hundred seed weight, seed yield, and harvest index. Whereas low genetic advance with high genetic advance as percent of mean was found on the number of branches per plant, and the number of seeds per pod.

A previous study by Reni and Rao (2013) also indicated high genetic advance as percent of mean for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, biological yield, harvest index, and seed yield, while moderate values for days to maturity, protein content and oil content. Along with this, Reni and Rao (2013) reported for days to 50% flowering, number of branches per plant, pod length, number of seeds per pod, hundred seed weight, biological yield, seed yield, protein content, and oil content low genetic advance.

As Sood and Sood (2001) indicated estimates of genetic parameters of high heritability accompanied with high genetic advance as percent of mean indicates the operation of

additive genes and provide possibilities for improvement of a trait via progeny selection, mass selection, and other suitable modified selection procedures directing to exploit the additive gene effects. It is also suggested the predominance of additive gene action in the expression of such traits (Bhakuni *et al*., 2017). Tadesse Ghiday *et al.* (2017) also reported high genetic advance as percent of mean for most of yield and yield-related traits while high genetic advance values for plant height, number of pods per plant and number of seeds per pod, and the low genetic advance was found for traits viz., number of branches per plant, harvest index, and seed yield.

2.8. Association of Traits

2.8.1 Phenotypic and genotypic correlations

Knowledge and understanding of the relationship among plant traits are useful while selecting traits for yield improvement. Searle (1961) described the mathematical implications of correlation at genotypic, phenotypic, and environmental levels. A correlation coefficient is very useful in quantifying the magnitude and direction of trait associations but can be misleading if the high correlation between two traits is a consequence of the indirect effect of other traits (Dewey and Lu, 1959). In a crop breeding program to improve crop yield, the breeder has the opportunity to select yield directly or indirectly via yield-related traits of a crop (Machikowa and Laosuwan, 2011). Arshad *et al*. (2006) indicated the correlations of yield with other components traits have been studied widely and served as an indicator to improve soybean yield. In soybean crop, studies associated with genotypic, phenotypic, and environmental correlations have variously reported about the evaluated traits from flowering to maturity; in those associated to yield and its components (Perini *et al*., 2012).

In a genotypic and phenotypic correlation analysis, when genotypic correlations are higher than their corresponding phenotypic correlations, which implies that the phenotypic expression is lowered by environmental influences (Searle, 1961; Machikowa and Laosuwan, 2011). Genetic correlations are more important in the selection procedures where in genetic correlations, environmental effects are not considered (Searle, 1961; Machikowa and Laosuwan, 2011). Akram *et al*. (2016) found seed yield was positively and significantly correlated with the number of branches per plant, pod length, number of

pods per plant, number of seeds per pod, and hundred seed weight, suggesting that as branch number and pod number increased, seed yield also increased, which contributed to higher yield. Chandrawat *et al*. (2015) indicated the genotypic correlations were higher than the phenotypic correlations revealing the more contribution of genetic factor in development of the seed yield. These authors also reported phenotypic and genotypic correlation of seed yield was positive and significant with hundred seed weight and harvest index while significant and negative association with protein content.

Studies conducted by Malek *et al*. (2014) and Bhuva *et al*. (2020) indicated that days to 50% flowering, plant height, and the number of pods per plant had positive significant associations with seed yield both phenotypically and genotypically. However, Malek *et al*. (2014) found significant positive correlations at phenotypic and genotypic levels of seed yield with days to maturity, number of branches per plant, number of seeds per pod. Positive significant phenotypic and genotypic correlations of seed yield with harvest index, positive non-significant with days to maturity, number of breaches per plant, number of seeds per pod, and pod length, while negative significant and negative non-significant correlations with hundred seed weight and oil content were reported by Bhuva *et al.* (2020).

Studies conducted by Aditya *et al*. (2011) indicated number of branches per plant, number of pods per plant, and harvest index had a significant correlation with seed yield both at phenotypic and genotypic levels. On the other way, Asmamaw Amogne *et al*. (2020) found significant phenotypic and genotypic correlations of seed yield with days to maturity and plant height, while non-significant associations with traits viz., days to 50% flowering, the number of seeds per pod, hundred seed weight, oil- and protein content. Similarly, Iqbal *et al*. (2010) also found seed yield had a significant and positive correlation with days to maturity, number of branches per plant, number of pods per plant, hundred seed weight, oil content, and harvest index.

2.8.2 Path coefficient analysis

Path coefficient analysis is understood as standard partial regression coefficient analysis and is unitless. It is estimated by considering the yield as the dependent variable to understand the causal factor and to identify the best components, which is contributing to

yield increment. Path analysis has been employed by plant breeders to locate traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959; Samonte *et al.*, 1998). Computation of direct and indirect effects of traits on yield is playing a significant role in the detailed understanding of the complex relationships between yield and other traits. Thus, path coefficient analysis as a statistical tool developed by Wright (1921) and is a useful technique designed to ascertain the path along which relationships among variables are oriented and facilitated the understanding of the causal relationship between the interrelated variables. It is done by using the phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield (Dewey and Lu, 1959).

In soybean, seed yield, as in other crops, is a complex trait because it results from the expression and association of different components. Partitioning of path correlation coefficients as direct and indirect effects offers information on the actual contribution of independent variables with respect to a dependent variable i.e., seed yield. Asmamaw Amogne *et al*. (2020) tested 81 soybean genotypes and found that number of pods per plant had higher positive direct effect followed by number of seeds per pod on seed yield. Phenotypically maximum direct effect on yield by the number of pods per plant followed by the number of branches per plant, and hundred seed weight were reported by Tadesse Ghiday *et al*. (2017). Similarly, Kumar *et al*. (2018b) reported that phenotypic path coefficients on seed yield that harvest index and biological yield had high and positive direct effects on seed yield. Traits that have direct positive effects on yield suggesting these traits are the major contributors to soybean yield. AS a result, during phenotypic selection, the principal emphasis should be given to such traits for producing high-yielding soybean genotypes. Supporting reports were also found on 41 genetically diverse genotypes of soybean by Jain *et al*. (2015).

It is obvious that the practice of selection for one trait may concurrently bring alteration in the other related traits. Hence, the information of the magnitude and direction of association among the component traits and partitioning of correlation coefficients as direct and indirect effects suggested the true nature of relationship noted among various traits for crop improvement (Kumar *et al*., 2018b). Deresse Hunde and Hirpa Legesse (2018) reported, high genotypic direct path values for hundred seed weight, number of pods per plant, days to maturity, and number of seeds per pod on seed yield. Whereas, the

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indirect influence of the number of pods per plant, number of seed per pod, and hundred seed weight was the maximum among the genotypic path indirect effects. Deresse Hunde and Hirpa Legesse (2018) also found that the highest phenotypic direct effect of the number of seed per pods accompanied by maximum indirect effects of other traits via number of branches per plant, number of pods per plant, and pod length, indicates these traits to be the most important component of seed yield.

2.9. Genetic Divergence and Cluster Analysis

The notion of genetic divergence (D^2) statistics was once at the start developed by Mahalanobis (1936). The application of this technique is the evaluation of genetic diversity in the field of plant breeding programs. This is one of the key strategies for measuring genetic divergence in different breeding materials. Mehetre *et al*. (1994) and Mishram *et al*. (2018) suggested that genetic divergence research is the vibrant technique for the evaluation of genotype and selection of parents for the breeding program.

Clustering using D^2 statics is greatly valuable for evaluating the divergence of the population to identify genotypic variability. The D^2 statistics is the technique of measuring the diversity at intra- and inter-cluster levels and determines the relative contribution of each component trait to the total divergence (Sharma, 2006). Clusters separated by the largest D^2 revealed the maximum divergence, while genotypes in the same clusters are less divergent (Singh and Choudhary, 1985). Moreover, genotypes having a place in the clusters with the most extreme inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce a wide range of variability with desirable segregants.

Based on D^2 values, Mishra *et al*. (2018) indicated 16 clusters, of which 6 clusters were polygenotypic while 10 clusters were monogenotypic. Iqbal *et al*. (2008) and Malek *et al*. (2014) similarly grouped soybean genotypes into 5 clusters based on quantitative traits. Oliveira *et al*. (2017) and Dubey *et al.* (2018a) examined the diversity of genotypes of soybean and grouped into 8 and 10 clusters based on similarity levels. Dubey *et al*. (2018a) also indicated diversity levels among the clusters ranged from 53.05 to 3181.79 inter-cluster distances. Furthermore, Mesfin Hailemariam (2018) found 7 clusters based on evaluated traits of soybean, indicated the existence of notable genetic divergence

2.10. Principal Component Analysis

Principal Component Analysis (PCA), a statistical technique that uses an orthogonal transformation to convert a collection of observations of possibly correlated variables into a set of values of linearly uncorrelated variables. Principal component analysis more explains the contribution of the most contributing traits that accounted for the total genetic variability (Noirot *et al.*, 1996). The principal components have both direction and magnitude; the direction represents across which principal axis the data is mostly distributed or has the most variance and the magnitude signifies the amount of variance that the PC captures of the data when projected onto that axis (Jolliffe, 2002). Using this method, it is possible to exclude less important traits in the group (Cruz and Carneiro, 2003), and simultaneously determine traits that are the most important. Traits having the highest absolute value closer to one within the first principal component influence the clustering more than those with a lower absolute value closer to zero (Chahal and Gosal, 2002). Moreover, an eigenvalue greater than one is considered, because components are with a significant amount of information from the original variables (Kaiser, 1958).

Principal component analysis, basically a well-known data reduction technique that identifies the minimum number of components, which can explain maximum variability out of the total variability (Jolliffe, 2002) and rank genotypes based on PC scores. Evaluating Eigenvalues is the primary step in PCA which is referred to as the amount of total variation indicated on the axis. The first PC indicates most of the variability present in the original data relative to all remaining PCs. While the second PC explains most of the variability which is not summarized by the first PC and uncorrelated with the first and so on (Jolliffe, 2002). Predominantly, it is applicable for the study of genetic divergence between genotypes which allows the identification and selection of important genotypes with desirable traits for improvement (Vianna *et al.*, 2013).

Vianna *et al.* (2013) found four Eigenvalues were greater than unity explaining 71.60% of the total variance. Of which PC1 retained 29.44% of the variance and the principal traits that explained this retention of variance were: number of seeds per pod, number of pods per plant, and number of branches per plant. Marconato *et al.* (2016) also reported PC1 accounted for 38.28% of the total variance explained by the most economical traits while PC2 accounted for 20.30% of the total variance explained by seed filling period and seed

yield. The first four principal components explain 82.00% of the total variation of soybean genotypes with Eigenvalues greater than one was also reported by Yechalew Sileshi *et al.* (2019).

Principal component analysis gives an information about certain traits and genotypes which helps as an indication to the breeding programs. Various research studies have been reported in PCA, Iqbal *et al.* (2008) and Salimi *et al.* (2012) found 3 and 5 PCs having greater than one Eigenvalue contributed 69.77 and 78.02% of the explained total variation. Dubey *et al.* (2018b) also reported five PCs explained about 73.44% variability among the evaluated economic traits. Based on these authors, the PC1, was mainly related with traits viz., days to maturity, plant height, number of nodes per plant, number of pods per plant, and seed yield.

Chapter 3. MATERIALS AND METHODS

3.1. Experimental Sites

An experiment was conducted at Metema and West Armachiho districts, Gondar Agricultural Research Center substations, West Gondar, Ethiopia during the main cropping season of 2019/2020. The experimental locations, Metema and West Armachiho, represent the lowland areas of the soybean growing area of West Gondar and are geographically located about 890 and 935 km Northwest of Addis Ababa and 340 km and 385 km from Bahir Dar, respectively.

Table 3.1. Descriptions of the experimental area

Location	Altitude (masl)	Longitude (N)	Latitude (E)	Average annual rainfall (mm)	Average daily temperature (°C)		Soil type
					Min	Max	
Metema	760	12° 47' 38″	36° 23' 41″	1030	16 - 24	30 - 40	Clay loam
W/Armachiho	657	13° 28' 42″	36° 28' 23″	625-1100	22.1	36.3	Clay loam

Source: (Dereje Ayalew *et al*., 2012
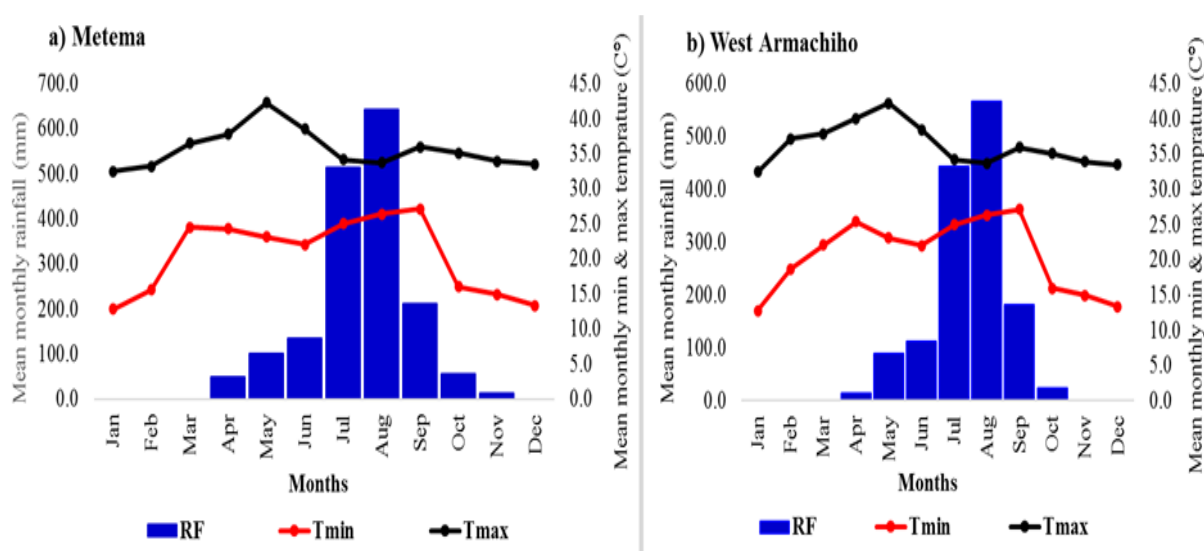
Figure 3.2. Meteorological data of Metema and West Armachiho for growing season (2020) (NMA, 2020)
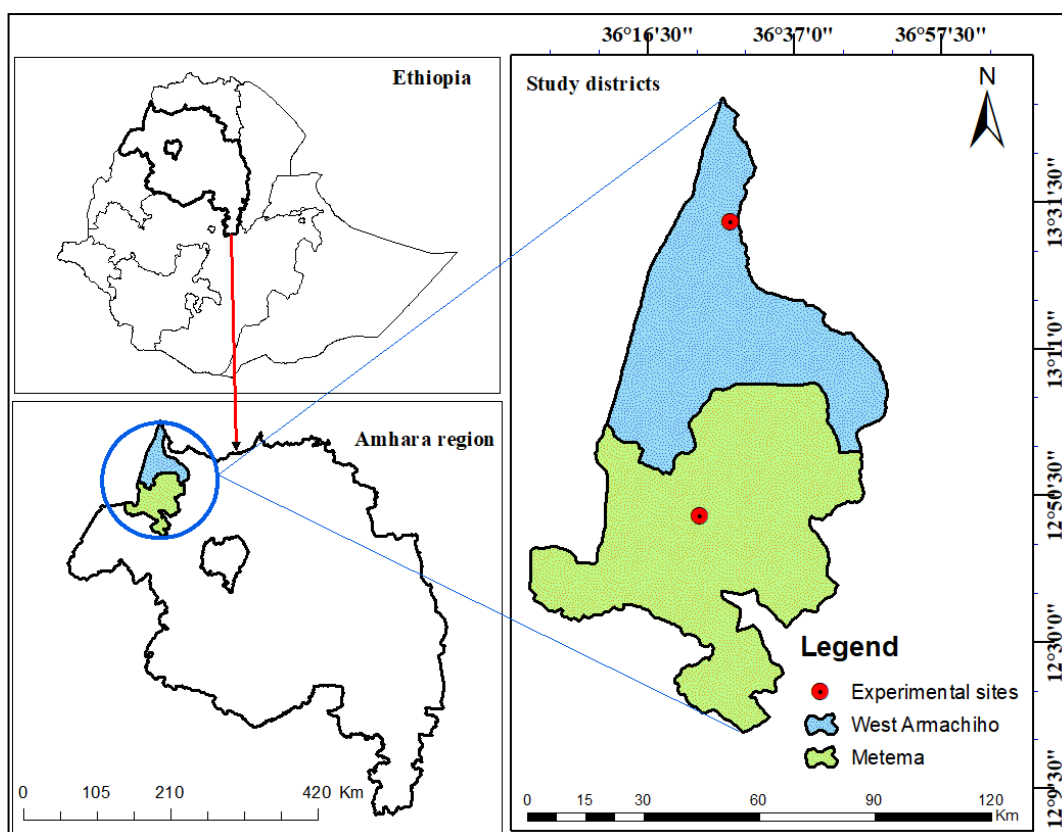
Figure 3.3. Geographical map of Metema and West Armachiho districts, Northwestern Ethiopia

3.2. Experimental Materials

Seventy-two soybean genotypes and nine released varieties were evaluated under this experiment. The genotypes and varieties were obtained from Pawe, Jimma and Gondar Agricultural Research Centers, Ethiopia. The list and detail of tested materials are presented in Appendix Table 1.

3.3. Experimental Design and Management

The experiment was carried out in a 9 x 9 simple lattice design. The experimental plot was 1.2 and 3 m length and width, respectively, with gross plot size of 3.6 m^2. Each plot consisted of two rows with 60 and 5 cm row and plant spacing, respectively. Spacing between plots, blocks and replications were 0.6, 1 and 2 m, respectively. Each genotype was randomly assigned to each experimental plot. Both rows were considered for both plant base and plot base data.

The experimental land was prepared using conventional practices. Planting was done on 01 and 02 July 2020 and sowing was made manually. To ensure uniform stand two seeds per hill were sown at a spacing of 5 and 60 cm between plants and rows, respectively. Thinning was done after two weeks of emergence. The recommended fertilizer rate, 121 kg NPS (19 N, 38 P_2O_5, and 7 S) per hectare, was used fully during sowing. Hand weeding was done uniformly to all experimental plots at early-, mid-, and before flowering- stage of the crop. Insect pests and diseases were not occurred during the crop growing season. Harvesting was done manually using hand sickles at harvesting stage.

3.4. Data Collection

Data were recorded during the cropping season at field and after harvesting. Five plants per plot were taken randomly for plant-based trait data and net plot area for plot-based traits based on the descriptors of soybean (IBPGR, 1984).

3.4.1. Qualitative traits

Qualitative traits were recorded according to the IBPGR (1984) soybean descriptor:

Flower color: was recorded at vegetative stage (when flower open at one of the two upper most nodes as 1 = white, 2 = purple).

Pubescence presence: was recorded and scored at beginning of maturity (1 = present, 2 = absent).

Pubescence color: was recorded at seed setting stage (full size seed in top four nodes, 1= white, 2 = brown).

Pod pubescence color: was recorded at the beginning of maturity as 1 = white, 2 = brown.

Seed color: was scored after seed collection (1 = yellowish, 2 = yellow green).

Hilum color: it was recorded after seed collection as 1 = yellow, 2 = black, 3 = grey.

Seed luster: was also identified and recorded after seed collection as 1 = shinny, 2 = dull.

3.4.1. Quantitative traits

Data collected on plot basis:

Days to flowering (DF): the number of days from sowing to 50% of plants bears flower.

Days to physiological maturity (DM): the number of days from sowing to the stage when 95% of the plants in a plot have reached physiological maturity.

Seed filling period (GFP): the number of days from flowering to maturity (i.e., the number of days to maturity minus the number of days to flowering).

Hundred seed weight (HSW) (g): it was recorded by taking weight of hundred randomly sampled seeds from total harvest of each plot and adjusted to 13% moisture level calculated as (100-actual moisture) / (100- standard moisture) x unadjusted seed yield

Seed yield (GY) (kg ha^{-1}): seed seed yield in gram obtained from each plot was converted to kg per hectare and adjusted to13% moisture content using the following formula.

$$GYadj. (kg/ha) at\ 13\%MC = ((100 - AMC(\%)))/((100 - SMC(\%))) * GYunadj.$$

Where, GYadj. = adjusted seed yield at 13% moisture content, AMC = the actual seed moisture content of the sample, SMC = the standard moisture content of soybean (13%) and GYunadj. = unadjusted seed yield.

Harvest index (HI): calculated as the ratio of yield to above ground dry biological yield.

Protein and oil content: protein and oil analysis were done via taking 300 g of 162 soybean samples by Near-Infra-Red Spectroscopy (NIRS) at Amhara Regional Agricultural Research Institute (ARARI) laboratory, Bahir Dar. The NIR spectral data were collected using NIR analyzer in the reflectance mode of the tool. Scanning of the sample was done twice by 1100 - 2500 nm spectral range. Estimation accuracy of protein and oil content was considered as the reading indicating the same accuracy with a standard error of predication of 0.22% to earlier reading. The partial least square calibrations were executed with un-scrambler 7.6 CAMO, and Oslo regression method (Martens and Naes, 1989), was used to develop calibration models for determining the protein and oil content of the soybean samples based on calibration sample set.

Data collected on plant basis:

Plant height (PH) (cm): the average height of five randomly taken plants from each plot was measured from ground to tip of the shoot at physiological maturity.

Number of branches per plant (count): the pod bearing branches from five randomly taken plants were counted.

Number of pods per plant (count): the middle pods having seeds from five randomly taken plants were counted.

Number of seeds per pod (count): the total numbers of seeds in middle pods from five randomly taken plants were counted.

3.5. Data Analysis

The data obtained for different agronomic and quality traits from the two locations were subjected to analysis of variance, phenotypic and genotypic correlations, path analysis, cluster analysis, and principal component analysis by using SAS version 9.4 (SAS Institute Inc, 2013) and JMP version 14 Pro software (JMP, 2018).

3.5.1. Shannon-Weaver diversity index

Morphological diversity for qualitative traits such as flower color (purple or white), pubescence presence (present or absent), pubescence color (white or brown), pod pubescence color (white or brown), seed color (yellow or yellow-green), hilum color (yellow, black or grey) and seed luster (shiny or dull) was estimated using the Shannon-Weaver diversity index (H′) (Dong *et al*., 2004) and the dominant and unique traits observed were recorded from the plot basis. The Shannon-Weaver diversity index (H′) used to characterize the phenotypic frequencies of the characters was defined as follow:

$$H' = \sum_{i=1}^{n} Pi \ln Pi$$

Where, n is the number of phenotypic classes for a character and Pi was the frequency of the ith class of traits, and H' was estimated for each trait.

3.5.2. Analysis of variance

The efficiency of the simple lattice design relative to randomized complete block design (RCBD) was checked and in most of the response traits the lattice was found to be more efficient than that of the RCBD at two locations. Thus, the data of all experimental units were subjected to analysis of variance (ANOVA) and general linear models (Proc GLM) as per the simple lattice design procedures. After testing the ANOVA assumptions, test of homogeneity of error variance for the purpose of combining the two-location data was done using F-test (the ratio of the largest to the smallest error variance) and the result proved homogeneous error variance for the studied traits (Appendix Table 5). Consequently, the ANOVA was also run for the two locations separately and combined over locations since all the evaluated traits indicated homogeneity of error variance. Thus, the results of the two locations were interpreted and presented in combination. Tukey's honest significance test (Tukey's HSD) at 5% and 1% level of significance was used for genotypes mean comparisons, when genotype differences were found to be significant. Analysis of variance for individual and over location was computed considering the general linear model for simple lattice is given below.

The ANOVA model for individual location analysis

$$P_{ijk} = \mu + g_i + b_{k(j)} + r_j + e_{ijk}$$

Where, P_{ijk} = phenotypic value of ith genotype under j^{th} replication and k^{th} incomplete block within replication j; μ = grand mean; g_i = the effect of ith genotype; $B_{k(j)}$ = the effect of incomplete block k within replication j; R_j = the effect of replication j; and E_{ijk} = the residual or effect of random error.

The ANOVA model for over location analysis

$$P_{ijkz} = \mu + g_i + B_{k(j)(z)} + R_{j(z)} + L_z + (gl)_{iz} + E_{ijkz}$$

Where, P_{ijkz} = phenotypic value of ith genotype under j^{th} replication at z^{th} location and k^{th} incomplete block within replication j and location z; μ = grand mean; g_i = the effect of ith genotype; $B_{k(j)(z)}$ = the effect of incomplete block k within replication j and location z; $R_{j(z)}$

= the effect of replication j within location z; l_z = the effect of location z; $(gl)_{iz}$ = the interaction effects between genotype and location; and E_{ijkz} = the residual or effect of random error.

Table 3.2. The structure of ANOVA for individual location for simple lattice design (Gomez and Gomez, 1984)

Source of variation	Degrees of freedom	Sum of squares (SS)	Mean square (MS)	F-value
Replication (r)	r-1	SSr	MSr	MSr/MSE
Genotypes (g unadj.)	g-1	SSg (unadj.)	MSg (unadj.)	MSg/MSE
Genotypes (adj.)	g-1	SSg(adj.)	MSg (adj.)	MSg/MSE
Block within replication (adj.)	r(b-1)	SSb (adj.)	MSb (adj.)	MSb/MSE
Intra–block error	(b-1) (rb-b-1)	SSe	MSe	
Total	rg-1	SST		

• *r = number of replications; g = N*<u>o</u>*. of genotypes and b = number of plots in a block/block size*

Table 3.3. Analysis of variances for combined over locations for simple lattice design

Source of variation	Degree of freedom	Mean square (MS)	Expected mean square (EMS)
Location (l)	l-1	MSl	$\sigma^2e + r\sigma^2gl + rg\sigma^2l$
Replication within location(r)	l (r-1)	MSr	$\sigma^2e + g\sigma^2rl$
Blocks within replication(b)	r(b-1)	MSb	$\sigma^2e + r\sigma^2gl + r\sigma^2 g$
Genotypes (g)	g-1	MSg	$\sigma^2e + r\sigma^2gl + rl\sigma^2g$
g x l interaction (i)	(g-1) (l-1)	MSgl	$\sigma^2e + r\sigma^2gl$
Error (e)	lg(r-1) - (rb-1) -(l -1)	MSe	σ^2e
Total	Lrb^2-1		

Where, b=intra blocks; σ^2g= genotypic variance, σ^2e = environmental variance, σ^2l=location variance, σ^2r = replication variance, and σ^2gl = genotype x location interaction variance, l = number of locations, g = number of genotypes and r = number of replications.

3.5.3. Estimation of phenotypic and genetic parameters

The phenotypic and genotypic variance components and coefficient of phenotypic and genotypic variability were estimated by utilizing the respective mean square values using the method suggested by Burton and Devane (1953). Partitioning of the total variance into components due to genotype (σ^2g), genotype by location interaction (σ^2gl) and

environment (σ^2e) variances were performed by assuming observed mean squares equal to their expected mean squares as suggested by Singh and Choudhary (1985) and Sharma (1998).

Environmental variance (σ^2e) = error mean square = MSe (individual location)

Environmental variance (σ^2e) = error mean square = MSe (combined over locations)

Genotypic variance (σ^2g) = (MSg - MSgl)/rl (combined over locations)

Genotypic variance (σ^2g) = (MSg - MSe)/r (individual location)

Phenotypic variance (σ^2p) = (σ^2g) + (σ^2e) (individual location)

Phenotypic variance (σ^2p) = σ^2g + σ^2gl/l + σ^2e/rl (combined over locations)

Genotype x location interaction variance (σ^2gl) = (MSgl-MSe/r)

where: MSgl = mean square due to genotypes by location interaction, MSg = mean square due to genotypes, r = number of replications, l = number of locations.

The coefficient of variation at phenotypic and genotypic levels was estimated using the methods suggested by Singh and Choudhary (1985) and Deshmukh *et al*. (1986).

Phenotypic Coefficient of Variation (PCV) = $\dfrac{\sqrt{\sigma^2 p}}{\bar{\chi}}$ x 100

Genotypic Coefficient of Variation (GCV) = $\dfrac{\sqrt{\sigma^2 g}}{\bar{\chi}}$ x 100

Where: $\bar{\chi}$ = grand mean of the character under study. The classification for GCV and PCV given by Deshmukh *et al.* (1986) as low (<10%), moderate (10-20%), and high (>20%).

3.5.4. Estimation of heritability in broad sense and genetic advance

Heritability in broad sense (H^2b) is expressed as a percentage of the ratio of the genotypic variance (σ^2g) to the phenotypic variance (σ^2p) estimated by using a method proposed by Hanson *et al*. (1956) and Allard (1960).

Heritability (H^2b) = $\dfrac{\sigma^2 g}{\sigma^2 p}$ x 100

Where, H^2b = heritability in broad sense, σ^2p = phenotypic components of variance, σ^2g = genotypic components of variance. As demonstrated by Robinson *et al*. (1949),

heritability can be categorized as low (0-30%), moderate (30 -60%), and high (60% and above).

Expected genetic advance (GA) for desirable traits under selection was computed by the formulae described by Johnson *et al*. (1955).

Expected genetic advance$(GA) = H^2b * k * \sigma\rho$

Genetic advance as percent of mean (GAM) was computed to compare the extent of the predicted advance of different traits under selection using the formula suggested by Johnson *et al*. (1955) and classified as low (<10%), moderate (10-20%) and high (>20%).

Expected genetic advance $(GAM) = \dfrac{GA}{\mu}$ x 100

Where, $\sigma\rho$ = phenotypic standard deviation on mean basis, H^2b = heritability in broad sense, k = selection differential (where k = 2.06 at 5% selection intensity) and μ = grand mean of the trait under consideration.

3.5.5. Phenotypic and genotypic correlation coefficient analysis

The genotypic and phenotypic correlation for all possible trait combinations were computed by using the formula suggested by Weber and Moorthy (1952) and Miller *et al*. (1958). The genotypic and phenotypic covariance components between two traits were found within the same way as for the corresponding variance components. These co-variance components are used for estimating the genotypic and phenotypic correlation between the pairs of traits. The covariance components between all pairs of characters were estimates as:

Genotypic covariance $(GCOVg_{xy}) = \dfrac{MSPg - MSPe}{r}$

Phenotypic covariance (PCOVpxy) $= COVgxy + \dfrac{\sigma exy}{r}$

Where: MSPe = mean sum of cross product for error, MSPg = mean sum of cross products for genotypes, COVexy (σexy) = environmental covariance between characters x and y, and r = number of replications.

To estimate phenotypic and genotypic correlation coefficients,

Phenotypic correlation coefficient between x and y $(rp_{xy}) = \dfrac{PCOVxy}{\sqrt{(\sigma^2px * \sigma^2py)}}$

Genotypic correlation coefficient between character x and y $(rg_{xy}) = \dfrac{GCOVxy}{\sqrt{(\sigma^2gx * \sigma^2gy)}}$

Where, PCOVxy and GCOVxy = phenotypic and genotypic covariance between variables x and y, respectively; σ^2gx and σ^2px = genotypic and phenotypic variance for trait x; and σ^2gy and σ^2py = genotypic and phenotypic variance for trait y, respectively.

The correlation coefficients were carried out to determine the degree of association of a character with yield and among the yield component traits. Estimates of genotypic and phenotypic correlation coefficients were tested against t-values given in (Fisher and Yates, 1963) table at n-2 degrees of freedom, at the probability levels of 5% and1% to test the significance, where n is the number of genotypes under studied. Thus, to test the significance of phenotypic correlation coefficients, the formula developed by Sharma (1998) was adopted.

$$t = rp_{xy} / SE_{rpxy}$$

Where, rp_{xy} = Phenotypic correlation; SE_{rpxy} = Standard errors of phenotypic correlation and

$$SErpxy = \sqrt{\dfrac{1 - r^2p}{n - 2}}$$

Where, r^2p is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were tested for their significance using the formula described by Robertson (1959) as indicated below:

$$t = \dfrac{rgxy}{SErgxy}$$

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n = number of genotypes.

$$SErgxy = \dfrac{(\sqrt{1 - r^2gxy})}{\sqrt{2Hx * Hy}}$$

Where, SErgxy is the standard error of genotypic correlation coefficient, Hx and Hy are heritability for traits x and y, respectively.

3.5.6. Path coefficient analysis

Path coefficient analysis is a standardized partial regression coefficient analysis that provides effective means of finding out direct and indirect causes of association, and it is unitless. The analysis measures the direct influence of one variable upon the other and permits the separation of phenotypic and genotypic correlations partitioned into direct and indirect effects using seed yield as a dependent (resultant) and other trait as an independent (causal) variable. Traits that had a significant relationship with seed yield were only considered in the path analysis. This analysis leads to the identification of important component traits useful for indirect selection of complex traits such as seed yield (Dewey and Lu, 1959) and path coefficient classified as negligible (0.00 - 0.09), low (0.1 - 0.19), moderate (0.2 - 0.29), high (0.3 - 0.99) and very high (> 1.00) (Lenka and Misra, 1973). Therefore, direct and indirect effects of the independent traits on soybean yield were estimated by the simultaneous equations suggested by Dewey and Lu (1959).

$$r_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where, r_{ij} =association between the independent variable/trait (i) and dependent variable/trait (j) as measured by correlation coefficient; P_{ij} = components of direct effects of the independent variable (i) on the dependent variable (j) as measured by path coefficient; and $\sum r_{ik}.P_{kj}$ is summation of components of indirect effect of a given independent variable (i) on a given dependent variable (j) via all other independent variables (k). To determine Pij values square matrices of the correlation coefficients between independent variables in all possible pairs were inverted and then multiplied by the correlation coefficient between independent and dependent variables. Therefore, the path analysis based on the genotypic and phenotypic correlation coefficients were estimated using SAS software (SAS Institute Inc., 2013). From the analysis, the R^2 value indicated the proportion of the variance accounted by the independent variables and U, the residuals which is not explained by the model and / or the contribution of the remaining unknown factor was measured as the residual effect also estimated as described by Dewey and Lu (1959).

$$U = \sqrt{(1-R^2)}; \text{ where } R^2 = \Sigma r_{ij} P_{ij},$$

The magnitude of R^2 indicates how best the causal factors account for the variability of the dependent variable seed yield. It is considered that if the R^2 value is small (e.g., nearly zero) the dependent variable (seed yield) is entirely explained by the variability in the independent variables, whereas higher values of R^2 indicated that some other factors which have not been included, needed to be considered in the analysis to account fully the variation in the dependent variable (seed yield).

3.5.7. Cluster analysis

Cluster analysis is one of the most common and efficient methods of multivariate statistical analysis techniques for grouping breeding materials from germplasms, accessions, and other lines, into distinct and variable groups depending on the genotype performance. Clustering of genotypes was performed using the proc cluster procedure of SAS software version 9.4 (SAS Institute Inc., 2013). The cut-off points where local peaks of the pseudo-F statistic join with small values of the pseudo t^2 statistic followed by a larger pseudo t^2 for the next cluster fusion was examined to decide the number of clusters. Agglomerative hierarchical cluster analysis approach was used. The trait means data values were standardized to have a mean of zero and variance of unity before cluster analysis to eliminate the biases due to differences in the scale of measurement. Clustering of genotypes was performed by average linkage and squared Euclidean distance method using Minitab software version 19.0 (Minitab, 2019). The dendrogram was constructed as a measure of dissimilarity technique using JMP software version 14 pro (JMP, 2018).

The Mahalanobis's D^2 statistics (Mahalanobis, 1936) was used to examine the genetic distance between populations. The generalized distance between any two populations and / or squared distances (D^2) for each pair of genotype combinations were computed using the following formula:

$D^2\text{ij} = (\text{xi} - \text{xj}) \text{ cov}^{-1} (\text{xi} - \text{xj})$

where, $D^2\text{ij}$ = the distance between cases i and j; xi and xj = vectors of the values of the variables for cases i and j; and cov^{-1} = the pooled within groups variance-covariance matrix.

The D^2 values obtained for pairs of clusters were considered as the calculated values of Chi-square (x^2) and were tested for significance at (1% and 5%) probability levels against the tabulated value of (x^2) for 'p' degree of freedom, where p is the number of traits considered. Average intra and inter cluster D^2 values were estimated using the formula given by Singh and Choudhary (1985),

Average intra-cluster $D^2 = \frac{\sum D_i^2}{n}$; where, $\sum D^2_i$ is the sum of distance between all possible combinations, (n) is the population/genotypes included in a cluster.

Average inter cluster $D^2 = \sum D^2_i$ / ninj; Where; $\sum D^2_i$ = sum of distance between all possible combinations, ni and nj = number of genotypes in cluster i and j, respectively.

3.5.8. Principal component analysis

Principal component analysis (PCA) was computed to find out the traits, which accounted more for the total variation (Jeffers, 1967). The data were standardized to mean zero and variance of one before proceeding with the principal component analysis. The principal component based on the correlation matrix was calculated using Past software version 4.03 (Hammer *et al*., 2020). In principal component analysis, eigenvalues greater than or equal to one were considered important to explain the observed variability (Jeffers, 1967). The correlations between the original traits and the respective PCs were also estimated. The principal component analysis was computed using the following equation:

PC1= b11(x1) + b12 + b1p = xp

Where, PC1 = the subjects score on PC1 (the first component extracted), b1p = the regression coefficient (weight) for observed variable p, as used in creating principal component 1 and xp = the subjects score on observed variable p.

Chapter 4. RESULTS AND DISCUSSION

4.1. Variability of Qualitative Traits

The genetic similarity of 81 soybean genotype analysis using the Shannon diversity index (H′), as a measure of phenotypic diversity of qualitative traits is presented in Table 4.4. The average Shannon genetic diversity index was 0.496. Hilum color revealed the highest (0.865) variation among the evaluated seven qualitative traits, followed by seed luster (0.680) and seed color (0.530) Pubescence presence had not any variation, that all the genotypes exhibited pubescence in their morphology (Table 4.4).

Based on the qualitative trait analysis, 82.72% (67 genotypes) exhibited purple flower color while the remaining 14 genotypes had white flower color. Regarding pubescence color, 65 genotypes (80.25%) exhibited brown while the 16 genotypes had white color with a diversity index of 0.497. Pod pubescence color also had a diversity of 0.440 with 68 genotypes characterized by brown color and 13 genotypes with white color. The high diversity indices for the qualitative traits showed the existence of high diversity in the tested soybean genotypes and the cluster analysis supported this finding. The current result was supported by Kumar *et al*. (2018) evaluated soybean genotypes and indicated presence of purple and white flower color. Dong *et al*. (2001, 2004) similarly found high phenotypic diversity indexes (H′) for qualitative traits viz., flower color, pubescence color, seed color, and hilum color. In fact, qualitative traits are mostly considered as marker traits in the identification of soybean varieties, which are less influenced by environmental variations. Gupta *et al*. (2010) indicated that soybean qualitative traits such as flower color, seed color, presence, and absence of pod pubescence were the most stable traits across various environments.

Table 4.4. Qualitative-based trait diversity in soybean with estimated phenotypic diversity index (H′)

Morphological traits	Category	Genotypes (No.)	Frequency (%)	Diversity Index (H′)
Flower color	White	14	17.28	0.460
	purple	67	82.72	
Pubescence presence	present	81	100.00	0.000
	absent	0	0.00	
Pubescence color	White	16	19.75	0.497
	brown	65	80.25	
Pod pubescence color	White	13	16.05	0.440
	brown	68	83.95	
Seed color	Yellow	18	22.22	0.530
	Yellow green	63	77.78	
Hilum color	yellow	15	18.52	0.865
	black	12	14.82	
	grey	54	66.66	
Seed luster	shiny	34	41.98	0.680
	dull	47	58.02	

4.2. Analysis of Variance, Range and Mean Performances

The combined analysis of variance over the two locations of 13 quantitative traits for the 81 genotypes revealed that mean squares due to genotypes were highly significant (P ≤ 0.01) for all the studied traits (Table 4.5, Appendix Table 4). The results indicated that the tested genotypes had adequate genetic variations concerning the traits under the study which can be exploited through selection. Hence, this result provides insight for soybean breeders to improve those traits via selection. The analysis of variance for 13 traits at separate locations of Metema and West Armachiho was also highly significant (P ≤ 0.01) among 81 genotypes (Appendix Table 2 & 3). Similarly, the existence of variability among soybean genotypes for different traits had been reported by Aditya *et al*. (2011), Akram *et al*. (2016), Guleria *et al*. (2019), and Yechalew Sileshi (2019). In addition, considerable differences and high genetic variability in soybean genotypes for different quantitative traits were also reported by Jain *et al*. (2018) and Shilpashree *et al*. (2021).

The mean squares due to genotype x location interaction was highly significant (p ≤ 0.01) except for hundred seed weight (p ≤ 0.05), number of seeds per pod and oil content (p ≥ 0.05) (Table 4.5). This significance of genotype (G) x location (L) interactions (MSgl)

suggests a differential response of the genotypes over the two locations for the considered traits (Table 4.5). A correspondent finding was reported by Mwiinga (2018). The mean squares due to locations (MSl) were also revealed as highly significant (p ≤ 0.01) for 12 evaluated traits and significant (p ≤ 0.05) for only oil content (Table 4.5). This suggests that the phenotypic expression of significant traits was different over the two locations. On the other way, it reveals, the location had significant effects on the performance of the tested soybean genotypes which might arise from the environmental variations of the two locations. The soybean crop has a differential response to climate variability in the different agroecology will associates with the growth stage of the crop (Molua, 2009).

Table 4.5. Combined analysis of variance (ANOVA) for 13 traits in 81 soybean genotypes tested at two locations in2020

Source of Var.	Mean Squares						
	MSl (1)	MSg (80)	MSgl (80)	Rep within Location (2)	Block within Rep (16)	MSe (144)	CV (%)
DF	1995.11**	264.40**	13.64**	17.83**	2.52^{ns}	1.79	2.55
DM	474.27**	185.83**	21.69**	8.34^{ns}	8.47**	3.27	1.61
GFP	523.90**	132.07**	38.17**	1.78^{ns}	7.49*	4.52	3.57
PH	50545.03**	1057.78**	83.27**	100.89^{ns}	100.7**	34.71	7.37
BPP	143.87**	6.20**	1.18**	11.29**	1.46**	0.36	13.45
PPP	73441.0**	1386.59**	389.66**	258.49^{ns}	231.75**	89.57	15.86
SPP	0.96**	0.11**	0.08^{ns}	0.047^{ns}	0.058**	0.06	9.46
PL	11.07**	0.19**	0.18**	0.23^{ns}	0.13^{ns}	0.12	9.62
GY	217633797.5**	4093634**	661101.3**	118301.6^{ns}	89986.8^{ns}	62893.7	9.36
HSW	1134.48**	14.45**	2.15*	0.51^{ns}	5.51**	1.51	8.08
HI	0.026**	0.018**	0.0096**	0.0041*	0.0012^{ns}	0.00099	8.15
OC	4.044*	8.77**	1.09^{ns}	1.00^{ns}	0.81^{ns}	0.93	4.58
PC	124.94**	15.54**	2.38**	10.31**	1.27^{ns}	1.39	2.77

*Note *, **significant at 0.05 and 0.01 probability levels, respectively; NS = Non-Significant, figures in parenthesis indicate degrees of freedom; MSl = Mean Square of Location, MSg = Mean Squares of Genotypes; MSgl = Mean Square Due to Genotype by Location, MSe = Mean Squares of Error; CV = coefficient of variation(%), DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH = Plant height(cm), BPP = Branches per Plant, PPP = Pods per Plant, SPP = Seed per Pod, PL = Pod Length(cm), GY = Seed Yield(kg/ha), HSW = Hundred Seed Weight (g), HI = Harvest Index, OC = Oil content, and PC = Protein Content, Number in parenthesis show respective degrees of freedom.*

Range and mean values of the 13 traits with the respective coefficient of variations combined over the two locations are presented in Table 4.6. The combined and separate

location mean performance of the 81 genotypes for the evaluated 13 traits are presented in Appendix Tables 4, 2, and 3, respectively.

In the combined mean performances of each trait over locations, a highly significant difference was observed on the number of days to heading among the tested genotypes, ranging from 34.75 to 65.25 days with a grand mean of 52.57 days. The earlier days to heading were found at genotype F6LG04-6000XLG04-5187-03 while the latest was recorded from the TGX2004-13F genotype. The mean value for the number of days to maturity ranged from 97.25 to 125.00 days among the tested genotypes. The late maturity date was recorded from genotypes TGX2004-13F (125.00), TGX2011-6F (124.75), TGX 2009-16F (124.75) while the early were found from F6LG04-6000XLG04-5187-03 (97.25) and F6LG04-6000XLG04-5187-04 (98.00) (Appendix Table 4).

The existence of wide variation among the tested genotypes for days to maturity provides an opportunity for the development of soybean varieties for different agro-ecologies. Consequently, early, and late-maturing soybean varieties can be developed based on the agroecological conditions which are mainly characterized by rainfall distribution. A similar finding had been reported by Yechalew Sileshi (2019) on days to maturity among soybean genotypes. Liu *et al*. (2017) also evaluated a total of 512 world soybean varieties and found different maturity groups. Seed filling period had also considerable estimated mean ranges 41.25 (Pawe-03) - 71.75 (CRFRD-15-SB). Similar report was demonstrated by Diriba Beyene and Negash Geleta (2021) .

The growth trait plant height exhibited high mean ranges from 40.70 to 116.37. The maximum plant height was obtained from genotype TGX2023-3E (116.37 cm) followed by TGX1993-4FN (115.15 cm), and TGX2017-5E (113.22 cm) Minimum plant height records were found in genotypes F6U03-300134XLG04-5187 (40.70 cm) followed by CRFRD-15-SE-2 (43.97 cm), F6LG04-6000XLG04-5187-06 (44.25 cm), and F6LG06-5920XU03-100612-03 (44.95 cm). Hence, under breeding for longer plant height, it is noted that the listed genotype could be considered. In agreement with the present finding, Viotto *et al*. (2020) and Shilpashree *et al.* (2021) found variations in plant height among tested soybean genotypes.

The number of branches per plant, pods per plant, seeds per pod, and pod length also showed significant differences among the tested genotypes with a range of 1.10 - 7.20, 22.40 - 104.75, 2.25 - 3.05, 3.05 - 4.13, and mean of 4.49, 59.66, 2.62 and 3.57, respectively (Table 4.6). The maximum branches per plant (7.2), pods per plant (104.75), seeds per pod (3.05), and pod length (4.13 cm) were recorded in the genotypes Pawe-01, TGX 2025-6E, Pawe-03, and TGX2009-14F, while minimum values were found in genotypes F6LG06-5920XU03-100612-01, F6LG04-6000XLG04-5187-04, CRFRD-15-SE-2, and CRFRD-15-SE-2, respectively. It was estimated that 50.61% of the tested genotypes had greater than the grand mean in the number of pods per plant. Consequently, this result verified the existence of genetic variability for these traits, suggesting the possibility of selection among soybean genotypes. Kumar *et al*. (2018b) reported variations for the number of branches per plant, number of pods per plant, and number of seeds per pod in soybean genotypes. Kumar *et al*. (2014) and Kumar *et al*. (2014) also found similar results on the variation of such traits of soybean.

The highest seed yield (4499.00 kg ha^{-1}) was recorded from genotype TGX1951-4F followed by TGX2010-5F (4267.50 kg ha^{-1}), Tgx-1990-5FP (4248.90 kg ha^{-1}), Gishama (4240.4 kg ha^{-1}), and TGX1993-4FN (4235.10 kg ha^{-1}). While the minimum seed yield was obtained from genotype G-49 (341.80 kg ha^{-1}) followed by G-14 (477.80 kg ha^{-1}) and G-74 (544.20 kg ha^{-1}). Based on the mean performance of 81 genotypes, TGX1951-4F, TGX2010-5F, Tgx-1990-5FP, Gishama, TGX1993-4FN, and TGX 2025-6E were found to be the best performing genotypes for seed yield. Generally, the seed yield was ranged from 341.80 to 4499.00 kg ha^{-1} and about 61.73% of the genotypes gave greater than the grand mean (2679.13 kg ha^{-1}) (Appendix Table 4). The variation of genotypes in producing seed yield indicates the existence of sufficient genetic variability in the tested genotypes and the potential of the genotypes for soybean yield improvement through direct selection. In accordant to the present study, significant variation was reported for seed yield by Kumar *et al*. (2014), Besufikad Enideg (2018), Yechalew Sileshi (2019), and Diriba Beyene and Negash Geleta (2021).

From agronomic traits, harvest index followed by hundred seed weight had considerable mean ranges while the quality traits oil content and protein content also exhibited significant mean ranges. As indicated from the results, these traits were revealed variations in the tested genotypes which could be important for future soybean breeding programs.

Harvest index, hundred seed weight, oil content, and protein content had a mean range of 0.2312 - 0.5002, 10.96 - 19.12 g, 17.97 - 24.45%, and 37.20 - 46.75% respectively. The highest harvest index (0.5002) was found at genotype Tgx-1919-22F followed by Gishama (0.4912), while the lowest value (0.2312) was recorded from genotype F6LG04-6000XLG04-5187-04 followed by F6LG04-6000XLG04-5187-05 (0.2357). The highest hundred seed weight was recorded in genotype CRFRD-15-SB (19.12 g), followed by F6LG04-6000XLG04-5187-02 (19.07 g), and F6LG04-6000XLG04-5187-01 (19.06 g), whereas the minimum records found from Pawe-03 (10.96 g) and Tgx-1889-62f (11.01 g) Aditya *et al.* (2011) found a similar variation for harvest index and hundred seed weight. A hundred seed weight variation ranged from 12.50 - 14.77 g was also previously reported by Rasyad *et al*. (2017).

For the two quality traits, oil and protein content maximum record was obtained from genotypes F6LG06-5920XU03-100612-03 (24.45%) and TGX1987-10F (46.75%) followed by CRFRD-15-SB (17.97%) and H3-15-SF-2 (18.00%) for oil content, and TGX2007-3F (46.30%) and Pawe-03 (46.15%) for protein content, respectively. This implies that significant variations existed among the tested genotypes for these traits. Such variation is crucial for the plant breeder and selection is possibly effective under the magnitude of variability in the breeding population is sufficient. Hence, if the breeding objective is targeted to improve the aforementioned traits, the respective genotypes should be given due attention. Rasyad *et al*. (2017) found a similar trend of variation for oil-and protein content. Similarly, Ramteke *et al*. (2010) indicated a significant mean variation of hundred seed weight, oil- and protein content. Generally, the range and mean values for various evaluated traits in the current study indicate the existence of adequate variability among the tested soybean genotypes.

Table 4.6. Descriptive statistics for 13 traits in 81 soybean genotypes tested over locations in 2020

| Traits | Statistics | | | |
	Mean ± SE mean	Range	CV (%)	R^2
DF	52.57±0.07	34.75 - 65.25	2.55	99.02
DM	112.13±0.10	97.25 – 125.00	1.61	97.45
GFP	59.56±0.12	41.25 - 71.75	3.57	95.90
PH	79.90±0.33	40.70 - 116.37	7.37	96.88
BPP	4.49±0.03	1.10 - 7.20	13.45	94.27
PPP	59.66±0.52	22.40 - 104.75	15.86	94.63
SPP	2.62±0.01	2.25 - 3.05	9.46	66.41
PL	3.57±0.02	3.05 - 4.13	9.62	72.92
GY	2679.13±13.93	341.80 - 4499.00	9.36	98.57
HSW	15.20±0.07	10.96 - 19.12	8.08	92.66
HI	0.3866±0.002	0.2312 - 0.5002	8.15	94.41
OC	21.00±0.05	17.97 - 24.45	4.58	86.71
PC	42.59±0.06	37.20 - 46.75	2.77	89.81

SE = Standard Error, CV = Coefficient of Variation (%), R^2 = Coefficient of Determination, DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH = Plant height(cm), BPP = Branches per Plant, PPP = Pods per Plant, SPP=Seed per Pod, PL= Pod Length(cm), GY = Seed Yield(kg ha⁻¹), HSW = Hundred Seed Weight(g), HI = Harvest Index, OC = Oil content, and PC = Protein Content

4.3. Estimates of Genetic Parameters

4.3.1. Estimates of variance components

The extent of traits assessed in estimates of phenotypic ($\sigma^2 p$), genotypic ($\sigma^2 g$) and environmental ($\sigma^2 e$) variances and genotypic (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability (H^2), genetic advance (GA) and genetic advance as percent of the mean (GAM) of all studied traits of combined over locations are presented in Table 4.7. The result indicated that estimates of phenotypic coefficients of variation were slightly higher than the corresponding genotypic coefficients of variation (Table 4.7) which demonstrated the slight influence of environment on the expression of studied traits. The smaller the differences between the values of GCV and PCV indicated a higher contribution of genetic factors and less environmental influences for the variations among genotypes for the studied traits. In agreement with the current result, Bisht *et al*. (2018) in days to flowering, plant height, number of pod per plant, seed yield and hundred seed weight; Guleria *et al*. (2019) found a smaller variation between PCV and GCV for

days to flowering, days to maturity, plant height, number of branch per plant, number of pods per plant, pod length, number of seed per pod and hundred seed weight of soybean genotypes.

According to Deshmukh *et al*. (1986) the classification for PCV and GCV values considered as low (< 10%), moderate/medium (10 - 20%), and high (> 20%). Based on this, for the present study of traits, the PCV ranged from 4.63 and 37.76% for protein content and seed yield, whereas the GCV ranged from 1.24 to 34.58% for pod length and seed yield, respectively (Table 4.7). Traits including plant height, number of branches per plant, number of pods per plant, and seed yield exhibited higher PCV values. Intermediate PCVs were observed on the days to flowering, hundred seed weight, and harvest index while low values were found from the days to maturity, seed filling period, number of seed per pod, pod length, oil content, and protein content traits.

Plant height, number of branches per plant, number of pods per plant, and seed yield had a higher PCV value. These high estimates of the genetic parameters allow breeders to enable direct selection to improve yield. A similar finding was reported by Guleria *et al*. (2019) for the number of branches per plant, the number of pods per plant, seed yield, and hundred seed weight of PCV of soybean genotypes evaluated at different locations Similarly, Besufikad Enideg (2018) from plant height, number of pods per plant, and seed yield; Bisht *et al*. (2018) from the number of pods per plant and seed yield obtained high PCV values. Medium PCV values were found from traits of days to flowering, hundred seed weight, and harvest index indicated, a considerable amount of phenotypic variation is presented among the tested genotypes and suggests the possibilities of yield improvement through phenotypic selection for these traits. Bisht *et al*. (2018) in plant height, number of branch per plant, number of seed per pod, and hundred seed weight; Kumar *et al*. (2018b) in days to 50% flowering and hundred seed weight; Guleria *et al*. (2019) in pod length and number of seed per pod found moderate PCV values among soybean genotypes.

Days to maturity, seed filling period, number of seed per pod, pod length, oil content, and protein content had low PCV value indicating the presence of low phenotypic variation among the tested genotypes and improvement of these traits through the phenotypic selection might be difficult. Therefore, an improvement on such traits should employ alternative methods like inducing genetic variability by crossing or induced mutagenesis

followed by selection. In harmony with this result, Baraskar *et al.* (2014) in days to maturity, oil content and protein content; Besufikad Enideg (2018) in days to maturity; Kumar *et al.* (2018b) in days to maturity and number of seed per pod; Guleria *et al.* (2019) in days to maturity reported low PCV score in a variability study of soybean genotypes. In contrast to the present result, Bisht *et al.* (2018) (in days to 50% flowering) and Guleria *et al.* (2019) (in days to 50% flowering and plant height) reported low PCV values.

Traits showing high GCV value include the number of branches per plant, number of pods per plant, and seed yield while days to 50% flowering, plant height, hundred seed weight, and harvest index were categorized under the medium GCV. The studied traits which had low GCV were included days to maturity, seed filling period, the number of seeds per pod, pod length, oil content, and protein content (Table 4.7). The higher the estimate of GCV of these traits indicating the presence of high genetic variability within the tested genotypes; and the possibility of improving these traits through selection. In agreement with the present finding, Besufikad Enideg (2018) for the number of pod per plant and seed yield Guleria *et al.* (2019) reported higher GCV for the number of branches per plant, the number of pods per plant, and seed yield; Yechalew Sileshi (2019) for seed yield of soybean genotypes. Furthermore, as similar with this study, Reni and Rao (2013) (in days to 50% flowering, plant height, and hundred seed weight); Besufikad Enideg (2018) (in days to 50% flowering and hundred seed weight) and Kumar *et al.* (2018b) (in days to 50% flowering, plant height, and hundred seed weight) indicated moderate GCV values among tested genotypes of soybean. Reni and Rao (2013) also found similar results of low GCV on oil and protein contents.

In contrary to the present finding, Aditya *et al.* (2011) in days to 50% flowering , number of branches per plant, and harvest index; Reni and Rao (2013) in harvest index, pod length, number of seeds per pod; Akram *et al.* (2016) in days to 50% flowering, plant height, number of branches per plant, pod length and hundred seed weight and Besufikad Enideg (2018) in plant height, pod length and harvest index reported a disagree point. In general, traits having low PCV and GCV values (Table 4.7) indicating a narrow range of variability, suggesting the limited scope for improvement of these traits through selection thus other means of creating variability is important. Moreover, the presence of high PCV, GCV, heritability in broad sense, and genetic advance could indicate the probability of trait selection based on genotypic variation (Baraskar *et al.*, 2014).

4.3.2. Estimates of broad sense heritability and genetic advance

Heritability in broad sense (H^2b) and genetic advance (GA) for the 13 quantitative traits using the combined data are presented in Table 4.6. Estimated heritability in broad sense ranged between 4.03% (pod length) to 94.84% (days to flowering) for the combined data (Table 4.6). According to Robinson *et al*. (1949) heritability estimates were classified as low (<30%), medium (30-60%), and high (≥60%). Considering this delineation, days to flowering (94.84%) followed by plant height (92.13%), days to maturity (88.32%), oil content (87.49%), hundred seed weight (85.12%), protein content (84.68%), seed yield (83.85%), number of branches per plant (80.89%), number of pods per plant (71.90%), and seed filling period (71.09%) had high heritability in broad sense while moderate heritability (48.08%) were observed on harvest index. High and moderate heritability in broad sense values indicates that the traits under study are less influenced by the environment or the predominance of genetic factors in their expression. In other ways, it indicates that the presence of a considerable heritable portion of variation can be exploited via the direct selection of superior genotypes based on the phenotypic performance of these traits.

High heritability estimates in days to 50% flowering, days to maturity, plant height, number of pods per plant, hundred seed weight, seed yield, and oil content has been reported by Reni and Rao (2013) and Ali *et al*. (2016). Chandrawat *et al*. (2017) and Bisht *et al*. (2018) found similar results of high heritability on days to 50% flowering, plant height, the number of branches per plant, seed yield, and hundred seed weight whereas high and moderate heritability on harvest index and the number of seed per pod disagrees with the present results. Similarly, as reported by Chandrawat *et al*. (2017) and Shilpashree *et al*. (2021) high heritability in broad sense is found on days to 50% flowering, plant height, protein, and oil content. However, these authors reported high heritability in pod length contrary to the current result. Aditya *et al*. (2011); Neelima *et al*. (2018) and Adetiloye *et al*. (2020) experimented on variability, heritability, and trait association of soybean genotypes and found similar results of high broad sense heritability on days to 50% flowering, days to maturity, plant height, number of pods per plant, seed yield, and hundred seed weight. In contrast, Agdew Bekele *et al*. (2012) demonstrated that medium heritability on days to 50% flowering, days to maturity, plant height, hundred seed weight, oil content, low heritability on seed filling period, number of branches per plant, number of

pod per plant, harvest index, seed yield and protein content. Reni and Rao (2013) also indicated a contrast result on the heritability in broad sense of the number of seeds per pod, pod length, and harvest index.

The combined genetic estimation result indicated that the estimated expected genetic advance, expressed as a percentage of the mean was in the range between 0.51% (pod length) and 65.22% (seed yield) (Table 4.7). The estimates of the range of genetic advance as percent of mean were classified as low (< 10%), moderate (10-20%), and high (>20%) as demonstrated by Johnson *et al.* (1955). Thus, based on this classification, a high estimate of genetic advance as percent of mean were observed for days to 50% flowering (30.21%), plant height (38.63%), number of branches per plant (46.15%), number of pods per plant (46.22%), hundred seed weight (21.93%) and seed yield (65.22%). Days to maturity, seed filling period, harvest index, and oil content had moderate genetic advance as percent of the mean, while the number of seeds per pod, pod length, and protein content exhibited a low value of genetic advance as percent of mean (Table 4.7). The high estimate of genetic advances for those traits revealed the possibility of improving the populations through selection.

High values of genetic advance are indicative of additive gene action while low values are suggestive of non-additive gene action (Singh and Narayanan, 1993). In agreement with this result, Neelima *et al.* (2018) reported high genetic advance for plant height; moderate genetic advance for days to maturity; and low genetic advance for the number of branches per plant, hundred seed weight, oil content, and protein content. Likely, Mesfin Hailemariam (2018) reported on plant height, the number of branches per plant, pod length, harvest index, seed yield, and hundred seed weight, whereas contradicting result of low genetic advance on days to maturity and number of pods per plant. This finding is also comparable with the results previously published by Malek *et al.* (2014) on plant height and the number of pods per plant and Chandrawat *et al.* (2017) on the number of branches per plant, seed yield, hundred seed weight, oil- and protein- content. However, Chandrawat *et al.* (2017) found a contrast result of genetic advance on days to 50% flowering, days to maturity, plant height, the number of pods per plant, and harvest index of soybean genotypes.

In the present study, high heritability coupled with high genetic advance observed for the

traits viz., plant height, number of pods per plant, and seed yield which indicates the presence of additive gene action and suggests the best possibility for improvement of these traits by various selection methods. High heritability coupled with moderate genetic advance was recorded for traits viz., days to 50% flowering and days to maturity, indicates these traits were less influenced by the environment but governed by additive and non-additive gene action. Moreover, high heritability coupled with low genetic advance were found from seed filling period, branch number per plant, hundred seed weight, oil- and protein content; indicates the presence of non-additive gene action and selection is not rewarding for these traits rather recombination breeding and recurrent selection may be employed for such type of traits for population improvement (Hakim and Suyamto, 2017).

In conformity, Shilpashree *et al*. (2021) reported high heritability coupled with a high genetic advance on plant height and number of pods per plant; high heritability with a low genetic advance on pod length. A contradicting report on days to 50% flowering and maturity (high H^2 and low GA), and protein content (high H^2 with high GA) were also demonstrated by these authors. Jain *et al*. (2018) indicated dissimilar report where moderate heritability together with a high genetic advance on days to maturity, plant height, number of pods per plant, hundred seed weight, harvest index, and seed yield; moderate heritability coupled with a moderate genetic advance on days to 50% flowering; moderately heritability with a low genetic advance on the number of branches per plant and number of seed per pod of twenty-four soybean genotype.

Table 4.7. Variance, heritability, genotypic and phenotypic coefficient of variation, and genetic advance for the 13 traits of 81 soybean genotypes combined over location, 2020

Traits	σ^2g	σ^2gl	σ^2p	σ^2e	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
DF	62.69	5.92	66.10	1.79	15.06	15.46	94.84	15.88	30.21
DM	41.03	9.21	46.46	3.27	5.71	6.08	88.32	12.40	11.06
GFP	23.47	16.83	33.02	4.52	8.13	9.65	71.09	8.41	14.13
PH	243.63	24.28	264.44	34.71	19.54	20.35	92.13	30.86	38.63
BPP	1.25	0.41	1.55	0.36	24.91	27.69	80.89	2.07	46.15
PPP	249.23	150.04	346.65	89.57	26.46	31.21	71.90	27.57	46.22
SPP	0.007	0.01	0.03	0.06	3.11	6.34	24.03	0.08	3.14
PL	0.002	0.03	0.05	0.12	1.24	6.16	4.03	0.02	0.51
GY	858133.35	299103.80	1023408.67	62893.70	34.58	37.76	83.85	1747.42	65.22
HSW	3.08	0.32	3.61	1.51	11.54	12.51	85.12	3.33	21.93
HI	0.002	0.004	0.005	0.001	12.20	17.59	48.08	0.07	17.42
OC	1.92	0.08	2.19	0.93	6.60	7.05	87.49	2.67	12.71
PC	3.29	0.49	3.88	1.39	4.26	4.63	84.68	3.44	8.07

σ^2p = Phenotypic variation, σ^2g = Genotypic variation, σ^2gl = Variance for genotype x location interaction, σ^2e = Environmental variance, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, H^2(%) =Broad sense heritability, GA (5%) = genetic advance at 5% selection intensity, GAM =Genetic advance as percent of mean, DF = Days to 50% Flowering (days), DM = Days to Maturity (days), GFP = Seed Filling Period (days), PH= Plant Height (cm), BPP = Number of Branches per Plant (No.), PPP = Number of Pods per Plant (No.), PL = Pod Length (cm), HSW(g) = Hundred Seed Weight, HI = Harvest Index (%), PC = protein Content (%)

4.4. Correlation among Yield and Yield Components

The genotypic and phenotypic correlation coefficients for yield and yield-related traits combined over location are presented in Table 4.8. Generally, in the present study, the genotypic correlation coefficients were higher in magnitude than their respective phenotypic correlation coefficient for most of the trait pairs, indicating the presence of a strong inherent genetic association between two corresponding traits (Table 4.8). According to Almeida *et al.* (2010), this verifies that genetic factors contributed more than the environmental factor to the trait correlations. Similar findings were reported by Sousa *et al*. (2015) and Machado *et al*. (2017) who reported higher genotypic correlation values rather than phenotypic ones to nearly all traits. In most of the trait combinations, the directions of phenotypic and genotypic correlation coefficients were similar (Table 4.8). Aditya *et al*. (2011), and Machikowa and Laosuwan (2011) reported a similar result.

4.4.1. Genotypic and phenotypic correlation of seed yield with other traits

In the present study, seed yield revealed highly significant (p ≤ 0.01) positive genotypic correlation with days to 50% flowering (rg = 0.678), days to maturity (rg = 0.550), plant height (rg = 0.749), number of branches per plant (rg = 0.578), number of pods per plant (rg = 0.674), harvest index (rg = 0.881) and protein content (rg = 0.557) while significant positive correlation at 5% were found for pod length (rg = 0.229) (Table 4.8). Such a result indicates the existence of the inherited relationship between traits and improving these traits may result in the improvement of seed yield as the result of a positive and strong correlation. Moreover, traits having a highly and positively genotypic correlation with seed yield indicating the importance of those traits for yield improvement in soybean crops. Therefore, the indirect selection for higher yield based on-and by- consideration of highly positively correlated traits would be effective. Viotto *et al*. (2020) reported a similar result on days to maturity, number of branches per plant, and number of pods per plant with seed yield while a disagreed with the genotypic correlation of oil- and protein content.

Similarly, Balla and Ibrahim (2017) reported on seed yield with days to maturity, plant height and the number of pod per plant and Machado *et al*. (2017) on seed yield had positively and significantly correlated with the number of branches per plant and number of pods per plant. Dissimilar finding had declared by Chandrawat *et al*. (2015) on plant

height, number of branches per plant, number of pods per plant, hundred seed weight, and protein content.

At phenotypic level, seed yield had positive and highly significant correlations with days to 50% flowering (rp = 0.637), days to maturity (rp = 0.451), plant height (rp = 0.779), number of branches per plant (rp = 0.592), number of pods per plant (rp = 0.692), pod length (rp = 0.303), harvest index (rp = 0.686) and protein content (rp = 0.517) (Table 4.8). In such cases, priority should be given to these traits, while during indirect selection for soybean yield improvement. The result of the positive and significant phenotypic correlation of yield with other component traits directed that improving seed yield of soybean through selection would be practical with simultaneous consideration of seed yield with these traits by indirect selection through phenotypic performance. The corresponding finding was noticed by Malek *et al*. (2014), indicated seed yield had positively and significantly correlated with number of branches per plant, number of pods per plant, and number of seed per pod at the phenotypic level. However, Malek *et al*. (2014) on hundred seed weight; Kumar *et al*. (2018b) on days to maturity, plant height, number of pod per plant, number of seed per pod, and hundred seed weight demonstrated dissimilar phenotypic correlation results.

Moreover, disagree with the current study, Chandrawat *et al*. (2015) indicted negative and positive non-significant phenotypic correlations of seed yield with days to 50% flowering, days to maturity, plant height, number of pods per plant, and protein contents. Aditya *et al*. (2011) found the same result on the number of pods per plant and harvest index while contradicting results on days to 50% flowering, plant height, and hundred seed weight. A positive significant phenotypic correlation was also observed between seed yield and hundred seed weight (rp = 0.135). Kumar *et al*. (2018b) reported contradicting results on hundred seed weight.

4.4.2. Genotypic and phenotypic correlation among yield-related traits

Genotypically, the number of branches per plant indicated a positive and significant association with the number of pods per plant, pod length, harvest index, and protein content, while the significant negative correlation with hundred seed weight and non-significantly with the number of seeds per pod and oil content. In harmony with this

result, Malek *et al*. (2014) and Kumar *et al*. (2018b) indicated similar results on pod number per plant and hundred seed weight while contradicting results on seed number per plant and harvest index.

The number of pods per plant showed highly significant positive genotypic correlations with harvest index and protein content whereas a highly significant negative correlation was observed with a hundred seed weight. The number of seeds per pod, pod length, and oil content had a non-significant genotypic correlation with pod number per plant. Malek *et al*. (2014) and Kumar *et al*. (2018b) reported similar results on hundred seed weight but differed on seed number per pod and harvest index. A similar report on pod length and harvest index was demonstrated by Kumar *et al*. (2013).

The number of seeds per pod showed a non-significant genotypic correlation with hundred seed weight, harvest index, oil content, and protein content while highly significantly positively correlated with pod length. In line with the current result, Kumar *et al*. (2018b) for hundred seed weight and harvest index. Hundred seed weight indicated a highly significant positive genotypic correlation with oil content and negatively with harvest index and protein content. Kumar *et al.* (2018b) indicated dissimilar results in soybean genotypic correlation study between hundred seed weight and harvest index. Harvest index with protein content had a highly significant positive correlation while oil content had non-significant associations. The two quality traits had negatively significant genotypic correlations with each other which was supported by Asmamaw Amogne *et al*. (2020) who indicated a negative and significant association of oil and protein content.

Days to maturity were positively and significantly correlated with seed filling period, plant height, number of branches per plant, number of pods per plant, pod length, harvest index, and protein content at phenotypic levels. However, it displayed a negative and significant association with oil content, indicates the improvement of this character will antagonistically affect the other. This result is in line with Malek *et al.* (2014) who reported that days to maturity were positively and significantly correlated with plant height and number of branches per plant; a non-significant similar result on seed number per pod and hundred seed weight. In addition, Malek *et al*. (2014) and Machado *et al.* (2017) obtained a non-significant correlation between days to maturity and number of pods per plant which contradicts with the current result.

Pod number per plant had a positive significant association with pod length, harvest index, and protein content whereas it was negatively and significantly correlated with oil content; and non-significantly with the number of seeds per pod and hundred seed weight (positively). This result disagrees with the report of Malek *et al.* (2014) who indicated pod number per plant had positive and negative phenotypic correlation with the number of seeds per pod and hundred seed weight, respectively. Kumar *et al.* (2013) reported the same result on harvest index but contradict result on pod length. Aditya *et al.* (2011) also found similar reports on number of pods per plant with harvest index and number of seeds per pod.

The number of seeds per pod showed a non-significant phenotypic correlation with hundred seed weight, harvest index, oil- and protein content while significantly correlated with pod length. Pod length had a positive significant association with hundred seed weight and protein content while a positive non-significant correlation was observed with harvest index and oil content. A similar result was demonstrated by Kumar *et al.* (2013) on harvest index. The other important trait hundred seed weight indicated positively and negatively significant phenotypic associations with oil content (rp = 0.146), harvest index (rp = -0.148), and protein content (rp = -0.136). Machikowa and Laosuwan (2011) found similar reports that most of the economical traits were negatively correlated with hundred seed weight. The two-quality trait oil- and protein content indicated a negative significant phenotypic correlation. The negative correlation might be indicated that the traits contribute no or less values in the selection for seed yield improvement in soybean.

In conclusion, genotypic and phenotypic correlation of traits revealed that the existence of associations of each other. Traits which exhibited positive and significant correlation with other trait demonstrates improvement of pair of traits is likely possible. However, traits that had negatively significant correlations suggests improvement of one trait can possibly influence the other pair of traits. Moreover, pair of traits that demonstrate significant positive genotypic and phenotypic correlation indicates the possibility of simultaneous improvement of traits and fair indirect selection of genotypes (Ghodrati, 2013).

Table 4.8. Estimates of genotypic (rg) (above diagonal) and phenotypic (rp) (below diagonal) correlation coefficients for 13 traits of 81 genotypes studied at Metema and West Armachiho, 2020

Traits	DF	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
DF		0.716^{***}	-0.582^{***}	0.731^{***}	0.652^{***}	0.754^{***}	0.015^{ns}	0.102^{ns}	0.678^{***}	-0.636^{***}	0.624^{***}	-0.132^{ns}	0.485^{***}
DM	0.658^{***}		0.151^{ns}	0.591^{***}	0.633^{***}	0.645^{***}	-0.049^{ns}	0.288^{**}	0.550^{***}	-0.281^{*}	0.447^{***}	-0.243^{*}	0.205^{ns}
GFP	-0.582^{***}	0.228^{***}		-0.347^{**}	-0.186^{ns}	-0.311^{***}	-0.077^{ns}	0.191^{ns}	-0.319^{***}	0.574^{***}	-0.363^{***}	-0.096^{ns}	-0.448^{**}
PH	0.686^{***}	0.502^{***}	-0.345^{***}		0.663^{***}	0.742^{***}	0.158^{ns}	0.224^{*}	0.749^{***}	-0.539^{***}	0.666^{***}	-0.035^{ns}	0.367^{***}
BPP	0.614^{***}	0.536^{***}	-0.215^{***}	0.659^{***}		0.744^{***}	0.037^{ns}	0.283^{**}	0.578^{***}	-0.315^{***}	0.533^{***}	-0.022^{ns}	0.227^{*}
PPP	0.662^{***}	0.506^{***}	-0.309^{***}	0.730^{***}	0.689^{***}		0.054^{ns}	0.113^{ns}	0.674^{***}	-0.591^{***}	0.559^{***}	-0.119^{ns}	0.353^{***}
SPP	0.097^{ns}	0.042^{ns}	-0.004^{ns}	0.159^{***}	0.062^{ns}	0.108^{ns}		0.462^{***}	-0.013^{ns}	-0.094^{ns}	0.008^{ns}	0.010^{ns}	0.052^{ns}
PL	0.131^{*}	0.227^{***}	0.075^{ns}	0.329^{***}	0.247^{***}	0.211^{***}	0.577^{***}		0.229^{*}	0.138^{ns}	0.223^{*}	0.091^{ns}	0.106^{ns}
GY	0.637^{***}	0.451^{***}	-0.337^{***}	0.779^{***}	0.592^{***}	0.692^{***}	0.081^{ns}	0.303^{***}		-0.471^{***}	0.881^{***}	0.002^{ns}	0.557^{***}
HSW	-0.238^{***}	-0.074^{ns}	0.228^{***}	0.088^{ns}	0.090^{ns}	0.050^{ns}	0.072^{ns}	0.351^{***}	0.135^{*}		-0.468^{***}	0.302^{***}	-0.498^{**}
HI	0.493^{***}	0.297^{***}	-0.317^{***}	0.478^{***}	0.404^{***}	0.376^{***}	-0.027^{ns}	0.099^{ns}	0.686^{***}	-0.148^{***}		-0.058^{ns}	0.574^{***}
OC	-0.131^{*}	-0.188^{**}	-0.034^{ns}	-0.074^{ns}	-0.064^{ns}	-0.137^{*}	-0.005^{ns}	0.041^{ns}	-0.038^{ns}	0.146^{***}	-0.027^{ns}		-0.259^{*}
PC	0.459^{***}	0.199^{***}	-0.378^{**}	0.383^{***}	0.264^{***}	0.361^{***}	0.048^{ns}	0.127^{*}	0.517^{***}	-0.136^{*}	0.415^{***}	-0.248^{**}	

DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH= Plant Height (cm), BPP and PPP = Number of Branches and Pods per Plant (No.), SPP = Number of Seeds per Pod, PL = Pod Length (cm), HSW(g) = Hundred Seed Weight, HI = Harvest Index (%), PC and OC = Protein and Oil Content (%)

4.5. Path Coefficient Analysis

4.5.1. Direct and indirect effects of traits on seed yield at genotypic level

The combined genotypic direct and indirect effects of various traits on seed yield are presented in Table 4.9. The genotypic path coefficient analysis indicated that the harvest index exerted a positive and maximum direct effect (0.632) on seed yield followed by the number of pods per plant (0.217) and plant height (0.209). These traits exhibited positive and significant genotypic correlation with seed yield, thus, these traits may be considered as the most important yield contributing traits and due emphasis should be placed on these traits while breeding for high seed yield in soybean. A similar result has been reported for the number of pods per plant by Arshad *et al*. (2006) and Machikowa and Laosuwan (2011); for harvest index by Baraskar *et al*. (2015), Chandrawat *et al*. (2015) and Yechalew Sileshi (2019) and for the number of pods per plant by Bhuva *et al*. (2020). Deresse Hunde and Hirpa Legesse (2018) found a disagreement result on hundred seed weight (high and positive direct effect), harvest index (low positive direct effect), days to maturity (high positive direct effect), and from protein content (high and negative direct effect) on seed yield of sixteen soybean genotypes.

Traits like days to maturity, hundred seed weight, and protein content had low magnitude positive direct effects on seed yield, while days to 50% flowering, seed filling period, number of branches per plant, and pod length had negligible negative direct effects on the seed yield. The negative direct effect suggests that seed yield possibly increased with the reduction of these traits and/or improvement of these traits is essential before selecting them for higher seed yield. Thus, in the breeding program, considerations are also important to the negative direct and indirect effects that existed amongst the traits. The genotypic path analysis residual effect indicates how best the causal/independent variables account for the variability of the resultant/dependent variable i.e., seed yield. Its estimate of 0.15 indicated that the causal variables explained about 85% of the variability in seed yield and only 15% of the variability remained unexplored. Kumar *et al*. (2018b) found and stated 0.352 residual effects or 64.8% of the variation found in the dependent traits was well explained by the contributed nine quantitative traits studied.

Disagreement with the present result, Baraskar *et al*. (2015) reported a negative negligible direct effect of days to maturity, plant height, and hundred seed weight on seed yield while similar result on days to 50% flowering, number of branches per plant, and protein content. Arshad *et al*. (2006) indicated contradicting results on the number of branches per plant and pod length, while Machikowa and Laosuwan (2011) indicated dissimilar results on the number of branches per plant but similarly found moderate direct effects of seed filling period. Malik *et al*. (2007) also found a similar result of a negative direct effect of days to 50% flowering, number of branches per plant while results on days to maturity, hundred seed weight, and protein content disagrees with the present findings. In addition, Deresse Hunde and Hirpa Legesse (2018) and Bhuva *et al*. (2020) support the present result via the finding of the positive direct contribution of pods per plant and harvest index on seed yield. However, Bhuva *et al*. (2020) reported a contradictory record via effects of plant height, number of branches per plant, pod length, and hundred seed weight on seed yield.

Moreover, Mesfin Hailemariam (2018) reported similar results having magnitude variations of direct effects of days to maturity (high positive), plant height (negligible positive), hundred seed eight (low positive), number of branches per plant (low negative), number of pods per plant (low positive), pod length (moderate negative). However, this author also declared a contradicting result on the direct effect of harvest index on seed yield. Datta *et al*. (2005) also reported high and positive direct effects of days to maturity, pod per plant, and hundred seed weight which differs from the current result only by values of ranges/magnitude. In addition, Arshad *et al*. (2006) supported that via the direct effects of same findings of days to 50% flowering, days to maturity, the number of pods per plant, and hundred seed weight.

Furthermore, days to 50% flowering (0.395), protein content (0.363), number of branches per plant (0.337), and days to maturity (0.283) contributed positive and high indirect effects through the harvest index (Table 4.9). Such a result indicates that, the importance of the trait harvest index as an indirect selection criterion for a successful soybean seed yield improvement program. Hence, considerations should be given for traits that depicted considerable positive indirect effects through other traits have to be taken simultaneously as indirect selection criteria for yield improvement.

Disagreement with the current result, Baraskar *et al*. (2015) found days to 50% flowering, days to maturity, plant height (no effect), and protein content exhibited negligible negative indirect effects on seed yield through harvest index. Deresse Hunde and Hirpa Legesse (2018) also indicated a negligible negative indirect effect of days to 50% flowering and days to maturity through harvest index while the number of branches per plant and pod length had a high positive indirect effect on seed yield through the number of pods per plant. A highly positive indirect effect of days to 50% flowering, days to maturity, and plant height through the number of pods per plant; plant height and days to 50% flowering through days to maturity were reported by Datta *et al*. (2005) which contradicted the present findings that had low and negligible indirect effects of these traits. Machikowa and Laosuwan (2011) found dissimilar results on seed filling period and similar records on days to 50% flowering, number of branches per plant, and hundred seed weight which had indirect effects via the number of pods per plant. Moreover, in agreement Iqbal *et al*. (2003) revealed the same result on plant height and hundred seed weight.

4.5.2. Direct and indirect effects of traits on seed yield at phenotypic level

The result of phenotypic correlation coefficients was partitioned into direct and indirect effects through various yield contributing traits (Table 4.10). The direct effects of days to maturity, plant height, and harvest index were high positive, while the number of pods per plant exhibited a positive direct effect classified as moderate. Traits like hundred seed weight and protein content had low positive direct effects whereas pod length exhibited positive negligible direct effects. On the other way, days to 50% flowering and seed filling period had a highly negative direct effect on seed yield. The phenotypic path coefficient analysis revealed that days to maturity exerted positive and maximum direct effect (0.652) on seed yield followed by harvest index (0.391). The maximum negative direct effect was contributed by days to 50% flowering (-0.697) followed by seed filling period (-0.583) while negligible negative direct effects were exhibited by the number of branches per plant (-0.041).

The highest phenotypic direct effect on days to maturity, followed by harvest index accompanied by maximum indirect effects of other traits via days to 50% flowering, plant height, the number of branches per plant, and the number of pods per plant (Table 4.10), established this trait to be the most important component trait of seed yield. Consequently,

such traits that had a positive direct effect, positive and significant phenotypic correlation with seed yield require considerable attention in the selection program. In the phenotypic path analysis, the residual effect (0.192) indicates that traits considered in the phenotypic path analysis could explain only 80.8% of the total variation in seed yield. The rest variation (19.2%) was contributed by other factors which are not considered in the current study. Similarly, Balla and Ibrahim (2017) indicated that considering five quantitative traits in path analysis and could sufficiently explained the variation in seed yield of studied soybean genotypes. Kumar *et al*. (2018b) also reported ten quantitative traits could well explained the total variation of the tested genotypes.

Previous research results indicated maximum phenotypic positive and negative direct effects on seed yield among soybean genotypes were recorded at the number of pods per plant and pod length, respectively by Deresse Hunde and Hirpa Legesse (2018). In disagreement with the present result, Satpute *et al*. (2016) made a report on days to 50% flowering (+), days to maturity (-), plant height (-), and the number of branches per plant (+), whereas similar results on the number of pods per plant and hundred seed weight. Aondover *et al*. (2013) indicated a similar report on days to 50% flowering and plant height, and a disagreement report on days to maturity, the number of branches per plant, and the number of pods per plant. Jain *et al*. (2015) and Mesfin Hailemariam (2018) reported similar findings of phenotypic direct effect with different magnitude of days to 50% flowering, days to maturity, number of pods per plant, and hundred seed weight on seed yield of soybean. A contrary report also made by, Jain *et al.* (2015) on plant height and number of branches per plant, Leite *et al*. (2016) on days to maturity and hundred seed weight, Deresse Hunde and Hirpa Legesse (2018) on days to 50% flowering, plant height, number of branches per plant, pod length, and harvest index, and Mesfin Hailemariam (2018) on harvest index.

In the present study, a high positive indirect effect was recorded from days to 50% flowering (0.429), plant height (0.327), number of branches per plant (0.350), and number of pods per plant (0.330) through the trait days to maturity. Furthermore, the current path analysis indicated, seed yield was positively and moderately indirectly affected by days to 50% flowering, number of branches per plant, and number of pods per plant through the trait plant height. Dissimilar results on the indirect phenotypic effect of plant height, number of pods per plant, pod length, and harvest index via days to maturity were

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reported by Deresse Hunde and Hirpa Legesse (2018). However, these authors also reported that days to 50% flowering and hundred seed weight had indirect effects through days to maturity. Contradict findings were also reported by Satpute *et al.* (2016) on the indirect effects of days to 50% flowering, and number of branches per plant via days to maturity; and days to 50% flowering and number of pods per plant through plant height. In harmony with the present result, Jain *et al.* (2015) on days to maturity, number of branches per plant, and number of pod per plant; Satpute *et al.* (2016) on hundred seed weight demonstrated phenotypic indirect effects via plant height.

Table 4.9. Estimates of direct (bold diagonal and underlined) and indirect effect (off diagonal) at genotypic level of 10 traits on seed yield in 81 soybean genotypes tested at Metema and West Armachiho in 2020

Traits	DF	DM	GFP	PH	BPP	PPP	PL	HSW	HI	PC	r_g
DF	**-0.034**	0.067	0.005	0.153	-0.057	0.164	-0.001	-0.065	0.395	0.051	0.678[***]
DM	-0.024	**0.093**	-0.001	0.123	-0.056	0.141	-0.002	-0.028	0.283	0.022	0.550[***]
GFP	0.020	0.014	**-0.009**	-0.073	0.016	-0.068	-0.001	0.058	-0.230	-0.047	-0.319[***]
PH	-0.025	0.055	0.003	**0.209**	-0.058	0.161	-0.001	-0.055	0.421	0.039	0.749[***]
BPP	-0.022	0.059	0.002	0.139	**-0.088**	0.162	-0.001	-0.032	0.337	0.024	0.578[***]
PPP	-0.025	0.060	0.003	0.155	-0.065	**0.217**	-0.001	-0.060	0.353	0.037	0.674[***]
PL	-0.003	0.027	-0.002	0.047	-0.025	0.024	**-0.005**	0.014	0.141	0.011	0.229[*]
HSW	0.021	-0.026	-0.005	-0.113	0.028	-0.128	-0.001	**0.101**	-0.296	-0.052	-0.471[***]
HI	-0.021	0.042	0.003	0.139	-0.047	0.121	-0.001	-0.047	**0.632**	0.060	0.881[***]
PC	-0.016	0.019	0.004	0.077	-0.020	0.077	-0.001	-0.051	0.363	**0.105**	0.557[***]
h^2	0.150										
r^2	0.850										

DF = Days to 50% Flowering, DM = Days to Maturity), GFP = Seed Filling Period (days), PH= Plant Height (cm), BPP = Number of Branches per Plant (No.), PPP = Number of Pods per Plant (No.), PL = Pod Length (cm), HSW(g) = Hundred Seed Weight, HI = Harvest Index (%), PC = protein Content (%), H^2 = Residual Effect, r^2 = Coefficient of Determination

Table 4.10. Estimates of direct (bold diagonal and underlined) and indirect effect (off diagonal) at phenotypic level of 10 traits on seed yield in 81 soybean genotypes tested at Metema and West Armachiho in 2020

Traits	DF	DM	GFP	PH	BPP	PPP	PL	HSW	HI	PC	r_p
DF	**-0.697**	0.429	0.340	0.227	-0.025	0.141	0.003	-0.044	0.193	0.071	0.637***
DM	-0.458	**0.652**	-0.133	0.166	-0.022	0.108	0.005	-0.014	0.116	0.031	0.451***
GFP	0.406	0.149	**-0.583**	-0.114	0.009	-0.066	0.002	0.042	-0.124	-0.058	-0.337***
PH	-0.478	0.327	0.201	**0.331**	-0.027	0.156	0.007	0.016	0.187	0.059	0.779***
BPP	-0.428	0.350	0.126	0.218	**-0.041**	0.147	0.006	0.017	0.158	0.041	0.553***
PPP	-0.461	0.330	0.181	0.241	-0.028	**0.213**	0.005	0.009	0.147	0.055	0.692***
PL	-0.092	0.148	-0.044	0.109	-0.010	0.045	**0.023**	0.065	0.039	0.019	0.303***
HSW	0.166	-0.049	-0.133	0.029	-0.004	0.011	0.008	**0.185**	-0.058	-0.021	0.135*
HI	-0.343	0.194	0.185	0.158	-0.017	0.080	0.002	-0.027	**0.391**	0.064	0.686***
PC	-0.320	0.130	0.220	0.127	-0.011	0.077	0.003	-0.025	0.162	**0.154**	0.517***
h^2	0.192										
r^2	0.808										

DF = Days to 50% Flowering, DM = Days to Maturity), GFP = Seed Filling Period (days), PH= Plant Height (cm), BPP = Number of Branches per Plant (No.), PPP = Number of Pods per Plant (No.), PL = Pod Length (cm), HSW(g) = Hundred Seed Weight, HI = Harvest Index (%), PC = protein Content (%), H^2 = Residual Effect, r^2 = Coefficient of Determination

4.6. Multivariate Analysis

4.6.1. Clustering of genotypes

The distribution of 81 tested soybean genotypes was partitioned into six distinct groups according to their similarities based on quantitative traits over the location (Table 4.11 and Figure 4.4). This result revealed that the existence of diversity among the studied genotypes. Cluster I was the largest cluster which consisted of 51 (62.96%) genotypes, followed by clusters III, II, IV, and VI comprised of 9 (11.11%), 8 (9.88%), 7 (8.64%), and 5 (6.17%) genotypes, respectively (Table 4.11 and Figure 4.4). The lowest number of genotypes in the cluster was recorded from cluster I which had only one genotype (singleton). The present finding demonstrated the presence of a high degree of divergence in the tested soybean genotypes.

Previous research work indicated the existence of diversity among soybean genotypes grouped in a different number of distinct clusters. Iqbal *et al*. (2008) and Oliveira *et al*. (2017) studied the genetic diversity of soybean genotypes using multivariate analysis and reported the soybean genotypes were originated from different sources. Marconato *et al*. (2016) examined soybean genotypes having a different origin and grouped them into 8 clusters and confirmed the diversity of the tested genotypes. Singh and Shrestha (2019) reported 5 clusters under testing soybean breeding lines. Similarly, six and eight clusters for soybean genotypes were reported by Dayaman (2007) and Varnica *et al*. (2018), respectively, indicating notable genetic divergence. Assessing the relationship between genetic diversity and relationships among genotypes simplifies the selection of parents with different genetic bases important for the breeding program (Souza and Sorrells, 1991). Genotypes grouped in a particular cluster signify their intimate relationship among themselves as compared to the other cluster groups. Hence, it could be likely that genotypes within a cluster are less genetically different from each other and diverse from the genotypes belonging to other clusters. The distribution of genotypes in the cluster and the relationships as displayed via dendrogram are presented in Table 4.11 and Figure 4.4.

Table 4.11. Distribution of genotypes into 6 clusters based on D^2 analysis for 81 soybean genotypes combined over location, 2020

Cluster	No. of genotypes	Proportion (%)	Genotypes/cluster membership
I	51	62.96	TGX2009-14F, Gishama, TGX2025-9E, TGX2016-2E, TGX2025-19E, Tgx-1990-40f, TGX2018-5E, TGX2013-2F, TGX2009-1F, TGX2027-4E, TGX2010-11F, TGX 2025-6E, TGX1988-5F, TGX2007-1F, TGX1993-4FN, TGX 2009-16F, TGX2020-1E, TGX2023-4E,TGX2017-5E, Tgx-1989-65f, TGX1951-4F, TGX2019-1E, TGX2011-6F, TGX2025-16E, TGX2016-3E, TGX1987-14F, Tgx-1987-28f, TGX2017-6E, TGX2016-4E, T34-15-T73-16-SD1, TGX2004-7F, TGX2025-10E, Tgx-1835-10E, Tgx-1919-22F, TGX2015-1E, TGX-1987-11F, Belessa-95, STGX2025-14E,TGX2023-1E, TGX2027-1E, TGX2008-4F, Tgx-1989-40F, Gizo,Tgx-1987-18F, Tgx-1988-5E,TGX1485-1D, TGX2022-4E, TGX2023-3E, TGX2004-13F, TGX2010-5F, Tgx-1990-5FP
II	8	9.88	TGX2007-3F, TGX1835-10E, TGX1989-19F, Tgx-1889-62F, Pawe-03, TGX2010-14F, TGX1987-10F, TGX2027-7E
III	9	11.11	T34-15-T72-16-Sc1, JM-ALM/H3-15-SC-1, Hawassa-04, Pawe-1, T44-15-T105-16Sc1, T47-15-T126-16-SF1, Afgat, Gozela, G7955-C3RPP(C1)
IV	7	8.64	F6U03-300134XLG04-5187, F6LG06-5920XU03-100612-03, F6LG04-6000XLG04-5187-04, F6LG04-6000XLG04-5187-03, F6LG06-5920XU03-100612-01, F6LG046000XLG04-5187-02, F6LG04-6000XLG04-5187-01
V	1	1.24	Andinet
VI	5	6.17	F6LG04-6000XLG04-5187-05, F6LG04-6000XLG04-5187-06, CRFRD-15-SE-2, CRFRD-15-SB, H3-15-SF-2
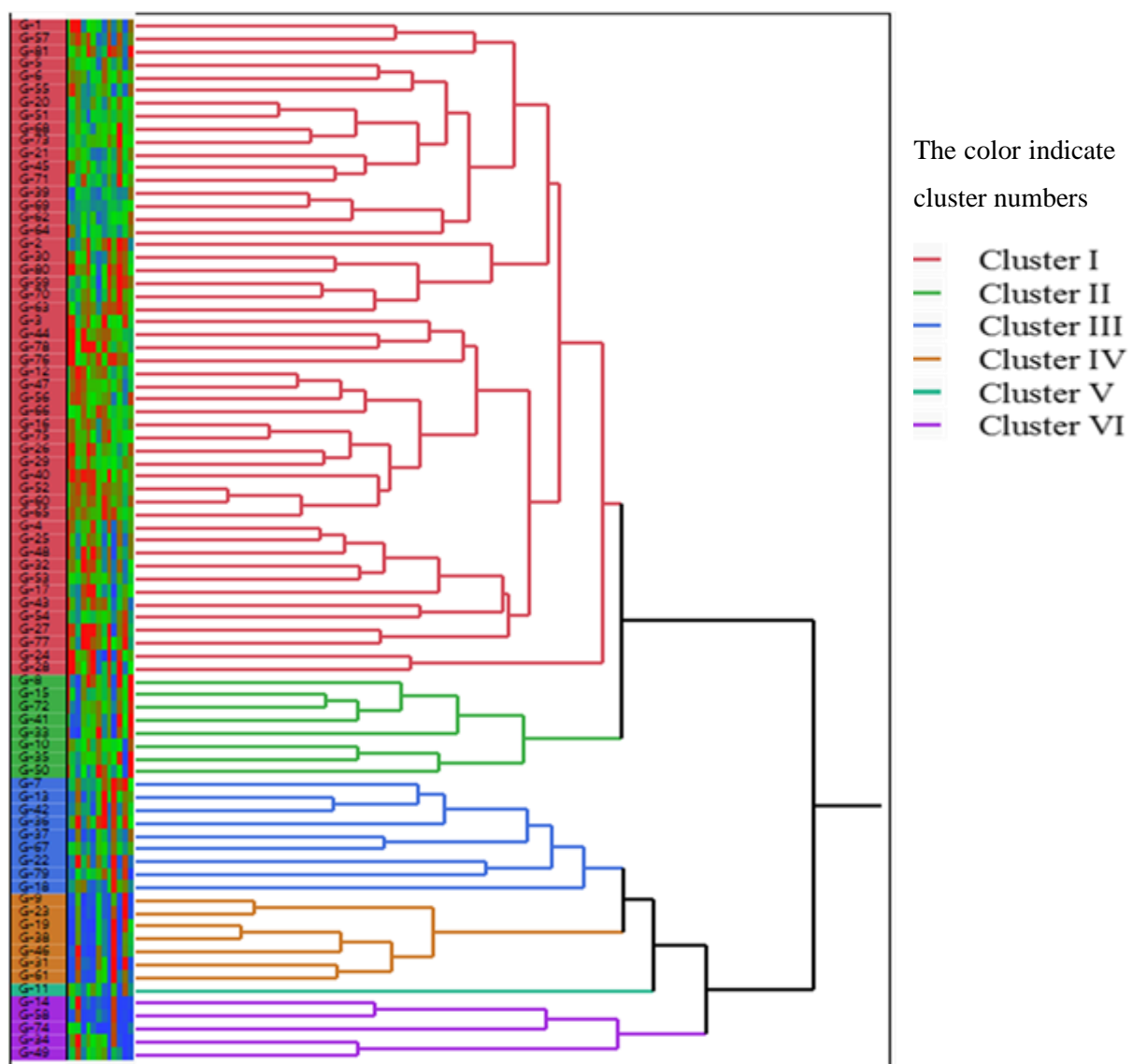
Figure 4.4. Dendrogram showing relationships among 81 soybean genotypes

4.6.2. Cluster means and distance analysis

The standardized Mahalanobis D^2 statistics revealed the presence of genetic differences between pairs of clusters, and the divergences between all pairs were significant and highly significant ($p \leq 0.05$ and $p \leq 0.01$) while intra-cluster divergences revealed a non-significant difference. The average intra- and inter-cluster D^2 values with their corresponding intra- and inter-cluster distance are presented in Table 4.12. The intra-cluster distance values were ranged from 1.91 (cluster IV) to 3.94 (cluster VI). All the intra-cluster distances were indicated a low D^2 value, indicated that there were more similarities than diversification within groups. In other ways, the genotypes grouped in a similar cluster are less divergent than those which are placed in a different cluster. In agreement with this result, Sharma *et al*. (2005) evaluated 62 Indian soybean varieties and found an intra-cluster distance of 0.0 to 4.43 D^2 values.

In inter-cluster distance analysis, the maximum inter-cluster distance was obtained in between cluster II and VI (D^2 =154.64[**]) followed by cluster II and IV (D^2 = 132.39[**]), cluster II and V (111.52[**]), and cluster I and VI (D^2 = 93.32[**]) (Table 4.12). The existence of a higher and significant inter-cluster distance between clusters in this study indicates the presence of considerable wider genetic diversity among the tested soybean genotypes. Moreover, it signifies genotypes grouped under maximum genetic diversity can be exploited in the future soybean selection and crossing programs to develop breeding lines with diverse genetic backgrounds. Thus, the genetic divergence detected in this study provides insights for the breeder to exploit the existing genetic variability for the improvement of soybean in the country.

The minimum inter-cluster distance (D^2 = 22.53[*]) was observed between clusters I and III, and cluster III and IV (D^2 =23.23[*]) followed by cluster I and II (D^2 = 23.70[*]), indicating the presence of closer proximity between these clusters (Table 4.12). Based on Dayaman (2007) were analyzed soybean genotypes in D^2 statistics using 22 morphological traits and grouped into 6 clusters, Salimi *et al*. (2012), reported 7 clusters of soybean genotypes based on nine agro-morphological and two qualitative seed traits, and successfully identified two drought-tolerant genotypes, and these genotypes could be exploited as a source of germplasm for drought tolerance soybean breeding. Adie and Krisnawati (2017) also clustered soybean genotypes in 10 clusters. Sharma *et al*. (2005) also found 15

clusters from soybean varieties and grouped 32 varieties in one group. In conclusion, genotypes in the cluster I, II and IV will potentially use as gene source for the development of soybean variety through hybridization.

Table 4.12. Pair-wise generalized intra- (bolded diagonal) and- inter (off-diagonal)-cluster distances (D^2) between cluster values of 81 soybean genotypes

Cluster	I	II	III	IV	V	VI
I	**2.53**					
II	23.70[*]	**2.53**				
III	22.53[*]	59.78[**]	**3.94**			
IV	77.35[**]	132.39[**]	23.23[*]	**1.91**		
V	64.04[**]	111.52[**]	35.18[**]	27.55[**]	**0**	
VI	93.32[**]	154.64[**]	63.21[**]	62.77[**]	56.84[**]	**3.08**

*= Significant at $p < 0.05$ for $x^2 = 21.03$; ** = significant at $p < 0.01$ for $x^2 = 26.22$ and ns = non-significant*

The mean value of all the 13 traits in each cluster group is presented in Table 4.13. The present cluster mean values indicated variations among the six clusters for different traits. Cluster I was mainly characterized by moderate mean values of traits and the highest cluster means estimates were exhibited for days to maturity, plant height, number of branches per plant, and seed yield. Furthermore, cluster I were characterized by long days to 50% flowering and days to maturity records. Cluster II was the third-largest cluster and characterized by having higher cluster mean values for days to 50% flowering, number of seeds per pod, harvest index, and protein content whereas lower cluster means for seed filling period and hundred seed weight were recorded at this cluster group. Traits like plant height, number of branches per plant, and seed yield had the second highest mean values under this cluster II group. Cluster III was characterized by the highest mean values for pod length and the second low and high value for the number of pods per plant and hundred seed weight, respectively. It is a fact that this cluster was the second-largest cluster which contains 9 genotypes.

In the current cluster analysis, higher cluster mean values for hundred seed weight and oil content were found at cluster IV. In this cluster,7 genotypes were included, and most of the lowest cluster mean values of traits were observed under this group. Cluster V had solely one genotype and the highest cluster mean for the number of pods per plant was recorded at this cluster. In this cluster, the second-lowest cluster mean for days to 50%

flowering, days to maturity, seed filling period, pod length, seed yield, and harvest index were recorded. This indicates particularly based on phenological records, the genotype grouped under this cluster was short maturing and important for earliness soybean breeding.

On the other way, cluster VI had 5 genotypes and was characterized by the highest cluster mean for the seed-filling period. However, this cluster had the lowest cluster mean value for the number of seeds per pod, seed yield, oil content, and protein content. Generally, cluster analysis grouped accessions having better morphological similarity, hence representative accessions from a cluster of groups could be chosen for hybridization breeding. A similar report was found by Khan *et al*. (2014) who indicated six clusters in testing 115 soybean genotypes and the clusters differed in mean values for almost all the recorded traits. However, Tiago *et al*. (2016) reported five clusters under testing 13 soybean genotypes.

Table 4.13. Mean values of 13 quantitative traits of the six clusters of 81 soybean genotypes for combined data tested at Metema and West Armachiho

Traits	Clusters					
	I	II	III	IV	V	VI
DF	56.16	59.13^{**}	43.61	36.50^{*}	57.30	43.62
DM	115.53^{**}	107.69	107.44	100.24^{*}	113.30	109.78
GFP	59.40	48.59^{*}	63.84	63.79	56.00	65.58^{**}
PH	88.29^{**}	84.90	67.19	49.71^{*}	61.80	55.16
BPP	4.99^{**}	4.54	3.96	1.83^{*}	4.30	3.72
PPP	68.24	62.45	41.50	27.87^{*}	70.60^{**}	42.80
SPP	2.61	2.84^{**}	2.70	2.67	2.60	2.50^{*}
PL	3.59	3.54	3.73^{**}	3.43	3.30^{*}	3.38
GY	3228.96^{**}	3023.18	2006.83	923.27	782.90	578.30^{*}
HSW	14.56	12.99^{*}	17.44	17.98^{**}	15.71	16.62
HI	0.4167	0.4300^{**}	0.3598	0.2570^{*}	0.2573^{*}	0.2667
OC	20.94	20.05	22.03	23.04^{**}	22.60	18.18*
PC	43.04	45.59^{**}	41.83	40.14	41.00	38.38^{*}

* and ** = lowest and highest value of cluster mean, DF = days to 50% flowering, DM = days to maturity, GFP = Seed Filling Period, PH = Plant Heigh, BPP = Number

4.7. Principal Component Analysis

The four principal components, PC1 to PC4, have accounted for 77.98% of the total variation among 81 genotypes of soybean (Table 4.14, Figure 4.5). It was observed that principal components 1, 2, 3, and 4 with Eigenvalue of 5.88, 1.73, 1.49, and 1.04 contributed 45.25%, 13.29%, 11.44%, and 8.00% of the total variation, respectively (Table 4.14).

In agreement with the current result, Yechalew Sileshi *et al*. (2019) reported that 82% of the total variation was explained among tested soybean genotypes by the first four principal components using 14 morphological traits. These authors also indicated that out of the total principal components, the highest variation was found at PC1. In addition, Vianna *et al*. (2013) reported that only four principal component explaining 71.6o% of the variance in the 11 original variables among soybean genotypes. However, Dubey *et al*. (2018b) explained 73.44% of the variation of soybean genotypes by the first five PCs, and from the first principal component, greater contribution was recorded. In other ways, Arora *et al*. (2017) found three principal components and contributed 79.37% of the total variation amongst genotypes evaluated for nine traits.

The first principal component (PC1) which contributed the highest variation was typically associated with traits like days to 50% flowering, plant height, seed yield, number of pods per plant, harvest index, and number of branches per plant with correlation values with the principal component of 0.372, 0.357, 0.356, 0.355, 0.336 and 0.311, respectively (Table 4.14). This indicated that the population with greater PC1 value is considered high yielding and formed by having long days to 50% flowering and plant height, and more seed yield, number of pods per plant, harvest index, and number of branches per plant. According to Iqbal *et al*. (2008), it is obvious that quantitative traits contributed positively to the first three PCs, and accordingly these could be given considerable importance for the genetic material under study. Hence, selection for traits under the first PC may be desirable and consideration have to be given. Vianna *et al*. (2013) and Marconato *et al*. (2016) reported similar results with the current study i.e., 71.60% and 71.07% contribution of the total variability by the first three PC in soybean genotypes, respectively. Wang *et al.* (2013) and Peric *et al*. (2014) found four and three PCs with cumulative contribution rates of 79.20%

and 92.13% among the tested soybean genotypes having twelve and nine traits, respectively.

In agreement with the current finding, Iqbal *et al.* (2008) reported on seed yield and harvest index, Marconato *et al.* (2016) on plant height, number of branches per plant, and number of pods per plant, and Dubey *et al.* (2018b) on days to 50% flowering, plant height, number of branches per plant, number of pods per plant and seed yield great contributions for the first PC. Disagreement with this result, Vianna *et al.* (2013) and Khan *et al.* (2014) found a higher contribution of the number of seeds per pod for the first PC while Dubey *et al.* (2018b) found hundred seed weight had a high contribution for the fifth PC. Jha *et al.* (2016) found only five PCs exhibited more than 1 Eigenvalue and indicated about 72.17% variability among the traits considered and mainly associated with traits like the number of pods per plant, days to 50% flowering, days to maturity, and plant height.

The main variables which explained the second principal component (PC2) of 13.29% retention of variance were pod length, seed filling period, hundred seed weight, days to maturity, and protein content with correlation values with the principal component of 0.521, 0.468, 0.399, 0.328 and -0.297, respectively (Table 4.14). Similarly, this result is consistent with Marconato *et al.* (2016) who indicated 20.30% of the total variance explained in PC2 was majorly by the seed-filling period. A similar result on protein content was reported by Miladinovic *et al.* (2006), and on days to maturity and hundred seed weight by Iqbal *et al.* (2008).

The third principal component (PC3), dominated by traits like the number of seeds per pod (0.575), oil content (0.482), seed filling period (-0.384), days to maturity (-0.362), and pod length (0.357). The fourth principal component was more associated with oil content, the number of seeds per pod, and pod length i.e., 0.655, -0.568, and -0.238, respectively (Table 4.14). Likewise, Dubey *et al.* (2018b) and Yechalew Sileshi *et al.* (2019) observed a higher contribution of the number of seeds per pod in the third PC. Moreover, Jha *et al.* (2016) found five PCs and off which the third- and- fourth PCs accounted for the variation of 10.15% and 8.27% were associated with the number of branches per plant, hundred seed weight, and harvest index; and hundred seed weight and harvest index, respectively which is a contrary to the current results.

Considering the first two principal components, PC1 (45.25%) and PC2 (13.29%), the data were analyzed on a two-dimensional plane, in which the distribution of traits and genotypes were grouped based on the bi-plot analysis is presented in Figure 4.5. Among the tested 81 soybean genotypes the maximum principal component scores for all the evaluated traits were estimated in these four principal components (Table 4.14). These scores can be used as indications for selection and decided by variability explained by each of the PCs. The maximum score of PCs for specific components indicates high values for the traits in those specific genotypes.

The result indicated that soybean genotypes G-58, G-19, G-23, G-31, G-46, G-38, G-61, G-14, and G-9 in PC1 indicating these genotypes had a high value of days to 50% flowering, plant height, number of branches per plant, number of pods per plant, seed yield and harvest index. This result is in line with the report of Yechalew Sileshi *et al.* (2019) on days to 50% flowering and plant height. In PC2 soybean genotypes Pawe-03, Pawe-01, G-41, G-78, G-8, G-15, and G-34 had high value for the trait days to 50% flowering, seed filling period, pod length, and hundred seed weight. Similarly, Yechalew Sileshi *et al.* (2019) found similar results on hundred seed weight. In PC3 genotypes include G-74, Pawe-03, G-14, G-24, G-28, G-1, G-57, and G-34 exhibited high values for days to maturity, seed filling period, seed per pod, pod length, and oil content. In the last PC, PC4 genotypes like G-59, G-50, G-49, G-30, G-80, Gizo, G-34, and G-55 had high values for the number of seeds per pod and oil content.

In this PC biplot analysis, the aggregation of traits and genotypes has presented in Figure 4.5. Genotypes such as G-27, G-59, G-32, G-28, and G-30 could be directly selected for seed yield improvement while G-32, G-59, and G-24 for days to 50% flowering, and G-78, G-40, G-16, G-44, and G-60 can be used for days to maturity improvements. For economic trait improvements such as the number of branches per plant by genotypes G-40, G-77, G-16, and G-50, and for plant height and number of pods per plant genotypes like G-28, G-27, G-77, and G-30 could be exploited, respectively.

In the tested genotypes, G-29, G-75, and G-6 are important for the number of seeds per pod, while pod length could be improved by the utilization of G-65, G-3, Gishama, and G-6 genotypes. Genotype G-34, G-13, Gozela, Afgat, Hawassa-04, and G-49 for hundred seed weight; G-8, G-48, G-24, G-25, G-17, G-4, G-45, G-10, G-35, G-72, and G-15 are

categorized as key genotypes for these trait improvements. However, the genotypes G-74, G-69, G-37, G-39, G-58, G-9, G-23, and Andinet are found in the fourth quadrant despite diverging from the others and had no outstanding variable that grouped them. A similar report was demonstrated by Vianna *et al*. (2013) and Marconato *et al*. (2016), who demonstrated potentially important traits could be exploited through principal component analysis.

Table 4.14. Eigenvectors, variance explained and Eigenvalues of the first four PCs of soybean genotypes evaluated over location, 2020

| Traits | Eigenvectors | | | |
	PC1	PC2	PC3	PC4
Days to 50% flowering	0.372	-0.061	-0.026	0.024
Days to maturity	0.283	0.328	-0.362	-0.107
Seed filling period (days)	-0.197	0.468	-0.384	-0.159
Plant height (cm)	0.357	0.123	0.071	0.021
Branch per plant	0.311	0.273	-0.073	0.082
Pod per plant	0.355	0.077	-0.092	-0.028
Seed per pod	0.043	0.098	0.575	-0.568
Pod length (cm)	0.080	0.521	0.357	-0.238
Seed yield (kg ha^{-1})	0.356	0.057	0.016	0.227
Hundred seed weight(g)	-0.283	0.399	0.007	0.177
Harvest index (%)	0.336	-0.0001	0.049	0.187
Oil content (%)	-0.064	0.205	0.482	0.655
Protein content (%)	0.247	-0.297	0.098	-0.166
Eigenvalue	5.88	1.73	1.49	1.04
Explained variance (%)	45.25	13.29	11.44	8.00
Cumulative variance (%)	45.25	58.54	69.98	77.98

Table 4.15. Traits having values greater than 0.3 in each PCs over the combined location, 2020

PC1	PC2	PC3	PC4
Days to 50% flowering	Days to maturity	Days to maturity	Seed per pod
Plant height	Seed filling period	Seed filling period	Oil content
Branch per plant	Pod length	Seed per pod	-
Pod per plant	Hundred seed weight	Pod length	-
Seed yield	-	Oil content	-
Harvest index	-	-	-

Figure 4.5. Biplot of PC1 and PC2 showing the relationships of genotypes by traits. The red in circled color represents genotypes (n=81) and the black color represents the traits understudy. The number representation is as indicated in Appendix Table 1.
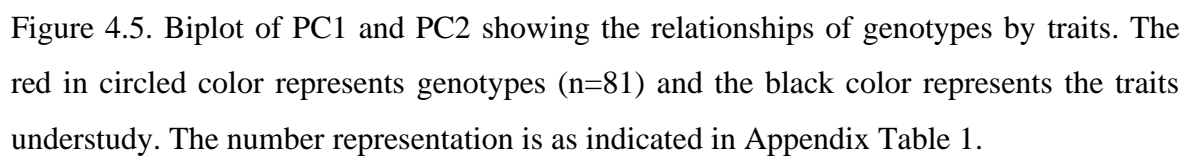
Chapter 5. CONCLUSION AND RECOMMENDATIONS

5.1. Conclusion

The results of Shannon diversity index for seven qualitative traits indicated that the average diversity index was 0.496, indicating the existence of adequate diversity on the tested genotypes.

The combined analysis of variances showed highly significant differences among the tested genotypes, indicating the presence of adequate genetic variability for improvement through selection. Hence, this provides an opportunity for future soybean improvement program and utilization of genotypes that were highly performing in economical traits genotypes. The genotype x location interaction effects were also highly significant for most of studied traits, suggesting a differential response of the genotypes and this might arise from the environmental variations of the two locations. So, evaluating soybean genotypes across location has to be taken consideration in future soybean breeding.

PCV was slightly higher than GCV for most of the studied traits, indicated the minimal influence of the environmental factors and presence of high genetic variability for the traits which is helpful to facilitate phenotypic selection. High values of PCV and GCV were obtained from traits viz., plant height, number of branches per plant, number of pods per plant, and seed yield. This confirms the existence of possibilities to improve these traits of the tested genotypes through phenotypic selection. High heritability estimates were observed for days to flowering, plant height, days to maturity, number of branches per plant, number of pods per plant, oil content, hundred seed weight, protein content and seed yield, hence, it can be suggested the possibilities for improvement of these traits by direct selection methods.

In combined correlation analysis, seed yield had positive and highly significant with days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, and protein content at phenotypic and genotypic correlations. This indicates that desirable traits could be improved simultaneously through indirect selection for soybean yield improvement. Path coefficient analysis both at phenotypic and genotypic level

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revealed high positive direct effect of plant height, number of pods per plant, and harvest index on seed yield, indicating major contribution of these traits in seed yield and would be considered to get desirable improvement in soybean.

The 81 soybean genotypes grouped into six clusters based on their similarity. The maximum inter-cluster distance was attained in between clusters II and VI. Therefore, cluster II and VI genotypes could be applied for the crossing program with considering other qualitative traits in soybean improvement. In principal component analysis, it was observed that the first four principal components accounted for 77.98% of the total variation among the tested 81 soybean genotypes. This indicates that evaluated traits could explain substantial portion of the overall diversity among the genotypes and confirms the potential for future improvement via directional selection and hybridization.

5.2. Recommendations

It can be recommended that intercrossing among the genotype belonging to genetically diverse clusters (II and VI) and genotypes showing superior mean performance could be applied for the improvement program with considering other qualitative traits in soybean improvement. Generally, in the current finding, genotypes showing superior mean performance were observed and should be considered for the improvement of soybean to increase production, particularly in West Gondar lowland areas. However, it is advisable that repeating over the season and exploring molecular means are required to make sound recommendations and confirmation of the present finding.

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APPENDIX

Appendix Table 1. List of 81 soybean genotypes used in the current study

Code	Genotype designation	Source/origin	Source of seed	Code	Genotype designation	Source/origin	Source of seed
G-1	TGX2009-14F	IITA	JARC	G-25	TGX1988-5F	IITA	JARC
G-2	Gishama	RV	GARC	G-26	TGX2007-1F	IITA	JARC
G-3	TGX2025-9E	IITA	JARC	G-27	TGX1993-4FN	IITA	JARC
G-4	TGX2016-2E	IITA	JARC	G-28	TGX 2009-16F	IITA	JARC
G-5	TGX2025-19E	IITA	JARC	G-29	TGX2020-1E	IITA	JARC
G-6	Tgx-1990-40f	IITA	PARC	G-30	TGX2023-4E	IITA	JARC
G-7	T34-15-T72-16-Sc1	IITA	PARC	G-31	F6LG04-6000XLG04-5187-02	IITA	JARC
G-8	TGX2007-3F	IITA	JARC	G-32	TGX2017-5E	IITA	JARC
G-9	F6U03-300134XLG04-5187	IITA	JARC	G-33	Pawe-03	RV	GARC
G-10	TGX2010-14F	IITA	JARC	G-34	CRFRD-15-SB	USA	PARC
G-11	Andinet	RV	PARC	G-35	TGX1987-10F	IITA	JARC
G-12	TGX2018-5E	IITA	JARC	G-36	Pawe-1	RV	PARC
G-13	JM-ALM/H3-15-SC-1	Jima	JARC	G-37	T44-15-T105-16Sc1	IITA	JARC
G-14	F6LG04-6000XLG04-5187-05	IITA	JARC	G-38	F6LG04-6000XLG04-5187-03	IITA	JARC
G-15	TGX1834-10E	IITA	PARC	G-39	Tgx-1989-65f	IITA	PARC
G-16	TGX2013-2F	IITA	JARC	G-40	TGX1951-4F	IITA	JARC
G-17	TGX2009-1F	IITA	JARC	G-41	Tgx-1889-62f	IITA	PARC
G-18	G7955-C3RPP(C1)	USA	Pawe	G-42	Hawassa-04	RV	GARC
G-19	F6LG04-6000XLG04-5187-04	IITA	JARC	G-43	TGX2019-1E	IITA	JARC
G-20	TGX2027-4E	IITA	JARC	G-44	TGX2011-6F	IITA	JARC
G-21	TGX2010-11F	IITA	JARC	G-45	TGX2025-16E	IITA	JARC
G-22	Afgat	RV	GARC	G-46	F6LG06-5920XU03-100612-01	IITA	JARC
G-23	F6LG06-5920XU03-100612-03	IITA	JARC	G-47	TGX2016-3E	IITA	JARC
G-24	TGX 2025-6E	IITA	JARC	G-48	TGX1987-14F	IITA	JARC

Appendix Table 1. List of 81 soybean genotypes used in the current study (Cont'd)

Code	Genotype designation	Source/origin	Source of seed	Code	Genotype designation	Source/origin	Source of seed
G-49	H3-15-SF-2	USA	PARC	G-73	Tgx-1988-5E	IITA	PARC
G-50	TGX2027-7E	IITA	JARC	G-74	CRFRD-15-SE-2	USA	PARC
G-51	Tgx-1987-28f	IITA	PARC	G-75	TGX1485-1D	IITA	JARC
G-52	TGX2017-6E	IITA	JARC	G-76	TGX2022-4E	IITA	JARC
G-53	TGX2016-4E	IITA	JARC	G-77	TGX2023-3E	IITA	JARC
G-54	T34-15-T73-16-SD1	IITA	JARC	G-78	TGX2004-13F	IITA	JARC
G-55	TGX2004-7F	IITA	JARC	G-79	Gozela	RV	PARC
G-56	TGX2025-10E	IITA	JARC	G-80	TGX2010-5F	IITA	JARC
G-57	Tgx-1835-10E	IITA	JARC	G-81	Tgx-1990-5FP	IITA	PARC
G-58	F6LG04-6000XLG04-5187-06	IITA	JARC				
G-59	Tgx-1919-22F	IIAT	PARC				
G-60	TGX2015-1E	IITA	PARC				
G-61	F6LG04-6000XLG04-5187-01	IITA	JARC				
G-62	TGX-1987-11F	IITA	PARC				
G-63	Belessa-95	RV	GARC				
G-64	TGX2025-14E	IITA	JARC				
G-65	TGX2023-1E	IITA	JARC				
G-66	TGX2027-1E	IITA	JARC				
G-67	T47-15-T126-16-SF1	IITA	JARC				
G-68	TGX2008-4F	IITA	JARC				
G-69	Tgx-1989-40F	IITA	IITA				
G-70	Gizo	RV	GARC				
G-71	Tgx-1987-18f	IITA	PARC				
G-72	TGX1989-19F	IITA	JARC				

RV = Released Variety in Ethiopia, GARC, JARC and PARC= Gondar, Jimma and Pawe Agricultural Research Center, respectively

Appendix Table 2. Mean performance values of 81 soybean genotypes tested at Metema

Gen	Trait												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-1	53.0	121.0	68.0	75.7	5.0	64.4	2.7	4.4	4917.6	15.7	0.443	18.4	46.0
G-2	53.5	107.0	53.5	108.0	6.3	78.0	2.6	3.7	5243.7	16.7	0.483	23.2	39.7
G-3	68.0	120.5	52.5	109.9	6.5	84.9	2.6	4.1	3810.8	17.6	0.413	22.4	43.0
G-4	65.0	116.5	51.5	91.9	5.7	103.4	2.6	3.4	4540.0	13.0	0.468	20.3	43.7
G-5	62.0	115.5	53.5	97.6	4.8	83.0	2.6	4.1	4544.6	16.3	0.468	19.0	44.8
G-6	56.0	115.0	59.0	101.8	3.6	81.9	2.7	4.1	4214.9	17.2	0.506	19.8	44.5
G-7	48.5	115.0	66.5	78.6	3.6	54.5	2.5	4.0	4087.7	20.0	0.446	23.3	42.4
G-8	67.0	109.5	42.5	112.6	6.9	120.7	2.7	3.5	4613.3	12.9	0.431	20.6	46.4
G-9	40.5	99.0	58.5	47.8	2.5	45.8	2.8	3.9	1587.2	17.2	0.282	24.3	38.1
G-10	63.0	114.0	51.0	95.6	5.9	71.7	2.7	3.6	4335.1	16.7	0.439	18.4	46.4
G-11	62.0	113.5	51.5	71.7	7.2	135.6	2.3	3.4	1041.4	17.6	0.283	23.0	42.5
G-12	49.5	115.0	65.5	113.3	5.1	112.9	2.6	3.9	4006.1	15.7	0.519	20.0	42.9
G-13	42.0	105.5	63.5	59.9	3.8	54.4	2.7	4.3	3946.0	20.0	0.436	22.7	43.7
G-14	41.0	108.5	67.5	61.7	3.1	37.9	2.4	3.2	633.4	21.0	0.225	18.4	38.9
G-15	68.0	114.5	46.5	107.4	3.7	69.2	2.7	3.7	3670.8	13.4	0.361	20.8	46.2
G-16	62.0	116.5	54.5	104.9	5.9	80.5	2.4	3.8	4560.0	17.0	0.523	20.3	44.1
G-17	60.5	105.0	44.5	114.3	6.2	99.8	2.6	3.5	2652.2	12.7	0.352	21.1	43.2
G-18	46.5	101.5	55.0	118.7	3.5	37.9	2.7	3.8	3778.4	20.4	0.450	21.4	41.5
G-19	39.0	99.5	60.5	55.5	1.1	24.7	2.9	3.9	1485.3	21.6	0.236	23.3	42.2
G-20	48.5	112.5	64.0	78.7	3.9	89.4	2.7	3.5	3933.6	16.4	0.380	20.4	43.8
G-21	51.0	113.0	62.0	89.3	4.4	46.1	2.3	3.4	4138.4	15.4	0.477	20.7	44.2
G-22	40.0	111.0	71.0	83.8	5.5	53.3	2.9	3.9	1948.9	19.7	0.305	24.1	41.2
G-23	37.5	103.0	65.5	53.4	2.7	37.9	3.0	4.0	1359.3	19.3	0.240	25.2	37.4
G-24	66.5	124.0	57.5	94.5	6.8	130.4	2.3	3.1	4675.9	13.5	0.506	20.6	44.3
G-25	66.0	115.5	49.5	90.6	4.7	91.3	2.6	3.4	3725.3	14.2	0.426	19.1	44.8
G-26	64.5	120.0	55.5	97.6	7.1	106.9	2.5	3.6	3549.7	17.7	0.320	20.4	45.8
G-27	67.00	121.0	54.0	124.9	6.6	119.0	2.9	3.7	4547.2	12.5	0.400	22.4	42.6

Appendix Table 2. Mean performance values of 81 soybean genotypes tested at Metema (Cont'd)

Gen	Trait												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-28	67.00	128.0	61.0	89.5	6.7	125.4	2.5	3.7	4798.5	15.5	0.501	19.4	42.8
G-29	65.50	120.5	55.0	100.9	6.1	70.4	2.8	4.0	3352.3	16.9	0.340	21.8	43.9
G-30	64.00	116.5	52.5	90.4	6.8	57.1	2.5	3.5	4786.4	17.2	0.488	22.7	41.8
G-31	38.50	106.0	67.5	63.4	2.3	31.0	3.0	4.0	1066.8	20.8	0.243	24.8	36.2
G-32	58.00	115.5	57.5	133.5	5.9	95.7	2.8	3.6	4132.2	15.8	0.458	19.3	44.0
G-33	63.00	104.0	41.0	92.3	4.2	72.4	3.1	3.7	3769.5	12.1	0.424	20.2	47.4
G-34	47.50	116.0	68.5	86.8	6.3	85.0	2.7	3.7	1041.7	20.0	0.244	17.8	38.6
G-35	59.00	114.5	55.5	95.8	4.9	90.8	2.9	3.6	4262.0	17.0	0.502	18.3	46.7
G-36	46.50	115.5	69.0	74.4	7.3	70.4	2.8	3.9	2737.0	21.3	0.364	22.6	44.6
G-37	39.50	103.0	63.5	58.1	3.2	34.1	3.1	4.2	2106.6	19.0	0.340	20.4	45.3
G-38	37.00	103.0	66.0	61.4	1.7	41.6	2.9	3.8	1335.7	20.5	0.226	22.2	42.4
G-39	44.50	103.5	59.0	83.2	3.6	50.7	2.6	3.9	3670.7	15.1	0.245	19.7	45.4
G-40	59.00	122.5	63.5	122.5	6.9	93.3	2.6	3.6	5666.8	16.7	0.519	21.1	43.7
G-41	54.50	107.5	53.0	93.6	4.7	85.4	3.0	3.6	3462.3	12.0	0.466	20.3	47.2
G-42	47.50	113.5	66.0	81.8	4.7	45.5	2.8	4.2	2228.1	19.7	0.349	23.2	43.8
G-43	65.50	114.0	48.5	113.6	5.8	109.9	2.7	3.8	3257.7	14.3	0.302	22.0	39.5
G-44	68.00	126.0	58.0	120.1	6.1	86.2	2.6	3.7	3872.3	18.5	0.383	20.0	42.9
G-45	65.00	118.5	53.5	97.6	7.0	82.9	2.6	3.5	4451.3	16.5	0.517	19.7	43.9
G-46	38.50	103.0	64.5	56.4	1.2	26.5	3.2	4.2	1487.6	20.5	0.277	22.4	43.4
G-47	53.00	118.0	65.0	112.2	6.2	82.9	2.8	3.9	4121.6	17.3	0.458	19.4	42.6
G-48	66.50	117.0	50.5	115.7	6.4	108.5	2.8	3.4	4014.7	12.7	0.412	20.1	45.1
G-49	48.00	111.0	63.0	69.6	5.2	72.1	2.8	3.6	393.2	14.4	0.229	18.0	38.1
G-50	64.00	112.5	48.5	93.0	3.6	64.5	3.2	3.9	3619.7	14.9	0.442	18.1	46.5
G-51	46.00	111.5	65.5	84.2	2.5	63.8	2.6	3.6	3384.7	16.2	0.343	20.1	43.9
G-52	52.00	118.0	66.0	98.4	6.6	99.2	2.7	3.7	4269.4	18.8	0.475	20.2	44.3
G-53	57.00	113.0	56.0	109.0	6.4	79.9	2.5	3.5	4154.7	15.8	0.467	20.0	42.3
G-54	59.50	107.5	48.0	100.9	5.6	65.6	2.7	3.7	3872.2	15.1	0.350	22.7	41.2

Appendix Table 2. Mean performance values of 81 soybean genotypes tested at Metema (Cont'd)

Gen	Trait												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-55	60.50	117.5	57.0	83.0	3.6	66.1	2.6	3.7	4654.2	14.7	0.459	19.3	44.9
G-56	54.50	118.0	63.5	102.4	5.3	75.7	2.6	3.9	3926.9	14.7	0.388	19.5	45.6
G-57	53.50	118.5	65.0	100.2	6.9	69.7	2.5	3.7	4262.7	15.1	0.512	19.8	44.1
G-58	39.00	102.0	63.0	51.9	2.3	39.9	2.8	3.6	1307.5	19.6	0.242	18.0	37.3
G-59	60.50	113.0	52.5	93.2	6.9	65.5	2.3	3.6	4747.5	18.1	0.526	22.7	45.0
G-60	53.50	118.5	65.0	95.6	6.8	88.8	2.6	3.9	3884.1	17.3	0.443	20.1	44.9
G-61	38.00	101.5	63.5	55.6	1.9	40.3	2.8	4.2	1482.5	20.6	0.223	22.9	41.0
G-62	55.00	109.5	54.5	96.6	4.2	82.3	2.6	3.6	2971.2	17.6	0.325	20.7	44.7
G-63	60.50	114.0	53.5	108.4	7.2	77.7	2.5	4.2	4218.8	18.9	0.444	22.2	42.7
G-64	67.50	118.5	51.0	95.3	4.0	87.0	2.4	3.5	3130.1	16.2	0.289	20.2	45.1
G-65	59.00	117.5	58.5	103.6	5.8	71.4	2.7	4.2	4396.8	19.0	0.500	20.5	44.0
G-66	50.00	114.5	64.5	111.8	5.2	77.9	2.8	4.0	3578.8	17.0	0.492	20.6	42.9
G-67	47.00	113.5	66.5	76.3	5.0	55.7	2.7	3.7	2908.0	19.2	0.361	20.7	45.2
G-68	50.00	114.5	64.5	85.5	5.0	55.6	2.6	3.7	4088.6	17.3	0.517	21.2	43.3
G-69	49.50	106.0	56.5	85.4	4.7	65.0	2.4	3.5	3424.3	16.7	0.371	21.5	43.1
G-70	51.50	113.5	62.0	99.9	6.9	80.9	2.5	3.9	4263.2	17.3	0.465	20.3	45.5
G-71	59.50	113.5	54.0	114.3	5.1	63.8	2.5	3.2	3978.8	16.2	0.482	20.4	43.6
G-72	63.00	107.5	44.5	99.6	5.7	81.0	2.8	3.5	3273.9	13.1	0.378	20.1	46.1
G-73	48.50	110.5	62.0	86.2	5.4	79.7	2.8	4.0	3815.0	17.7	0.427	20.9	42.8
G-74	55.00	115.5	60.5	52.5	3.9	42.0	2.4	3.4	388.9	19.1	0.221	18.0	40.0
G-75	61.00	118.0	57.0	101.0	6.0	67.0	2.5	4.1	4670.2	16.9	0.407	20.6	43.5
G-76	69.00	125.5	56.5	100.2	6.4	87.0	2.8	3.7	4622.8	20.1	0.436	21.5	44.2
G-77	66.00	114.0	48.0	130.6	7.5	83.3	2.6	3.8	3901.6	17.1	0.348	23.1	41.2
G-78	67.50	124.0	56.5	124.6	7.9	108.0	2.6	4.0	3651.5	17.7	0.464	21.3	41.7
G-79	45.50	107.5	62.0	86.7	5.4	85.0	2.9	4.2	3193.7	20.9	0.299	24.1	37.4
G-80	65.00	125.0	60.0	105.1	6.9	66.9	2.5	4.1	5089.3	18.8	0.481	22.7	42.0
G-81	48.00	117.0	69.0	99.8	6.3	82.9	2.6	4.0	4704.3	19.9	0.381	19.2	46.5

Appendix Table 2. Mean performance values of 81 soybean genotypes tested at Metema (Cont'd)

Gen	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
								Trait					
Mean	55.05	113.3	58.3	92.4	5.2	74.7	2.7	3.7	3498.7	8.3	0.395	20.9	43.2
CV (%)	2.18	1.7	3.8	6.8	13.3	12.3	9.8	9.8	6.2	17.1	4.8	5.2	2.4
$THSD_{0.05}$	5.33**	8.39**	10.00**	28.06**	3.05**	41.01**	1.16NS	1.64NS	958.87**	6.28**	0.085**	4.78**	4.65**

Gen = Genotypes, DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH = Plant height (cm), BPP = Branches per Plant, PPP = Pods per Plant, SPP = Seed per Pod, PL = Pod Length (cm), GY = Seed Yield (kg ha-1), HSW = Hundred Seed Weigh t(g), HI = Harvest Index, OC = Oil content, and PC = Protein Content, THSD = Tukey's Honestly Significant Difference, *, ** significant at 0.05 and 0.01 probability levels, respectively

Appendix Table 3. Mean performance values of 81 soybean genotypes tested at West Armachiho

Gen	Trait												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-1	53.0	122.0	69.0	51.8	4.0	59.6	2.9	3.9	1780.0	11.2	0.385	19.6	42.4
G-2	47.5	103.0	55.5	69.2	5.5	33.4	2.8	3.9	3237.1	15.2	0.500	22.6	41.4
G-3	59.0	119.5	60.5	68.1	4.9	36.4	2.8	3.9	1181.4	13.1	0.348	23.6	40.9
G-4	56.5	117.5	61.0	79.9	3.9	65.8	2.6	3.3	2661.0	12.6	0.386	20.3	43.0
G-5	53.0	114.5	61.5	66.5	4.0	29.1	2.2	3.6	1131.9	11.8	0.347	19.4	43.6
G-6	52.0	118.5	66.5	71.5	2.6	32.4	2.5	3.5	1485.3	12.8	0.340	21.8	41.9
G-7	44.0	104.5	60.5	58.7	3.7	43.1	2.6	3.7	1973.3	16.5	0.430	23.3	42.7
G-8	58.0	103.0	45.0	66.8	5.6	41.7	2.7	3.6	2441.4	11.3	0.500	20.9	46.2
G-9	40.5	104.5	64.0	33.6	2.1	21.6	2.3	2.6	501.8	14.5	0.253	23.2	38.2
G-10	54.0	116.5	62.5	62.9	4.7	32.1	2.8	3.5	1224.8	13.0	0.339	19.2	42.6
G-11	52.5	113.0	60.5	51.8	3.4	25.5	2.3	3.1	424.4	13.8	0.232	22.2	41.5
G-12	50.0	120.0	70.0	84.4	3.9	28.0	2.9	3.7	918.9	12.5	0.280	20.2	41.3
G-13	38.5	104.0	65.5	46.5	3.5	23.5	2.7	3.8	1018.3	15.3	0.319	21.5	43.0
G-14	37.5	112.0	74.5	45.9	2.9	22.4	2.4	3.2	322.2	13.5	0.247	18.1	37.5
G-15	59.0	107.5	48.5	75.2	3.7	36.9	2.6	3.4	2492.8	11.6	0.477	21.5	44.8
G-16	53.0	119.5	66.5	80.1	5.4	68.0	2.5	3.8	2051.8	12.6	0.268	20.4	43.6
G-17	51.5	111.5	60.0	82.4	5.9	79.2	2.5	3.3	1952.9	9.9	0.370	22.2	41.9
G-18	44.0	114.5	70.5	66.8	2.1	34.8	2.3	2.8	1141.5	14.9	0.363	22.7	39.9
G-19	32.5	96.5	64.0	43.3	1.5	20.1	2.3	2.8	385.8	16.0	0.227	22.6	42.1
G-20	48.5	110.0	61.5	57.2	2.8	52.8	2.4	3.3	2471.6	13.6	0.478	21.4	42.0
G-21	51.5	113.5	62.0	75.6	3.5	38.4	2.5	3.4	1487.5	12.7	0.405	20.8	43.6
G-22	36.0	103.0	67.0	62.8	5.2	23.3	2.7	3.1	507.5	15.8	0.257	21.5	38.3
G-23	37.0	96.0	59.0	36.5	2.1	18.4	2.2	2.6	488.2	14.7	0.243	23.7	40.1
G-24	57.5	122.0	64.5	77.9	4.2	79.1	2.4	3.2	3530.3	10.8	0.391	21.2	42.2
G-25	57.0	112.0	55.0	75.8	6.2	57.7	2.7	3.2	1834.3	10.2	0.440	19.8	43.2
G-26	55.0	122.5	67.5	77.0	5.2	58.6	2.7	3.9	2403.1	12.0	0.364	21.0	43.1
G-27	59.0	117.0	58.0	105.4	5.6	75.5	2.6	3.3	3923.0	10.7	0.450	23.6	40.5

Appendix Table 3. Mean performance values of 81 soybean genotypes tested at West Armachiho (Cont'd)

Gen	Trait												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-28	58.0	121.5	63.5	69.9	4.3	60.7	2.3	3.3	2468.4	12.9	0.471	19.6	42.3
G-29	56.5	116.5	60.0	71.1	5.3	62.9	2.4	3.3	1596.7	13.4	0.382	22.4	43.1
G-30	55.0	119.5	64.5	74.4	5.0	42.7	2.2	3.3	2269.9	14.6	0.411	22.1	42.3
G-31	32.0	96.0	64.0	53.5	2.6	27.1	2.5	3.3	505.8	17.3	0.230	22.8	41.2
G-32	53.5	117.5	64.0	93.0	5.2	70.4	2.5	3.2	2637.5	10.6	0.412	19.8	41.4
G-33	54.5	96.0	41.5	73.3	5.2	57.3	3.0	3.2	2510.8	9.8	0.445	21.5	44.9
G-34	39.5	114.5	75.0	54.2	5.5	24.3	2.8	3.8	385.2	18.2	0.304	18.2	37.2
G-35	53.5	105.0	51.5	72.8	4.3	35.8	2.6	3.4	1976.4	13.2	0.410	18.0	46.8
G-36	46.5	114.0	67.5	55.1	7.1	42.1	2.9	4.1	746.5	15.4	0.387	25.3	40.5
G-37	38.0	101.5	63.5	40.8	2.7	21.2	2.2	2.8	768.8	14.5	0.345	18.6	43.2
G-38	32.5	91.5	59.0	43.6	1.3	17.6	2.3	2.9	337.5	15.6	0.261	21.5	41.1
G-39	42.5	99.5	57.0	64.1	4.1	37.0	2.2	3.1	1338.0	13.3	0.409	20.2	42.9
G-40	54.5	120.5	66.0	84.9	4.8	80.1	2.8	3.7	3331.3	13.8	0.326	20.7	43.5
G-41	54.0	97.0	43.0	78.5	3.2	42.9	2.5	3.3	2649.0	10.0	0.456	21.7	44.4
G-42	39.5	99.5	60.0	57.4	2.6	21.3	2.6	3.8	608.9	15.1	0.300	21.6	40.5
G-43	57.0	114.5	57.5	77.0	4.0	56.6	2.8	3.7	1716.6	11.5	0.439	22.1	40.1
G-44	59.5	123.5	64.0	94.4	3.6	51.4	3.0	3.9	3017.7	12.8	0.409	20.9	40.1
G-45	56.0	116.0	60.0	65.9	3.3	32.6	2.4	3.4	1249.8	12.7	0.370	21.2	41.7
G-46	33.5	104.5	71.0	41.6	1.0	19.2	2.3	2.6	385.2	15.6	0.244	21.6	39.7
G-47	49.0	116.0	67.0	79.7	3.3	48.4	2.6	3.3	2107.5	12.6	0.373	19.7	40.9
G-48	58.0	115.0	57.0	91.7	3.5	78.7	2.7	3.4	2861.7	10.9	0.407	20.5	42.6
G-49	42.0	109.5	67.5	56.7	3.9	31.9	2.9	3.8	290.4	14.3	0.447	18.0	38.7
G-50	55.5	108.5	53.0	66.1	2.2	39.6	2.8	3.7	1256.7	12.7	0.327	19.5	44.4
G-51	48.5	107.5	59.0	60.6	2.2	49.4	2.6	3.5	2605.1	12.9	0.469	21.3	42.6
G-52	51.0	116.0	65.0	80.5	4.8	73.5	2.7	3.8	2537.3	13.5	0.367	20.8	42.6
G-53	53.5	112.5	59.0	69.5	4.8	52.5	2.8	3.8	2294.7	10.8	0.350	19.6	41.7
G-54	52.0	111.0	59.0	62.7	2.8	40.8	2.7	3.5	2048.7	12.2	0.494	23.0	40.9

Appendix Table 3. Mean performance values of 81 soybean genotypes tested at West Armachiho (Cont'd)

Gen	Trait												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-55	54.0	122.5	68.5	53.2	2.3	37.3	2.7	3.7	1002.1	10.4	0.269	19.2	43.7
G-56	51.0	119.0	68.0	84.9	4.1	44.8	2.8	3.6	2629.7	11.6	0.373	20.0	44.0
G-57	48.5	115.5	67.0	77.0	4.4	56.6	2.2	3.1	2904.4	10.7	0.372	20.0	43.4
G-58	34.5	101.0	66.5	36.6	1.0	18.3	2.2	3.0	321.0	15.0	0.233	19.0	37.1
G-59	51.5	107.0	55.5	69.5	3.3	42.6	2.2	3.6	2775.3	14.4	0.475	23.3	43.1
G-60	52.5	116.5	64.0	78.0	4.3	68.0	2.8	3.8	2779.2	14.0	0.396	20.6	43.9
G-61	33.5	99.0	65.5	50.3	1.4	18.0	2.5	3.0	517.4	17.6	0.416	21.7	38.3
G-62	51.5	105.0	53.5	67.3	3.0	46.6	2.1	3.1	1784.1	12.5	0.428	21.6	44.0
G-63	55.5	110.5	55.0	77.3	3.7	67.5	2.5	3.4	3014.6	15.1	0.474	22.7	43.0
G-64	58.5	114.0	55.5	64.6	2.7	27.4	2.7	3.3	1341.4	13.1	0.371	21.1	42.9
G-65	53.0	119.0	66.0	86.5	4.3	62.0	2.7	3.7	2284.5	15.6	0.301	21.0	42.4
G-66	53.0	109.0	56.0	79.3	4.0	54.4	2.9	3.7	1938.3	12.2	0.303	20.8	43.4
G-67	51.5	108.0	56.5	53.0	2.6	21.2	2.7	3.4	797.9	14.1	0.386	19.5	41.6
G-68	47.5	107.5	60.0	71.0	2.7	29.7	2.7	3.5	1826.9	13.1	0.434	20.2	43.0
G-69	50.5	103.5	53.0	59.0	2.6	27.4	2.5	3.3	1210.7	12.4	0.328	20.0	42.5
G-70	48.5	102.0	53.5	80.2	3.8	42.3	2.3	3.1	2990.5	14.5	0.501	23.2	40.7
G-71	54.0	110.5	56.5	82.1	3.1	41.9	2.7	3.6	2153.4	11.8	0.432	21.5	43.4
G-72	55.5	105.0	49.5	73.2	3.9	56.8	2.7	3.8	2812.2	14.1	0.485	21.4	44.0
G-73	49.0	108.5	59.5	56.7	4.2	54.1	2.6	3.3	2853.9	13.9	0.504	21.3	42.7
G-74	52.0	107.5	55.5	35.5	4.7	37.9	2.1	2.7	699.6	15.0	0.278	18.3	40.3
G-75	52.0	118.0	66.0	70.7	4.7	53.0	2.4	3.4	2847.6	12.7	0.396	21.2	41.4
G-76	61.5	122.0	60.5	65.0	4.4	51.3	2.9	3.5	2874.0	15.1	0.424	23.5	40.5
G-77	59.0	116.0	57.0	102.2	5.4	75.9	3.0	3.5	3648.8	13.1	0.471	23.4	41.1
G-78	63.0	126.0	63.0	92.3	5.8	73.3	2.8	3.7	2279.6	11.2	0.364	21.2	41.0
G-79	43.5	98.5	55.0	50.0	3.2	25.2	2.4	3.4	1626.1	14.2	0.345	21.9	37.5
G-80	58.0	122.5	64.5	75.3	4.4	51.8	2.3	3.1	3445.6	14.7	0.492	22.1	42.7
G-81	52.0	108.5	56.5	64.8	5.5	72.7	2.4	3.1	3793.5	14.7	0.480	20.1	45.1

Appendix Table 3. Mean performance values of 81 soybean genotypes tested at West Armachiho (Cont'd)

Gen	Traits												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
Mean	50.1	110.9	60.8	67.4	3.8	44.6	2.6	3.4	1859.5	13.3	0.377	21.1	41.9
CV (%)	2.6	1.6	1.9	7.9	14.0	20.9	9.4	7.1	13.6	8.0	10.7	3.9	2.9
$THSD_{0.05}$	5.88**	7.74**	8.65**	23.68**	2.38**	41.41**	1.07NS	1.06**	1123.10**	4.79**	0.18**	3.69**	5.52**
Mean	50.1	110.9	60.8	67.4	3.8	44.6	2.6	3.4	1859.5	13.3	0.377	21.1	41.9

Gen = Genotypes, DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH = Plant height (cm), BPP = Branches per Plant, PPP = Pods per Plant, SPP = Seed per Pod, PL = Pod Length (cm), GY = Seed Yield (kg ha-1), HSW = Hundred Seed Weigh t(g), HI = Harvest Index, OC = Oil content, and PC = Protein Content, THSD = Tukey's Honestly Significant Difference, *, ** significant at 0.05 and 0.01 probability levels, respectively

Appendix Table 4. The combined mean performance values of 81 soybean genotypes

							Traits						
Gen	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-1	53.0^{p-u}	121.5^{a-d}	68.5^{a-d}	63.8^{s-z}	4.5^{d-s}	62.0^{e-u}	2.8^{abc}	4.1^{a}	3348.8^{c-j}	13.4^{l-v}	0.414^{a-p}	19.0^{n-s}	44.2^{a-i}
G-2	50.5^{r-y}	105.0^{a-gyz}	54.5^{p-u}	88.6^{f-l}	5.9^{a-g}	55.7^{j-x}	2.7^{abc}	3.8^{ab}	4240.4^{ab}	16.0^{a-p}	0.491^{ab}	22.9^{a-f}	40.6^{j-t}
G-3	63.5^{abc}	120.0^{a-e}	56.5^{k-u}	89.0^{f-l}	5.7^{a-h}	60.7^{f-u}	2.7^{abc}	4.0^{ab}	2496.1^{k-q}	15.3^{b-s}	0.381^{d-p}	23.0^{a-f}	42.0^{e-p}
G-4	60.7^{b-i}	117.0^{d-k}	56.3^{l-u}	85.9^{f-q}	4.8^{c-p}	84.6^{a-i}	2.6^{abc}	3.4^{ab}	3600.5^{b-g}	12.8^{o-v}	0.427^{a-l}	20.3^{f-s}	43.4^{a-l}
G-5	57.5^{g-n}	115.0^{e-q}	57.5^{i-t}	82.0^{g-r}	4.4^{e-s}	56.1^{i-x}	2.4^{abc}	3.8^{ab}	2838.2^{g-p}	14.1^{g-v}	0.407^{a-p}	19.2^{m-s}	44.2^{a-i}
G-6	54.0^{m-s}	116.8^{e-l}	62.8^{c-k}	86.7^{f-m}	3.1^{o-x}	57.2^{i-v}	2.6^{abc}	3.8^{ab}	2850.1^{g-p}	15.0^{d-u}	0.423^{a-m}	20.8^{e-s}	43.2^{a-n}
G-7	46.2^{a-dz}	109.8^{p-z}	63.5^{c-i}	68.6^{n-y}	3.7^{l-v}	48.8^{o-z}	2.6^{abc}	3.8^{ab}	3030.5^{d-o}	18.3^{a-e}	0.438^{a-j}	23.3^{a-e}	42.6^{d-n}
G-8	62.5^{a-e}	106.3^{a-fxyz}	43.8^{yz}	89.7^{e-k}	6.3^{a-d}	81.2^{a-l}	2.7^{abc}	3.5^{ab}	3527.3^{b-i}	12.1^{r-v}	0.466^{a-e}	20.8^{e-s}	46.3^{ab}
G-9	40.5^{e-g}	101.8^{d-i}	61.3^{g-n}	40.7^{b}	2.3^{v-y}	33.7^{u-z}	2.6^{abc}	3.3^{ab}	1044.5^{s-v}	15.8^{a-r}	0.267^{s-x}	23.8^{a-d}	38.2^{rst}
G-10	58.5^{e-l}	115.3^{e-p}	56.8^{j-u}	79.2^{h-u}	5.3^{b-m}	51.9^{m-x}	2.8^{abc}	3.6^{ab}	2779.9^{i-p}	14.9^{d-u}	0.389^{c-p}	18.8^{o-s}	44.5^{a-h}
G-11	57.2^{h-n}	113.3^{g-t}	56.0^{m-u}	61.8^{au-z}	5.3^{b-m}	80.6^{a-m}	2.3^{abc}	3.3^{ab}	732.9^{tuv}	15.7^{a-r}	0.257^{t-x}	22.6^{a-i}	42.0^{e-o}
G-12	49.7^{u-z}	117.5^{c-i}	67.8^{a-f}	98.8^{a-g}	4.5^{d-s}	70.5^{b-q}	2.8^{abc}	3.8^{ab}	2462.5^{k-q}	14.1^{g-v}	0.399^{b-p}	20.1^{f-s}	42.1^{e-o}
G-13	40.2^{fg}	104.8^{a-gz}	64.5^{c-h}	53.2^{abx-z}	3.7^{l-v}	39.0^{s-z}	2.7^{abc}	4.1^{ab}	2482.2^{k-q}	17.6^{a-h}	0.377^{e-p}	22.1^{a-m}	43.4^{a-l}
G-14	39.2^{gh}	110.3^{p-z}	71.0^{ab}	53.8^{abw-z}	3.0^{p-x}	30.2^{v-z}	2.4^{abc}	3.2^{ab}	477.8^{uv}	17.2^{a-k}	0.236^{wx}	18.2^{qrs}	38.2^{q-t}
G-15	63.5^{abc}	111.0^{m-x}	47.5^{w-z}	91.3^{d-i}	3.7^{k-v}	53.1^{l-x}	2.7^{abc}	3.5^{ab}	3081.8^{d-n}	12.5^{p-v}	0.419^{a-o}	21.2^{b-q}	45.5^{a-e}
G-16	57.5^{gn}	118.0^{c-h}	60.5^{g-q}	92.5^{d-h}	5.7^{a-i}	74.3^{b-o}	2.5abc	3.8^{ab}	3305.9^{d-j}	14.8^{d-u}	0.395^{b-p}	20.4^{e-s}	43.9^{a-j}
G-17	56.0^{k-p}	108.3^{abs-z}	52.3^{t-x}	98.3^{b-g}	6.1^{a-f}	89.5^{a-f}	2.6^{abc}	3.4^{ab}	2302.5^{opq}	11.3^{uv}	0.361^{h-s}	21.7^{a-o}	42.6^{d-n}
G-18	45.2^{abc}	108.0^{abt-z}	62.8^{c-k}	92.8^{d-h}	2.8^{s-y}	36.4^{t-z}	2.5^{abc}	3.3^{ab}	2459.9^{k-q}	17.7^{a-h}	0.406^{a-p}	22.1^{a-m}	40.7^{i-t}
G-19	35.7^{hi}	98.0^{hi}	62.3^{d-m}	49.4^{abz}	1.3^{xy}	22.4^{z}	2.6^{a-c}	3.4^{ab}	935.5^{tuv}	18.8^{abc}	0.231^{x}	23.0^{a-f}	42.2^{e-o}
G-20	48.5^{abcw-z}	111.3^{l-x}	62.8^{c-k}	68.0^{q-y}	3.4^{n-w}	71.1^{b-q}	2.6^{abc}	3.4^{ab}	3202.6^{d-l}	15.0^{d-u}	0.429^{a-l}	20.9^{c-s}	42.9^{b-n}
G-21	51.2^{q-x}	113.3^{g-t}	62.0^{e-m}	82.4^{g-r}	4.0^{h-v}	42.3^{q-z}	2.4^{abc}	3.4^{ab}	2812.9^{i-p}	14.1^{g-v}	0.441^{a-i}	20.8^{e-s}	43.9^{a-j}
G-22	38.0^{ghi}	107.0^{a-ey-z}	69.0^{abc}	73.3^{j-v}	5.4^{b-m}	38.3^{s-z}	2.8^{abc}	3.5^{ab}	1228.2^{r-u}	17.8^{a-g}	0.281^{q-x}	22.8^{a-h}	39.8^{m-t}
G-23	37.2^{ghi}	99.5^{ghi}	62.3^{d-m}	45.0^{ab}	2.4^{u-y}	28.2^{w-z}	2.6^{abc}	3.3^{ab}	923.7^{tuv}	17.0^{a-l}	0.241^{wx}	24.5^{a}	38.8^{q-t}
G-24	62.0^{a-f}	123.0^{abc}	61.0^{g-o}	86.2^{f-o}	5.5^{a-k}	104.8^{a}	2.4^{abc}	3.1^{ab}	4103.1^{abc}	12.1^{q-v}	0.448^{a-h}	20.9^{c-s}	43.3^{a-m}
G-25	61.5^{a-g}	113.8^{f-s}	52.3^{t-x}	83.2^{g-q}	5.5^{a-l}	74.5^{b-o}	2.7^{abc}	3.3^{ab}	2779.8^{i-p}	12.2^{q-v}	0.433^{a-l}	19.4^{l-s}	44.0^{a-j}
G-26	59.7^{b-k}	121.3^{a-d}	61.5^{f-n}	87.3^{f-m}	6.2^{a-e}	82.8^{a-k}	2.6^{abc}	3.7^{ab}	2976.4^{f-p}	14.9^{d-u}	0.342^{k-u}	20.7^{e-s}	44.5^{a-h}
G-27	63.0^{a-d}	119.0^{b-f}	56.0^{m-u}	115.2^{ab}	6.1^{a-f}	97.3^{ab}	2.8^{abc}	3.5^{ab}	4235.1^{ab}	11.6^{tuv}	0.425^{a-m}	23.0^{a-f}	41.6^{f-r}

Appendix Table 4. The combined mean performance values of 81 soybean genotypes (Cont'd)

Gen	Traits												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-28	62.5$^{a\text{-}e}$	124.8^a	62.3$^{d\text{-}m}$	79.7$^{h\text{-}u}$	5.5$^{a\text{-}k}$	93.1$^{a\text{-}d}$	2.4^{abc}	3.5^{ab}	3633.5$^{b\text{-}f}$	14.2$^{g\text{-}v}$	0.486^{ab}	19.5$^{k\text{-}s}$	42.6$^{d\text{-}n}$
G-29	61.0$^{b\text{-}h}$	118.5$^{b\text{-}g}$	57.5$^{i\text{-}t}$	86.0$^{f\text{-}p}$	5.7$^{a\text{-}h}$	66.7$^{c\text{-}s}$	2.6^{abc}	3.6^{ab}	2474.5$^{k\text{-}q}$	15.1$^{c\text{-}t}$	0.361$^{g\text{-}s}$	22.1$^{a\text{-}m}$	43.5$^{a\text{-}k}$
G-30	59.5$^{c\text{-}k}$	118.0$^{c\text{-}h}$	58.5$^{h\text{-}t}$	82.4$^{g\text{-}r}$	5.9$^{a\text{-}g}$	49.9$^{n\text{-}z}$	2.4^{abc}	3.4^{ab}	3528.2$^{b\text{-}i}$	15.9$^{a\text{-}p}$	0.449$^{a\text{-}h}$	22.4$^{a\text{-}k}$	42.1$^{e\text{-}o}$
G-31	35.3^{hi}	101.0$^{f\text{-}i}$	65.8$^{a\text{-}g}$	58.5$^{abv\text{-}z}$	2.5$^{t\text{-}y}$	29.1$^{v\text{-}z}$	2.8^{abc}	3.6^{ab}	786.3^{tuv}	19.1^{ab}	0.236^{wx}	23.8^{abc}	38.7$^{o\text{-}t}$
G-32	55.8^{kp}	116.5$^{d\text{-}m}$	60.8$^{g\text{-}p}$	113.2^{abc}	5.6$^{a\text{-}j}$	83.1$^{a\text{-}j}$	2.7^{abc}	3.4^{ab}	3384.8$^{c\text{-}j}$	13.2$^{m\text{-}v}$	0.435$^{a\text{-}k}$	19.6$^{k\text{-}s}$	42.7$^{c\text{-}n}$
G-33	58.8$^{e\text{-}l}$	100.0^{ghi}	41.3^{z}	82.8$^{g\text{-}q}$	4.7$^{c\text{-}r}$	64.9$^{c\text{-}t}$	3.1^{a}	3.4^{ab}	3140.2$^{d\text{-}m}$	11.0^{v}	0.435$^{a\text{-}k}$	20.8$^{d\text{-}s}$	46.2^{abc}
G-34	43.5^{def}	115.3$^{e\text{-}p}$	71.8^{a}	70.5$^{m\text{-}x}$	5.9$^{a\text{-}g}$	54.7$^{j\text{-}x}$	2.8^{abc}	3.7^{ab}	713.5^{tuv}	19.1^{a}	0.274$^{r\text{-}x}$	18.0^{s}	37.9st
G-35	56.3$^{k\text{-}p}$	109.8$^{p\text{-}z}$	53.5$^{s\text{-}w}$	84.3$^{g\text{-}q}$	4.6$^{d\text{-}s}$	63.3$^{e\text{-}t}$	2.8^{abc}	3.5^{ab}	3119.2$^{d\text{-}m}$	15.1$^{c\text{-}t}$	0.456$^{a\text{-}h}$	18.2^{rs}	46.8^{a}
G-36	46.5$^{a\text{-}dyz}$	114.8$^{e\text{-}r}$	68.3$^{a\text{-}e}$	64.7$^{r\text{-}z}$	7.2^{a}	56.3$^{i\text{-}x}$	2.9^{abc}	4.0^{ab}	1741.7^{qrs}	18.3$^{a\text{-}d}$	0.375$^{e\text{-}q}$	23.9^{abc}	42.6$^{d\text{-}n}$
G-37	38.8^{ghi}	102.3$^{c\text{-}i}$	63.5$^{c\text{-}i}$	49.5^{abz}	3.0$^{q\text{-}x}$	27.7^{xyz}	2.7^{abc}	3.5^{ab}	1437.7^{rst}	16.8$^{a\text{-}m}$	0.343$^{j\text{-}u}$	19.5$^{k\text{-}s}$	44.3$^{a\text{-}i}$
G-38	34.8^{i}	97.3^{i}	62.5$^{d\text{-}l}$	52.5^{abyz}	1.5^{xy}	29.6$^{v\text{-}z}$	2.6^{abc}	3.4^{ab}	836.6^{tuv}	18.1$^{a\text{-}f}$	0.243^{vwx}	21.9$^{a\text{-}n}$	41.8$^{f\text{-}q}$
G-39	43.5^{def}	101.5$^{e\text{-}i}$	58.0$^{i\text{-}t}$	73.7$^{i\text{-}v}$	3.9$^{i\text{-}v}$	43.9$^{p\text{-}z}$	2.4^{abc}	3.5^{ab}	2504.3$^{k\text{-}q}$	14.2$^{g\text{-}v}$	0.327$^{n\text{-}x}$	20.0$^{g\text{-}s}$	44.2$^{a\text{-}i}$
G-40	56.8$^{i\text{-}p}$	121.5$^{a\text{-}d}$	64.8$^{b\text{-}h}$	103.7$^{a\text{-}f}$	5.9$^{a\text{-}g}$	86.7$^{a\text{-}g}$	2.7^{abc}	3.6^{ab}	4499.0^{a}	15.2$^{c\text{-}t}$	0.422$^{a\text{-}n}$	20.9$^{c\text{-}s}$	43.6$^{a\text{-}k}$
G-41	54.3$^{m\text{-}r}$	102.3$^{c\text{-}i}$	48.0$^{v\text{-}y}$	86.0$^{f\text{-}p}$	4.0$^{h\text{-}v}$	64.2$^{e\text{-}t}$	2.8^{abc}	3.4^{ab}	3055.7$^{d\text{-}o}$	11.0^{v}	0.461$^{a\text{-}e}$	21.0$^{b\text{-}r}$	45.8$^{a\text{-}d}$
G-42	43.5^{def}	106.5$^{a\text{-}fw\text{-}z}$	63.0$^{c\text{-}j}$	69.6$^{m\text{-}y}$	3.7$^{l\text{-}v}$	33.4$^{u\text{-}z}$	2.7^{abc}	4.0^{ab}	1418.5^{rst}	17.4$^{a\text{-}j}$	0.324$^{o\text{-}x}$	22.4$^{a\text{-}k}$	42.2$^{e\text{-}o}$
G-43	61.3$^{a\text{-}h}$	114.3$^{f\text{-}r}$	53.0$^{t\text{-}x}$	95.3$^{c\text{-}h}$	4.9$^{c\text{-}o}$	83.3$^{a\text{-}j}$	2.8^{abc}	3.8^{ab}	2487.1$^{k\text{-}q}$	12.9$^{n\text{-}v}$	0.371$^{e\text{-}q}$	22.1$^{a\text{-}m}$	39.8$^{l\text{-}t}$
G-44	63.8^{ab}	124.8^{a}	61.0$^{g\text{-}o}$	107.3$^{a\text{-}e}$	4.9$^{c\text{-}o}$	68.8$^{b\text{-}r}$	2.8^{abc}	3.8^{ab}	3445.0$^{c\text{-}j}$	15.7$^{a\text{-}r}$	0.396$^{b\text{-}p}$	20.5$^{e\text{-}s}$	41.5$^{f\text{-}r}$
G-45	60.5$^{b\text{-}j}$	117.3$^{d\text{-}j}$	56.8$^{j\text{-}u}$	81.7$^{g\text{-}s}$	5.2$^{b\text{-}n}$	57.8$^{h\text{-}v}$	2.5^{abc}	3.5^{ab}	2850.5$^{g\text{-}p}$	14.6$^{e\text{-}v}$	0.443$^{a\text{-}i}$	20.5$^{e\text{-}s}$	42.8$^{b\text{-}n}$
G-46	36.0^{hi}	103.8$^{d\text{-}k}$	67.8$^{a\text{-}f}$	49.0^{abz}	1.1^{y}	22.9^{yz}	2.8^{abc}	3.4^{ab}	936.4^{tuv}	18.1$^{a\text{-}f}$	0.261$^{t\text{-}x}$	22.0$^{a\text{-}m}$	41.6$^{f\text{-}r}$
G-47	51.0$^{r\text{-}x}$	117.0$^{d\text{-}k}$	66.0$^{a\text{-}g}$	96.0$^{c\text{-}h}$	4.8$^{c\text{-}q}$	65.7$^{c\text{-}s}$	2.7^{abc}	3.6^{ab}	3114.5$^{d\text{-}m}$	14.9$^{d\text{-}u}$	0.415$^{a\text{-}p}$	19.5$^{k\text{-}s}$	41.8$^{f\text{-}r}$
G-48	62.3$^{a\text{-}e}$	116.0$^{d\text{-}o}$	53.8$^{s\text{-}w}$	103.7$^{a\text{-}f}$	5.0$^{c\text{-}n}$	93.6^{abc}	2.8^{abc}	3.4^{ab}	3438.2$^{c\text{-}j}$	11.8$^{s\text{-}v}$	0.409$^{a\text{-}p}$	20.3$^{f\text{-}s}$	43.9$^{a\text{-}j}$
G-49	45.0^{bcd}	110.3$^{p\text{-}z}$	65.3$^{b\text{-}g}$	63.2$^{t\text{-}z}$	4.6$^{d\text{-}s}$	52.0$^{m\text{-}x}$	2.9^{abc}	3.7^{ab}	341.8^{v}	14.4$^{f\text{-}v}$	0.338$^{l\text{-}v}$	18.0^{s}	38.4$^{p\text{-}t}$
G-50	59.8$^{b\text{-}k}$	110.5$^{o\text{-}y}$	50.8$^{u\text{-}x}$	79.5$^{h\text{-}u}$	2.9$^{r\text{-}y}$	52.1$^{m\text{-}x}$	3.0^{ab}	3.8^{ab}	2438.2$^{l\text{-}q}$	13.8$^{i\text{-}v}$	0.384$^{d\text{-}p}$	18.8$^{o\text{-}s}$	45.5$^{a\text{-}e}$
G-51	47.3$^{a\text{-}dxz}$	109.5$^{q\text{-}z}$	62.3$^{d\text{-}m}$	72.4$^{j\text{-}v}$	2.4$^{v\text{-}y}$	56.6$^{i\text{-}w}$	2.6^{abc}	3.5^{ab}	2994.9$^{e\text{-}p}$	14.5$^{e\text{-}v}$	0.406$^{a\text{-}p}$	20.7$^{e\text{-}s}$	43.3$^{a\text{-}m}$
G-52	51.5$^{q\text{-}w}$	117.0$^{d\text{-}k}$	65.5$^{a\text{-}g}$	89.4$^{e\text{-}k}$	5.7$^{a\text{-}h}$	86.4$^{a\text{-}h}$	2.7^{abc}	3.8^{ab}	3403.3$^{c\text{-}j}$	16.1$^{a\text{-}p}$	0.421$^{a\text{-}n}$	20.5$^{e\text{-}s}$	43.5$^{a\text{-}k}$
G-53	55.3$^{l\text{-}q}$	112.8$^{h\text{-}u}$	57.5$^{i\text{-}t}$	89.3$^{f\text{-}l}$	5.6$^{a\text{-}j}$	66.2$^{c\text{-}s}$	2.7^{abc}	3.6^{ab}	3224.7$^{d\text{-}k}$	13.3$^{l\text{-}v}$	0.408$^{a\text{-}p}$	19.8$^{i\text{-}s}$	42.0$^{e\text{-}o}$
G-54	55.8$^{k\text{-}p}$	109.3$^{ar\text{-}z}$	53.5$^{s\text{-}w}$	81.8$^{g\text{-}r}$	4.2$^{g\text{-}u}$	53.2$^{l\text{-}x}$	2.7^{abc}	3.6^{ab}	2960.4$^{f\text{-}p}$	13.6$^{j\text{-}v}$	0.422$^{a\text{-}n}$	22.9$^{a\text{-}g}$	41.1$^{h\text{-}s}$

Appendix Table 4. The combined mean performance values of 81 soybean genotypes (Cont'd)

Gen	Traits												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
G-55	57.3^{h-o}	120.0^{a-e}	62.8^{c-k}	68.1^{p-y}	3.0^{q-x}	51.7^{m-y}	2.7^{ab}c	3.7^{ab}	2828.1^{h-p}	12.5^{o-v}	0.364^{f-r}	19.3^{m-s}	44.3^{a-h}
G-56	52.8^{p-v}	118.5^{b-f}	65.8^{a-g}	93.6^{d-h}	4.7^{c-r}	60.3^{g-u}	2.7^{abc}	3.7^{ab}	3278.3^{d-j}	13.2^{m-v}	0.380^{d-p}	19.8^{i-s}	44.8^{a-g}
G-57	51.0^{r-x}	117.0^{d-k}	66.0^{a-g}	88.6^{f-l}	5.7^{a-i}	63.2^{e-t}	2.4^{abc}	3.4^{ab}	3583.5^{b-h}	12.9^{o-v}	0.442^{a-i}	19.9^{h-s}	43.8^{a-j}
G-58	36.8^{ghi}	101.5^{f-i}	64.8^{b-h}	44.2^{ab}	1.7^{wxy}	29.1^{v-z}	2.5^{abc}	3.3^{ab}	814.2^{tuv}	17.3^{a-j}	0.237^{wx}	18.5^{p-s}	37.2^{t}
G-59	56.0^{k-p}	110.0^{p-z}	54.0^{r-v}	81.3^{g-s}	5.1^{b-n}	54.1^{k-x}	2.3^{bc}	3.6^{ab}	3761.4^{a-d}	16.3^{a-o}	0.500^{a}	23.0^{a-f}	44.1^{a-j}
G-60	53.0^{p-u}	117.5^{c-i}	64.5^{c-h}	86.8^{f-m}	5.6^{a-j}	78.4^{a-n}	2.7^{abc}	3.9^{ab}	3331.6^{d-j}	15.7^{a-r}	0.419^{a-o}	20.4^{e-s}	44.4^{a-h}
G-61	35.8^{hi}	100.3^{ghi}	64.5^{c-h}	52.9^{abxyz}	1.7^{wxy}	29.2^{v-z}	2.7^{abc}	3.6^{ab}	999.9^{s-v}	19.1^{ab}	0.319^{p-x}	22.3^{a-l}	39.7^{n-t}
G-62	53.3^{o-u}	107.3^{a-du-z}	54.0^{r-v}	81.9^{g-r}	3.6^{m-v}	64.5^{d-t}	2.4^{abc}	3.4^{ab}	2377.6^{m-q}	15.1^{c-t}	0.376^{e-q}	21.2^{b-q}	44.4^{a-h}
G-63	58.0^{f-m}	112.3^{i-v}	54.3^{q-v}	92.8^{d-h}	5.5^{a-l}	72.6^{b-p}	2.5^{abc}	3.8^{ab}	3616.7^{b-f}	17.0^{a-l}	0.459^{a-f}	22.4^{a-k}	42.9^{b-n}
G-64	63.0^{a-d}	116.3^{d-n}	53.3^{t-x}	79.9^{h-t}	3.4^{n-w}	57.2^{i-v}	2.6^{abc}	3.4^{ab}	2235.8^{pq}	14.6^{d-v}	0.330^{m-w}	20.7^{e-s}	44.0^{a-j}
G-65	56.0^{k-p}	118.3^{b-h}	62.3^{d-m}	95.0^{d-h}	5.1^{b-n}	66.7^{c-s}	2.7^{abc}	3.9^{ab}	3340.6^{c-j}	17.3^{a-k}	0.401^{b-p}	20.8^{e-s}	43.2^{a-n}
G-66	51.5^{q-w}	111.8^{j-x}	60.3^{g-r}	95.5^{c-h}	4.6^{d-s}	66.2^{c-s}	2.9^{abc}	3.8^{ab}	2758.5^{j-p}	14.6^{e-v}	0.397^{b-p}	20.7^{f-s}	43.2^{b-n}
G-67	49.3^{au-z}	110.8^{n-x}	61.5^{f-n}	64.6^{r-z}	3.8^{j-v}	38.5^{s-z}	2.7^{abc}	3.6^{ab}	1852.9^{qr}	16.6^{a-n}	0.373^{e-q}	20.1^{f-s}	43.4^{a-k}
G-68	48.8^{abv-z}	111.0^{m-x}	62.3^{d-m}	78.2^{h-u}	3.9^{i-v}	42.7^{q-z}	2.7^{abc}	3.6^{ab}	2957.7^{f-p}	15.2^{c-t}	0.475^{a-d}	20.7^{e-s}	43.2^{b-n}
G-69	50.0^{s-z}	104.8^{a-gz}	54.8^{o-u}	72.2^{k-v}	3.7^{l-v}	46.2^{o-z}	2.5^{abc}	3.4^{ab}	2317.5^{n-q}	14.5^{e-v}	0.349^{i-t}	20.8^{e-s}	42.8^{b-n}
G-70	50.0^{s-z}	107.8^{abct-z}	57.8^{i-t}	90.0^{e-k}	5.4^{b-m}	61.6^{f-u}	2.4^{abc}	3.5^{ab}	3626.9^{b-f}	15.9^{a-q}	0.483^{abc}	21.8^{a-n}	43.1^{b-n}
G-71	56.8^{i-p}	112.0^{i-w}	55.3^{n-u}	98.2^{b-g}	4.1^{g-v}	52.9^{l-x}	2.6^{abc}	3.4^{ab}	3066.1^{d-o}	14.0^{h-v}	0.457^{a-g}	21.0^{c-r}	43.5^{a-k}
G-72	59.3^{d-i}	106.3^{a-fxyz}	47.0^{xyz}	86.4^{f-n}	4.8^{c-p}	68.9^{b-q}	2.8^{abc}	3.6^{ab}	3043.1^{d-o}	13.6^{k-v}	0.431^{a-l}	20.8^{e-s}	45.1^{a-f}
G-73	48.8^{abv-z}	109.5^{q-z}	60.8^{g-p}	71.4^{l-w}	4.8^{c-p}	66.9^{c-s}	2.7^{abc}	3.6^{ab}	3334.4^{d-j}	15.8^{a-r}	0.465^{a-e}	21.1^{b-r}	42.8^{b-n}
G-74	53.5^{n-t}	111.5^{k-x}	58.0^{i-t}	43.9^{ab}	4.3^{f-t}	40.0^{r-z}	2.2^{c}	3.1^{b}	544.2^{uv}	17.0^{a-l}	0.249^{u-x}	18.2^{rs}	40.2^{k-t}
G-75	56.5^{j-p}	118.0^{c-h}	61.5^{f-n}	85.8^{f-q}	5.4^{b-m}	60.0^{g-u}	2.5^{abc}	3.8^{ab}	3758.9^{a-e}	14.8^{d-u}	0.402^{b-p}	20.9^{c-s}	42.5^{d-n}
G-76	65.3^{a}	123.8^{ab}	58.5^{h-t}	82.6^{g-r}	5.4^{a-m}	69.2^{b-q}	2.9^{abc}	3.6^{ab}	3748.4^{a-e}	17.6^{a-h}	0.430^{a-l}	22.5^{a-j}	42.4^{d-n}
G-77	62.5^{a-e}	115.0^{e-q}	52.5^{t-x}	116.4^{a}	6.5^{abc}	79.6^{a-m}	2.8^{abc}	3.6^{ab}	3775.2^{a-d}	15.1^{c-t}	0.409^{a-p}	23.3^{a-e}	41.2^{h-s}
G-78	65.3^{a}	125.0^{a}	59.8^{g-s}	108.4^{a-d}	6.9^{ab}	90.7^{a-e}	2.7^{abc}	3.9^{ab}	2965.5^{f-p}	14.4^{f-v}	0.414^{a-p}	21.3^{b-p}	41.4^{g-s}
G-79	44.5^{c-e}	103.0^{b-h}	58.5^{h-t}	68.3^{o-y}	4.3^{f-s}	55.1^{j-x}	2.7^{abc}	3.8^{ab}	2409.9^{m-q}	17.5^{a-i}	0.322^{p-x}	23.0^{a-f}	37.5^{t}
G-80	61.5^{aa-g}	123.8^{ab}	62.3^{d-m}	90.2^{e-j}	5.7^{a-i}	59.4^{g-u}	2.4^{abc}	3.6^{ab}	4267.5^{ab}	16.8^{a-m}	0.48^{6ab}	22.4^{a-k}	42.4^{d-n}
G-81	50.0^{s-z}	112.8^{h-u}	62.8^{c-k}	82.3^{g-r}	5.9^{a-g}	77.8^{a-n}	2.5^{abc}	3.5^{ab}	4248.9^{ab}	17.3^{a-k}	0.430^{a-l}	19.6^{j-s}	45.8^{a-d}

Appendix Table 4. The combined mean performance values of 81 soybean genotypes (Cont'd)

Gen	Traits												
	DH	DM	GFP	PH	BPP	PPP	SPP	PL	GY	HSW	HI	OC	PC
Mean	52.5	112.1	59.5	79.9	4.5	59.6	2.6	3.57	2679.1	15.2	0.386	21.0	42.6
CV (%)	2.5	1.6	3.6	7.4	13.4	15.8	9.4	9.6	9.4	8.1	8.1	4.6	2.8
$THSD_{0.05}$	4.09**	5.52**	6.49**	17.98**	1.84**	28.89**	0.76**	1.05**	765.5**	3.75**	0.096**	2.94**	3.59**

Gen = Genotypes, DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH = Plant height (cm), BPP = Branches per Plant, PPP = Pods per Plant, SPP = Seed per Pod, PL = Pod Length (cm), GY = Seed Yield (kg ha^{-1}), HSW = Hundred Seed Weigh t(g), HI = Harvest Index, OC = Oil content, and PC = Protein Content, THSD = Tukey's Honestly Significant Difference, *, ** significant at 0.05 and 0.01 probability levels, respectively

Appendix Table 5. Results of homogeneity test for combined analysis of soybean genotypes

Traits	Variances		DFE	F-Cal.	F-Tab.		Homogeneity status
	Metema	W/Armachiho			0.01	0.05	
DF	1.44	1.75	64	1.22	1.821	1.520	Homogeneous
DM	3.56	3.03	64	1.18	1.821	1.520	Homogeneous
GFP	5.06	3.79	64	1.34	1.821	1.520	Homogeneous
PH	39.82	28.36	64	1.40	1.821	1.520	Homogeneous
BPP	0.47	0.29	64	1.64	1.821	1.520	Homogeneous
PPP	85.04	86.72	64	1.02	1.821	1.520	Homogeneous
SPP	0.07	0.06	64	1.27	1.821	1.520	Homogeneous
PL	0.15	0.09	64	1.67	1.821	1.520	Homogeneous
GY	46487.10	63777.40	64	1.37	1.821	1.520	Homogeneous
HSW	2.00	1.16	64	1.72	1.821	1.520	Homogeneous
HI	0.0003	0.0004	64	1.33	1.821	1.520	Homogeneous
OC	1.16	0.69	64	1.68	1.821	1.520	Homogeneous
PC	1.09	1.54	64	1.41	1.821	1.520	Homogeneous

DF = Days to 50% Flowering, DM = Days to Maturity, GFP = Seed Filling Period, PH = Plant height (cm), BPP = Branches per Plant, PPP = Pods per Plant, SPP = Seed per Pod, PL = Pod Length (cm), GY = Seed Yield (kg ha^{-1}), HSW = Hundred Seed Weigh t(g), HI = Harvest Index, OC = Oil content, and PC = Protein Content ,DFE = Degree Freedom for the Error, F-cal. and F-tab. = F-calculated and F-tabulated

BIOGRAPHICAL SKETCH

The author, Gobezie Chakelie was born on January 15, 1987, in Amhara Region, Ethiopia. He completed his primary education at Guhala Elementary and Junior Secondary School in Central Gondar and high school at Fasiledess Comprehensive Secondary School at Gondar Town. Following the completion of his high school education, he joined the then Hawassa University in October 2008 and graduated with a Degree of Bachelor Science in Plant Science in July 2011.

Soon after graduation, he joined the Amhara National Regional State, Bureau of Agriculture and served as crop production expert in East Belessa Woreda Agricultural Office for 2 years. Then he joined Amhara Regional Agricultural Research Institute (ARARI) in January 2014 and has worked at Adet Agricultural Research Center (AARC) as a junior researcher in the Agronomy position for 2 years and 5 months. For personal reasons, he left AARC and stayed away for 7 months. Then, he was again employed by ARARI and positioned at Gondar Agricultural Research Center as a junior and assistant researcher where he has been serving from January 16 until he joined the School of Graduate Studies at Bahir Dar University in September 2019 to pursue his MSc. Degree in Plant Breeding.