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# Genetic Variability and Association of Traits in Soybean (Glycine Max L.) Genotypes at pawe Agricultural Research Center, North-Western Ethiopia

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# BAHIR DAR UNIVERSITY

## COLLEGE OF AGRICULTURE AND ENVIROMENTAL SCIENCES

## PROGRAM PLANT BREEDING

# GENETIC VARIABILITY AND ASSOCIATION OF TRAITS IN SOYBEAN (*Glycine max* L.) GENOTYPES AT PAWE AGRICULTURAL RESEARCH CENTER, NORTH-WESTERN ETHIOPIA

**MSc. Thesis**

**By:**

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**June 2024**

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

**June 2024**

**Bahir Dar, Ethiopia**

# THESIS APPROVAL SHEET

As member of the Board of Examiners of the Master of Sciences (MSc.) thesis open defense examination, we read and evaluated the thesis prepared by Mr **Anbesaw Gate Atanaw** entitled '**Genetic Variability and Association of Traits in Soybean *(Glycine max L.)* Genotypes at Pawe Agricultural Research Center, North-Western Ethiopia** '. We hereby certify that, the thesis is accepted for fulfilling the requirements for the award of the Degree of Master of Sciences (MSc.) in **PLANT BREEDING.**

**Board of Examiners**

| | | |
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| Name of Internal Examiner | Signature | Date |
| Wossen Tarekegne(PhD) | | 7/10/2024 |
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# DECLARATION

This is to certify that this thesis entitled "**Genetic Variability and Association of Traits in Soybean** *(Glycine Max* **L.) Genotypes in Pawe Agricultural Research Center, North-West 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 carried out by Mr. Anbesaw Gate Atanaw (ID: BDU1500067) was an authentic work carried out by him under our guidance. The matter embodied in this project work has not been submitted earlier for the award of any degree or diploma to the best of our knowledge and belief. Therefore, we recommend that it could be accepted as fulfilling the thesis requirements for the degree of Master of Science in Plant breeding.

Anbesaw Gate Atanaw ........................ 06/06/2024
Name of the student Signature Date

Dr. Alemu Abate ........................ 20/May, 2024
Name of advisor Signature Date

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Name of advisor Signature Date

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# DEDICATION

Dedicated to my beloved family and almighty God, who gave me all strength and courage

# LIST OF ABBREVIATIONS AND ACRONYMS

| | |
|---|---|
| AARC | Awassa Agricultural Research Center |
| ANOVA | Analysis of Variance |
| CADU | Chilalo Agricultural Development Unite |
| CSA | Central Statistical Agency |
| DAP | Di Ammonium Phosphate |
| DZARC | Debre Zeit Agricultural Research Center |
| ENI | Ethiopian Nutrition Institute |
| FAO | Food and Agricultural Organization |
| IAR/EIAR | Institute of Agricultural Research |
| INRA | Institute National de la Recherché Agronomies |
| LSD | Least Significant Difference |
| P2O5 | Phosphorus Pentoxide |
| RAPD | Random Amplified Polymorphic DNA |
| SRARC | Southern Regional Agricultural Research Center |
| SSR | Simple Sequence Repeats |
| USDA | United State Department of Agriculture |

## Genetic Variability and Association of Traits in Soybean (*Glycine max* L.) Genotypes at Pawe Agricultural Research Center, North-Western Ethiopia

**By**

Anbesaw gate, Alemu Abate and Muluken Bantayehu

# ABSTRACTS

*Soybean is a multipurpose leguminous oil crop with high grain nutritional and industrial value. However, the crop has a narrow genetic base in Ethiopia, which makes it susceptible to different diseases, insects, and abiotic stresses. Therefore, the research was initiated to evaluate genetic variability, and trait association, with one hundred fifty soybean genotypes in a 10x15 alpha lattice design with two replications at the Pawe Agricultural Research Center during the main cropping season of 2023. Data analyses were don SAS 9.4 version software. The result of analysis of variance revealed highly significant different ($P<0.01$) among genotypes for most studied traits and significant different ($P<0.05$) among genotypes for number of branch per plant.* The result of *phenotypic coefficient of variation values varied from 2.56% for protein content to 51.84% for loading, while genotypic coefficient of variation values ranged from 1.70% for protein content to 44.96% for lodging. High heritability coupled with high genetic advance as percent of mean was recorded for days to flowering, number of pods per plant, days to maturity, oil yield, biomass yield, number of seeds per pod, grain yield, plant height, and hundred seed weight, indicating the possibility of improving these traits through direct selection. Grain yield showed positive and highly significant phenotypic and genotypic correlation coefficient with days to flowering, days to maturity, plant height, pods per plant, seeds per plant, hundred seed weight, and biomass yield. The divergence analysis grouped the 150 genotypes into seven distinct clusters based on 19 traits. The maximum inter cluster distance was observed from cluster VI and cluster VII ($D^2 = 547.84$) followed by cluster V and cluster VI ($D^2 =386.76$). Largest cluster distance indicated that the existence of large variability among the genotypes with in that cluster. The principal component analysis revealed that the five PCA with Eigen values of greater than one accounted for 69.27% of the total variation. Generally, the present study indicated existence of reasonable variability among genotypes, and this variability shall be exploited for future soybean improvement program.*

**Key words:** Alpha lattice, *Correlation, Genetic divergence, Heritability, PCA*

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# Chapter 1. INTRODUCTION

## 1.1. Background and Justification

Soybean (*Glycine max L.*, 2n=40) is a self-pollinating crop but natural crosspollination has also been observed with a rate of 0.03–1.14% in cultivated species (Chiang and Kiang, 1987) and it belongs to the genus *Glycine* in the family *Leguminasae* (Masreshaw Yirga *et al.*, 2022). It is reported to be domesticated in Asia, probably in north eastern China (Singh and Hymowitz, 1999).

Soybean is a warm season (tropical) crop however; its cultivation now extends to subtropics and temperate climates (Grassini *et al.*, 2021). It is drought tolerant and grows to a height of 60–120 cm, maturing in 3 to 6 months depending on variety, climate, and location (Belete Woundefiraw and Birhanu Argaw, 2023). Soybean is farmed in a larger range of agro-ecologies in Ethiopia and is most widely cultivated in rain-fed agriculture (Fageria *et al.*, 2006), with a focus on low to mid altitude regions (1300 to 1700 m.a.s.l) with moderate annual rainfall (500-1500mm) (Fekadu Gurmu *et al.*, 2009). It can tolerate low and extremely high temperatures, despite its development rate is slower at above 35°C and below 18°C. The optimal temperature for growth between planting and flowering is 30°C, while the minimum temperature for growth is approximately 10°C (Roberts and Schlenker, 2011).

Soybean may be cultivated on a variety of well-drained soils, clay loams soil are the best for it (Popović *et al.*, 2017). The pH range between 6 and 6.5 is ideal for the growth of soybeans (Cartter and Hartwig, 1962). When compared to other oil crops, soybean is classified as a crop with a moderate tolerance to salt; the reported salinity threshold is around 5 dS m-1. Shallow water tables can have a negative impact on the yield, especially in the early stages of growth. Waterlogging can damage the crop, especially in the early stages (Rhine *et al.*, 2010).

It is a crucial leguminous and oil crop having a global impact as a food and market crop. Its high grain nutritional value, consists of 40% protein and 20% oil (Vollmann, 2016) hence, it serves as a crucial raw material for the food and oil processing industries. Additionally, Soybeans are a crucial crop in the battle against global food scarcity and malnutrition issues (Islam *et al.*, 2022). This is because they offer health benefits when consumed, and many food supplies provided to displaced and malnourished people are fortified with soybeans as a result.

It is an important and cheap source of vegetable proteins and oils. It is the cheapest, richest, and most convenient source of high-quality fat and protein. It is known as a "wonder crop" because of the variety of uses it has in both food and industrial products (Dangi and Sharma, 2021). Soybean is a good source of fibre, protein, lipids, minerals, and carbohydrates (Lokuruka, 2010). The oil of soybean consists the three fatty acids which are linoleic / linolenic/, and oleic (Pham *et al.*, 2012).

Soybean produced in different countries of the world, the overall soybean production in 2022 in the world is 348.56 million tons from 130.48 million ha of area cultivated (FAO, 2022). The most producer of soybean in the continent are America more than of 85 % of soybean produced in the continent, 10% of soybean produced in Asia, 3.7 % produced in Europe and less than 1.3% of the soybeans produced around the world are produced in Africa. Brazil is the biggest producer; it produces 120.70 million tonnes from 40.89 million ha of area coverage, providing 34.6% of world soybean production. It is followed by the United States, which produces 116.38 million tons from 34.94 million ha of land coverage and provides 33.4% of world soybean production (FAO, 2022).

According to FAO (2022) Brazil, the United States, Argentina, and China account for more than 86% of global production as the leading producers and suppliers. Soybean produced 4538839.28 ton in Africa from 3,859,178 ha of area cultivated (FAO, 2022). The top three soybean producers on the continent are South Africa, Nigeria, and Zambia, while Ethiopia is the sixth producer on the continent (Cornelius and Goldsmith, 2019).

The area of production of soybean in Ethiopia is increased due to increasing demands of soy cooking oil, soy fortified food, animal feed, and improving human nutrition and soil fertility (Deresse Hunde, 2017). However, its cultivation is still not spread much as compared to another crop grown during the same season. In Ethiopia pulses is the second food crops in terms of food behind cereals, covers 14% of the total cultivated land and contribute to making up 10% of the country's agricultural production (CSA, 2022). One of the most significant pulse crops in the nation is soybean, which produced 1,855,222,32 quintals of soybeans form 75,938.88 hectare area of cultivated with the productivity of 24.43 quintal per hectare (CSA, 2022).

Subsistence farmers in different parts of the country who have been engaged in soybean production are benefiting from the multiple uses of the crop (Rehima Mussema *et al.*, 2022). The crop contributes approximately 25% of the country's total oil crop production but accounts for only 14.5% of the country's overall oil crop cultivation (CSA, 2022). Northwest, western, and southwest regions are the key locations now soybeans being widely farming in Ethiopia. In particular, the main soybean-producing regions were Amhara (39%), Benishangul Gumuz (35%), and Oromia (26%) (CSA, 2022).

Variability is the occurrence of differences among individuals that are caused by their genetic make-up and environment during development (Allard, 1960). The development of an effective plant breeding programme is dependent upon the existence of genetic variability. The effectiveness of selection or choice of individuals with desirable traits largely depends upon the degree of genetic variability present in the plant population (Bankapur *et al.*, 2018). The choice of promising genotypes from diverse genetic base, and their subsequent utilization for hybridization is one of the strategies for improving the productivity of soybean.

Genetic variability studies have been conducted in Ethiopia by considerable member of research on soybean. Inadequacy of improved varieties and absence of disease resistance varieties of soybean is the main problem for production in the study area. For this reason, assessing variability is fundamental to identify important traits for soybean improvement and to identify adaptable genotype to the study area. Knowledge generated on genetic variability, heritability, and correlation coefficients help to improve the grain yield through directed selection of component traits. So, the present study is proposed to understand extent of genetic variability, heritability, genetic advance and association of important traits of soybean genotypes.

## 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 0.186 million tons of harvest with average productivity of 2.44 ton per hectare in 2019 (CSA, 2022), which is very low as compared to the productivity of 2.61 ton per hectare the crop in the world (FAO, 2022). Currently, in Ethiopia the demand for soybean product is increasing as a result of increasing population growth, agro processing and urbanization (Afework Hagos and Adam Bekele, 2018). Though, its production and productivity in Ethiopia remains low due to lack of diversified soybean materials and genetic potential reductions of released varieties (Mesfin Hailemariam and Abush Tesfaye, 2018).

In addition, the crop has a narrow genetic base in Ethiopia, which makes it susceptible to different diseases, insects, and abiotic stresses. Hence, inadequacy of high-yielding and better resistance varieties to diseases, insect pests, and other abiotic factors have been the major production and productivity constraints of soybean in Ethiopia, in the region, specifically in the study area. In such cases, continuous introduction and characterization of genotypes would be the primarily option to be considered to cope up with the above-mentioned challenges. Knowledge of the extent and pattern of genetic variability present within the population is definitely essential for further improvement of the crop. Therefore, the present variability study was proposed on newly advanced soybean genotypes which have not been undergone any variability tests.

## 1.3. Objectives of the Study

### 1.3.1. General objective

To assess the genetic variability and association of traits among crossed soybean genotypes to contribute for future soybean improvement program

### 1.3.2. Specific objectives

The specific objectives were:
To evaluate the genetic variability among soybean genotypes;
to estimate heritability and genetic advance of traits;
to determine the extent of association among traits;
to determine relationship among genotypes; and
to identify promising genotypes for future soybean breeding program

# Chapter 2. LITERATURE REVIEW

## 2.1. Genetics, Origin and Distribution of Soybean

Soybean *[Glycine max (*L.*)* Merr.; 2n = 40] is important crop that produces both protein and oils. It was originated in north-eastern China, however currently grown in many different climates throughout the world (Zsögön *et al.*, 2022). It spread to several other nations, producing landraces and secondary gene centres in North India, Japan, Indonesia, the Philippines, Vietnam, Thailand, Malaysia, Myanmar, and the Philippines (Rathod *et al.*, 2017). Soybean were imported to Europe in the 17th century, and it was introduced in the United States in 1765 (Hymowitz, 2004).

It may have been introduced to Africa in the nineteenth century by Chinese traders across the east coast of Africa (Khojely *et al.*, 2018). Finally soybean was introduced to Ethiopia for the first time in the 1950s (Yifru Abera, 2019). A few trials were conducted in Ethiopia's agricultural experimental stations over the following years, but it wasn't until the 1970s, with the introduction of high-yielding soybean varieties from Europe and the USA, that true soybean production began (Tsedeke Abate *et al.*, 2012). The production of the crop at farm level could not take place until recently. Now soybean widely distributed and cultivated in 35 countries in worldwide including some regions of Ethiopia.

Soybeans have a complex genetic makeup that influences various traits such as yield, disease resistance, and nutritional content. The genetic diversity of soybeans is vast, with thousands of different varieties cultivated worldwide (Sammour, 2011). Plant breeders utilize this diversity to develop new cultivars with desired characteristics through selective breeding and genetic engineering techniques. Key genes related to soybean traits such as seed composition, plant architecture, and response to environmental stress have been identified and studied to improve soybean productivity and resilience. Soybean genetics, cytogenetic, molecular genetics, and genomics have made important contributions to soybean breeding and soybean production. Understanding the genetic makeup of soybeans has allowed breeders to accelerate the development of new varieties (Orf, 2008), that can meet the evolving needs of farmers and consumers, ultimately contributing to the sustainability and productivity of soybean production in Ethiopia and beyond.

## 2.2. Taxonomy and Botany of Soybean

The soybean is an economically very important leguminous seed crop for feed and food products that is rich in seed protein (about 40%) and oil (about 20%). Taxonomy of the genus Glycine Wild is well defined based on morphological features, cytogenetic and molecular methods. The taxonomy of wild annual and cultivated soybean is as follows: kingdom: Plantae, Order: Fabales, Family: Fabaceae (Leguminasae), Subfamily: Papilionoideae, Tribe: Phaseoleae, Sub tribe: Glycininae, Genus: *Glycine Wild,* Subgenus: *Soja* (Moench) F.J. Herm and Species of: Glycine soja Sieb. & Zucc and Species: Glycine max L. Merr (Singh, 2017).The subgenus Glycine is perennial, and comprises about 18 species; while Soja is an annual soybean (Rathod *et al.*, 2017). The sub genus Soja is also classified in to two species i.e., *Glycine soja* which is a wild soybean, and *Glycine max* L., which is the cultivated soybean. Initially, the crop develops taproot growth, however latter it begins to forms a significant number of secondary roots. Through the development of root nodules, Brady rhizobium japonicum, a bacterium that fixes nitrogen, establishes a symbiotic association with the roots. There are three different stem types: determinate, semi-determinate, and indeterminate.

The development of soybean is categorized into vegetative growth (leaves and nodes) and reproductive growth (flowers, pods and seeds) (Guriqbal Singh, 2010). Flowering usually begins 25–50 days after planting and lasts for 20–40 days. Early-maturing soybean varieties' flowering is mostly influenced by accumulated heat units, whereas later-maturing soybean varieties' blooming is predominantly impacted by day duration.

Soybeans will produce four to seven trifoliate leaves before the flowering stage (anthesis) starts when they are planted at the right time. Flower clusters are visible on the stem node. The fifth or sixth node is where the first node with a flower cluster can be found. Flower buds can occur on the terminal or auxiliary racemes, depending on the growth habit—determinate or indeterminate. The inflorescence, called a raceme, initially contains about 3 to 35 single flower buds. There may be up to 90% floral abortion, leaving only a few flowers per node (Singh *et al.*, 2007). The stigma is receptive to pollen approximately 24 hours before anthesis and remains receptive 48 hours after anthesis.

Soybean is highly self-pollinated with natural crossing usually below 1% because the stamens are elevated so that the anthers form a ring around the stigma (Singh, 2017). Cross-pollination in plants at 10 m or more from the source pollen is absent or very rare (Caviness, 1966). Pollen tubes pass through the style and enter the filiform apparatus, where the pollen tube tip explodes and releases two sperm nuclei. The first sperm nucleus joins with the egg to create a zygote, while the second sperm nucleus joins with the secondary nucleus to develop the endosperm. Each node's inflorescence may develop into one to twenty pods, giving rise to a maximum of 400 pods per plant. Pods typically appear 4 to 14 days after the beginning of flowering and reach their maximum length after 15 to 20 days (Cober, 2011).

When the plant reaches maturity, pods typically shift from green to yellow to brown. The pod is straight or slightly curved and ranges in length from 2 to 7 cm (TeKrony *et al.*, 1979). After fertilisation, seeds need between 30 and 50 days to mature. When mature, pods typically have 2 to 3 seeds but may have more than 5. The oval or spherical seed is made up of a seed coat that encloses a sizable embryo. Mature seeds of common varieties are often yellow, but they can also be green, brown, black, or bicolour (Song *et al.*, 2016). The hilum, which is part of the seed coat, can vary in size, colour, and shape depending on the environment, illnesses, and genetics of the plant. Yellow, black, brown, grey, or buff is attainable colours for the hilum.

## 2.3. Ecological Requirement of Soybean

The production of soybeans depends on the genetics of the crop and the environment. Soybeans are mainly grown during the main wet season (MWS) and are suitable for upland crop rotations alongside maize, pigeon pea, sesame, and groundnuts. This crop grows well in warm conditions found in the tropics, subtropics, and temperate climates. Soybeans show relative resistance to both low and very high temperatures, although growth rates may decrease above 35°C and below 18°C. Ideal growth conditions for soybeans include warm and moist climates, with temperatures ranging from 26 to 30°C being optimal for most varieties (Sato and Ikeda, 1979). Temperatures below 21°C and above 32°C can hinder flowering and pod development. Additionally, extreme temperatures exceeding 40°C can be detrimental to seed production (Rienke and Joke, 2005).

Soybeans need 400 to 500 mm of water throughout the season to produce a good crop. Adequate moisture is crucial during germination, flowering, and pod formation stages. Conversely, dry weather is essential for ripening. While soybeans can withstand short periods of waterlogging, seed damage due to excessive rain is a significant concern during the rainy season. It can also be grown in an area receiving 450 to 1500 mm annual rainfall; however, soybean requires a minimum of 500 mm annual rainfall to grow very well, and for optimum yields (Tesfaye Abush *et al.*, 2017).

According to 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 favor warm, moist, and well-drained fertile loamy soils, which supply adequate nutrients (Hans *et al.*, 1997). The most suitable soils for cultivating soybeans are well-drained and fertile loam soils with a pH level ranging from 6.5 to 7.0 (Karthikeyan *et al.*, 2013). Sodic and saline soils can impede seed germination, while waterlogging poses a threat to the crop. Soybeans can withstand slightly acidic soil, with the optimal pH range being 5.5 to 6.5. However, they are intolerant of strongly acidic soils below a pH level of 4.5, as this can lead to issues with aluminium (Al) and manganese (Mn) toxicity. Similarly, soils with a pH exceeding 8 may result in micronutrient deficiencies, such as zinc (Zn) and iron (Fe).

### 2.4. Importance of the Crop

Soybean is a multipurpose crop. It is useful for the preparation of different kinds of foods, prevention of chronic human diseases, crop rotation, improving soil fertility, and raw material for oil and concentrates food-producing factories. It is one of the most nutritious food crops; its protein has a good balance of the essential amino acids.

Approximately, it has 40% protein, and 20% oil (Vollmann, 2016). The sulphur amino acids viz., methionine, and cysteine are in low concentration, while lysine and tryptophan are in high concentration. This indicates the possibility of obtaining balanced diet by combining soybean, and cereal foods in the diet, since cereals contain the reverse essential amino acid concentration. Thus, soybean is easily available, cheap, and a rich source of protein for poor farmers, who have less access to animal source protein due to their low purchasing capacity.

Due to its nutritional composition, it also helps to prevent human diseases, especially those arising from unbalanced diet. According Birt *et al.* (2004), soybean consumption can prevent some chronic human diseases. The authors reported that there is strong evidence to conclude that soybean consumption can prevent heart disease risk factor, and bone sparing. Even though, the available evidence is not conclusive enough, they also noted the availability of reports that associate soybean diet with reduced cancer and diabetes.

Soybean is also used as an animal fodder. Ruminant animals need high fibre content in their feed. Soybean hulls are extensively and exclusively used for roughage in feeding livestock (Löest *et al.*, 2001). This feed stuff is a source of highly digestible fibre that does not contain starch (Coverdale *et al.*, 2004). Soy protein concentrates are preferred because the absence of water-soluble carbohydrates not only increases the protein content, but also keep the flatulence problem under control. Soybean meals play an important role in the production of fish feed and pet foods. Soybean proteins and the linoleic and linolenic acids present in full-fat soybean meal may even improve for quality of milk. Soybean meal represents one of the major feed ingredients for cattle, especially during winter.

As a leguminous crop, soybean is important for crop rotation in areas where cereal sole cropping is a common practice. It favours soil fertility and soil structure, increases crop yield, leaves nitrogen in the soil, helps to reduce soil erosion, and soybean crop rotation with maize shows positive effects in pest and disease management, reduces the stress of weeds (Mesfin Hailemariam *et al.*, 2021).

Soybean also plays an important role in increasing household income; as it is a source of cash for subsistence farmers. Recently, there has been an increase in the demand and market value of soybeans due to the crop's use as a raw material for the production of oil, margarine, and food concentrates, as well as the growth of soybean processing facilities in the country.

## 2.5. Soybean Production and Production Constraints in Ethiopia

### 2.5.1. Soybean production and productivity

Soybeans are the most important grains among legumes produced by small scale holders both for subsistence and cash. On average soybean production accounts for 5.9 % of pulse production form 4.5 % of land area coverage in Ethiopia in 2021/22 and it is mainly source of income and food. Soybean is the first most important oil crop used for oil production industry in Ethiopia. Soybean contributes nearly 25.5% to the country’s total oil crop production and accounts for only 14.5% of oil crops area under smallholders (CSA, 2022).

Soybean is used to make a variety of local foods as well as a corn-soy blend for emergency food assistance programs and as the livestock sector, particularly the poultry sector demands more soybean meal. The productivity and production of soybeans are increasing with time. The productivity of soybean increased from 0.3 tons per hectare in 2004/05 to 2.43 tons per hectare in 2021/22 (CSA, 2022). According to CSA (2022), enhancements in productivity may be attributed to the utilisation of better technologies, an increase in the area planted, and the adoption of best practises by smallholder farmers, among other variables.

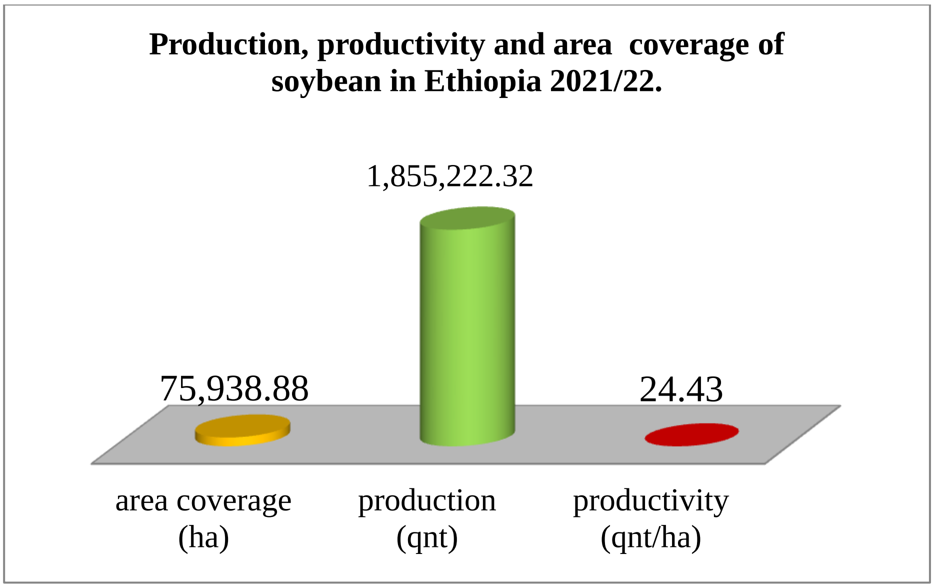

Figure 1. Area coverage, production, and productivity of soybean in Ethiopia in 2021/22

Source: CSA 2022

According to CSA (2022) the area covered by oil crop production in Ethiopia in 2022 was 598,088.16 ha (5 %), where Sesame accounted for 204,511.91 ha (34%), Neug accounted for 179,827.91 ha (30%), Groundnut accounted for 77,283.21 ha (13%) and soybean accounted for 75,938.88 ha (12%). Thus, soybean ranks the fourth next to groundnut among oil crops produced in Ethiopia (CSA, 2022). The major areas currently growing the soybean are Northwest, Western, and Southwest part of Ethiopia (CSA, 2022). In terms of geographical distribution of production soybean produced in three national regions of Ethiopia. It is most dominantly grown in Amhara regions of Ethiopia it accounted for 60 % of production followed by Benishangul region accounted for 34 % and the rest Oromia region accounted for 6 % of soybean in Ethiopia (CSA, 2022).

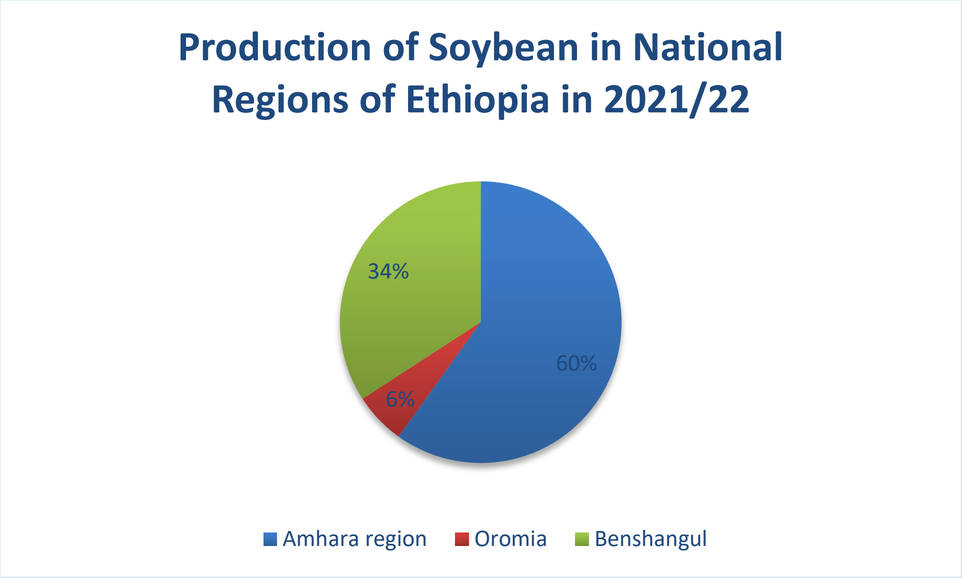

Figure 2. Regional total Soybean Production in Ethiopia in percent

Source: CSA, 2022

### 2.4.2. Soybean production constraints in Ethiopia

Soybean is a crucial economic crop due to its protein and oil content, but its production in Ethiopia remains low. The low yields are attributed to various challenges, including biotic, socioeconomic, and abiotic factors (Meaza Tadesse, 2019). Weather-related issues like extreme temperatures, drought, waterlogging, and frost, as well as soil nutrient deficiencies and salinity, are the primary abiotic constraints affecting soybean production (Hartman *et al.*, 2011).

In addition to environmental challenges, socio-economic factors such as limited access to high-yielding varieties, poor farming practices(crop rotation, planting, application of fertilizer, spraying of herbicides and pesticides, weeding and other management practices), inadequate knowledge of soybean processing and utilization, market limitations, lack of inputs (fertilizers, herbicides, and pesticides), and insufficient government support policies hinder soybean production (Meaza Tadesse, 2019). Biotic constraints like insect pests (aphids, mites, and birds) (Heinrichs and Muniappan, 2019), diseases (Asian Soybean Rust, brown spot, soybean mosaic virus, red leaf blotch, downy mildew, frogeye leaf spot, and bacterial blight), and weeds also pose significant threats to soybean cultivation, leading to reduced yields (Singh *et al.*, 2020).

## 2.6. Soybean Breeding History in Ethiopia

Breeding work on the soybean plant was started in the 1950s and was characterized by plant introduction (Deresse Hunde, 2019). The introductions were assessed to find viable varieties that could adapt to Ethiopia's various conditions as well as to find potential regions for the country's soybean production. The first variety trial was took place at Jimma College of Agriculture in 1956 (Hammer and Haraldson, 1975). Then, from 1958 to 1963, the variety experiments were carried out at the Debre Zeit Agricultural Research Centre (DZARC). The breeding work was discontinued for some time. After that, from 1967 to 1970, trials on a few newly introduced varieties from Germany and America were carried out at CADU (Chilalo Agricultural Development Unit). A cooperative introduction programme was started in 1971 by CADU and ENI (Ethiopian Nutrition Institute), with the main goals of replacing imported soybean flour and introducing the crop into the diet and farming practises of peasant farmers.

In 1971, the programme conducted a variety trial with 63 entries from the FAO and 112 introduced species from Uganda (Deresse Hunde, 2019). The collaborative programme also assessed the resources that were distributed from West Africa, Indonesia, the United States, and Japan in various locations in 1972. In 1974, the Institute of Agricultural Research (IAR), as it was known at the time, began a nationally coordinated soybean research project. The Awassa Agricultural Research Centre (AWARC) of the current SARI (Southern Agricultural Research Institute) has been coordinating the national work on soybean genetic improvement both before and after the decentralisation of agricultural research in the 1990s.The breeding techniques used included plant introduction and, to some extent, selection from introductions. With Jimma and other collaborative centres, the Pawe Agricultural Research Centre in particular was conducting research on soybeans including variety development research (breeding and genetics research) (Deresse Hunde, 2019).

A significant contribution to the advancement of soybean technology is made by soybean varietal development through traditional breeding techniques, which include the introduction of new germplasm, selection of existing germplasm, crossing and hybridization, and advancing generation. In order to promote genetic diversity in line with acceptable, stable, and new varietal development, crossing and hybridization of soybeans were initiated in Ethiopia in 2011–12, mainly at Jimma and Pawe (Deresse Hunde, 2019).

## 2.7. Genetic Diversity of Soybean

Genetic diversity is defined as genetic differences between species, sub species, varieties, populations or individuals. Species with higher genetic diversity are more likely than those with low genetic diversity to be able to adapt in response to a changing environment. In populations lacking genetic diversity, low fertility and high mortality among offspring may occur even in fairly stable environments. Cultivated soybean [*Glycine max* L. Merr.] is one of the most important crops grown for human and animal feed. Soybean is mostly grown in China, Brazil, Argentina, and the United States.

China was the site of the domestication of G. max from the wild species *(Glycine soja Sieb. and Zucc.)*; however, the precise location within China is unknown (Carter *et al.*, 2004; Wang *et al.*, 2016). *Glycine max* differs from *G. soja* by having smaller pods and seeds, viny, twining stems, and practically completes plant breakage at maturity. Hybridizations between wild and domesticated species produce fertile offspring. These fertile offspring forms were at one time called *G. gracilis*. However, Hermann (1962) applied traditional taxonomy to remove *G. gracilis* from the species rank and include it in *G. max*.

According to Carter *et al.* (2004) semi-wild accessions can be separated from G. max and G. soja based on either morphological or genotypic information but they do not always justify a separate species designation.

Utilising the coefficient of parentage, morphological features, and simple sequence repeat (SSR) markers, substantial research has been conducted on the amount or level of genetic diversity and geographic differentiation in Chinese cultivated soybean, demonstrating a definite geographic influence on genetic structure. A core collection of 2794 Chinese soybean accessions based on agronomic traits and SSR markers.

Genetic differences between Japanese and Chinese germplasm have been assessed using SSR markers, RAPD, and isozymes. Diverse Chinese germplasm pools have been used independently and repeatedly to introduce soybeans into South Asia, Japan, and Korea (Abe *et al.*, 2003).

Comparisons between the diversity of different samples of Asian soybean landraces and that of North American cultivars have shown a lower level of diversity in the American pools than in the Asian pools, using either phenotypic characterization or the coefficient of parentage. This reduced diversity was confirmed using sequence analyses to show successive genetic bottlenecks between wild and cultivated soybeans and between Asian landraces and North American cultivars (Hyten *et al.*, 2006).

The narrow genetic base of North American soybean cultivars has been indicated in numerous investigations by using pedigree analysis or molecular markers. According to Gizlice *et al.* (1994) reviewed now generally acknowledged that fewer than 20 progenitor lines represent more than 85% of the genetic base of current North American soybean cultivars; in contrast, the USDA Soybean Germplasm Collection holds nearly 17,000 accessions of *G. max*. Other American genetic pools have also been studied.

In G. max cultivation, soybean accessions present in European germplasm collections may be highly diversified, with genotypes acclimated to temperate conditions that may be useful for European breeding. At the INRA (Institute National de la Recherché Agronomies) in France, a collection of 2000 plant introductions are currently preserved in ex situ; it is made up of accessions derived through various scientific and exchange programmes with Asia and various nations of Europe.

## 2.8. Genetic Variability, Heritability and Genetic Advance

### 2.8.1. Genetic variability

Genetic variation can be defined as the genetic makeup of organisms within a population change (Tsegau Senbetay and Tegegn Belete, 2020). It refers to differences in the genetic makeup of individuals in a population. Genetic variation is necessary selection because if there is no variability among population no need to done selection. Genetic variability is a measure of the tendency of individual accessions in a population to vary from one another. Variability is the degree of variation present in a population, which is different from genetic diversity. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variation in populations is crucial for biodiversity because, without variability, it becomes hard for a population to adapt to environmental changes, which increases their risk of extinction.

Variability is a crucial factor in natural evolution because it influences an individual's response to environmental stress, which can result in unequal survival of organisms within a population owing to natural selection of the fittest variants. As a result, variability is a significant aspect of evolution (Burt, 2000). Furthermore, phenotypic variability is the total variability, which is observable and consist both genotype and environmental variation. Such variation is measured in terms of phenotypic variation (Singh, 2000). The variability of a crop under study is better assessed from genotypic (GCV) and phenotypic (PCV) coefficients of variations, of which high genotypic coefficient variance is breeders usually focus for the traits of interest (Chekole Nigus *et al.*, 2016). Grain yield are the most economical traits and strongly influenced by a variety of environmental factors (Bello *et al.*, 2012).

The study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is highly helpful to evaluate the potential for improvement through selection, in addition to comparing the relative amounts of phenotypic and genotypic variations among different traits. The reliability of a parameter to be selected for a breeding programme, among other factors, is dependent on the magnitude of its coefficient of variation, particularly the genotypic coefficient of variance. However, differences between genotypic and phenotypic coefficients of variability show the influence of the environment. Whereas a lower value of coefficient of variance shows low variability among the tested sample; a high proportion genotypic coefficient variance to the phenotypic coefficient variance is desirable in breeding works (Bello *et al.*, 2012). Presence of high genotypic coefficient variance among the lines describes the possibility of selecting for some most important traits such as grain yield, panicle length, and harvest index (Habte Jifar *et al.*, 2015).

Masreshaw Yirga and Yechalew Sileshi (2023) reported that estimates of genotypic and phenotypic coefficient of variation were high for traits of days to flowering, days to maturity, pods per plant number of seeds per plant hundred seed weight and grain yield. high genotypic and phenotypic coefficient of variation directed the existence of considerable variability for those traits. In addition Yechalew Sileshi (2019) also found high phenotypic coefficient of variation for plant height, number of seed per plant, number of seed per pod, biomass yield, harvest index and grain yield. This author also found high genotypic coefficient of variation for traits of plant height, biomass yield and grain yield in eighteen genotypes.

### 2.8.2. Heritability

Heritability refers to the proportion of variation observed for a particular trait between individuals in a given population that is due to genetic factors. Another genetic parameter to be taken into consideration is heritability, which provides the genetic selection process with objective information by showing how much of the phenotypic variability has a genetic basis (Visscher *et al.*, 2008). Heritability estimates need to be considered together with genetic advance, which is more important than heritability alone to predict the resulting effect of selecting the best individuals. It had been generally believed that the higher the heritability estimates of given traits, the simpler the selection procedure and the better would be the response to selection.

Understanding the relationships between various agronomic characteristics and how they directly and indirectly affect the production of grains can help breeders improve the productivity of crops. There are two types of heritability: broad- and narrow-sense heritability. Broad-sense heritability is the degree to which a trait is genetically determined. it is estimated as the ratio of the total genetic variance (additive and non-additive) to the phenotypic variance ( phenotypic variance) (Kumar *et al.*, 2014). It is the portion of overall or phenotypic variability that can be explained by genetics. It estimates the degree of phenotypic variation caused by gene activity. Narrow-sense heritability is the amount of a trait that is passed from one parent to the progeny or offspring, and it is measured as the ratio of additive genetic variance to total phenotypic variance (Burton and Devane, 1953).

Heritability is of interest to plant breeders mainly as a measure of the effectiveness of selection for a certain trait in different kinds of progenies and as an indicator of transmissibility (Dutta *et al.*, 2018). According to Singh (2001), selection for a trait whose heritability is very high, say, 80% or more, would be relatively simple because genotype and phenotype closely match because the environment has a little impact on phenotype. However, selection may be very challenging or practically impossible for characteristics with low heritability, say 40% or less, due to the environment's ability to mask traits. A trait having high heritability, it indicates that the influence of the environment on the trait is less (Allard, 1960).

Diriba Beyene and Negash Geleta (2021) examined 100 soybean genotypes and he found highly traits of days to flowering, days to emergence, days to maturity, hundred seed weight, biomass yield and grain yield. Jandong *et al.* (2020) also reported high heritability for traits of days to flowering, plant height, branch number, pods per plant and pod weight. Heritability values vary with the nature of the test materials and the area where the experiment is conducted (Ayalew Habtamu *et al.*, 2011). Heritability plays an important role in deciding the suitability and strategy for selection of a character.

### 2.8.3. Genetic Advance

Genetic advance refers to the improvement of mean genotypic value of a population for particular trait towards the desired path as a result of selection (Bello *et al.*, 2012). It measures the genetic gain that would result from selecting the best performing genotype for a given trait (Deresse Hunde, 2017). According to Allard (1960) the success of genetic advance depends on genetic variability, heritability, and selection intensity. When heritability is mainly due to dominance and epitasis, the genetic advance would be low, whereas if heritability is mainly due to the additive gene effect, the genetic advance would be high (significant) (Das *et al.*, 2012).

Genetic variability, heritability, and genetic progress are typically prerequisites for breeding programmes that provide the chance to plant breeders to select genotypes with high yields or to combine or transfer genes with desirable traits (Negi *et al.*, 2017). Heritability and genetic advance are important aspects to determine the success of selection in breeding programs.

Masreshaw Yirga *et al.* (2022) reported of high genetic advance as percent of mean for traits of plant height, pods per plant, seed per plant, number of branches per plant, frogeye leaf spot, hundred seed weight and grain yield and moderate genetic advance as percent of mean reported for lodging, whereas he also found low genetic advance as percent of mean for days to flowering and days to flowering. High genetic advance as percent of mean for plant height, and pod length, moderate genetic advance as percent of mean for pods per plant, and number of seeds per pod, and low genetic advance as percent of mean for traits of days to flowering, days to maturity, branch per plant, and hundred seed weight revealed by the studies of Deresse Hunde (2017).

The genetic gain that can be expected for a particular character through selection is the product of heritability, phenotypic standard deviation and selection differentials. High genetic advance and high heritability is the outcome of additive gene action and the reverse indicates the presence of more non-additive gene action. The traits are expected to be controlled more by additive gene effect and improvement could be through selection in the existing material. However traits like Protein content and oil content improved through hybridization followed by selection are expected to produce some good recombinants (Panse and Sukhatme, 1957).

## 2.9. Association of Traits

### 2.9.1 Correlation analysis

In plant breeding, the degree of correlation between the traits is important. Correlation is a tool that can be used for indirect selection. Correlation studies help the plant breeder gain an understanding of yield components during selection. Correlation co-efficient between grain yield and its component characters is essential for yield improvement, since grain yield in soybean is a complex entity and is highly influenced by several component characters (Mahmudul Hasan, 2018). Studies on path co-efficient are also helpful to understand the direct and indirect effects of various grain yield component characteristics, which help breeders, provide appropriate selection criteria for yield improvement. The estimation of correlation coefficients is an essential statistical approach for assessing characteristics' contributions to seed yield (Rameeh, 2015).

According to Ali *et al.* (2002) reported that pods per plant, seeds per plant and 100-seed weight traits have  positively correlated with seed yield. All these traits influence the yield of soybean directly and indirectly. Likewise Masreshaw Yirga *et al.* (2022) found grain yield was positive and highly significant correlation with days to maturity, plant height, pods per plant, number of seeds per pod number of branches per plant, and hundred seed weight.

Analysis of correlation coefficients determines the component characters on which selection can be utilised for genetic yield improvement by measuring the natural relations between various plant characters. The breeder is always concerned for the selection of superior genotype on the basis of phenotypic expression. However, for the quantitative characters, genotypes are influenced by environment, thereby effecting the phenotypic expression. Information regarding the nature and extent of association of morphological character would be helpful in developing suitable plant type, in addition to the improvement of yield a complex character for which direct selection is not effective.

### 2.9.2. Path coefficient analysis

Path coefficient analysis is a very important statistical tool that indicates which variable exerts influence on another variable. A path coefficient is simply a standardized partial regression coefficient and measures the direct influence of one variable upon another and permits the separation of the correlation in to components of direct and indirect effect. Path coefficient analysis specifies the cause and measures the relative importance of characters, while correlation measures only mutual association without considering causation (Azeb Hailu *et al.*, 2016).

In any breeding programs of complex character such as yield of which direct selection is not effective, it become essential to measures the contribution of each the component variables to the observed correlation and the partition of the correlation into components of direct and indirect effect. Gravois and Helms (1992) showed that path analysis has proven useful providing additional information that describes causes and effect relationships, such as between yield and yield component. Therefore, it is essential to identify degree of association of various quantitative traits in ordered to initiate an effective selection program aimed at genetic improvement of crop yield.

Path co-efficient analysis is a useful tool for identifying the direct and indirect causes of associations. It also offers a critical analysis of the particular forces at play in a given correlation and estimates the amount of significance that each causative factor contributes to the association (Kishore *et al.*, 2015). Correlation estimates are useful in determining the components that influence a trait either positively or negatively. However, they don't give precise information about the relative importance of the direct and indirect effects of component traits on complex traits like yield (Nigus Belay, 2018). Path analysis provides more information among variables than do correlation coefficients.

Path coefficient analysis is a standardized partial regression coefficient is used to partition the correlation coefficients of the grain yield attributing traits into direct and indirect effects on grain yield and to determine the degree of relationship between grain yield and its components (Dewey and Lu, 1959). In path coefficient analysis, grain yield is considered as dependent variable and the remaining traits are considered as independent variables (Singh and Chaudhary, 1979). Thus, it is essential to study the association of yield components with yield and their direct and indirect effect on grain yield through path coefficient analysis.

Asmamaw Amogne *et al.* (2020) studied on eighty one genotypes and found that number of pods per plant was the higher positive direct effect on yield followed by hundred seed weight, seed per plant and oil content, whereas traits of days to flowering, plant height, number of branch per plant and protein content had negative direct effects on grain yield. Gobezie Chakelie (2022) also reported protein content, harvest index, hundred seed weight, number of pods per plant, plant height and days to maturity had positive direct effects on grain yield, whereas days to flowering, grain feeling period, branch per plant and pod length had negative direct effects on grain yield.

### 2.9.3. Cluster analysis

Clustering is the process of grouping a set of data objects into multiple groups or clusters so that objects within a cluster have high similarity, but dissimilar objects grouped in to other clusters. Assessment of similarities and dissimilarities is based on attribute values that describe the objects, and it often involves using distance measurements. The cluster analysis is a method of classification and hierarchy in which the studied population is divided into a number of groups called clusters. It is a multivariate method that aims to divide a sample of subjects into various groups based on a set of measured factors, and similar individuals are placed in the same group. Cluster analysis is a type of exploratory analysis that tries to identify structures within the data.

Cluster analysis is also called segmentation analysis or taxonomy analysis (Taha *et al.*, 2018). More specifically, it aims to identify homogeneous sets of events, such as observations, participants, and responders. Cluster analysis is used to identify groups of cases if the grouping is not previously known. Because of its explorative nature, it does not distinguish between dependent and independent variables. The different cluster analysis methods that SPSS offers can handle binary, nominal, ordinal, and scale (interval or ratio) data. According to Dimitrov *et al.* (2021) the study of breeding materials through the cluster analysis allows breeders to plan and make more effective decisions for the development of their breeding programs. The samples can be divided by genotype, depending on the phenotypic expression of a particular trait or group of traits, using clustering. Classifying genotypes based on their agronomic traits with multivariate techniques could reduce the time period and expenditure for crop improvement.

Based on $D^2$ values Wakjira Getachew (2021) grouped 49 soybean genotypes in to five cluster based on 17 phenotypic traits. Besufikad Enideg (2018) examined the genetic variability and character association in soybean genotypes and grouped 49 genotypes in to three clusters based on 14 phenotypic traits. Sivabharathi *et al.* (2023) also grouped 135 soybean genotypes in to twelve clusters based on ten quantitative traits.

## 2.10. Genetic Divergence

The concept of genetic divergence ($D^2$) statistics was once at the start developed by Mahalanobis (1936). Genetic divergence refers to the statistical separation between genotypes and is identified through cluster analysis, a method that categorizes genotypes into distinct groups (Singh and Chaudhary, 1977). Selection, whether direct or indirect, can effectively target the heritable variability already present in a population.

Additionally, variability can be artificially introduced through hybridization techniques by crossing genetically distant parents. However, the success of this process relies on the genetic divergence among the crossed lines. Greater genetic divergence increases the likelihood of developing high-yielding genotypes. Mahalanobis's $D^2$ analysis offers a method to group genotypes based on their genetic differences (Mahalanobis, 1936), underscoring the critical importance of estimating divergence among the lines.

Crossing genotypes from the same cluster is unlikely to produce desirable recombinants. Therefore, a breeding program should be designed such that parents come from different clusters. The greater the diversity among parents, within certain fitness parameters, the higher the chances of achieving increased hetrotic expression in F1 hybrids and a wide range of variability in segregating populations (Rao *et al.*, 1981). The utilization of the $D^2$ statistic (Mahalanobis, 1936) stands out as a key biometrical technique for assessing genetic divergences within a population.

Utilizing the $D^2$ matrix for clustering based on genetic distance is valuable in assessing population divergence and identifying genotypic variability. The $D^2$ statistics evaluate differentiation forces at intra- and inter-cluster levels, determining the contribution of each trait component to overall divergence (Sharma, 2001). Clusters with the greatest $D^2$ distances exhibit the highest levels of divergence, while genotypes within the same clusters display lower divergence (Singh and Chaudhary, 1977).

Based on $D^2$ value Neelima and Narkhede (2017) grouped 132 soybean genotypes in to five clusters based on 11 quantitative and quality traits and he found that maximum inter cluster distance was between cluster IV and V (D=66.15) followed by cluster II and V (D=58.81) and cluster III and IV (D=57.05). The minimum inter cluster distance was observed for clusters I and III (D=33.73) and cluster III and V (D=33.82). Similarly Kumawat *et al.* (2024) examined 25 soybean genotypes and grouped in to three clusters based on 8 traits. This author found that the highest (D= 4.440) inter cluster distance was observed between cluster II and I, followed by, cluster III and II (3.142), cluster III and I (2.913), indicating wide diversity between genotypes in these clusters. However, the highest (D = 2.081) intra-cluster distance was found for cluster I, followed by, cluster II (1.961), cluster III (1.913). It is suggested that the genetic materials belonging to these clusters may be used as parents for hybridization programme to develop desirable variety.

## 2.11. Principal Component Analysis

Principal component analysis explains the contribution of the most important traits that account for the total genetic variability (Sharma, 2001). 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. The first step in PCA is to see Eigen values, which define the amount of total variation that is displayed on the PC axis. The first PC summarizes most of the variability present in the original data relative to all remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on.

Gada Gudina *et al.* (2023) found that 71.25 % of the total variation was explained among 100 tested soybean recombinant inbred lines by the first four principal components with Eigen values more than one using 12 quantitative traits and also his result implied that the highest variation was found in principal component one (28.4%). Dunna *et al.* (2023) examined thirty three soybean genotypes and he found that 81.748% of the total variability by seven principal components with Eigen values more than one using 14 traits.

Principal component analysis (PCA) has various applications such as the study of genetic divergence between genotypes which permits the identification and selection of the most promising genotypes for cultivation and improvement, besides using in evaluating the relative importance of characters in the total variation available among genotypes (Vianna *et al.*, 2013).

# Chapter 3. MATERIALS AND METHODS

## 3.1. Description of the Study Area

The experiment was conducted at Pawe Agricultural Research Center, North West Ethiopia in 2023 main cropping season. The experimental site is located 575 km to Pawe from Addis Ababa. Pawe Agricultural Research Center is located at 11°17’30”-11°22’30” N latitude and 36°20’30” -36°25’30” E longitude. The average temperature ranges between 19.4 ℃ to 37.6 ℃ and the altitude ranges from 1120 m.a.s.l. The annual rainfall is 1586 mm and the soil type is vertisol. Agriculture is the economic sector in the study area and the major crops cultivated in the study area are maize, sesame, and soybean (PARC, 2023).

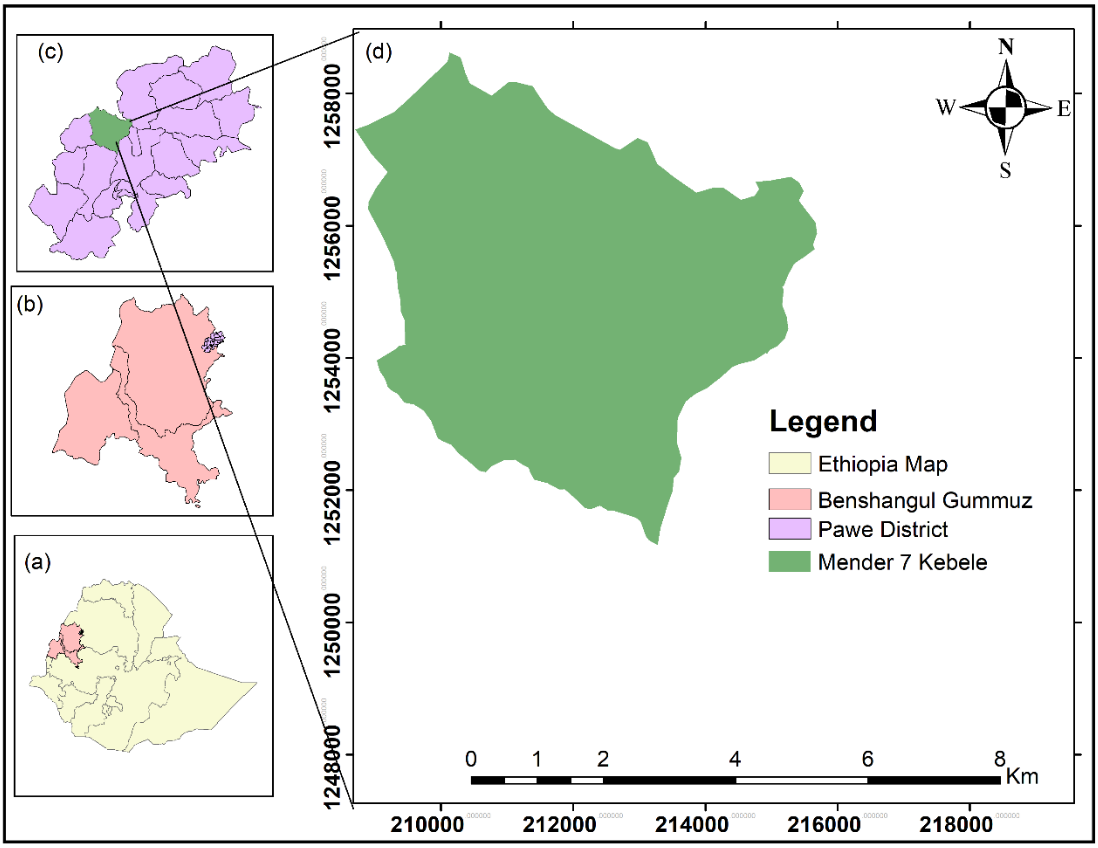

Figure 3. Map of the study area

### 3.2. Experimental Materials and Designs

The experiment was conducted on 150 soybean genotypes (Appendix Table 4). Out of which 147 genotypes were fixed lines obtained from crossed genotypes and the remaining 3 were standard checks. All genotypes were obtained from Pawe Agricultural Research Center.

Design of the experiment was 15x10 alpha lattice designs with two replications. A plot had 4 rows; each 4 m long and 2.4 m wide (9.6 $m^2$) with 0.6 m of row spacing. Distance between plots was 0.6 m and 1.5 m between replications. The total experimental area was 53.5 m x 90.3 m. The seed rate was 16.8 g per row and 67.2 g per plot on the basis of the 70 kg per ha recommended rate (Keerthana *et al.*, 2021). The NPS fertilizer was applied at the recommend rate of 100 kg per ha (Asmachew Agegn *et al.*, 2022). The NPS fertilizer was applied after planting. All other agronomic (pre- and post-management) practises were applied uniformly in accordance with the recommendations made for the crop.

### 3.3. Data to be collected

Data were collected from the two middle rows on plot and plant basis.

#### 3.3.1. Data collected on plot basis

**Days to 50% flowering:** The numbers of days was recorded from planting to 50% of plants open (starts) first flower.

**Days to maturity:** Number of days was recorded from planting until the attainment of physiological maturity of 95% of the stand in each plot as judged by the turning of the vegetative parts of the plants into light yellow color.

**Biomass yield (gram /plot):** Above ground total biomass of all the plants in each plot was weighted at harvest after sun dried and attained constant weight.

**Hundred seed weight (gram):** One hundred randomly counted seeds were weighted after threshing using sensitive balance.

**Grain yield (gram /plot):** The weight of the air-dried seeds harvested from each plot was recorded.

**Harvest index (%):** The ratio of grain yield per plot to biological yield per plot expressed in percent was recorded.

**Shattering:** the data was taken from ten days to 2 weeks after harvest date using 1-5 scoring scale. Where 1= No pods shattered,2=25% of pods shattered,3=50% of pods shattered, 4= 75% of pods shattered,5= all plants shattered.

**Lodging:** the data regarding to lodging was counted the plants lying on the ground per plot using 1-5 scoring scale. Where 1= all plants erect,2=25% op plants lodged,3=50% of plants lodged, 4= 75% of plants lodged,5= all plants lodged.

### 3.3.2. Data collected on plant basis

**Plant height (cm):** Height of the plant in centimetre was recorded from the base of the main stem to the tip of inflorescence as the average of five randomly taken plants from the central two rows in each plot.

**Number of branches per plant**: The pod bearing branches of five randomly taken plants were counted from the middle two rows.

**Numbers of pods per plant:** All seed contained pods of five randomly taken plants were counted from the middle two rows.

**Number of seeds per plant:** The total numbers of seeds per plant was counted as an average of five randomly taken plants from the middle two rows.

**Numbers of seed per pod:** was recorded by dividing the total number of seeds per plant to total number of pods.

### 3.3.3. Quality traits

**Oil content per gram:** The oil content of the grain of soybean genotypes were determined by NIRS after harvesting. For determination of the quantity of oil, one hundred thirty grams of dried seed samples from each genotype was grinded using grinder (Mill 120) at laboratory room. Then, two to three grams of seed flour was taken using small cups (internal diameter of 35 mm and depth of 8 mm) and scanned by Near infrared spectroscopy (NIRS) monochromator model FOSS 6500 (FOSS NIR

Systems, Inc., Silver Spring, Denmark) to estimate the percentage of oil and protein contents.

**Protein content per gram:** The protein content of the grain was also determined by NIRS after harvested. The procedure was the same as of oil content determination.

### 3.3.4. Disease data

Most common and economically importance fungal disease (Frog eye leaf spot), bacterial disease (Bacterial blight), brown spot, and red leaf blotch were happened in the experimental field. The data regarding to those diseases were recorded by visual observation using 1-5 scoring scale (Zubaidah and Kuswantoro, 2016), where 1=no spot, 2=few spot on some plant, 3=some spot on most plant, 4=several spots, and 5=several infection with leaf abscission.

## 3.4. Data Analysis

### 3.4.1. Analysis of variance

The data were checked for its normal distribution using Shapiro Wilk's test (Shapiro and Wilk, 1965) before proceeding to analysis. All data were found normal, but loading, shattering and disease data were transformed by log transformation. Test of homogeneity of error variance was done using Bartlett test (Snedecor and Cochran, 1989). Analysis of variance (ANOVA) was computed for each traits of soybean to test the presence or absence of significance difference among the genotype. Then the genotypes showed a significance difference subjected to mean separation by using Duncan's multiple range test (DMRT). The relevant values generated on plot and plant basis was subjected to analysis of variance (ANOVA) using the linear model: SAS software version 9.4.

$Yij = \mu + G\ Yij = \mu + Gi + Bj + eij$

Where: Yij= observed value of variety i in block j;

$\mu$ = grand mean of the experiment;

Gi= effect of genotype I;

Bj= effect of block j, e and

ij = error (residual) effect of i genotype in j the block to determine the differences existing among the genotypes of soybean i + Bj+ eij.

Table 1. Structure of ANOVA for Alpha lattice design

| **Source of variation** | **DF** | **SS** | **MS** | **F** |
|---|---|---|---|---|
| **Replications** | r-1 | SSr | MSr | |
| **Block within replicates** | rs-r | SSb | MSb | |
| **Treatments (adjusted for block)** | t-1 | SSt | MSt | Fo |
| **Error** | rt-rs-t+1 | SSe | MSb | |
| **Total** | n-1 | SSc | | |

Note: SS=Sum of square; MS= Mean of square; r= Replication; b=Block; s= is the number of blocks per replicate; and t= Treatment.

### 3.4.2. Phenotypic and genotypic variance

The variability present in the population was estimated to identify the genetic variability among the genotypes and to determine the extent of environmental effect on several traits. The phenotypic and genotypic variance was computed for traits showed a significance difference among genotypes according to the methods suggested by Burton and De Vane (1953). Genotypic variance is the variance present due to genotype in the population, was calculated according to the formula suggested by Burton and De Vane (1953). A measurement of variance which is independent of the unit of measurement is provided by the standard deviation expressed as percentage of mean this is known as coefficient of variation (CV). According to Deshmukh *et al.* (1986)The value of phenotypic and genotypic coefficient of variance classified as, low PCV and GCV value (<10%), moderate value (10%-20%) and high PCV and GCV value (>20%). The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were calculated by the formula given Burton (1952).

$\sigma^2g = \frac{Mg-Me}{r}$

Where; $\sigma^2g$ = Genotypic variance;
Mg = Genotypic mean square and
$\sigma^2e$ = Environmental variance (Error mean square)
$\sigma^2P = \sigma^2g + \sigma^2e$
Where, $\sigma^2g$ = genotypic variance;
$\sigma^2P$ = Phenotypic variance; and
$\sigma^2e$ = Error variance.

Phenotypic coefficient of variation, PCV= $\frac{\sqrt{\sigma^2 P}}{X}\ x\ 100$;

Genotypic coefficient of variation, GCV= $\frac{\sqrt{\sigma^2 g}}{X}\ x\ 100$;

Where, X = population mean

Environmental coefficient of variance, ECV= $\frac{\sqrt{\sigma^2 E}}{X}\ x\ 100.$

### 3.4.3. Heritability in broad sense

Heritability in Broad sense ($H^2b$) for all traits showed a significance difference were estimated using the formula of ratio of genotypic variance ($\sigma^2g$ ) to the phenotypic variance ($\sigma^2P$) based on genotype mean according to (Allard, 1960; Falconer, 1990) as follows:

$H2= \frac{\sigma 2g}{\sigma 2P}$

$\sigma^2p = \sigma^2g + \sigma^2e$
Where, $\sigma^2g$=genotypic variance;
$\sigma^2p$ = phenotypic variance; and
$\sigma^2e$ = error variance.

According to Robinson *et al.* (1949) the values of heritability in broad sense for traits were categorized in to three groups, namely low heritability (<30%), moderate (30%-60%) and high (>60%).

### 3.4.4 Estimation of genetic advance

Johnson *et al.* (1955) demonstrated that estimates of genetic advance as percent of mean classified as low (<10%), moderate (10% - 20%) and high (>20%). Genetic advance (GA) and Genetic advance (GA%) as present of the mean for each traits showed a significance difference were calculated based on the methods illustrated by (Fisher, 1987; Falconer, 1990).

$GA = (K) X (Sph) X H^2$

$GA\,\% = \frac{GA}{X} X\ 100$

Where, k= selection differential (k= 2.06);

Sph= phenotypic standard deviation;

$H^2$= heritability (Broad sense); and

X= Grand mean.

### 3.5. Correlation Analysis

Phenotypic and genotypic correlations between yield, yield related, quality and disease traits showed a significance diference were estimated using the method described by Miller *et al.* (1958). Phenotypic correlation, is the observable correlation between variables, wchich is the sum of genotypic and phenotypic effects were estimated from variance components as follow:

$$\text{rpxy} = \frac{COV\ pxy}{\sqrt{\boldsymbol{\sigma}^2 px.\sigma^2 py}}$$

Where, phenotypic correlation coefficient between character x and y;

$COV_{pxy}$= phenotypic covariance between character x and y;

$\sigma^2 px$= phenotypic variance for character x; and

$\sigma^2 py$= phenotypic variance for character y.

$$\text{rgxy} = \frac{COV\ gxy}{\sqrt{\boldsymbol{\sigma}^2 gx.\sigma^2 gy}}$$

Where, rgxy = genotypic correlation coefficient between character x and y;

COV gxy = genotypic covariance between character of xand y;

$\boldsymbol{\sigma}^2 gx$ = genotypic variance for character of x; and

$\sigma^2 g$ = genotypic variance for character of y;

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. Hence, to test the significance of phenotypic correlation coefficients, the formula developed by Sharma (1998).

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

Where, rpxy = Phenotypic correlation; and SErpxy = Standard errors of phenotypic correlation. And

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

Where, $r^2p$ is phenotypic correlation coefficient. Whereas the coefficients of correlations at genotypic levels were tested for their significance using the formula described by Robertson (1959) as indicated below:

$$t = \frac{\text{rgxy}}{\text{SErgxy}}$$

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

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

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

### 3.6. Path Coefficient Analysis

Path-coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into the measures of direct and indirect effects (Dewey and Lu, 1959). Both the traits showed significant and non-significance correlations between the traits in correlation coefficient analysis were subjected to path coefficient analysis. Depend on genotypic correlation, path coefficient which refers to the direct and indirect effect of yield attributing traits (independent character) on grain yield (dependant character) was estimated as the method adopted by Dewey and Lu (1959). The path coefficient analysis was done by SAS software analysis.

$rij = Pij + \sum rikpkj$

Where, rij = Mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients; Pij = Components of direct effects of the independent character (i) as measured by the path coefficients; and ∑rikpkj = summation of components of indirect effect of a given independent character (i) on a given dependent character (j) via all other independent characters (k).

The contribution of the remaining unknown factor was measured as the residual factor (Pr) which determines how best the causal factors account for the variability of the dependant factor of yield, will be calculated as: Pr = $\sqrt{(\mathbf{1} - \sum \boldsymbol{r_{ij}p_{ij}})}$ (Singh and Chaudhary, 1979).

If Pr value is small (for instance, nearly zero) the dependent character considered (seed yield) is fully explained by the variability in the independent characters, whereas higher Pr value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (seed yield).

### 3.7. Genetic Divergence Analysis

Genetic divergence analysis was calculated for traits showed a significance difference using Mahalanobis's $D^2$statics developed by Mahalanobis (2018) by SAS 9.4 version.

#### 3.7.1. Estimation of square distance

Square distance ($D^2$) for each pair of genotype combination was estimated using the formula as follow:

$D^2ij = (Xi – Xj)\ S^{-1}\ (Xi – Xj)$

Where, $D^2ij$ = the square distance between any two genotypes of i and j; Xi and Xj = the vectors for genotype $i^{th}$ and $j^{th}$ genotype; and $S^{-1}$ = the inverse of pooled variance covariance matrix.

### 3.7.2. Clustering of analysis (Genotype)

Before running multivariate analysis, the data was standardized to mean zero and variance 1. Cluster analysis is a multivariate method which aims to classify a sample of subjects on the basis of a set of measured variables into a number of different groups such that similar subjects are placed in the same group. Based on square distance ($D^2$) the genotypes were clustered to the same group by using Tocher's method suggested by Singh and Chaudhary (1979).

### 3.7.3. Estimation of intra and inter cluster square distance

Average intra and inter cluster $D^2$ values was estimated using the formula $\frac{ED^2i}{n}$ where, $\sum D_i^2$ is the sum of distance between all possible combinations (n) of the genotypes included in a cluster. Significance of the squared distances for each clusters were tested against the tabulated χ2 values at p degree of freedom at 5% probability level. Where, p = number of characters used for clustering genotypes.

Average intra and inter cluster $D^2$ values were estimated using the formula given by Singh and Choudhary (1985),

Intra Cluster Distance $D^2 = \frac{\sum Di^2}{n}$

Inter Cluster Distance $D^2 = \frac{\sum Di^2}{ninj}$

Where, $\sum Di^2$ =is the sum of distance between all n possible combinations; (n) is the population/genotypes included in a cluster; and ni and nj = number of genotypes in cluster i and j respectively.

## 3.8. Principal Component Analysis

Principal component analysis (PCA) is probably the most popular multivariate statistical technique and it is used by almost all scientific disciplines and PC has inherently more information than would any single variable alone (Iezzoni and Pritts, 1991). The principal components are used to interpret based on finding which variables are most strongly correlated with each component. The principal components may then be used as predictor or criterion variables in subsequent analyses. PCA was computed for all traits showed a significance difference to identify the character, which accounted more to the total variation. Before proceeding PCA estimated the data was standardized to mean zero and variance one. The principal component analysis was calculated based on correlation matrix using SAS 9.4 software.

# Chapter 4. RESULTS AND DISCUSSION

## 4.1. Analysis of Variance (ANOVA) Yield, Yield Related, Quality and Disease Traits

The results of analysis of variance in present study for nineteen quantitative traits including, quality, and disease traits are presented bellow in table 2. The result showed there was highly significant different (P<0.01) among 150 soybean genotypes in days to flowering, days to maturity, lodging, shattering, plant height, hundred seed weight, average grain yield, number of pods per plant, total seed per plant, number seeds per pod, biomass and harvest index, protein content, oil content, frogeye leaf spot, bacterial blight, brown spot, and red leaf blotch and significant different (P<0.05) among genotypes for number of branch per plant.

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. Similarly, highly significant difference (p<0.01) results among soybean genotypes have been reported for days to flowering, days to maturity, plant height, number of branch per plant, hundred seed weight, average grain yield, number of pods per plant, total seed per plant, number seeds per pod (Jandong *et al.*, 2020; Diriba Beyene *et al.*, 2021), for Biomass yield and harvest index (Kumar *et al.*, 2020).

In addition, significant difference was reported for shattering and lodging among soybean genotypes (Masreshaw Yirga *et al.*, 2022). Similarly, Masreshaw Yirga *et al.* (2022) reported a highly significant difference among 100 soybean genotypes for frog eye leaf spot, however in disagreement with the present result, non-significant difference was reported for bacterial blight. Highly significant difference among soybean genotypes was reported for red leaf blotch (Murithi *et al.*, 2022).

Table 2. Mean square for nineteen traits of soybean genotypes recorded at PARC

| **S.NO** | **Traits** | **Mean Square** | | | | **CV (%)** | **R-square** |
|---|---|---|---|---|---|---|---|
| | | Rep | Block(Rep) | Genotype | Error | | |
| | DF | 1 | 18 | 149 | 131 | | |
| **1** | DTF | 5.60$^{ns}$ | 2.06$^{ns}$ | 109.86$^{**}$ | 1.55 | 2.72 | 98.86 |
| **2** | DTM | 33.33$^{ns}$ | 10.37$^{ns}$ | 114.22$^{**}$ | 11.85 | 3.16 | 92.05 |
| **3** | LDG | 0.00$^{ns}$ | 0.12$^{ns}$ | 0.99$^{**}$ | 0.14 | 25.36 | 89.79 |
| **4** | STG | 0.013$^{ns}$ | 0.17$^{ns}$ | 1.33$^{**}$ | 0.21 | 19.03 | 88.42 |
| **5** | PH | 75.00$^{ns}$ | 52.54$^{ns}$ | 293.67$^{**}$ | 55.79 | 11.43 | 86.51 |
| **6** | BPP | 11.21$^{*}$ | 0.71$^{ns}$ | 1.37$^{*}$ | 0.84 | 16.41 | 67.70 |
| **7** | HSW | 0.96$^{ns}$ | 1.67$^{ns}$ | 9.96$^{**}$ | 1.90 | 9.32 | 86.64 |
| **8** | GY | 20294.20$^{ns}$ | 45277.87$^{ns}$ | 426906.10$^{**}$ | 63022.91 | 11.04 | 89.06 |
| **9** | PPP | 298.80$^{*}$ | 50.61$^{ns}$ | 521.09$^{**}$ | 44.18 | 8.46 | 93.32 |
| **10** | SdPP | 1778.77$^{*}$ | 522.17$^{ns}$ | 3113.17$^{**}$ | 426.71 | 12.33 | 89.73 |
| **11** | SedPP | 0.002$^{ns}$ | 0.056$^{ns}$ | 0.10$^{**}$ | 0.04 | 9.73 | 74.16 |
| **12** | PC | 8.88$^{*}$ | 0.93$^{ns}$ | 1.59$^{**}$ | 0.62 | 1.92 | 78.01 |
| **13** | OC | 4.30$^{**}$ | 0.46$^{*}$ | 1.78$^{**}$ | 0.22 | 2.03 | 91.46 |
| **14** | BM | 437007.6$^{ns}$ | 2123504.40$^{ns}$ | 2123504.4$^{**}$ | 261135.00 | 11.08 | 90.81 |
| **15** | HI | 18.47$^{ns}$ | 32.68$^{ns}$ | 72.20$^{**}$ | 36.78 | 12.09 | 70.64 |
| **16** | FLS | 0.037$^{ns}$ | 0.058$^{ns}$ | 0.744$^{**}$ | 0.106 | 19.87 | 89.76 |
| **17** | BBL | 0.941* | 0.183$^{ns}$ | 0.665$^{**}$ | 0.122 | 13.52 | 87.17 |
| **18** | BS | 0.875* | 0.174$^{ns}$ | 0.878$^{**}$ | 0.225 | 18.35 | 83.34 |
| **19** | RLB | 1.08* | 0.128$^{ns}$ | 0.856$^{**}$ | 0.084 | 11.03 | 92.75 |

*Note: *, ** Significant at 0.05 and 0.01 probability levels, respectively. Ns=non-significant at 0.05 probability level. CV=coefficient of variance;* $R^2$*=coefficient of determination; DF=degree of freedom. DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC= Protein content; OC= Oil content; FLS=frog eye leaf spot; BB=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

## 4.2. Mean and Range Values of Yield, Yield Related and Quality Traits

The mean and range values of thirteen yield and yield related, and two quality traits are presented in Table 3. The mean performance of 150 genotypes for 15 traits is also presented in Appendix table 3. The 150 soybean genotypes showed wide range of variability for all traits except lodging. The highest and lowest range values showed that genotypes had different performances in yield, yield related traits, and quality traits. Usually, the range and mean values for traits evaluated in the present study showed the existence of adequate variability among the tested soybean genotypes. Similarly, wide range of variation on days to 50% flowering, days to maturity, lodging, Shattering, plant height, branch number plant, hundred seed weight, grain yield, pod number per plant, and seed number per plant was reported by Masreshaw Yirga *et al.* (2022).

The mean values of days of 50% flowering and days to maturity ranged from 34.5 to 60.5 and 78.5 to 125.5, respectively (Table 3). The earliest days to heading were recorded from genotypes PW06_18_S_14 and PW10_18_S_25 (34.5 days) while the latest was recorded from the genotype PW13_17_S_31 (60.5 days) and PW05_17_S_13 (60.5 days) and PW04_17_S_35 (60.5 days) (Appendix table 3). The number of days to maturity ranged from 97.25 to 125.00 days among the tested genotypes. The early maturity date was recorded from genotypes PW17_18_S_14 (78.5 days), while the late matured were found from SC_Signal (125.5 days), followed by genotype PW03_17_S_21 (125.5 days).

The present study conducted on 150 soybean genotypes out of which 19 genotypes were early matured, 101 genotypes were found for medium maturity group and 30 genotypes were late matured group (Appendix table 3). 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 agro ecological conditions which are mainly characterized by rainfall distribution. Similar result with wide ranges of variation for traits days to flowering and days to maturity have been reported (Saini *et al.*, 2020), and also Yechalew Sileshi (2019) found variations in days to flowering and days to maturity.

The grain yield ranged from 1167.81 kg/ha to 3593.62 kg/ ha and the highest grain yield was recorded from PW09_18_S_15_2 (3593.62 kg/ha) followed by genotype PW21_18_S_23_1 (3519.17 kg/ha), PW04_17_S_11 (3291.17 kg/ha) and SC_Signal (3186.77 kg/ha), while the lowest yield was recorded from the genotype PW06_18_S_35 (1167.81 kg/ha), followed by genotype PW10_18_S_25 (1242.72 kg/ha) and PW09_18_S_11 (1424.29 kg/ha) (Appendix table 3). If the breeding objective is to improve grain yield, genotypes with high yield in this study needs further work. Diriba Beyene *et al.* (2022) found variations in grain yield among soybean genotypes. Kumar *et al.* (2020) and (Adhikari *et al.*, 2018) reported variation for such soybean traits.

Protein content and oil content are another most important trait in quality and showed mean value of 41 % and 22.91 % respectively and the value ranged from 37.55 % to 43.25 % and 20.25 % to 24.95 % for protein content and oil content respectively (table 3). The highest protein yield was found for genotype PW09_18_S_25_1 (43.25 %) and followed by genotype PW04_17_S_32 (42.95 %), PW11_18_S_23 (42.8), whereas the lowest value was recorded for genotype SC_Signal (37.55 %) followed by genotype PW04_17_S_12 (37.95 %) and PW01_18_S_13_2 (38.1 %) (Appendix table 3). Similarly

The maximum oil yield was obtained from genotype PW16_18_S_23 (24.95 %) followed by PW11_18_S_21 (24.8 %) and PW16_18_S_22 (24.7 %), however the minimum oil yield found for genotype PW04_17_S_32 (20.25 %) followed by genotype PW08_17_S_11 (20.3 %) and genotype PW05_17_S_11 (20.75 %) (Appendix table 3). Well performed genotypes in protein content and oil yield were found in the current study, therefore if the breeding program needs to improve oil yield and protein content those genotypes needs further work. Similar findings reported, Gobezie Chakelie (2022) tested 81 soybean genotypes and found wide variations for traits oil yield and protein content and Dutta *et al.* (2021) found wide ranges of variations among soybean genotypes for oil content.

Number of branch per plant and number of pods per plant are the most yield contributing traits. It ranged from 3.2 to 8.2 and 37.6 to 136.9 respectively (table 3). The highest number of branch per plant was obtained from genotype, PW07_17_S_21 (8.2), followed by genotype, PW09_18_S_15_1 (7.7), PW01_17_S_25 (7.5) and genotype PW01_17_S_33 (7.4) whereas the lowest branch per plant was obtained from genotype PW06_18_S_14 (3.2) followed by genotype, PW01_18_S_13_2 (3.8), and genotype PW09_18_S_11 (4) (Appendix table 3).

The highest pods per plant was recorded from genotype PW13_17_S_11 (136.9) followed by PW07_17_S_21 (133), and PW16_18_S_35_2 (118.9) genotypes, while the minimum pods per plant was recorded from genotype PW06_18_S_14 (37.6) followed by genotype, PW06_18_S_13 (41.6), PW09_18_S_11 (41.8) (Appendix table 3). If the breeding program needs to improve the number of branch per plant and number of pods per plant these genotypes further test will be considered.

Plant height and hundred seed weight showed mean value of 65.35cm and 14.20 gram respectively and it ranged from 27cm to 93.2 cm and 9 gram to 19.25 gram respectively (table 3). The highest plant height was obtained from genotype PW01_17_S_32 (93.2 cm) followed by genotype PW19_18_S_25 (92.6 cm) and PW01_17_S_12 (91.7 cm), whereas the lowest plant height value was recorded from genotype PW06_18_S_13 (27 cm) followed by genotype PW10_18_S_22 (29.4 cm) and PW06_18_S_14 (31.5) (Appendix table 3).

The higher hundred seed weight was recorded from genotype PW09_18_S_25_1 (20 gram) followed by genotype PW20_18_S_44 (19.25 gram) and PW10_18_S_22 (18.85 gram), while the minimum value was recorded from genotype PW05_17_S_11 (9 gram) followed by PW05_17_S_13 (9.25 gram) and PW13_17_S_11 (9.25 gram). Therefor if the breeding programs and plant breeding experts needs to improve traits like plant height and hundred seed weight above mentioned genotypes in this finding needs further work. A similar finding had been reported by Kuswantoro *et al.* (2021) and Guleria *et al.* (2019) on plant height and hundred seed weight. Gada Gudina *et al.* (2023) evaluated 97 soybean recombinant inbred lines and found wide ranges of variation for plant height and hundred seed weight.

Seed per plant and seed per pod are yield contributing trait which showed mean value of 167.49 and 2.13 respectively and ranged from 75.1 to 308.8 and 1.3 to 2.74 respectively (table 3). The highest seed per plant was obtained from PW13_17_S_11 (308.8) genotype, followed by genotype PW09_18_S_15_1 (268.5) and genotype PW01_17_S_33 (256.9), however the lowest value was found from genotype PW06_18_S_14 (75.1) followed by genotype PW10_18_S_22 (83.4) and PW06_18_S_13 (88) (Appendix table 3).

The highest seeds per pod were found from genotype PW06_18_S_35 (2.73) followed by genotype PW01_17_S_33 (2.61) and PW11_18_S_21 (2.57), whereas the minimum values was obtained from PW16_18_S_43 (1.3) genotype followed by PW16_18_S_15 (1.46) and PW02_18_S_25 (1.64) genotype. In general, the results showed that there was a large range of variance among the soybean genotypes in these traits, which may be used in a breeding program to improve seed per plant and seed per pod.

On the other hand biomass yield and harvest index showed mean value of 4611.11 kg/ha and 50.13% respectively and performance of genotypes ranged from 1979.2 kg/ha to 7395.8 kg/ha and 32.28% to 73.89 % biomass yield and harvest index respectively (table 3). The maximum biomass yield was obtained from genotype PW13_17_S_11 (7395.833 kg/ha) followed by genotype PW09_18_S_15_2 (6875 kg/ha) and PW01_17_S_13 (6770.83 kg/ha), however the minimum value was obtained from PW10_18_S_25 (1979.17 kg/ha) followed by genotype PW06_18_S_35 (2291.67 kg/ha) and PW20_18_S_21 (2604.17 kg/ha) (Appendix table 3). The maximum harvest index was recorded for PW13_17_S_21 (73.89 %) followed by genotype PW09_18_S_12 (70.20%) and PW04_17_S_13 (68.57%) whereas the lowest value was found from genotype PW14_17_S_21 (32.28%) followed by PW01_17_S_33 (35.59%) and PW15_17_S_11 (37.43 %) (Appendix table 3). The performance of genotypes widely ranged for crop lodging and shattering from 1 to 3.5 and 1 to 4 respectively.

### 4.2.1. Mean and ranges of diseases traits

The mean and range values of four disease traits are presented in a Table 3. The mean performance and disease reactions of 150 genotypes for four major disease traits are presented in Appendix Tables1 and 2. Disease scoring for all traits was done through visual observation in plot bases in two rounds. The first round was conducted after flowering, and the second round of records was taken two weeks after the first round. The present findings consist of 150 soybean genotypes, including three checks.

The mean value for frog eye leaf spot was 1.54, with a range of 1 to 3. Evaluating soybean genotypes for their reactions to frog eye leaf spot is seen as the most feasible and durable solution for controlling FLS disease in soybeans. The study revealed that the majority of genotypes fell under the categories of resistant (50.7%) and moderately resistant (40.7%) (Figure 4). Out of the 150 genotypes studied, 76 were classified as resistant to frog eye leaf spot, 61 as moderately resistant, and the remaining 13 as moderately susceptible (Appendix table 1). None of the test genotypes were observed to be susceptible and highly susceptible to frog eye leaf spot.

Das *et al.* (2017) screened twenty six different soybean verities to find the resistance potential of genotypes against frog eye leaf spot and his result also showed maximum number of genotypes grouped as resistance and moderately resistance. This author reported fifteen varieties resistant, eight varieties rated as moderately resistant; two varieties were categorized under moderately susceptible and only one genotype showed susceptible for frog eye leaf spot. Sharma *et al.* (2023) also screened 200 soybean germplasms against frog eye leaf spot. Out of 200 genotypes, five were having absolute resistance, 20 were highly resistant, 74 were moderately resistant, 70 were moderately susceptible, 28 were in category of susceptible and three were highly susceptible. These resistant and moderately resistant varieties can be used as good donor for evolving resistant varieties against Frogeye leaf spot disease in soybean.

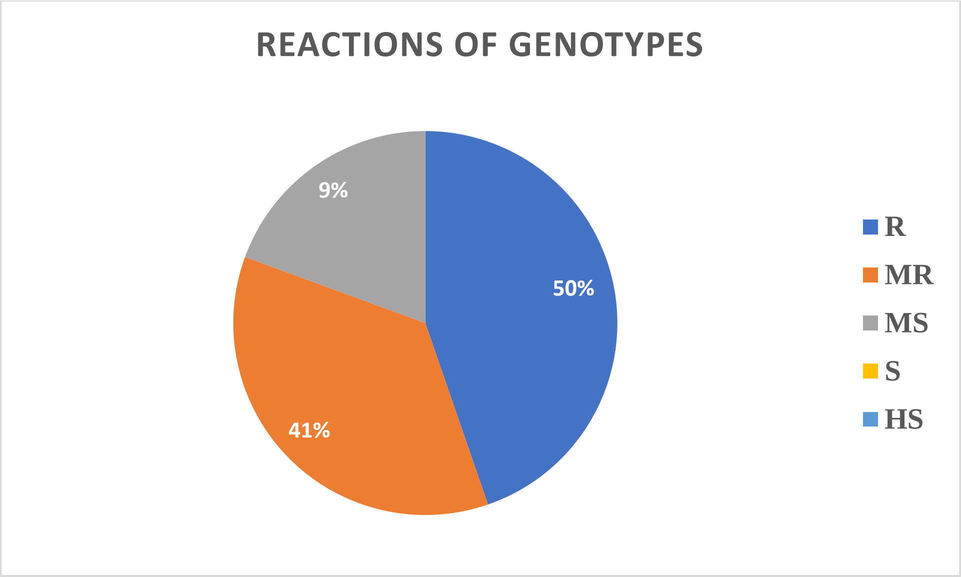

Figure 4. Reactions of soybean genotypes for frog eye leaf spot

Where R= resistance; MR= Moderately resistance; MS= Moderately susceptible; S= Susceptible; HS= Highly susceptible.

The mean value of bacterial blight was 2.58 and also it ranged from 1 to 3.9 (Table 3). Out of the 150 tested soybean genotypes, most showed moderate susceptibility (70.7%) and moderate resistance (16.7%) (Figure 5). Among these findings, 10 genotypes were found to be resistant to bacterial blight, 25 were rated as moderately resistant, and the majority (106) were categorized as moderately susceptible. The remaining nine genotypes showed susceptible reactions to bacterial blight. However, none of the genotypes exhibited highly susceptible reactions in the study (Appendix table 1).

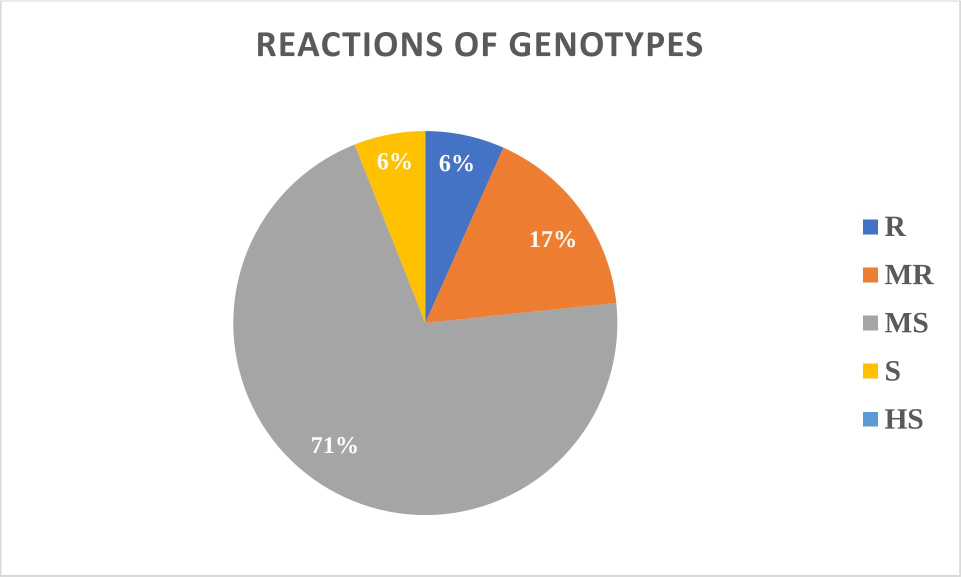

Figure 5. Reactions of soybean genotypes for bacterial blight

Where R= resistance; MR= Moderately resistance; MS= Moderately susceptible; S= Susceptible; HS= Highly susceptible.

Brown spot is yield influencing traits which showed mean values of 2.56 and the mean values ranged from 1 to 4.4 (Table 3). The present finding studied on the reactions of soybean genotypes against brown spot. The outcomes of the findings showed that most of the genotypes reacted for moderately susceptible (58.7%) and moderately resistance (29.3%) (Figure 6). The study consisted of 150 soybean genotypes out of which 10 resistance genotypes were found against brown spot. The maximum numbers of genotypes were categorized in to moderately resistance (44) and moderately susceptible (88). Eight genotypes were found susceptible for brown spot. However similarly to above mentioned disease none of genotypes was found highly sucipitabel to brown spot (Appendix table 2).

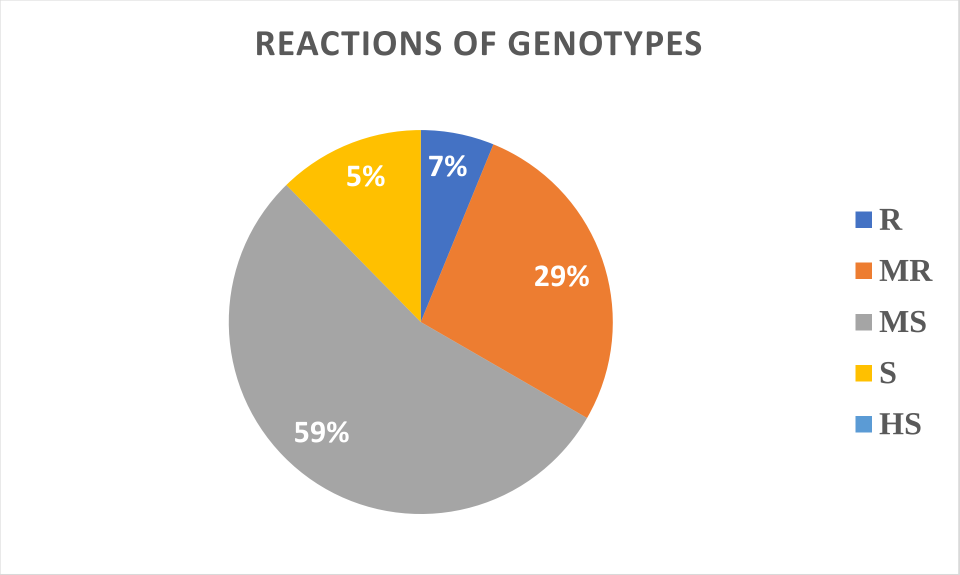

Figure 6. Reactions of soybean genotypes for brown spot

Where R= resistance; MR= Moderately resistance; MS= Moderately susceptible; S= Susceptible; HS= Highly susceptible.

In the study, another influential disease trait affecting yield was red leaf blotch. Red leaf blotch had a mean value of 2.63, with range values varied from 1 to 3.9 (Table 3). The reaction of genotypes to red leaf blotch was observed in the field. Among 150 soybean genotypes, the majority showed susceptibility, with 13.3% being susceptible and 64.7% moderately susceptible (Figure 7). The results indicated that 15 genotypes were resistant to red leaf blotch, while 18 genotypes showed moderate resistance (Appendix table 2). Additionally, 97 genotypes were classified as moderately susceptible and 20 genotypes as susceptible to red leaf blotch. None of the genotypes were highly susceptible to red leaf blotch.

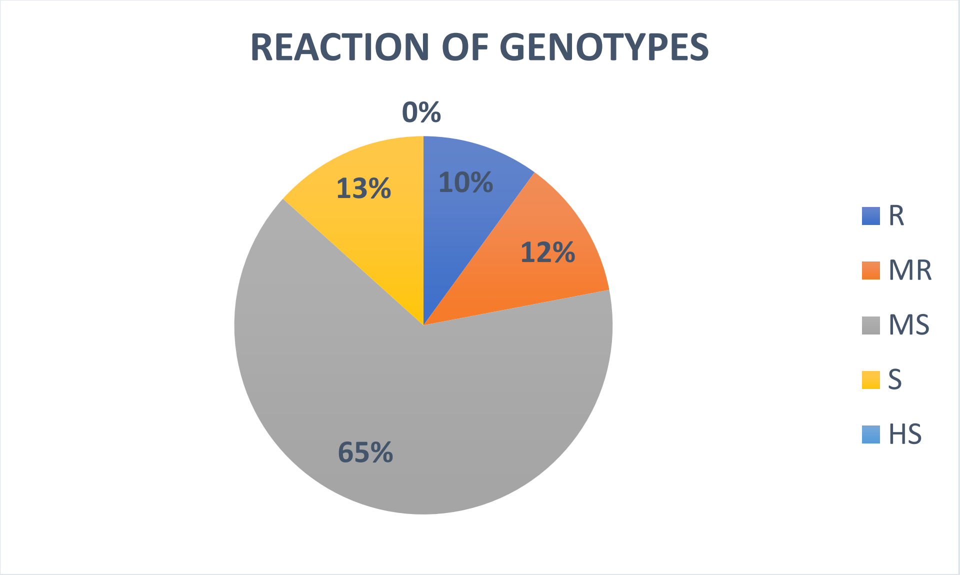

Figure 7. Reactions of soybean genotypes for red leaf blotch

Where R= resistance; MR= Moderately resistance; MS= Moderately susceptible; S= Susceptible; HS= Highly susceptible.

In general, the reactions of genotypes varied for different diseases. This result indicated the presence of resistant and moderately resistant genotypes for frog eye leaf spot, bacterial blight, brown spot, and red leaf blotch. Therefore, if breeders or breeding programs aim to enhance the resistance or performance of soybean genotypes, these specific genotypes require further attention and work.

Table 3. Mean and range performance of nineteen traits

| Traits | Mean ± SD | Range |  | CV (%) | $R^2$ (%) |
|---|---|---|---|---|---|
|  |  | Minimum | Maximum |  |  |
| DTF | 45.66 ± 1.24 | 34.5 | 60.5 | 2.72 | 98.86 |
| DTM | 109.05 ± 3.44 | 78.5 | 125.5 | 3.16 | 92.05 |
| LDG | 1.45 ± 0.37 | 1 | 3.5 | 25.36 | 89.79 |
| SHG | 2.43 ± 0.46 | 1 | 4 | 19.03 | 88.42 |
| PH | 65.35 ± 7.47 | 27 | 93.2 | 11.43 | 86.51 |
| BPP | 5.59 ± 0.92 | 3.2 | 8.2 | 16.41 | 67.70 |
| HSW | 14.79 ± 1.38 | 9 | 20.75 | 9.32 | 86.64 |
| GY | 2274.64 ± 251.04 | 1167.81 | 3593.62 | 11.04 | 89.06 |
| PPP | 78.56 ± 6.65 | 37.6 | 136.9 | 8.46 | 93.32 |
| SdPP | 167.49 ± 20.66 | 75.1 | 308.8 | 12.33 | 89.73 |
| SedPP | 2.13 ± 0.21 | 1.3 | 2.735 | 9.73 | 74.16 |
| BM | 4611.11 ± 511.01 | 1979.2 | 7395.8 | 11.08 | 90.81 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| HI | 50.13 ± 6.07 | 32.28 | 73.89 | 12.09 | 70.64 |
| PC | 41.00 ± 0.79 | 37.55 | 43.25 | 1.92 | 78.01 |
| OC | 22.91± 0.46 | 20.25 | 24.95 | 2.03 | 91.46 |
| FLS | 1.64 ± 0.33 | 1 | 3 | 19.87 | 89.76 |
| BBL | 2.58 ± 0.35 | 1 | 4 | 13.52 | 87.17 |
| BS | 2.59 ± 0.47 | 1 | 4.4 | 18.35 | 83.34 |
| RLB | 2.63 ± 0.29 | 1 | 3.9 | 11.03 | 92.75 |

*CV=coefficient of variance; $R^2$= coefficient of determination; SD=standard deviation. DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC=Protein content; OC= Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

## 4.3. Estimation of Genetic Parameters

### 4.3.1. Estimates of variance components

The estimated of genetic variance, phenotypic variance, phenotypic coefficient of variance and genotypic coefficient variance for all traits considered are presented in Table 4. Estimates of genetic and phenotypic variance under the study ranged from 0.03 for number of seeds per pod to 931184.70 for biomass yield, and 0.07 numbers of seeds per pod to 1192319 for biomass yield respectively. The highest genetic variance was observed from biomass yield (931184.7) followed by grain yield (181941.60), number of seeds per plant (1343.23), number of pods per plant (238.46) and plant height (118.94). The minimum genetic variance was found for number of seeds per pod (0.03) followed by number of branch per plant (0.27), bacterial blight (0.27), frogeye leaf spot (0.32) and brown spot (0.33).

The highest phenotypic variance was record for biomass yield (1192319) followed by grain yield (244964.51), number of seeds per pod (1769.94), number of pod per plant (282.63) and plant height (174.73), whereas the lowest phenotypic variance was recorded from number of seeds per pod (0.07) followed by bacterial blight (0.39), frogeye leaf spot (0.43), and red leaf blotch (0.47).

Similarly high genetic variance and phenotypic variance have been reported for days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per plant, biomass yield, grain yield and harvest index (Yechalew Sileshi, 2019; Tesfaye Belay *et al.*, 2022). The result of variance component for traits of days to 50% of flowering, days to maturity, lodging, shattering, plant height, number of pods per plant, branch number plant, hundred seed weight, grain yield, seed number per plant, number of seeds per pod, biomass yield, harvest index, frog eye leaf spot, bacterial blight, brown spot, and red leaf blotch implied that genotypic variance were higher than environmental variance. The presences of higher genotypic variance could be these traits are more affected by genetic factor and less affected by the environment influences and it could be improved through selection.

Phenotypic coefficient of variation values varied from 2.56% for protein content to 51.84 % for lodging, while genotypic coefficient of variation values ranged from 1.70 % for protein content to 44.96% for lodging. Traits loading, shattering, plant height, grain yield, number of pods per plant, number of seeds per plant, biomass yield, frog eye leaf spot, bacterial blight, brown spot and red leaf blotch represented high PCV value (Table 4).

Similar high PCV values have also been reported (Besufikad Enideg, 2019; Habte Berhanu *et al.*, 2023) for traits of plant height, grain yield, number of pods per plant, Diriba Beyene *et al.* (2021) for biomass yield and Yechalew Sileshi (2019) for number of seeds per plant. Similarly, Masreshaw Yirga *et al.* (2022) reported high PCV values for frog eye leaf spot. High values of phenotypic coefficient of variation suggested the existence of considerable variability for the traits. Moderate phenotypic coefficient of variation for days to 50% of flowering, number of branches per plant, number of seeds per pod, hundred seed weight, and harvest index showed a considerable amount of phenotypic variation among the genotypes, therefore, improvement is possible through phenotypic selection for the traits. The present result is in agreement with Gobezie Chakelie (2022) who found moderate PCV values for traits of days to 50% of flowering, number of seeds per pod, hundred seed weight and harvest index. Kuswantoro *et al.* (2018) had reported moderate PCV value for number of branches per plant which is in line with the present finding.

Low phenotypic coefficient of variation was reported for days to maturity, protein content and oil yield. Similar results have been reported (Gobezie Chakelie, 2022) for days to maturity, protein content and oil yield among soybean genotypes.

Higher genotypic coefficient variation values were found for lodging, shattering, seeds per plant, biomass yield, frog eye leaf spot, bacterial blight, brown spot, and red leaf blotch. The presence of high GCV for these traits indicated the possibility of improving these traits through selection. Similar result was obtained by Masreshaw Yirga *et al.* (2022) who reported high genotypic coefficient of variation for frog eye leaf spot, lodging and number seeds per plant and also high genotypic coefficient of variation on lodging and number seeds per plant and biomass yield in soybean genotypes, have been reported by Diriba Beyene *et al.* (2022). Moderate GCV values were recorded on days to flowering, plant height, hundred seed weight, grain yield and pods per plant.

The present finding is in agreement with Koraddi and Basavaraja (2019) who found moderate GCV values for days to flowering, hundred seed weight, pods per plant and also moderate GCV values on plant height and grain yield were reported in soybean genotypes (Gada Gudina *et al.*, 2023). In contrary with present finding Besufikad Enideg (2018) who had high GCV values in soybean genotypes on days to flowering, plant height, hundred seed weight, grain yield and pods per plant. Traits like days to maturity, branches per plant, seeds per pod, harvest index, protein content and oil yield had low GCV values. Similar result in soybean genotypes for days to maturity with low GCV has been reported by Adhikari *et al.* (2018) and low GCV values on seeds per pod, oil yield and protein content were recorded by (Gobezie Chakelie, 2022). On the contrary Jandong *et al.* (2020) reported moderate GCV value for number of branch per plant among twenty soybean genotypes.

### 4.3.2. Estimation of heritability and genetic advance

Estimates of heritability in broad sense, genetic advance and genetic advance as percent of mean for traits considered are presented in Table 4. Estimates of heritability in broad sense ranged from 24.12% for number of branches per plant to 97.22% for days to flowering.

The highest values of heritability in broad sense was recorded from days to flowering (97.22%), followed by, number of pods per plant (84.37%), red leaf blotch (82.13%), days to maturity (81.2%), oil yield (78.35%), biomass yield (78.1%), number of seeds per pod (75.89%), frog eye leaf spot (75.06%), grain yield (74.27%), shattering (72.73%), lodging (75.22%), bacterial blight (69%), plant height (68.07%), and hundred seed weight (67.96). Traits with high heritability estimates values indicated that a larger proportion of the total phenotypic variation is due to genetic factors rather than environmental influences.

Traits such as days to flowering, pods per plant, days to maturity, oil yield, biomass yield, seeds per pod, grain yield, shattering, loading, plant height and hundred seed weight had high heritability estimates, suggesting that these traits are predominantly controlled by the genetic makeup of the plants rather than external factors (environmental factor). High heritability values for certain traits imply that selection based on phenotypic performance could be more likely to result in significant genetic gains in subsequent generations. This means that breeding efforts will be focused on these traits have a higher probability of success in improving the desired traits in soybean genotypes.

Similar results to the present finding with high heritability estimates have been reported (Koraddi and Basavaraja, 2019; Masreshaw Yirga *et al.*, 2022; Tesfaye Belay *et al.*, 2022) for number of pods per plant, days to maturity, hundred seed weight and plant height and for oil yield (Gobezie Chakelie, 2022). Prathima *et al.* (2022) also reported high heritability estimate for shattering, days to flowering, days to maturity, plant height, pods per plant, and hundred seed weight. Contrary to the current result with moderate heritability estimates for grain yield (39.22%) and number of seeds per plant (48.56%) and low heritability estimates on days to flowering (26.14%) and lodging (27.27%) were reported by Masreshaw Yirga *et al.* (2022).

Moderate heritability values were found on brown spot (59.20%), protein content (44.2%), number of seeds per pod (37.88%) and harvesting index (32.5%) this suggesting that there is a balance between genetic and environmental influences on the traits. In agreement with in this results, moderate heritability have been reported (Abush Tesfaye *et al.*, 2017; Wakjira Getachew, 2021) for protein content, number of seeds per pod reported and for harvest index (Koraddi and Basavaraja, 2019; Gobezie Chakelie, 2022). On the other hand contrary results with low heritability estimates for number of seeds per pod and harvest index was reported (Yechalew Sileshi, 2019).

Traits with medium heritability estimates values indicated that a moderate proportion of the total phenotypic variation is attributed to genetic factors, while the remaining variation is influenced by environmental factors and Traits with medium heritability values implied a balance between genetic control and environmental influence, making them suitable targets for selective breeding programs. While these traits may not be as strongly determined by genetics as high heritability traits, they still offer potential for improvement through targeted breeding efforts and selection strategies.

The measure of low heritability value was obtained for number of branches per plant which is similar to the result obtained by Kuswantoro (2017). The presence of low heritability for traits indicated that selection could be significantly difficult or almost impractical due to masking effect of the genotype or environmental factors play a significant role in this trait. Traits with low heritability estimates values indicated that a smaller proportion of the total phenotypic variation is due to genetic factors, while a larger proportion is attributed to environmental influences. In the situation traits of branch number per plant have low heritability estimates, suggesting that these traits are heavily influenced by external factors such as growing conditions, management practices, and other environmental variables rather than genetic factors.

Low heritability values for certain traits imply that selection based solely on phenotypic performance may not lead to significant improvements in subsequent generations. Instead, it may be more effective to focus on other breeding strategies that can account for the environmental influences on these traits, such as multi-environment trials, hybridization or incorporating genomic information into breeding programs.

The estimates of genetic advance as present of mean ranged from 2.33% on protein content to 80.33% for loading. High genetic advance as percent of mean was recorded on lodging (80.33%), frog eye leaf spot (61.46%), shattering (54.10%),red leaf blotch (44.10%), number of seeds per plant (39.27%), number of pods per plant (37.19%), brown spot (34.57%), bacterial blight (34.56%), grain yield (33.29%), days to flowering (32%), plant height (28.36%), and hundred seed weight (23.05%). Similar result was found with high genetic advance as percent of mean on number of pods per plant, plant height, days to flowering, and grain yield (Jandong *et al.*, 2020), seeds per plant and hundred seed weight (Yechalew Sileshi, 2019; Tesfaye Belay *et al.*, 2022) and shattering (Prathima *et al.*, 2022).

In contrast to the present result, moderate genetic advance as percent of means was reported for hundred seed weight, and days to flowering (Diriba Beyene *et al.*, 2022). The presence of high genetic advance as a percent of the mean (GAM) values indicated that a considerable potential genetic variability for soybean improvement through direct selection. High GAM values for above mentioned traits indicated that there is a strong genetic component influencing the expression of these traits, making them promising targets for genetic enhancement. Traits with high GAM percentages for those traits offer breeders and the opportunity to make significant genetic gains in a relatively short period through selective breeding strategies.

On the other hand moderate genetic advance as percent of mean was recorded for days to maturity (12.18%). Moderate genetic advance as percent of mean for days to maturity was reported (Besufikad Enideg, 2019; Kumar *et al.*, 2020). On the other hand contrary with the current finding, Habte Berhanu *et al.* (2023) reported high genetic advance as percent of mean for days maturity (23.23%). The existence of moderate genetic advance suggesting that targeted breeding efforts could lead to substantial enhancements in these traits

Low genetic advance as percent of the means were reported for branches per plant (9.36%), seeds per pod (9.63%), harvest index (9.86%) oil yield (7%) and protein content (2.33%). The current result in agreement with Gobezie Chakelie (2022) who found low genetic advance as percent of mean on seeds per pod and protein content, Wakjira Getachew (2021) who reported low genetic advance as percent of for oil yield. Genetic advance as percent of mean for branches per plant in this study showed low, while Neelima *et al.* (2018) reported high GAM. Traits with low genetic advance as a percent of the mean (GAM) may indicate limited genetic variability within the population or low heritability, making it challenging to achieve significant improvements through conventional breeding methods.

Additionally, traits with low GAM percentages may also be controlled by a large number of genes with small effects, making it difficult to make substantial genetic gains through traditional breeding practices. In such cases, alternative breeding strategies such as marker-assisted selection or genomic selection may be more effective in improving these traits. Understanding the limitations posed by low GAM values for certain traits can help breeders and researchers to prioritize their efforts and resources towards traits with higher genetic potential for improvement.

Table 4. Variances and Genetic parameters of 19 soybean traits

| Traits | $\sigma^2 g$ | $\sigma^2 e$ | $\sigma^2 p$ | GCV (%) | PCV (%) | $H^2$ (%) | GA | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| DTF | 54.16 | 1.55 | 55.70 | 16.12 | 16.34 | 97.24 | 14.95 | 32.73 |
| DTM | 51.19 | 11.85 | 63.04 | 6.56 | 7.28 | 81.20 | 13.28 | 12.18 |
| LDG | 0.43 | 0.14 | 0.57 | 44.96 | 51.84 | 75.22 | 1.16 | 80.33 |
| STG | 0.56 | 0.21 | 0.77 | 30.8 | 36.11 | 72.73 | 1.31 | 54.10 |
| PH | 118.94 | 55.79 | 174.73 | 16.69 | 20.23 | 68.07 | 18.54 | 28.36 |
| BPP | 0.27 | 0.84 | 1.11 | 9.25 | 18.83 | 24.12 | 0.52 | 9.36 |
| HSW | 4.03 | 1.9 | 5.93 | 13.57 | 16.46 | 67.96 | 3.41 | 23.05 |
| GY | 181941.60 | 63022.91 | 244964.51 | 18.75 | 21.76 | 74.27 | 757.26 | 33.29 |
| PPP | 238.46 | 44.18 | 282.63 | 19.66 | 21.40 | 84.37 | 29.22 | 37.19 |
| SdPP | 1343.23 | 426.71 | 1769.94 | 21.88 | 25.12 | 75.89 | 65.77 | 39.27 |
| SedPP | 0.03 | 0.04 | 0.07 | 7.60 | 12.34 | 37.88 | 0.21 | 9.63 |
| BM | 931184.7 | 261135 | 1192319.7 | 20.93 | 23.68 | 78.10 | 1756.74 | 38.10 |
| HI | 17.71 | 36.78 | 54.49 | 8.39 | 14.73 | 32.50 | 4.94 | 9.86 |
| PC | 0.49 | 0.62 | 1.10 | 1.70 | 2.56 | 44.20 | 0.96 | 2.33 |
| OC | 0.78 | 0.22 | 1.00 | 3.85 | 4.35 | 78.35 | 1.60 | 7 |
| FLS | 0.32 | 0.106 | 0.43 | 34.44 | 39.75 | 75.06 | 1.01 | 61.46 |
| BBL | 0.27 | 0.122 | 0.39 | 20.20 | 24.31 | 69.00 | 0.89 | 34.56 |
| BS | 0.33 | 0.225 | 0.55 | 22.06 | 28.67 | 59.20 | 0.91 | 34.97 |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| RLB | 0.39 | 0.084 | 0.47 | 23.62 | 26.07 | 82.13 | 1.16 | 44.10 |

*DF=degree of freedom. DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC= Protein content; OC= Oil content; FLS=frog eye leaf spot; BB=bacterial blight; BS=brown spot; and RLB=red leaf blotch.* $\sigma^2g$*= Genetic variance;* $\sigma^2e$*= environmental variance;* $\sigma^2p$*=phenotypic variance; GCV (%)= genotypic coefficient of variance; PCV (%)= phenotypic coefficient of variance;* $H^2$ *(%)= heritability in broad sense in percent; GA= genetic advance; and GAM=genetic advance as present of mean.*

## 4.4. Correlation Traits

### 4.4.1. Phenotypic correlation

The estimates of phenotypic correlation coefficient between grain yield and other traits are presented in Table 5 and table 6. Grain yield showed positive and highly significant ($p<0.01$) phenotypic correlation with days to flowering (0.52), days to maturity (0.47), plant height (0.48), number of pods per plant (0.40), number of seeds per plant (0.47), number of seeds per pod (0.25), hundred seed weight (0.54), biomass yield (0.81, number of branches per plant (0.22) and harvest index (0.13).

Grain yield showed positive but non-significant phenotypic correlation with protein content (0.2) and showed negative but non-significant phenotypic association with oil content(-0.06). Gobezie Chakelie (2022) also found positive and highly significant phenotypic correlation of grain yield with days to flowering, days to maturity, plant height, pods per plant, and hundred seed weight. In agreement with the present findings, positive and highly significant phenotypic correlation was reported between seed yield with seeds per plant, and seeds per pod (Pawar *et al.*, 2020) and with biomass yield (Dubey *et al.*, 2015).

These results suggested that these traits may play a crucial role in influencing grain yield and it would be advised to use them for indirect selection in future soybean improvement program. However, seed yield showed negative and highly significant ($p<0.01$) phenotypic correlation coefficient with lodging (-0.24), frogeye leaf spot (-0.45), bacterial blight (-0.44), brown spot (-0.44) and red leaf blotch (-0.63) and it also had negative and significant ($p<0.05$) correlation with shattering (-0.12). The traits showed negative correlations make difficult for the simultaneous improvement of those traits.

Biomass yield showed positive and highly significant (<0.01) phenotypic correlation coefficient with, days to flowering (0.55), days to maturity (0.45), plant height (0.52), pods per plant (0.43), seeds per plant (0.51), seeds per pod (0.25), branch per plant (0.26) hundred seed weight (0.44). Whereas, it had negative and highly significant (<0.01) phenotypic correlation coefficient with harvest index (-0.45), which is similar the result reported by Deresse Hunde and Hirpa Legesse (2018). Supportive to the present findings, Yechalew Sileshi (2019) reported positive and highly significant phenotypic correlation for days to flowering, days to maturity, plant height and hundred seed weight. In addition biomass had negative and highly significant (<0.01) phenotypic correlation coefficient with, frogeye leaf spot (-0.37), bacterial blight (-0.35), brown spot (-0.39) and red leaf blotch (-0.57).

The current finding showed harvest index had negative and significant ($p<0.05$) phenotypic correlation with, days to flowering (-0.13), lodging (-0.12), shattering (-0.21), plant height (-0.20), pods per plant (-0.12) and seeds per plant (-0.12) in soybean genotypes.

Hundred seed weight showed positively and significant ($p<0.05$) phenotypic correlation coefficient with days to flowering (0.15), days to maturity (0.21), plant height (0.12), pods per plant (0.19), seeds per plant (0.21) and branches per plant (0.13). This result is in harmony with the finding of Deresse Hunde and Hirpa Legesse (2018) who reported positive association of hundred seed weight with branches per plant.

Number of branches per plant had positive and highly significant (<0.01) phenotypic correlation coefficient with plant height (0.37), number of pods per plant (0.57) and number of seeds per plant (0.54), in addition it showed positive and significant

($p<0.05$) phenotypic correlation coefficient with days to flowering (0.16) and oil content (0.21). Similarly positive and significant phenotypic correlation for number of pods per plant and number of seeds per plant with number of branches per plant was reported (Mesfin Hailemariam, 2018; Gada Gudina *et al.*, 2023).

Days to 50% of flowering showed positive and highly significant (<0.01) phenotypic correlation with days to maturity (0.60), plant height (0.41), pods per plant (0.48), seeds per plant (0.56) and seeds per pod (0.29), and similarly positive and significant ($p<0.05$) correlation with protein content (0.16) was found. However, It showed negative and highly significant phenotypic correlation with oil yield (-0.46). Similar results, positive and high significant PCV for days to maturity, plant height and seeds per pod with days to flowering was recorded by Pawar *et al.* (2020).

Days to maturity had positive and highly (<0.01) significant phenotypic correlation coefficient with plant height (0.33), seeds per plant (0.35), seeds per pod (0.34) and it also had positive and significant ($p<0.05$) correlation with pods per plant (0.21). Days to maturity showed negative and significant correlation with oil content (-0.20). Positive and highly significant phenotypic correlation for plant height with days to maturity has been reported (Gada Gudina *et al.*, 2023).

Plant height showed positive and highly significant (<0.01) phenotypic correlation with pods per plant (0.49), number of seeds per plant (0.48) and it had positive and significant phenotypic correlation coefficient with shattering, Number of seeds per pod and hundred seed weight and in agreement with this result, positive and highly significant phenotypic correlation coefficient of plant height with pods per plant and number of seeds per plant was obtained by Masreshaw Yirga *et al.* (2022).

Plant height also had positive and significant ($p<0.05$) value with number of seeds per pod (0.11), oil content (0.11) and shattering (0.13), whereas it had negative and highly significant (<0.01) correlation with protein content (-0.14). Pods per plant showed positive and significant ($p<0.05$) phenotypic correlation coefficient with shattering (0.13). As the result showed protein content had negative and highly significant (<0.01) phenotypic correlation coefficient with oil yield (0.51), which is similar with the result reported by Asmamaw Amogne *et al.* (2020).

### 4.4.2. Genotypic correlation

The genotypic correlations of traits are given in Table 5 and table 6. Grain yield showed positive and highly significant ($p<0.01$) genotypic correlation coefficient with days to flowering (0.56), days to maturity (0.54), plant height (0.55), pods per plant (0.42), seeds per plant (0.51), hundred seed weight (0.55), biomass yield (0.86) and similarly positive and significant ($p<0.05$) genotypic correlation coefficient was found with seeds per pod (0.30). Gobezie Chakelie (2022) reported a similar result of positive and highly significant genotypic correlation of days to flowering, days to maturity, plant height and pods per plant with grain yield. However, the present finding in contrary with this author for seeds per plant, seeds per pod, hundred seed weight with grain yield.

Grain yield showed negative and highly significant genotypic correlation with lodging (-0.37), frogeye leaf spot (-0.53), bacterial blight (-0.53), brown spot (-0.52), and red leaf blotch (-0.71). And also it had negative and non-significant genotypic correlation coefficient with protein content (-0.04) and oil yield (-0.03). In concurrence with the present findings, negative and non-significant genotypic correlation coefficient of grain yield with protein content (-0.2) and oil yield (-0. 157) have been reported (Asmamaw Amogne *et al.*, 2020; Shete *et al.*, 2023). Gobezie Chakelie (2022) reported the same result on oil yield (-0.038) and found negative and non-significant genotypic correlation coefficient with grain yield.

Biomass yield showed positive and highly significant genotypic correlation with days to flowering (0.58), days to maturity (0.51), plant height (0.58), pods per plant (0.46), number of seeds per plant (0.53), branches per plant (0.32), hundred seed weight (0.47) and it had positive and significant correlation with number of seeds per pod (0.27). However, biomass yield had negative and highly significant genotypic correlation with harvest index (-0.45) and similar result found by Yechalew Sileshi (2019). It also had negative and highly significant genotypic correlation with frog eye leaf spot (-0.43), bacterial blight (-0.41), brown spot (-0.45) and red leaf blotch (-0.66).

Harvest index had positive and significant genotypic correlation coefficient with hundred seed weight while harvest index had negative and significant genotypic correlation coefficient with days to flowering (-0.16), shattering (-0.24), plant height (-0.24) and pods per plant (-0.16). Deresse Hunde and Hirpa Legesse (2018) who reported contrary result in this finding, negative and non-significant genotypic correlation for days to flowering (-0.08), plant height (-0.32) and positive and non-significant genotypic correlation coefficient of pods per plant (0.17) with harvest index.

Hundred seed weight showed positive and significant genotypic correlation with days to flowering (0.17), days to maturity (0.24), number of pods per plant (0.20), number of seeds per plant (0.23) and number of branches per plant (0.16), and it also showed negative and significant genotypic correlation coefficient with lodging (-0.27). contrary results in the current findings, on days to flowering, days to maturity, number of pods per plant, number of seeds per pod and branch number plant with hundred seed weight was reported (Wakjira Getachew, 2021; Gada Gudina *et al.*, 2023).

Branch number per plant showed positive and highly significant genotypic correlation with plant height (0.45), pod number per plant (0.68), seed number per plant (0.61). Gada Gudina *et al.* (2023) obtained a similar results on pods number per plant, seed number per plant, and plant height with branch number per plant. Similarly branch number per plant showed positive and significant genotypic correlation with days to flowering (0.22) and oil yield (0.26).

Days to maturity had positive and highly significant genotypic correlation with days to flowering (0.63), plant height (0.37), number of seeds per plant (0.39) and number of seeds per pod (0.42). In addition it showed positive and significant correlation with number of pods per plant (0.24), and it also showed negative and significant genotypic correlation with oil content (-0.22). Shete *et al.* (2023) who had positive and highly significant genotypic correlation of days to flowering, plant height with days to maturity which is in line with this finding.

The current finding showed days to flowering had positive and highly significant genotypic correlation with, plant height (0.45), pods per plant (0.51), seed number per plant (0.61), seed per pod (0.35), and it had positive and significant genotypic correlation with protein content (0.19). On the other hand days to flowering showed negative and highly significant correlation with oil content (-0.50). Similarly, positive and highly significant genotypic correlation of plant height and number of seeds per pod with days to flowering have been reported by Pawar *et al.* (2020), while disagreed with genotypic correlation of pods per plant, seed number per plant, protein content and oil content.

Plant height exhibited a positive and highly significant genotypic correlation with the number of pods per plant (0.54) and the number of seeds per plant (0.52) which is similar the result reported by Masreshaw Yirga *et al.* (2022). It also displayed a positive and significant genotypic correlation with shattering (0.16), while it had a negative and significant genotypic correlation coefficient with protein content (-0.17).

Number of pods per plant showed positive and highly significant genotypic correlation coefficient with number of seeds per pod (0.89), which is in agreement with the result found by Habte Berhanu *et al.* (2021). Shattering had positive and highly significant genotypic correlation coefficient through protein content (0.31). Protein content had negative and highly significant genotypic correlation coefficient with oil content (-0.45).

Table 5. Genotypic (bellow diagonal) and phenotypic (above diagonal) correlation coefficients 19 traits of 150 soybean genotypes

| Variable | DTF | DTM | LDG | STG | PH | PPP | SdPP | SedPP | BPP | HSW |
|---|---|---|---|---|---|---|---|---|---|---|
| DTF | 1 | $0.60^{**}$ | $0.01^{ns}$ | $0.08^{ns}$ | $0.41^{**}$ | $0.48^{**}$ | $0.56^{**}$ | $0.29^{**}$ | $0.16^{*}$ | $0.15^{*}$ |
| DTM | $0.63^{**}$ | 1 | $-0.08^{ns}$ | $-0.11^{ns}$ | $0.33^{**}$ | $0.21^{*}$ | $0.35^{**}$ | $0.34^{**}$ | $0.09^{ns}$ | $0.21^{*}$ |
| LDG | $0.01^{ns}$ | $-0.09^{ns}$ | 1 | $0.06^{ns}$ | $0.07^{ns}$ | $0.04^{ns}$ | $0.03^{ns}$ | $-0.01^{ns}$ | $0.04^{ns}$ | $-0.23^{**}$ |
| STG | $0.09^{ns}$ | $-0.12^{ns}$ | $0.07^{ns}$ | 1 | $0.13^{*}$ | $0.13^{*}$ | $0.07^{ns}$ | $-0.09^{ns}$ | $0.10^{ns}$ | $-0.11^{*}$ |
| PH | $0.45^{**}$ | $0.37^{**}$ | $0.06^{ns}$ | $0.16^{*}$ | 1 | $0.49^{**}$ | $0.48^{**}$ | $0.11^{*}$ | $0.37^{**}$ | $0.12^{*}$ |
| PPP | $0.51^{**}$ | $0.24^{*}$ | $0.05^{ns}$ | $0.14^{ns}$ | $0.54^{**}$ | 1 | $0.86^{**}$ | $0.003^{ns}$ | $0.57^{**}$ | $0.19^{*}$ |
| SdPP | $0.61^{**}$ | $0.39^{**}$ | $0.04^{ns}$ | $0.07^{ns}$ | $0.52^{**}$ | $0.89^{**}$ | 1 | $0.50^{**}$ | $0.54^{**}$ | $0.21^{*}$ |
| SedPP | $0.35^{**}$ | $0.42^{**}$ | $-0.03^{ns}$ | $-0.12^{ns}$ | $0.11^{ns}$ | $0.03^{ns}$ | $0.47^{**}$ | 1 | $0.11^{ns}$ | $0.09^{ns}$ |
| BPP | $0.22^{*}$ | $0.12^{ns}$ | $0.02^{ns}$ | $0.10^{ns}$ | $0.45^{**}$ | $0.68^{**}$ | $0.61^{**}$ | $0.05^{ns}$ | 1 | $0.13^{*}$ |
| HSW | $0.17^{*}$ | $0.24^{*}$ | $-0.27^{*}$ | $-0.12^{ns}$ | $0.14^{ns}$ | $0.20^{*}$ | $0.23^{*}$ | $0.13^{ns}$ | $0.16^{*}$ | 1 |
| GY | $0.56^{**}$ | $0.54^{**}$ | $-0.37^{**}$ | $-0.10^{ns}$ | $0.55^{**}$ | $0.42^{**}$ | $0.51^{**}$ | $0.30^{*}$ | $0.30^{*}$ | $0.55^{**}$ |
| BM | $0.58^{**}$ | $0.51^{*}$ | $-0.26^{*}$ | $0.05^{ns}$ | $0.58^{**}$ | $0.46^{**}$ | $0.53^{**}$ | $0.27^{*}$ | $0.32^{**}$ | $0.47^{**}$ |
| HI | $-0.16^{*}$ | $-0.02^{ns}$ | $-0.15^{ns}$ | $-0.28^{*}$ | $-0.26^{*}$ | $-0.17^{*}$ | $-0.15^{ns}$ | $0.01^{ns}$ | $-0.11^{ns}$ | $0.07^{*}$ |
| PC | $0.19^{*}$ | $-0.11^{ns}$ | $-0.07^{ns}$ | $0.31^{**}$ | $-0.17^{*}$ | $-0.03^{ns}$ | $-0.01^{ns}$ | $0.06^{ns}$ | $-0.12^{ns}$ | $0.04^{ns}$ |
| OC | $-0.50^{**}$ | $-0.22^{*}$ | $-0.07^{ns}$ | $0.07^{ns}$ | $0.13^{ns}$ | $0.01^{ns}$ | $-0.12^{ns}$ | $-0.27^{*}$ | $0.26^{*}$ | $-0.01^{ns}$ |
| FLS | $-0.33^{**}$ | $-0.30^{*}$ | $0.21^{*}$ | $0.06^{ns}$ | $-0.27^{*}$ | $-0.37^{**}$ | $-0.41^{**}$ | $-0.22^{*}$ | $-0.24^{*}$ | $-0.40^{**}$ |
| BBL | $-0.29^{*}$ | $-0.16^{*}$ | $0.22^{*}$ | $-0.01^{ns}$ | $-0.15^{ns}$ | $-0.08^{ns}$ | $-0.17^{*}$ | $-0.20^{*}$ | $0.08^{ns}$ | $-0.35^{**}$ |
| BS | $-0.35^{**}$ | $-0.34^{**}$ | $0.19^{*}$ | $0.23^{*}$ | $-0.07^{ns}$ | $-0.05^{ns}$ | $-0.20^{*}$ | $-0.34^{**}$ | $0.06^{ns}$ | $-0.38^{**}$ |
| RLB | $-0.47^{**}$ | $-0.53^{**}$ | $0.12^{ns}$ | $0.12^{ns}$ | $-0.57^{**}$ | $-0.32^{**}$ | $-0.39^{**}$ | $-0.24^{*}$ | $-0.24^{*}$ | $-0.41^{**}$ |

*DF=degree of freedom. DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC= Protein content; OC= Oil content; FLS=frog eye leaf spot; BB=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

Table 6. Table 5 continued

| Variable | GY | BM | HI | PC | OC | FLS | BBL | BS | RLB |
|---|---|---|---|---|---|---|---|---|---|
| DTF | $0.52^{**}$ | $0.55^{**}$ | $-0.13^{*}$ | $0.16^{*}$ | $-0.46^{**}$ | $-0.31^{**}$ | $-0.27^{*}$ | $-0.32^{**}$ | $-0.45^{**}$ |
| DTM | $0.47^{**}$ | $0.45^{**}$ | $-0.03^{ns}$ | $-0.09^{ns}$ | $-0.20^{*}$ | $-0.27^{*}$ | $-0.13^{*}$ | $-0.28^{**}$ | $-0.48^{**}$ |
| LDG | $-0.34^{**}$ | $-0.24^{**}$ | $-0.12^{*}$ | $-0.04^{ns}$ | $-0.07^{ns}$ | $0.19^{*}$ | $0.19^{*}$ | $0.15^{*}$ | $0.11^{ns}$ |
| STG | $-0.11^{*}$ | $0.02^{ns}$ | $-0.21^{*}$ | $0.23^{**}$ | $0.07^{ns}$ | $0.04^{ns}$ | $-0.01^{ns}$ | $0.17^{*}$ | $0.09^{ns}$ |
| PH | $0.48^{**}$ | $0.52^{**}$ | $-0.20^{*}$ | $-0.14^{*}$ | $0.11^{*}$ | $-0.24^{*}$ | $-0.14^{ns}$ | $-0.08^{ns}$ | $-0.48^{**}$ |
| PPP | $0.40^{**}$ | $0.43^{**}$ | $-0.12^{*}$ | $-0.02^{ns}$ | $0.01^{ns}$ | $-0.33^{**}$ | $-0.08^{ns}$ | $-0.04^{ns}$ | $-0.28^{**}$ |
| SdPP | $0.47^{**}$ | $0.51^{**}$ | $-0.12^{*}$ | $-0.002^{ns}$ | $-0.10^{ns}$ | $-0.37^{**}$ | $-0.15^{*}$ | $-0.17^{*}$ | $-0.33^{**}$ |
| SedPP | $0.25^{**}$ | $0.25^{**}$ | $-0.02^{ns}$ | $0.04^{ns}$ | $-0.21^{*}$ | $-0.17^{*}$ | $-0.15^{*}$ | $-0.26^{**}$ | $-0.17^{*}$ |
| BPP | $0.22^{*}$ | $0.26^{**}$ | $-0.09^{ns}$ | $-0.10^{ns}$ | $0.21^{*}$ | $-0.19^{*}$ | $0.08^{ns}$ | $0.07^{ns}$ | $-0.17^{*}$ |
| HSW | $0.54^{**}$ | $0.44^{**}$ | $0.09^{ns}$ | $0.06^{ns}$ | $-0.02^{ns}$ | $-0.32^{**}$ | $-0.29^{**}$ | $-0.32^{**}$ | $-0.36^{**}$ |
| GY | 1 | $0.81^{**}$ | $0.14^{*}$ | $0.02^{ns}$ | $-0.06^{ns}$ | $-0.45^{**}$ | $-0.44^{**}$ | $-0.44^{**}$ | $-0.63^{**}$ |
| BM | $0.86^{**}$ | 1 | $-0.45^{**}$ | $0.04^{ns}$ | $-0.07^{ns}$ | $-0.37^{**}$ | $-0.35^{**}$ | $-0.39^{**}$ | $-0.57^{**}$ |
| HI | $0.05^{ns}$ | $-0.45^{**}$ | 1 | $-0.04^{ns}$ | $0.01^{ns}$ | $-0.08^{ns}$ | $-0.05^{ns}$ | $-0.03^{ns}$ | $0.04^{ns}$ |
| PC | $-0.04^{ns}$ | $0.02^{ns}$ | $-0.09^{ns}$ | 1 | $-0.51^{**}$ | $0.01^{ns}$ | $-0.06^{ns}$ | $0.05^{ns}$ | $0.10^{ns}$ |
| OC | $-0.03^{ns}$ | $-0.06^{ns}$ | $0.03^{ns}$ | $-0.45^{**}$ | 1 | $-0.06^{ns}$ | $0.07^{ns}$ | $0.22^{*}$ | $0.01^{ns}$ |
| FLS | $-0.53^{**}$ | $-0.43^{**}$ | $-0.09^{ns}$ | $-0.01^{ns}$ | $-0.05^{ns}$ | 1 | $0.11^{ns}$ | $0.18^{*}$ | $0.39^{**}$ |
| BBL | $-0.53^{**}$ | $-0.41^{**}$ | $-0.08^{ns}$ | $-0.13^{ns}$ | $0.11^{ns}$ | $0.13^{ns}$ | 1 | $0.37^{**}$ | $0.27^{**}$ |
| BS | $-0.52^{**}$ | $-0.45^{**}$ | $-0.05^{ns}$ | $0.03^{ns}$ | $0.28^{*}$ | $0.21^{*}$ | $0.42^{**}$ | 1 | $0.30^{**}$ |
| RLB | $-0.71^{**}$ | $-0.66^{**}$ | $0.08^{ns}$ | $0.14^{ns}$ | $0.00^{ns}$ | $0.42^{**}$ | $0.32^{**}$ | 0.37 | $1^{**}$ |

*DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC= Protein content; OC=Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

## 4.5. Path Coefficient Analysis

### 4.5.1. Phenotypic direct and indirect effects

The phenotypic direct and indirect effects of traits on grain yield are presented in table 7 and table 8. The path coefficient analysis revealed that biomass yield (0.999) had the highest positive direct effect on grain yield followed by harvest index (0.591), number of pods per plant (0.107), plant height (0.071), number of seeds per pod (0.062), days to flowering (0.025), oil content (0.025), protein content (0.024), hundred seed weight (0.010) and frogeye leaf spot (0.003) showed positive phenotypic direct effect on grain yield. This indicated the importance of the traits in influencing grain yield and these results suggest that focusing on improving biomass yield, along with other traits mentioned, can potentially enhance grain yield through indirect selection.

Similarly, positive phenotypic direct effects of plant height, number of pods per plant, hundred seed weight on grain yield have been reported (Asmamaw Amogne *et al.*, 2020; Masreshaw Yirga *et al.*, 2022). Additionally, Deresse Hunde and Hirpa Legesse (2018) who had positive phenotypic direct effects of biomass yield, days to flowering, and number of seeds per pod on grain yield, while he found disagreement result of negative phenotypic direct effect on plant height (-0.09) and harvest index (-0.018) on grain yield in soybean genotypes.

Conversely negative direct effect on grain yield observed from brown spot (-0.009), branch per plant (-0.011), days to maturity (-0.017), shattering (-0.018), lodging (-0.024), bacterial blight (-0.029), red leaf blotch (-0.035) and number of seeds per plant (-0.135). It appears that traits such as branch per plant, days to maturity, shattering, loading, and number of seeds per plant have a negative impact on grain yield. It is important to consider these factors when aiming to improve grain yield. Similarly negative phenotypic direct effect of number of branches per plant and days to maturity on grain yield were reported by Kuswantoro *et al.* (2022). In contrary Masreshaw Yirga *et al.* (2022) reported positive direct phenotypic effects of lodging (0.028), and shattering (0.282) on grain.

The maximum positive phenotypic indirect effects was observed from biomass yield through days to flowering (0.547), plant height (0.514), number of seeds per plant (0.507), days to maturity (0.453), hundred seed weight (0.437), and number of pods per plant (0.434) on soybean grain yield. The second positive phenotypic indirect effects recorded for number of pods per plant via number of seeds per plant (0.092), branch per plant (0.061), plant height (0.053) and days to flowering (0.052). This suggested that improving these factors can potentially lead to an increase in soybean grain yield by positively influencing biomass yield. Therefore, focusing on optimizing these factors may enhance overall grain yield and productivity.

Table 7. Direct (bold diagonal) and indirect effects (off diagonal) at phenotypic level of 18 traits on grain yield in 150 soybean genotypes

| Variable | DTF | DTM | LDG | STG | PH | PPP | SdPP | SedPP | BPP | HSW | rp |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DTF | **0.025** | -0.010 | -0.0002 | -0.001 | 0.029 | 0.052 | -0.076 | 0.018 | -0.002 | 0.002 | 0.521 |
| DTM | 0.015 | **-0.017** | 0.002 | 0.002 | 0.023 | 0.023 | -0.048 | 0.021 | -0.001 | 0.002 | 0.475 |
| LDG | 0.0002 | 0.001 | **-0.024** | -0.001 | 0.005 | 0.004 | -0.004 | -0.001 | -0.0004 | -0.002 | -0.340 |
| STG | 0.002 | 0.002 | -0.002 | **-0.018** | 0.009 | 0.014 | -0.010 | -0.006 | -0.001 | -0.001 | -0.113 |
| PH | 0.010 | -0.006 | -0.002 | -0.002 | **0.071** | 0.053 | -0.065 | 0.007 | -0.004 | 0.001 | 0.478 |
| PPP | 0.012 | -0.004 | -0.001 | -0.002 | 0.035 | **0.107** | -0.116 | 0.0002 | -0.006 | 0.002 | 0.400 |
| SdPP | 0.014 | -0.006 | -0.001 | -0.001 | 0.034 | 0.092 | **-0.135** | 0.031 | -0.006 | 0.002 | 0.474 |
| SedPP | 0.007 | -0.006 | 0.000 | 0.002 | 0.008 | 0.0003 | -0.068 | **0.062** | -0.001 | 0.001 | 0.250 |
| BPP | 0.004 | -0.002 | -0.001 | -0.002 | 0.026 | 0.061 | -0.073 | 0.007 | **-0.011** | 0.001 | 0.215 |
| HSW | 0.004 | -0.004 | 0.006 | 0.002 | 0.008 | 0.020 | -0.028 | 0.006 | -0.001 | **0.010** | 0.537 |
| BM | 0.014 | -0.008 | 0.006 | -0.0003 | 0.037 | 0.047 | -0.069 | 0.016 | -0.003 | 0.004 | 0.808 |
| HI | -0.003 | 0.0005 | 0.003 | 0.004 | -0.015 | -0.013 | 0.016 | -0.001 | 0.001 | 0.001 | 0.135 |
| PC | 0.004 | 0.001 | 0.001 | -0.004 | -0.010 | -0.002 | 0.0002 | 0.002 | 0.001 | 0.001 | 0.019 |
| OC | -0.012 | 0.003 | 0.002 | -0.001 | 0.008 | 0.001 | 0.014 | -0.013 | -0.002 | -0.0002 | -0.060 |
| FLS | -0.008 | 0.005 | -0.005 | -0.001 | -0.017 | -0.036 | 0.049 | -0.011 | 0.002 | -0.003 | -0.451 |
| BBL | -0.007 | 0.002 | -0.005 | 0.0002 | -0.010 | -0.008 | 0.020 | -0.009 | -0.001 | -0.003 | -0.440 |
| BS | -0.008 | 0.005 | -0.004 | -0.003 | -0.006 | -0.005 | 0.023 | -0.016 | -0.001 | -0.003 | -0.443 |
| RLB | -0.011 | 0.008 | -0.003 | -0.002 | -0.034 | -0.030 | 0.044 | -0.011 | 0.002 | -0.004 | -0.629 |

*DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC=Protein content; OC=Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

Table 8. Table 7 Continued

| Variable | BM | HI | PC | OC | FLS | BBL | BS | RLB | GY |
|---|---|---|---|---|---|---|---|---|---|
| DTF | 0.547 | -0.079 | 0.004 | -0.011 | -0.001 | 0.008 | 0.003 | 0.016 | 0.521 |
| DTM | 0.453 | -0.016 | -0.002 | -0.005 | -0.001 | 0.004 | 0.002 | 0.017 | 0.475 |
| LDG | -0.236 | -0.068 | -0.001 | -0.002 | 0.0005 | -0.005 | -0.001 | -0.004 | -0.340 |
| STG | 0.019 | -0.124 | 0.005 | 0.002 | 0.0001 | 0.0003 | -0.001 | -0.003 | -0.113 |
| PH | 0.514 | -0.121 | -0.003 | 0.003 | -0.001 | 0.004 | 0.001 | 0.017 | 0.478 |
| PPP | 0.434 | -0.073 | -0.0005 | 0.0003 | -0.001 | 0.002 | 0.0004 | 0.010 | 0.400 |
| SdPP | 0.507 | -0.072 | -0.00004 | -0.003 | -0.001 | 0.004 | 0.001 | 0.011 | 0.474 |
| SedPP | 0.249 | -0.012 | 0.001 | -0.005 | -0.0004 | 0.004 | 0.002 | 0.006 | 0.250 |
| BPP | 0.255 | -0.056 | -0.002 | 0.005 | -0.0005 | -0.002 | -0.001 | 0.006 | 0.215 |
| HSW | 0.437 | 0.054 | 0.001 | -0.0005 | -0.001 | 0.008 | 0.003 | 0.013 | 0.537 |
| BM | **0.999** | -0.265 | 0.001 | -0.002 | -0.001 | 0.010 | 0.003 | 0.020 | 0.808 |
| HI | -0.448 | **0.591** | -0.001 | 0.0002 | -0.0002 | 0.001 | 0.0002 | -0.002 | 0.135 |
| PC | 0.036 | -0.021 | **0.024** | -0.013 | 0.00001 | 0.002 | -0.0004 | -0.004 | 0.019 |
| OC | -0.072 | 0.004 | -0.012 | **0.025** | -0.0001 | -0.002 | -0.002 | -0.0004 | -0.060 |
| FLS | -0.365 | -0.046 | 0.0001 | -0.001 | **0.003** | -0.003 | -0.002 | -0.014 | -0.451 |
| BBL | -0.350 | -0.029 | -0.001 | 0.002 | 0.0003 | **-0.029** | -0.003 | -0.010 | -0.440 |
| BS | -0.386 | -0.016 | 0.001 | 0.005 | 0.0005 | -0.011 | **-0.009** | -0.011 | -0.443 |
| RLB | -0.573 | 0.026 | 0.002 | 0.0003 | 0.001 | -0.008 | -0.003 | **-0.035** | -0.629 |

*DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC=Protein content; OC=oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

### 4.5.2. Genotypic direct and indirect effects

Genotypic direct and indirect effects of traits on grain yield are presented in table 9 and table 10. The genotypic path coefficient analysis showed that biomass yield (0.956), harvest index (0.493), pods per plant (0.188), number of seeds per pod (0.111), plant height (0.089), days to flowering (0.046), oil yield (0.026), hundred seed weight (0.012), and protein content (0.009) had positive genotypic direct effects on grain yield. These results implied the complex interplay of various traits in influencing grain yield. By focusing on enhancing these traits through targeted breeding, it may be possible to enhance grain yield potential.

Similarly, positive genotypic direct effects of plant height, hundred seed weight and number of pods per plant on grain yield was reported (Pawar *et al.*, 2020; Mesfin Hailemariam *et al.*, 2021), and Habte Berhanu *et al.* (2021) also found positive genotypic direct effects of plant height, days to flowering, hundred seed weight, pods per plant, number of seeds per pod on grain yield.

In addition positive genotypic direct effects for traits of harvest index and protein content on soybean grain yield have been reported by Gobezie Chakelie (2022). On the other hand positive genotypic direct effects of biomass yield, harvest index, days to flowering, number of seeds per pod, hundred seed weight were reported by Yechalew Sileshi (2019).

Negative genotypic direct effect observed from number of branch per plant (-0.004), frogeye leaf spot (-0.007), brown spot (-0.011), shattering (-0.015), days to maturity (-0.028), lodging (-0.037), red leaf blotch (-0.044), bacterial blight (-0.045) number of seeds per plant (-0.239). Kuswantoro *et al.* (2022) was reported negative genotypic direct effects of number of branches per plant and number of seeds per pod on soybean grain yield. Negative direct effects indicated that an increase in these particular traits may lead to a decrease in grain yield. Understanding these negative relationships is crucial for breeding program. This highlights the importance of considering not only positive but also negative trait interactions in crop improvement efforts.

The maximum positive genotypic indirect effects was manifested from biomass yield via days to flowering (0.556), plant height (0.556), seeds per plant (0.512), days to maturity (0.486), hundred seed weight (0.447), pods per plant (0.442), branch per plant (0.307) and seeds per pod (0.259), followed by, number of pods per plant through number of seeds per plant (0.167), number of branches per plant (0.127), plant height (0.101) days to flowering (0.096) and biomass yield (0.087) and plant height via biomass yield (0.052), pods per plant (0.048), seeds per plant (0.047), branch per plant (0.040), and days to flowering (0.040) on soybean grain yield. This indicated that these traits play crucial roles in influencing soybean grain yield. Therefore it is important to consider these indirect effects when evaluating and improving soybean grain yield.

Table 9. Direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of 18 traits on yield of 150 soybean genotypes

| Variable | DTF | DTM | LDG | STG | PH | PPP | SdPP | SedPP | BPP | HSW | gp |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DTF | **0.046** | -0.018 | -0.0003 | -0.001 | 0.040 | 0.096 | -0.145 | 0.039 | -0.001 | 0.002 | 0.562 |
| DTM | 0.029 | **-0.028** | 0.003 | 0.002 | 0.033 | 0.045 | -0.094 | 0.047 | -0.001 | 0.003 | 0.545 |
| LDG | 0.0004 | 0.003 | **-0.037** | -0.001 | 0.005 | 0.010 | -0.009 | -0.003 | -0.0001 | -0.003 | -0.374 |
| STG | 0.004 | 0.003 | -0.003 | **-0.015** | 0.015 | 0.027 | -0.017 | -0.014 | -0.0004 | -0.001 | -0.097 |
| PH | 0.020 | -0.011 | -0.002 | -0.002 | **0.089** | 0.101 | -0.125 | 0.012 | -0.002 | 0.002 | 0.547 |
| PPP | 0.023 | -0.007 | -0.002 | -0.002 | 0.048 | **0.188** | -0.212 | 0.003 | -0.003 | 0.002 | 0.419 |
| SdPP | 0.028 | -0.011 | -0.001 | -0.001 | 0.047 | 0.167 | **-0.239** | 0.053 | -0.003 | 0.003 | 0.508 |
| SedPP | 0.016 | -0.012 | 0.001 | 0.002 | 0.010 | 0.005 | -0.113 | **0.111** | -0.0002 | 0.002 | 0.302 |
| BPP | 0.010 | -0.003 | -0.001 | -0.002 | 0.040 | 0.127 | -0.146 | 0.005 | **-0.004** | 0.002 | 0.295 |
| HSW | 0.008 | -0.007 | 0.010 | 0.002 | 0.012 | 0.038 | -0.056 | 0.014 | -0.001 | **0.012** | 0.553 |
| BM | 0.027 | -0.014 | 0.010 | -0.001 | 0.052 | 0.087 | -0.128 | 0.030 | -0.001 | 0.006 | 0.855 |
| HI | -0.007 | 0.001 | 0.005 | 0.004 | -0.023 | -0.031 | 0.035 | 0.001 | 0.0004 | 0.001 | 0.051 |
| PC | 0.009 | 0.003 | 0.002 | -0.005 | -0.015 | -0.005 | 0.001 | 0.006 | 0.0005 | 0.001 | -0.036 |
| OC | -0.023 | 0.006 | 0.003 | -0.001 | 0.011 | 0.002 | 0.029 | -0.030 | -0.001 | -0.0001 | -0.034 |
| FLS | -0.015 | 0.009 | -0.008 | -0.001 | -0.024 | -0.069 | 0.098 | -0.024 | 0.001 | -0.005 | -0.532 |
| BBL | -0.013 | 0.004 | -0.008 | 0.0001 | -0.013 | -0.015 | 0.039 | -0.023 | -0.0003 | -0.004 | -0.527 |
| BS | -0.016 | 0.010 | -0.007 | -0.003 | -0.006 | -0.010 | 0.047 | -0.037 | -0.0003 | -0.005 | -0.522 |
| RLB | -0.022 | 0.015 | -0.005 | -0.002 | -0.051 | -0.061 | 0.094 | -0.026 | 0.001 | -0.005 | -0.713 |

*DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC=Protein content; OC=Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

Table 10. Table 9 Continued

| Variable | BM | HI | PC | OC | FLS | BBL | BS | RLB | gp |
|---|---|---|---|---|---|---|---|---|---|
| DTF | 0.556 | -0.079 | 0.002 | -0.013 | 0.002 | 0.013 | 0.004 | 0.021 | 0.562 |
| DTM | 0.486 | -0.010 | -0.001 | -0.006 | 0.002 | 0.007 | 0.004 | 0.023 | 0.545 |
| LDG | -0.246 | -0.072 | -0.001 | -0.002 | -0.002 | -0.010 | -0.002 | -0.005 | -0.374 |
| STG | 0.044 | -0.136 | 0.003 | 0.002 | -0.0004 | 0.0003 | -0.003 | -0.005 | -0.097 |
| PH | 0.556 | -0.126 | -0.001 | 0.003 | 0.002 | 0.007 | 0.001 | 0.025 | 0.547 |
| PPP | 0.442 | -0.082 | -0.0002 | 0.0003 | 0.003 | 0.003 | 0.001 | 0.014 | 0.419 |
| SdPP | 0.512 | -0.072 | -0.00005 | -0.003 | 0.003 | 0.007 | 0.002 | 0.017 | 0.508 |
| SedPP | 0.259 | 0.003 | 0.001 | -0.007 | 0.002 | 0.009 | 0.004 | 0.010 | 0.302 |
| BPP | 0.307 | -0.054 | -0.001 | 0.007 | 0.002 | -0.004 | -0.001 | 0.011 | 0.295 |
| HSW | 0.447 | 0.033 | 0.0004 | 0.000 | 0.003 | 0.016 | 0.004 | 0.018 | 0.553 |
| BM | **0.956** | -0.221 | 0.0001 | -0.002 | 0.003 | 0.018 | 0.005 | 0.029 | 0.855 |
| HI | -0.429 | **0.493** | -0.001 | 0.001 | 0.001 | 0.003 | 0.001 | -0.004 | 0.051 |
| PC | 0.016 | -0.046 | **0.009** | -0.012 | 0.0001 | 0.006 | -0.0003 | -0.006 | -0.036 |
| OC | -0.060 | 0.015 | -0.004 | **0.026** | 0.0004 | -0.005 | -0.003 | 0.0001 | -0.034 |
| FLS | -0.413 | -0.046 | -0.0001 | -0.001 | **-0.007** | -0.006 | -0.002 | -0.018 | -0.532 |
| BBL | -0.394 | -0.037 | -0.001 | 0.003 | -0.001 | **-0.045** | -0.005 | -0.014 | -0.527 |
| BS | -0.427 | -0.026 | 0.0002 | 0.007 | -0.002 | -0.019 | **-0.011** | -0.016 | -0.522 |
| RLB | -0.629 | 0.041 | 0.001 | -0.0001 | -0.003 | -0.014 | -0.004 | **-0.044** | -0.713 |

*DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Loading; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC=Protein content; OC=Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

### 4.6. Clustering of Genotypes

The distribution of 150 genotypes were divided into seven distinct clusters based on 19 quantitative, including quality and disease traits (Table 11 and Figure 8), indicating the existence of considerable genetic diversity. Cluster III was the largest cluster which consisted 43 (28.67%) genotypes, followed by cluster I which consisted of 40 (26.67%) genotypes, cluster II consisted 31 (20.67%) genotypes, cluster IV which comprised 25 (16.67%) genotypes and cluster V which contained 8 (5.33%) genotypes. The lowest number of genotypes was clustered in cluster VII which consisted of only one genotypes (0.67%) followed by cluster VI which comprised of two genotypes (1.33%). Similarly Masreshaw Yirga *et al.* (2022) studied 100 soybean genotypes and clustered them into five groups. The largest cluster, Cluster I, consisted of 57% of the genotypes, while the smallest cluster, Cluster V, had only one genotype.

Earlier studied on soybean genotypes have been indicated the existence of genetic divergence among soybean genotypes and those genotypes were portioned to different cluster. Diriba Beyene and Negash Geleta (2021) studied the existence of genetic diversity among 100 soybean genotypes and reported ten clusters under the studied soybean genotypes. Similarly, Asmamaw Amogne (2023) examined the existence of genetic divergence among 81 soybean and he reported four clusters in tested soybean genotypes.

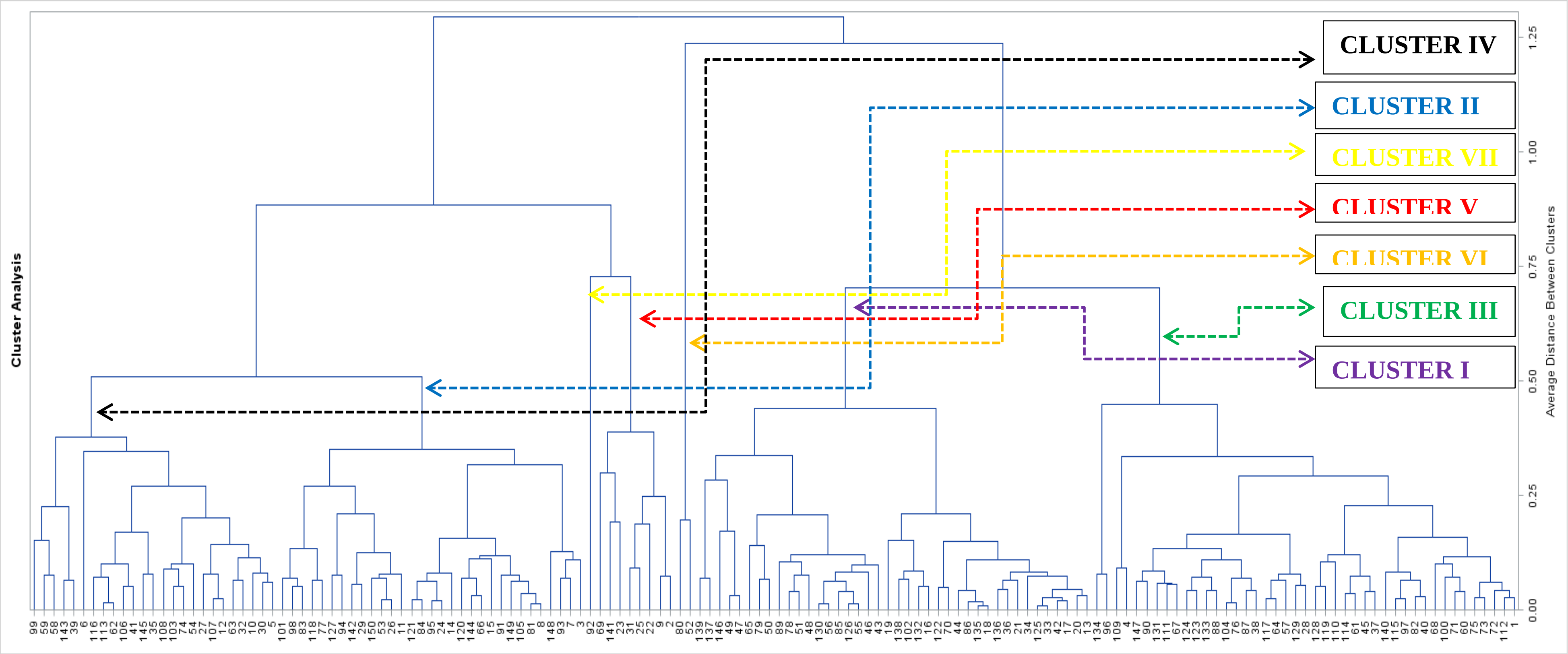

Figure 8. Dendrogram for one hundred fifty soybean genotypes

Table 11. Distribution of genotypes in to seven clusters based on $D^2$ analysis for 150 soybean genotypes studied at PARC

| Clusters | N0.of genotypes | Genotypes included |
|---|---|---|
| **I** | 40 | PW01_18_S_13_2,PW02_18_S_15,PW02_18_S_21,PW02_18_S_22, PW02_18_S_23, PW02_18_S_24, PW02_18_S_25, PW04_18_S_32, PW04_18_S_33, PW04_18_S_35, PW05_18_S_21, PW05_18_S_51, PW05_18_S_52, PW06_18_S_11, PW06_18_S_13, PW06_18_S_14, PW06_18_S_15, PW06_18_S_31, PW06_18_S_34, PW07_18_S_33, PW07_18_S_55, PW09_18_S_11, PW09_18_S_23, PW10_18_S_11, PW10_18_S_22, PW11_18_S_21, PW11_18_S_23, PW11_18_S_51, PW14_18_S_13, PW16_18_S_41, PW16_18_S_44, PW16_18_S_45, PW17_18_S_13, PW17_18_S_41, PW19_18_S_15, PW19_18_S_25, PW20_18_S_21, PW20_18_S_31, PW20_18_S_44, PW21_18_S_31. |
| **II** | 31 | PW01_17_S_14, PW01_17_S_25, PW01_17_S_31, PW01_17_S_34, PW02_17_S_31, PW02_17_S_35, PW04_17_S_12, PW04_17_S_14, PW04_17_S_32, PW07_17_S_11, PW09_18_S_12, PW10_17_S_21, PW11_17_S_11, PW11_17_S_21, PW11_17_S_31, PW12_17_S_21, PW13_17_S_21, PW13_17_S_22, PW13_17_S_31, PW14_17_S_21, PW14_18_S_12_2,PW14_18_S_21,PW16_18_S_24,PW16_18_S_31,PW16_18_S_35_2,PW16_18_S_51_1, PW21_18_S_23_2, PW21_18_S_24_2, SC_Signal, SCS_1, Tana Beles |
| **III** | 43 | PW01_17_S_12, PW01_17_S_15, PW04_17_S_31, PW04_18_S_52, PW05_17_S_11, PW05_17_S_13, PW05_18_S_53, PW08_17_S_11, PW08_17_S_23, PW08_17_S_31, PW09_17_S_31, PW09_18_S_13, PW09_18_S_15_1,PW09_18_S_23_1,PW09_18_S_23_2,PW09_18_S_25_1, PW09_18_S_44_2, PW10_17_S_11, PW11_17_S_12, PW11_18_S_25, PW11_18_S_33_1, PW12_17_S_11, PW13_18_S_21, PW14_17_S_11, PW14_18_S_12_1, PW14_18_S_15_2, PW15_17_S_11, PW15_17_S_21, PW15_17_S_31, PW16_18_S_12, PW16_18_S_15, PW16_18_S_21, PW16_18_S_23, PW16_18_S_25, PW16_18_S_42, PW16_18_S_43, PW16_18_S_52_1, PW16_18_S_53, PW17_18_S_14, PW17_18_S_43, PW17_18_S_44, PW21_18_S_22, PW21_18_S_33 |

| | | |
|---|---|---|
| **IV** | 25 | PW01_17_S_22, PW01_17_S_23, PW01_17_S_33, PW01_18_S_13_1, PW04_17_S_23, PW04_17_S_33, PW04_18_S_25, PW04_18_S_34, PW05_17_S_12, PW05_17_S_21, PW07_17_S_21, PW08_17_S_12, PW08_17_S_21, PW09_17_S_11, PW09_17_S_21, PW09_18_S_44_1, PW14_17_S_31, PW14_18_S_15_1, PW14_18_S_22, PW14_18_S_44, PW14_18_S_45, PW16_18_S_14, PW16_18_S_22, PW21_18_S_24_1, PW21_18_S_25_2. |
| **V** | 8 | PW01_17_S_13, PW01_17_S_32, PW03_17_S_21, PW04_17_S_11, PW04_17_S_13, PW04_17_S_35, PW09_18_S_15_2, PW21_18_S_23_1 |
| **VI** | 2 | PW06_18_S_35 and PW10_18_S_25 |
| **VII** | 1 | PW13_17_S_11 |

### 4.7. Genetic Distance between Clusters

The intra-cluster and inter cluster distance of genotypes are presented in Table 12. The standardized Mahalanobis $D^2$ statistics indicated the presence of genetic differences between pairs of clusters. The genetic divergence between pairs of CI and CII, CI and CIV, CI and CV, CI and CVI, CI and CVII, CII and CII, CII and CV, CII and CVI, CII and CVII, CIII and CV, CIII and CVI, CIII and CVII, CIV and CV, CIV and CVI, CIV and CVII, CV and CVI, CV and CVII and CVI and CVII were significant and highly significant ($p \leq 0.05$ and $p \leq 0.01$). In addition non-significant genetic divergence were found between pairs of cluster I and cluster III, cluster II and cluster IV, cluster II and cluster V and cluster III and cluster IV. Intra-cluster divergences revealed a non-significant difference. In agreement with this finding Gada Gudina *et al.* (2023) reported significant and non-significant genetic divergences between pairs of inter clusters in 100 testing soybean genotypes.

The intra cluster distance between genotypes within cluster was ranged from $D^2$ =2.5 for cluster III to $D^2$ = 10.02 for cluster VII. The intra cluster value showed low this revealed that the genotypes grouped in the same cluster were less divergent than the genotypes grouped in different cluster. Similar results of low $D^2$ value within the same cluster have been reported (Masreshaw Yirga *et al.*, 2022).

The inter cluster distance between genotypes was varied from $D^2$ = 11.27 between cluster II and cluster IV to $D^2$ = 547.84 between cluster VI and cluster VII. The maximum inter cluster distance was observed from cluster VI and cluster VII ($D^2$ = 547.84) followed by cluster V and cluster VI ($D^2$ =386.76), cluster I and cluster VII ($D^2$ = 350.35), cluster II and cluster VI ($D^2$ =253.29), and cluster III and cluster VII ($D^2$ =383.72), while the minimum inter cluster distance was obtained on cluster II and cluster IV ($D^2$ = 11.27) followed by cluster III and cluster IV ($D^2$ = 13.15), cluster II and cluster V ($D^2$ = 19.54) and cluster I and cluster III ($D^2$ = 17.50). In harmony results of maximum inter cluster distance between pairs of clusters and minimum inter cluster distance for pairs of cluster were observed by Rohitash and Gaibriyal (2020).

Therefore clusters with largest cluster distance indicated that the existence of large variability among the genotypes with in that cluster. The presence of shortest inter cluster distance indicated that the presence of similarity between these clusters. Crossing of genotypes from distant inter clusters may produce higher amount of hetrotic expression in the first filial generations and wide range of variability in subsequent segregating populations (Ghaderi *et al.*, 1984). Hence, crossing between genotypes involving between cluster VI and cluster VII, cluster V and cluster VI and cluster I and cluster VII is suggested to exhibit high heterosis and could result in segregates with higher seed yield, i.e. better recombinants will be resulted in.

Table 12. Intra (bold diagonal) and inter Mahalanobis distance among 150 soybean genotypes at PARC

| Cluster | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | **2.64** | | | | | | |
| II | $113.18^{**}$ | **3.15** | | | | | |
| III | 17.50 | $45.89^{**}$ | **2.50** | | | | |
| IV | $57.89^{**}$ | 11.27 | 13.15 | **3.58** | | | |
| V | $212.99^{**}$ | 19.54 | $116.37^{**}$ | $55.10^{**}$ | **5.86** | | |
| VI | $44.69^{**}$ | $258.37^{**}$ | $103.65^{**}$ | $174.08^{**}$ | $386.76^{**}$ | **8.63** | |
| VII | $383.72^{**}$ | $139.01^{**}$ | $277.58^{**}$ | $196.13^{**}$ | $105.08^{**}$ | $547.84^{**}$ | **10.02** |

$\chi^2$= 30.14 and 36.19 at 5%, 1% probability level respectively.

### 4.8. Cluster Mean Analysis

Estimates of cluster means for the traits are presented in Table 13. The current cluster mean values indicated variations among the seven clusters for different traits. Genotypes in Cluster I was characterized by the highest mean value of brown spot and the second-highest mean values of oil content, harvest index, frogeye leaf spot, bacterial blight and red leaf blotch. They also had the lowest mean value for the number of seeds per pod and days to maturity, as well as the second-lowest mean values for days to flowering, biomass yield, grain yield, hundred seed weight, number of pods per plant, number of branches per plant, and plant height. Rohitash and Gaibriyal (2020) who had a similar result with current findings of lowest mean values for number of seeds per pod in cluster VIII.

Cluster II was characterized by the lowest mean values of lodging, the second lowest mean values of bacterial blight, brown spot and red leaf blotch, the third-lowest mean values of protein content, and frogeye leaf spot, the second-highest mean values of plant height and number of pods per plant, and the third-highest mean values of days to flowering, days to maturity, shattering, hundred seed weight, seeds per plant, and biomass yield. Similar result of the second highest mean value of plant height have been reported by Gobezie Chakelie (2022).

In Cluster III, traits such as days to maturity and number of seeds per pod had the second-lowest mean value, Additionally, they also had the third-lowest mean values for days to flowering, number of branches per plant, hundred seed weight, grain yield, pods per plant, number of seeds per plant, and biomass yield, while lodging had the highest mean value, protein content, and brown spot had the second-highest mean value among the traits in this cluster and it also had the third-highest mean value of harvest index, oil content, frogeye leaf spot, bacterial blight, and red leaf blotch. The second highest mean values of days to maturity and number of seeds per pod under cluster I were reported (Asmamaw Amogne, 2023).

Cluster IV was characterized by the highest mean value of oil content, the second-highest mean value of shattering and number of branches per plant, the third-highest mean value of plant height, hundred seed weight, grain yield, number of pods per plant, protein content, and brown spot. Additionally, it had the second-lowest mean values of the number of seeds per pod and the third-lowest mean values of lodging. Similar results the highest mean values of oil content under cluster IV have been reported by Neelima and Narkhede (2017).

In cluster V, genotypes were characterized by the highest mean values for days to maturity, plant height, hundred seed weight, and grain yield. They also had the second-highest mean values for days to flowering, number of seeds per plant, number of seeds per pod, and biomass yield. Additionally, they had the third-highest mean values for the number of branches per plant and harvest index, as well as the second-lowest mean values for lodging, shattering, and oil content and the lowest mean values for bacterial blight, brown spot, and red leaf blotch. In agreement with the present findings, the highest mean values of days to maturity and plant height in Cluster II were reported (Kumawat *et al.*, 2024).

Cluster VI had two genotypes that were characterized by the lowest mean values for days to flowering, shattering, plant height, number of branches per plant, hundred seed weight, grain yield, number of pods per plant, number of seeds per pod, biomass yield, and protein content. They also had the second-lowest mean values for oil content and the third-lowest mean values for days to maturity. They also characterized by the highest mean values for lodging, harvest index, frogeye leaf spot, bacterial blight and red leaf blotch, and the second-highest mean values for the number of seeds per plant. Similarly Nag and Sarawgi (2021) reported lowest mean values of days to maturity in cluster III, days to maturity, number of seeds per plant and plant height in cluster I, pods per plant and hundred seed weight in cluster IV and protein content in cluster VI.

Cluster VII included only one genotype characterized by the highest mean values for days to flowering, lodging, number of branches per plant, number of pods per plant, number of seeds per plant, biomass yield, and protein content which. Similarly, highest mean values of days to flowering in cluster VIII, number of branches per plant in cluster II and number of pods per plant have been reported by Joshi *et al.* (2018). It also had the second-highest mean values for days to maturity and hundred seed weight, the third-highest mean values for shattering and number of seeds per pod. In addition Cluster VII characterized by the lowest mean values for harvest index, oil content and frogeye leaf spot, and the third-lowest mean value for plant height, bacterial blight, brown spot and red leaf blotch.

Table 13. Cluster means of nineteen traits in 150 soybean genotypes

| | Clusters | | | | | | |
|---|---|---|---|---|---|---|---|
| Traits | **I** | **II** | **III** | **IV** | **V** | **VI** | **VII** |
| DTF | 38.91 | 50.19 | 46.36 | 48.06 | 51.38 | 35.75 | 59.50 |
| DTM | 102.48 | 112.76 | 108.80 | 111.98 | 118.56 | 111.00 | 114.00 |
| LDG | 1.65 | 1.06 | 1.56 | 1.36 | 1.13 | 3.00 | 3.00 |
| STG | 2.26 | 2.32 | 2.67 | 2.64 | 1.81 | 1.75 | 2.50 |
| PH | 55.39 | 70.64 | 67.51 | 68.42 | 77.90 | 46.25 | 67.10 |
| BPP | 5.21 | 5.68 | 5.60 | 5.93 | 5.88 | 5.10 | 7.00 |
| HSW | 13.59 | 15.76 | 14.55 | 15.09 | 18.00 | 11.75 | 16.50 |
| GY | 1753.86 | 2712.30 | 2203.31 | 2493.86 | 3134.54 | 1205.27 | 2384.71 |
| PPP | 68.32 | 84.30 | 79.33 | 84.21 | 83.13 | 59.70 | 136.90 |
| SdPP | 138.98 | 187.43 | 166.07 | 178.53 | 194.95 | 140.50 | 308.80 |
| SedPP | 2.05 | 2.22 | 2.09 | 2.13 | 2.34 | 2.37 | 2.25 |
| BM | 3406.25 | 5735.89 | 4338.66 | 5079.17 | 6549.48 | 2135.42 | 7395.83 |
| HI | 52.09 | 47.52 | 51.05 | 49.57 | 47.84 | 57.02 | 32.28 |
| PC | 40.94 | 40.88 | 41.12 | 41.10 | 40.87 | 40.70 | 41.30 |
| OC | 22.94 | 22.80 | 22.93 | 23.16 | 22.61 | 22.58 | 21.40 |
| FLS | 2.03 | 1.40 | 1.53 | 1.44 | 1.14 | 2.50 | 1.00 |
| BBL | 2.83 | 2.35 | 2.68 | 2.53 | 1.60 | 3.19 | 2.50 |
| BS | 2.90 | 2.06 | 2.85 | 2.56 | 1.57 | 2.50 | 2.13 |
| RLB | 3.22 | 2.17 | 2.67 | 2.47 | 1.40 | 3.32 | 2.38 |

*DF=degree of freedom. DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP=*

*Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC= Protein content; OC= Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

### 4.9. Principal Component Analyses

The estimates of principal component for traits of soybean genotypes are presented in Table 14. The result revealed that the first five PCA components: PCA 1 to PCA 5 with egen values of 6.08, 2.45, 1.94, 1.45, and 1.25, respectively, accounted for 69.27% to the total variation. From the total variation 32.02% was explained by PCA I, followed by 12.92% by PCA II, 10.22% by PCA III, 7.62% by PCA IV and 6.48% by PCA V.

Gada Gudina *et al.* (2023) reported similar result with current finding that 71.25 % of the total variation was explained among 100 tested soybean recombinant inbred lines by the first four principal components using 12 quantitative traits and also his result implied that the highest variation was found in principal component one (28.4%). In addition Saraswat and Sharma (2021) reported that 77.48% of the total variation was explained among thirty soybean genotypes by the first four principal components using 16 morphological traits and he also found the highest genetic variation in the first principal component. Dubey *et al.* (2018) reported that 73.44% the total variability explained among eighteen soybean genotypes by five principal components.

In this result ten character had positive contribution to PCA I which accounted for 32.02% of the total variation, whereas the remaining nine characters had negative contribution to PCA I. PCA I contributes the largest variation in the principal component and grain yield (0.360) had maximum contribution in this PCA followed by biomass yield (0.352), number of seeds per plant (0.311), and days to flowering (0.303). Similarly Dubey *et al.* (2018) found similar result with the current finding reported that 37.13% of total variation was contributed in the first principal components and associated with days to flowering, and number of seeds per plant. In addition Asmamaw Amogne (2023) reported 27% of total variation was contributed by principal component one associated with days to flowering. Likewise Upadhyay *et* *al.* (2022) observed a highest total variability contribution in the first PC and this author also found higher contribution of days to flowering, number of seeds per plant and biomass yield to the first PC.

Eleven traits had positive contribution in the second PC while eight traits had negative contribution in this PC. About 12.92% of the total variation among 150 tested soybean genotypes was contributed by PCA II, with the number of branches per plant being the largest contributor in this PCA followed by number of pods per plant and brown spot. It has a load value of 0.404, 0.364 and 0.354 respectively, similar to the result reported by Asmamaw Amogne (2023) where 16% of the total variability was contributed in this PC associated with the number of branches per plant and number of pods per plant.

The third principal component had eleven positive and eight negative contributors and was more dominated by traits like days to flowering (0.337), and protein content (0.463). It contributes 10.22% of the total variability among the genotypes. Gobezie Chakelie (2022) reported 8% of the total variation was contributed in principal component three related with protein content. Similarly PCA four had ten positive contributors' traits whereas nine traits had negative contribution in this PCA. Traits which explained in the fourth principal components were loading (0.344) and number of seeds per pod (0.329).

Principal components five explained the smallest contribution to the total variation among 150 testing genotypes. It comprised ten positive contributing traits and nine negative contributing traits. The fifth principal component exhibited the highest contribution from harvest index (0.508); followed by protein content (0.321). The outcomes of Dubey *et al.* (2018) were similar with the present study of 6.88% of total variation was contributed in this principal component associated with protein content and Sivabharathi *et al.* (2023) found 8.98% of total variation was contributed in principal component five on number of branches per plant.

In this PC biplot analysis, the contribution of traits to total variability and correlation between the traits presented in figure 9. Longer vectors indicated that traits that have a greater influence or contribution on the variability. Hence, traits such as pods per plant, branches per plant, plant height, biomass yield, number of seeds per plant, grain yield, and days to flowering made the greatest contributions to the total variation in principal component I and II. On the other hand, shattering, loading, harvest index, oil content and protein content exhibited the lowest contribution to the total variability in principal component I and II.

The angle between the trait vectors represents the correlation between the traits. If the angle is small (close to 0 degrees), the traits are positively correlated, meaning they change in a similar direction. If the angle is close to 90 degrees, the traits are uncorrelated, and if it is close to 180 degrees, they are negatively correlated, meaning they change in opposite directions. Based on the biplot results, grain yield exhibited a positive correlation with the number of seeds per plant, days to flowering, biomass yield, and hundred seed weight. The number of pods per plant displayed a positive correlation with plant height, branches per plant, and seeds per plant. A negative correlation was observed between grain yield and shattering and lodging. Additionally, a strong negative correlation was evident between oil content and protein content.

Table 14. Eigen vectors, total variance explained, cumulative and Eigen values of the first seven principal components (PCs) of soybean genotypes evaluated at PARC

| | Eigen vectors | | | | |
|---|---|---|---|---|---|
| Characters | PCA 1 | PCA 2 | PCA 3 | PCA 4 | PCA 5 |
| DTF | 0.303 | -0.012 | 0.337 | 0.114 | -0.007 |
| DTM | 0.266 | -0.110 | 0.071 | 0.291 | -0.186 |
| LDG | -0.082 | 0.246 | 0.234 | 0.344 | -0.185 |
| STG | -0.007 | 0.261 | 0.263 | -0.466 | -0.005 |
| PH | 0.267 | 0.277 | -0.056 | -0.014 | -0.263 |
| BPP | 0.185 | 0.404 | -0.136 | 0.037 | 0.263 |
| HSW | 0.211 | -0.196 | -0.207 | -0.221 | 0.172 |

| | | | | | |
|---|---|---|---|---|---|
| GY | 0.360 | -0.138 | -0.155 | -0.117 | -0.016 |
| PPP | 0.264 | 0.364 | 0.034 | 0.028 | 0.286 |
| SdPP | 0.311 | 0.241 | 0.118 | 0.174 | 0.273 |
| SedPP | 0.174 | -0.174 | 0.191 | 0.329 | 0.062 |
| BM | 0.352 | -0.006 | -0.005 | -0.217 | -0.251 |
| HI | -0.064 | -0.242 | -0.253 | 0.249 | 0.508 |
| PC | -0.004 | -0.106 | 0.463 | -0.386 | 0.321 |
| OC | -0.060 | 0.253 | -0.539 | -0.144 | -0.100 |
| FLS | -0.235 | 0.023 | 0.164 | 0.026 | -0.313 |
| BBL | -0.179 | 0.280 | 0.005 | 0.281 | 0.037 |
| BS | -0.203 | 0.354 | -0.004 | -0.055 | 0.088 |
| RLB | -0.307 | 0.048 | 0.146 | -0.024 | 0.248 |
| Eigen values | 6.08 | 2.45 | 1.94 | 1.45 | 1.23 |
| variance % | 32.02 | 12.92 | 10.22 | 7.62 | 6.48 |
| Cumulative | 32.02 | 44.94 | 55.16 | 62.78 | 69.27 |

*DF=degree of freedom. DTF=Days to 50% flowering; DTM=Days to maturity; LDG= Lodging; STG=Shattering; PH=Plant height; BPP= Branch number plant; HSW=Hundred seed weight; GY=Grain yield; PPP=Pod number per plant; SdPP= Seed number per plant; SedPP= Number of seeds per pod; BM=Biomass yield; HI=Harvest index; PC= Protein content; OC= Oil content; FLS=frog eye leaf spot; BBL=bacterial blight; BS=brown spot; and RLB=red leaf blotch.*

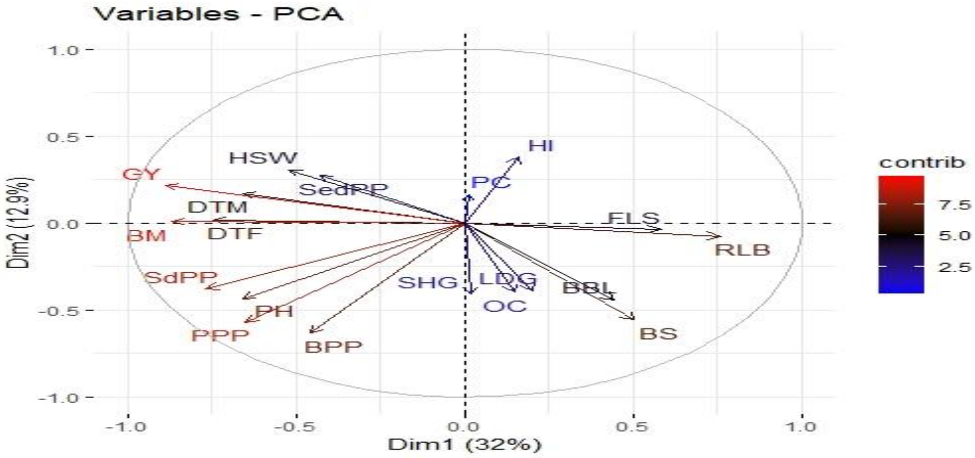

Figure 9. Biplot of PC1 and PC2 showing the contribution and correlation between the traits

# Chapter 5. CONCLUSIONS AND RECOMMENDATIONS

## 5.1. Conclusions

In this study, 150 soybean genotypes were examined to evaluate the genetic diversity and relationships among 13 quantitative traits, 2 quality attributes, and 4 disease reaction traits. The result of analysis of variance showed there was highly significant difference ($P<0.01$) for traits days to flowering, days to maturity, lodging, shattering, plant height, hundred seed weight, average grain yield, number of pods per plant, total seed per plant, number seeds per pod, biomass, harvest index, oil content, protein content, frogeye leaf spot, bacterial blight, brown spot and red leaf blotch and significant different ($P<0.05$) for number of branch per plant considered among 150 soybean genotypes.

Phenotypic coefficient of variation values varied from 2.56% for protein content to 51.84 % for lodging, while genotypic coefficient of variation values ranged from 1.70 % for protein content to 44.96% for loading. The highest phenotypic coefficient of variation were observed for lodging, shattering, plant height, grain yield, number of pods per plant, number of seeds per plant, biomass yield, frog eye leaf spot, bacterial blight, brown spot and red leaf blotch. The highest genotypic coefficient of variation were observed from lodging, shattering, number of seed per plant, biomass yield, frogeye leaf spot, bacterial blight, brown spot, and red leaf blotch. Whereas, low phenotypic and genotypic coefficient of variation values observed from days to maturity, protein content and oil yield.

High heritability coupled with high genetic advance as per cent of mean was recorded for days to flowering, number of pods per plant, red leaf blotch, oil yield, biomass yield, number of seeds per pod, frog eye leaf spot, grain yield, shattering, lodging, bacterial blight, plant height, and hundred seed weight.

Correlation analysis showed grain yield had positive significant genotypic and phenotypic associations with days to flowering, days to maturity, plant height, number of pods per plant, number of seeds per plant, number of seeds per pod, hundred seed weight, and biomass yield. The path coefficient analysis revealed that biomass yield, harvest index, number of pods per plant, plant height, number of seeds per pod, days to flowering, oil content, protein content and hundred seed weight showed positive phenotypic and genotypic direct effects on grain yield.

Based on squared distance values ($D^2$) 150 Soybean genotypes clustered in to seven distinct groups. The result of principal component analysis revealed five PCA components and the first five principal components accounted for about 69.27% contribution to the total variation. 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

The present study generally implied the presence of significant genetic variability among the tested genotypes. Thus, there is an opportunity to bring about improvement through direct selection or hybridization. It can be recommended that inter crossing among the genotype belonging to genetically diverse clusters (VII and VI ; V and VI) and also genotypes showing superior mean performance could be advanced for the improvement program with considering other quality traits in soybean improvement. Quantitative traits are polygenic and highly influenced by environmental factors and one-season experiment could not capture the variability of genotypes in response to the environmental changes. Therefore, a further experiment on these genotypes in different seasons is necessary.

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# APPENDIX

Appendix Table 1. Mean performance of 150 soybean genotypes for traits of frog eye leaf spot and bacterial blight studied at Pawe.

| Genotypes | FLS<br>disease score | disease grade | Genotypes | BBL<br>disease score | disease grade |
|---|---|---|---|---|---|
| PW01_17_S_22 | 1.0 | R | PW04_17_S_35 | 1.0 | R |
| PW01_17_S_33 | 1.0 | | PW09_18_S_15_2 | 1.0 | |
| PW01_17_S_34 | 1.0 | | PW21_18_S_23_1 | 1.0 | |
| PW02_17_S_31 | 1.0 | | PW04_17_S_31 | 1.1 | |
| PW02_17_S_35 | 1.0 | | PW13_17_S_21 | 1.3 | |
| PW03_17_S_21 | 1.0 | | PW01_17_S_34 | 1.3 | |
| PW04_17_S_14 | 1.0 | | PW17_18_S_13 | 1.3 | |
| PW04_17_S_32 | 1.0 | | PW15_17_S_11 | 1.4 | |
| PW04_17_S_33 | 1.0 | | PW01_17_S_32 | 1.4 | |
| PW04_18_S_52 | 1.0 | | PW17_18_S_14 | 1.4 | |
| PW05_17_S_13 | 1.0 | | PW02_17_S_31 | 1.6 | MR |
| PW06_18_S_13 | 1.0 | | PW04_17_S_13 | 1.6 | |
| PW06_18_S_15 | 1.0 | | PW04_17_S_33 | 1.7 | |
| PW08_17_S_21 | 1.0 | | PW04_18_S_25 | 1.7 | |
| PW08_17_S_31 | 1.0 | | PW13_17_S_31 | 1.7 | |
| PW09_17_S_21 | 1.0 | | PW01_18_S_13_1 | 1.8 | |
| PW09_18_S_13 | 1.0 | | PW04_17_S_11 | 1.8 | |
| PW09_18S_15_1 | 1.0 | | PW07_17_S_11 | 1.8 | |
| PW09_18_S_15_2 | 1.0 | | PW09_18_S_44_1 | 1.8 | |
| PW09_18_S_25_1 | 1.0 | | PW14_18_S_44 | 1.8 | |
| PW09_18_S_44_1 | 1.0 | | PW16_18_S_31 | 1.8 | |
| PW09_18_S_44_2 | 1.0 | | PW21_18_S_24_2 | 1.8 | |
| PW10_17_S_11 | 1.0 | | SC_Signal | 1.8 | |
| PW11_17_S_11 | 1.0 | | PW01_17_S_14 | 1.9 | |
| PW11_18_S_51 | 1.0 | | PW16_18_S_41 | 1.9 | |
| PW12_17_S_11 | 1.0 | | PW01_17_S_23 | 2.0 | |
| PW13_17_S_11 | 1.0 | | PW01_17_S_25 | 2.0 | |
| PW13_17_S_31 | 1.0 | | PW11_17_S_31 | 2.1 | |
| PW14_17_S_11 | 1.0 | | PW16_18_S_35_2 | 2.1 | |
| PW14_17_S_31 | 1.0 | | PW09_18_S_12 | 2.2 | |
| PW14_18_S_12_2 | 1.0 | | PW01_17_S_13 | 2.3 | |
| PW14_18_S_15_1 | 1.0 | | PW14_18_S_45 | 2.3 | |
| PW14_18_S_21 | 1.0 | | PW05_18_S_52 | 2.4 | |
| PW14_18_S_22 | 1.0 | | PW06_18_S_14 | 2.4 | |
| PW14_18_S_45 | 1.0 | | PW15_17_S_21 | 2.4 | |
| PW15_17_S_11 | 1.0 | | PW01_17_S_12 | 2.5 | MS |
| PW15_17_S_21 | 1.0 | | PW02_17_S_35 | 2.5 | |
| PW16_18_S_12 | 1.0 | | PW04_17_S_32 | 2.5 | |

| | | | | |
|---|---|---|---|---|
| PW16_18_S_14 | 1.0 | | PW04_18_S_32 | 2.5 |
| PW16_18_S_15 | 1.0 | | PW04_18_S_33 | 2.5 |
| PW16_18_S_21 | 1.0 | | PW04_18_S_35 | 2.5 |
| PW16_18_S_23 | 1.0 | | PW05_17_S_11 | 2.5 |
| PW16_18_S_24 | 1.0 | | PW05_17_S_13 | 2.5 |
| PW16_18_S_25 | 1.0 | | PW05_18_S_21 | 2.5 |
| PW16_18_S_31 | 1.0 | | PW06_18_S_13 | 2.5 |
| PW16_18_S_51_1 | 1.0 | | PW06_18_S_34 | 2.5 |
| PW16_18_S_52_1 | 1.0 | | PW07_17_S_21 | 2.5 |
| PW16_18_S_53 | 1.0 | | PW08_17_S_11 | 2.5 |
| PW19_18_S_25 | 1.0 | | PW09_17_S_31 | 2.5 |
| PW21_18_S_22 | 1.0 | | PW09_18_S_23 | 2.5 |
| PW21_18_S_23_1 | 1.0 | | PW09_18_S_23_1 | 2.5 |
| PW21_18_S_23_2 | 1.0 | | PW11_17_S_11 | 2.5 |
| PW21_18_S_33 | 1.0 | | PW11_17_S_12 | 2.5 |
| PW01_17_S_23 | 1.1 | | PW11_17_S_21 | 2.5 |
| PW02_18_S_21 | 1.1 | | PW12_17_S_21 | 2.5 |
| PW02_18_S_24 | 1.1 | | PW13_17_S_11 | 2.5 |
| PW04_17_S_11 | 1.1 | | PW14_17_S_11 | 2.5 |
| PW04_17_S_13 | 1.1 | | PW14_18_S_12_2 | 2.5 |
| PW05_18_S_53 | 1.1 | | PW16_18_S_42 | 2.5 |
| PW07_17_S_21 | 1.1 | | PW16_18_S_43 | 2.5 |
| PW08_17_S_23 | 1.1 | | PW16_18_S_44 | 2.5 |
| PW09_17_S_11 | 1.1 | | PW17_18_S_41 | 2.5 |
| PW09_18_S_12 | 1.1 | | PW17_18_S_43 | 2.5 |
| PW09_18_S_23 | 1.1 | | PW17_18_S_44 | 2.5 |
| PW10_17_S_21 | 1.1 | | PW19_18_S_15 | 2.5 |
| PW13_17_S_22 | 1.1 | | PW20_18_S_31 | 2.5 |
| PW14_17_S_21 | 1.1 | | PW21_18_S_24_1 | 2.5 |
| PW14_18_S_15_2 | 1.1 | | PW21_18_S_31 | 2.5 |
| PW01_17_S_13 | 1.3 | | PW21_18_S_33 | 2.5 |
| PW01_17_S_32 | 1.3 | | PW13_18_S_21 | 2.6 |
| PW04_17_S_23 | 1.3 | | PW01_17_S_22 | 2.6 |
| PW11_17_S_31 | 1.3 | | PW04_18_S_34 | 2.6 |
| PW13_17_S_21 | 1.3 | | PW08_17_S_21 | 2.6 |
| SC_Signal | 1.3 | | PW09_18_S_25_1 | 2.6 |
| PW04_17_S_35 | 1.4 | | PW10_17_S_11 | 2.6 |
| PW16_18_S_35_2 | 1.4 | | PW10_17_S_21 | 2.6 |
| PW01_17_S_25 | 1.5 | MR | PW10_18_S_25 | 2.6 |
| PW01_18_S_13_1 | 1.5 | | PW14_17_S_21 | 2.6 |
| PW04_18_S_25 | 1.5 | | PW16_18_S_45 | 2.6 |
| PW12_17_S_21 | 1.5 | | PW21_18_S_23_2 | 2.6 |
| PW01_18_S_13_2 | 1.6 | | PW03_17_S_21 | 2.7 |
| PW05_17_S_11 | 1.6 | | PW01_17_S_31 | 2.8 |
| PW10_18_S_11 | 1.6 | | PW04_17_S_12 | 2.8 |
| PW11_18_S_33_1 | 1.6 | | PW04_18_S_52 | 2.8 |

| | | | |
|---|---|---|---|
| PW17_18_S_14 | 1.6 | PW05_17_S_12 | 2.8 |
| PW01_17_S_12 | 1.8 | PW05_17_S_21 | 2.8 |
| PW11_18_S_25 | 1.8 | PW05_18_S_51 | 2.8 |
| PW01_17_S_14 | 1.9 | PW06_18_S_11 | 2.8 |
| PW05_17_S_12 | 1.9 | PW06_18_S_15 | 2.8 |
| PW16_18_S_45 | 2.0 | PW08_17_S_23 | 2.8 |
| PW04_17_S_12 | 2.0 | PW09_17_S_11 | 2.8 |
| PW04_18_S_32 | 2.0 | PW09_17_S_21 | 2.8 |
| PW04_18_S_33 | 2.0 | PW09_18_S_11 | 2.8 |
| PW05_18_S_51 | 2.0 | PW09_18_S_23_2 | 2.8 |
| PW06_18_S_14 | 2.0 | PW10_18_S_11 | 2.8 |
| PW07_18_S_55 | 2.0 | PW11_18_S_23 | 2.8 |
| PW11_18_S_21 | 2.0 | PW13_17_S_22 | 2.8 |
| PW16_18_S_44 | 2.0 | PW14_17_S_31 | 2.8 |
| PW20_18_S_31 | 2.0 | PW14_18_S_12_1 | 2.8 |
| PW20_18_S_44 | 2.0 | PW14_18_S_15_2 | 2.8 |
| PW21_18_S_24_1 | 2.0 | PW14_18_S_21 | 2.8 |
| PW21_18_S_25_2 | 2.0 | PW16_18_S_23 | 2.8 |
| PW11_18_S_23 | 2.1 | PW16_18_S_51_1 | 2.8 |
| PW01_17_S_15 | 2.3 | PW16_18_S_52_1 | 2.8 |
| PW01_17_S_31 | 2.3 | PW19_18_S_25 | 2.8 |
| PW02_18_S_15 | 2.3 | PW20_18_S_44 | 2.8 |
| PW02_18_S_22 | 2.3 | PW21_18_S_22 | 2.8 |
| PW02_18_S_25 | 2.3 | PW21_18_S_25_2 | 2.8 |
| PW04_17_S_31 | 2.3 | SCS_1 | 2.8 |
| PW04_18_S_34 | 2.3 | PW14_18_S_13 | 2.8 |
| PW04_18_S_35 | 2.3 | PW15_17_S_31 | 2.8 |
| PW05_18_S_21 | 2.3 | PW05_18_S_53 | 2.9 |
| PW05_18_S_52 | 2.3 | PW08_17_S_12 | 2.9 |
| PW06_18_S_11 | 2.3 | PW10_18_S_22 | 2.9 |
| PW06_18_S_35 | 2.3 | PW16_18_S_14 | 2.9 |
| PW07_17_S_11 | 2.3 | PW01_17_S_33 | 3.0 |
| PW07_18_S_33 | 2.3 | PW01_18_S_13_2 | 3.0 |
| PW08_17_S_11 | 2.3 | PW04_17_S_23 | 3.0 |
| PW08_17_S_12 | 2.3 | PW08_17_S_31 | 3.0 |
| PW09_17_S_31 | 2.3 | PW09_18_S_15_1 | 3.0 |
| PW09_18_S_23_1 | 2.3 | PW09_18_S_44_2 | 3.0 |
| PW09_18_S_23_2 | 2.3 | PW11_18_S_21 | 3.0 |
| PW10_18_S_22 | 2.3 | PW11_18_S_33_1 | 3.0 |
| PW11_17_S_12 | 2.3 | PW14_18_S_15_1 | 3.0 |
| PW11_17_S_21 | 2.3 | PW14_18_S_22 | 3.0 |
| PW14_18_S_44 | 2.3 | PW16_18_S_12 | 3.0 |
| PW15_17_S_31 | 2.3 | PW16_18_S_25 | 3.0 |
| PW16_18_S_22 | 2.3 | PW02_18_S_25 | 3.1 |
| PW16_18_S_41 | 2.3 | PW16_18_S_22 | 3.1 |
| PW16_18_S_42 | 2.3 | PW01_17_S_15 | 3.3 |

| | | | | | |
|---|---|---|---|---|---|
| PW17_18_S_13 | 2.3 | | PW04_17_S_14 | 3.3 | |
| PW17_18_S_43 | 2.3 | | PW07_18_S_33 | 3.3 | |
| PW17_18_S_44 | 2.3 | | PW11_18_S_25 | 3.3 | |
| PW21_18_S_24_2 | 2.3 | | PW11_18_S_51 | 3.3 | |
| PW21_18_S_31 | 2.3 | | PW12_17_S_11 | 3.3 | |
| PW02_18_S_23 | 2.4 | | PW16_18_S_15 | 3.3 | |
| PW20_18_S_21 | 2.4 | | PW16_18_S_21 | 3.3 | |
| PW05_17_S_21 | 2.5 | MS | PW16_18_S_24 | 3.3 | |
| PW06_18_S_31 | 2.5 | | PW16_18_S_53 | 3.3 | |
| SCS_1 | 2.5 | | PW20_18_S_21 | 3.3 | |
| Tana Beles | 2.5 | | PW09_18_S_13 | 3.4 | |
| PW09_18_S_11 | 2.8 | | PW02_18_S_24 | 3.5 | S |
| PW10_18_S_25 | 2.8 | | PW07_18_S_55 | 3.5 | |
| PW13_18_S_21 | 2.8 | | PW06_18_S_31 | 3.7 | |
| PW14_18_S_12_1 | 2.8 | | PW02_18_S_15 | 3.8 | |
| PW16_18_S_43 | 2.8 | | PW02_18_S_21 | 3.8 | |
| PW17_18_S_41 | 2.8 | | PW02_18_S_22 | 3.8 | |
| PW19_18_S_15 | 2.8 | | PW06_18_S_35 | 3.8 | |
| PW14_18_S_13 | 2.8 | | Tana Beles | 3.9 | |
| PW06_18_S_34 | 3.0 | | PW02_18_S_23 | 4.0 | |

Appendix Table 2. Mean performance of soybean genotypes for traits of brown spot and red leaf blotch at Pawe

| Genotypes | Brown spot disease score | disease grade | Genotypes | Red leaf blotch disease score | disease grade |
|---|---|---|---|---|---|
| PW01_17_S_23 | 1.0 | R | PW01_17_S_13 | 1.0 | R |
| PW02_17_S_31 | 1.0 | | PW01_18_S_13_1 | 1.0 | |
| PW04_17_S_35 | 1.0 | | PW08_17_S_31 | 1.0 | |
| PW13_17_S_31 | 1.0 | | PW13_17_S_21 | 1.0 | |
| Tana Beles | 1.0 | | PW14_18_S_21 | 1.0 | |
| PW04_17_S_11 | 1.1 | | PW21_18_S_23_1 | 1.0 | |
| PW21_18_S_33 | 1.3 | | PW03_17_S_21 | 1.1 | |
| PW09_18_S_44_1 | 1.3 | | PW04_17_S_13 | 1.1 | |
| PW11_17_S_21 | 1.4 | | PW09_18_S_12 | 1.1 | |
| PW01_17_S_13 | 1.4 | | PW12_17_S_21 | 1.1 | |
| PW03_17_S_21 | 1.5 | MR | PW16_18_S_31 | 1.1 | |
| PW08_17_S_21 | 1.5 | | SC_Signal | 1.1 | |
| PW01_17_S_14 | 1.6 | | PW01_17_S_32 | 1.3 | |
| PW01_17_S_34 | 1.6 | | PW04_18_S_25 | 1.3 | |
| PW09_18_S_12 | 1.6 | | PW09_18_S_15_2 | 1.4 | |
| PW01_17_S_25 | 1.7 | | PW14_18_S_12_2 | 1.6 | MR |
| PW04_17_S_33 | 1.7 | | PW01_17_S_15 | 1.8 | |
| PW04_18_S_25 | 1.8 | | PW01_17_S_14 | 1.9 | |
| PW05_17_S_13 | 1.8 | | PW05_17_S_13 | 1.9 | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| PW05_18_S_53 | 1.8 |  | PW02_17_S_31 | 1.9 |  |
| PW11_17_S_11 | 1.8 |  | PW01_17_S_23 | 2.0 |  |
| PW21_18_S_23_1 | 1.8 |  | PW07_17_S_11 | 2.0 |  |
| PW21_18_S_31 | 1.8 |  | PW16_18_S_22 | 2.0 |  |
| PW01_17_S_32 | 1.8 |  | Tana Beles | 2.0 |  |
| PW07_17_S_11 | 1.8 |  | PW01_17_S_25 | 2.1 |  |
| PW09_18_S_15_2 | 1.8 |  | PW04_17_S_11 | 2.1 |  |
| PW14_18_S_21 | 1.8 |  | PW04_17_S_35 | 2.2 |  |
| SCS_1 | 1.8 |  | PW11_17_S_11 | 2.4 |  |
| PW21_18_S_24_2 | 1.9 |  | PW11_18_S_25 | 2.4 |  |
| PW01_18_S_13_1 | 1.9 |  | PW12_17_S_11 | 2.4 |  |
| PW09_17_S_21 | 1.9 |  | PW13_17_S_11 | 2.4 |  |
| PW13_17_S_21 | 1.9 |  | PW16_18_S_15 | 2.4 |  |
| PW16_18_S_24 | 1.9 |  | PW16_18_S_25 | 2.4 |  |
| PW16_18_S_51_1 | 1.9 |  | PW01_17_S_12 | 2.5 | MS |
| PW21_18_S_24_1 | 1.9 |  | PW01_17_S_34 | 2.5 |  |
| PW09_18_S_13 | 2.0 |  | PW01_18_S_13_2 | 2.5 |  |
| PW10_17_S_11 | 2.0 |  | PW04_17_S_12 | 2.5 |  |
| PW11_17_S_31 | 2.0 |  | PW04_17_S_23 | 2.5 |  |
| SC_Signal | 2.0 |  | PW04_17_S_32 | 2.5 |  |
| PW04_17_S_12 | 2.1 |  | PW04_17_S_33 | 2.5 |  |
| PW06_18_S_14 | 2.1 |  | PW04_18_S_52 | 2.5 |  |
| PW06_18_S_15 | 2.1 |  | PW05_17_S_11 | 2.5 |  |
| PW07_17_S_21 | 2.1 |  | PW05_17_S_12 | 2.5 |  |
| PW13_17_S_11 | 2.1 |  | PW05_17_S_21 | 2.5 |  |
| PW16_18_S_31 | 2.1 |  | PW07_17_S_21 | 2.5 |  |
| PW16_18_S_41 | 2.1 |  | PW08_17_S_23 | 2.5 |  |
| PW04_17_S_13 | 2.2 |  | PW09_17_S_11 | 2.5 |  |
| PW20_18_S_44 | 2.2 |  | PW09_17_S_21 | 2.5 |  |
| PW21_18_S_23_2 | 2.2 |  | PW09_17_S_31 | 2.5 |  |
| PW04_17_S_32 | 2.3 |  | PW09_18_S_44_2 | 2.5 |  |
| PW11_17_S_12 | 2.3 |  | PW11_17_S_21 | 2.5 |  |
| PW08_17_S_11 | 2.4 |  | PW11_17_S_31 | 2.5 |  |
| PW17_18_S_41 | 2.4 |  | PW11_18_S_33_1 | 2.5 |  |
| PW04_18_S_35 | 2.4 |  | PW13_17_S_22 | 2.5 |  |
| PW14_17_S_11 | 2.5 | MS | PW13_17_S_31 | 2.5 |  |
| PW04_17_S_14 | 2.5 |  | PW14_17_S_11 | 2.5 |  |
| PW05_18_S_51 | 2.5 |  | PW14_18_S_15_1 | 2.5 |  |
| PW06_18_S_35 | 2.5 |  | PW14_18_S_15_2 | 2.5 |  |
| PW09_17_S_11 | 2.5 |  | PW14_18_S_22 | 2.5 |  |
| PW09_18_S_11 | 2.5 |  | PW14_18_S_44 | 2.5 |  |
| PW09_18_S_23 | 2.5 |  | PW15_17_S_11 | 2.5 |  |
| PW10_17_S_21 | 2.5 |  | PW15_17_S_21 | 2.5 |  |
| PW10_18_S_22 | 2.5 |  | PW15_17_S_31 | 2.5 |  |
| PW10_18_S_25 | 2.5 |  | PW16_18_S_23 | 2.5 |  |
| PW12_17_S_21 | 2.5 |  | PW16_18_S_24 | 2.5 |  |

| | | | |
|---|---|---|---|
| PW17_18_S_13 | 2.5 | PW16_18_S_52_1 | 2.5 |
| PW01_17_S_22 | 2.6 | PW16_18_S_53 | 2.5 |
| PW04_17_S_31 | 2.6 | PW21_18_S_22 | 2.5 |
| PW09_17_S_31 | 2.6 | PW21_18_S_24_1 | 2.5 |
| PW09_18_S_25_1 | 2.6 | PW21_18_S_24_2 | 2.5 |
| PW06_18_S_31 | 2.7 | PW01_17_S_31 | 2.6 |
| PW01_17_S_12 | 2.8 | PW01_17_S_33 | 2.6 |
| PW01_17_S_31 | 2.8 | PW02_18_S_15 | 2.6 |
| PW02_17_S_35 | 2.8 | PW02_18_S_21 | 2.6 |
| PW09_18_S_23_1 | 2.8 | PW08_17_S_11 | 2.6 |
| PW09_18_S_23_2 | 2.8 | PW08_17_S_12 | 2.6 |
| PW14_17_S_21 | 2.8 | PW11_17_S_12 | 2.6 |
| PW14_18_S_13 | 2.8 | PW16_18_S_14 | 2.6 |
| PW14_18_S_15_2 | 2.8 | PW16_18_S_35_2 | 2.6 |
| PW16_18_S_35_2 | 2.8 | PW21_18_S_23_2 | 2.6 |
| PW16_18_S_43 | 2.8 | PW21_18_S_25_2 | 2.6 |
| PW16_18_S_45 | 2.8 | SCS_1 | 2.6 |
| PW16_18_S_52_1 | 2.8 | PW02_17_S_35 | 2.8 |
| PW17_18_S_43 | 2.8 | PW02_18_S_22 | 2.8 |
| PW20_18_S_21 | 2.8 | PW02_18_S_24 | 2.8 |
| PW20_18_S_31 | 2.8 | PW04_17_S_14 | 2.8 |
| PW21_18_S_25_2 | 2.8 | PW04_17_S_31 | 2.8 |
| PW07_18_S_33 | 2.8 | PW04_18_S_33 | 2.8 |
| PW01_17_S_33 | 2.9 | PW07_18_S_55 | 2.8 |
| PW08_17_S_12 | 2.9 | PW08_17_S_21 | 2.8 |
| PW11_18_S_51 | 2.9 | PW09_18_S_15_1 | 2.8 |
| PW16_18_S_23 | 2.9 | PW09_18_S_23 | 2.8 |
| PW01_17_S_15 | 3.0 | PW09_18_S_23_1 | 2.8 |
| PW02_18_S_21 | 3.0 | PW09_18_S_23_2 | 2.8 |
| PW02_18_S_22 | 3.0 | PW10_17_S_11 | 2.8 |
| PW02_18_S_23 | 3.0 | PW10_17_S_21 | 2.8 |
| PW07_18_S_55 | 3.0 | PW11_18_S_21 | 2.8 |
| PW11_18_S_33_1 | 3.0 | PW14_17_S_21 | 2.8 |
| PW12_17_S_11 | 3.0 | PW14_17_S_31 | 2.8 |
| PW14_18_S_12_1 | 3.0 | PW14_18_S_45 | 2.8 |
| PW14_18_S_15_1 | 3.0 | PW16_18_S_12 | 2.8 |
| PW14_18_S_45 | 3.0 | PW16_18_S_21 | 2.8 |
| PW15_17_S_31 | 3.0 | PW16_18_S_51_1 | 2.8 |
| PW16_18_S_12 | 3.0 | PW19_18_S_25 | 2.8 |
| PW16_18_S_15 | 3.0 | PW01_17_S_22 | 2.9 |
| PW16_18_S_44 | 3.0 | PW14_18_S_12_1 | 2.9 |
| PW16_18_S_53 | 3.0 | PW02_18_S_23 | 3.0 |
| PW19_18_S_25 | 3.0 | PW06_18_S_35 | 3.0 |
| PW04_18_S_32 | 3.1 | PW09_18_S_11 | 3.0 |
| PW17_18_S_14 | 3.1 | PW09_18_S_44_1 | 3.0 |
| PW02_18_S_25 | 3.1 | PW11_18_S_51 | 3.0 |

| | | | | | |
|---|---|---|---|---|---|
| PW08_17_S_23 | 3.1 | | PW14_18_S_13 | 3.0 | |
| PW16_18_S_14 | 3.1 | | PW16_18_S_43 | 3.0 | |
| PW16_18_S_22 | 3.1 | | PW17_18_S_13 | 3.0 | |
| PW04_18_S_52 | 3.2 | | PW17_18_S_44 | 3.0 | |
| PW01_18_S_13_2 | 3.3 | | PW05_18_S_53 | 3.1 | |
| PW02_18_S_15 | 3.3 | | PW06_18_S_14 | 3.1 | |
| PW04_17_S_23 | 3.3 | | PW09_18_S_13 | 3.1 | |
| PW05_17_S_11 | 3.3 | | PW11_18_S_23 | 3.1 | |
| PW05_17_S_12 | 3.3 | | PW04_18_S_32 | 3.3 | |
| PW05_17_S_21 | 3.3 | | PW05_18_S_52 | 3.3 | |
| PW05_18_S_21 | 3.3 | | PW06_18_S_11 | 3.3 | |
| PW06_18_S_11 | 3.3 | | PW06_18_S_31 | 3.3 | |
| PW06_18_S_13 | 3.3 | | PW16_18_S_41 | 3.3 | |
| PW06_18_S_34 | 3.3 | | PW17_18_S_14 | 3.3 | |
| PW09_18_S_15_1 | 3.3 | | PW17_18_S_43 | 3.3 | |
| PW09_18_S_44_2 | 3.3 | | PW19_18_S_15 | 3.3 | |
| PW11_18_S_21 | 3.3 | | PW20_18_S_31 | 3.3 | |
| PW11_18_S_23 | 3.3 | | PW21_18_S_33 | 3.3 | |
| PW11_18_S_25 | 3.3 | | PW04_18_S_34 | 3.4 | |
| PW13_17_S_22 | 3.3 | | PW02_18_S_25 | 3.5 | S |
| PW14_17_S_31 | 3.3 | | PW04_18_S_35 | 3.5 | |
| PW14_18_S_44 | 3.3 | | PW05_18_S_21 | 3.5 | |
| PW15_17_S_11 | 3.3 | | PW06_18_S_13 | 3.5 | |
| PW15_17_S_21 | 3.3 | | PW06_18_S_15 | 3.5 | |
| PW16_18_S_21 | 3.3 | | PW07_18_S_33 | 3.5 | |
| PW17_18_S_44 | 3.3 | | PW09_18_S_25_1 | 3.5 | |
| PW21_18_S_22 | 3.3 | | PW17_18_S_41 | 3.5 | |
| PW04_18_S_34 | 3.4 | | PW20_18_S_21 | 3.5 | |
| PW08_17_S_31 | 3.4 | | PW20_18_S_44 | 3.5 | |
| PW10_18_S_11 | 3.4 | | PW10_18_S_25 | 3.6 | |
| PW16_18_S_42 | 3.4 | | PW16_18_S_44 | 3.6 | |
| PW02_18_S_24 | 3.5 | S | PW21_18_S_31 | 3.6 | |
| PW14_18_S_22 | 3.5 | | PW05_18_S_51 | 3.8 | |
| PW16_18_S_25 | 3.5 | | PW06_18_S_34 | 3.8 | |
| PW14_18_S_12_2 | 3.8 | | PW10_18_S_22 | 3.8 | |
| PW19_18_S_15 | 3.8 | | PW16_18_S_45 | 3.8 | |
| PW04_18_S_33 | 3.9 | | PW10_18_S_11 | 3.9 | |
| PW13_18_S_21 | 3.9 | | PW13_18_S_21 | 3.9 | |
| PW05_18_S_52 | 4.4 | | PW16_18_S_42 | 3.9 | |

Appendix table 3. Mean values of 15 traits of soybean genotypes

| | | | | | Traits | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | DTF | DTM | LDG | SHG | PH | BPP | HSW | GY | PPP | SdPP | SedPP | BM | HI | PC | OC |
| PW01_17_S_12 | 52.5 | 102.5 | 1.0 | 2.0 | 91.70 | 6.60 | 13.00 | 2214.15 | 91.3 | 172.5 | 1.89 | 4479.17 | 49.48 | 40.55 | 22.85 |
| PW01_17_S_13 | 51.5 | 118.5 | 1.0 | 1.5 | 74.50 | 7.20 | 17.50 | 3008.23 | 91.3 | 229.4 | 2.51 | 6770.83 | 44.41 | 41.50 | 21.85 |
| PW01_17_S_14 | 52.5 | 118.0 | 1.0 | 3.0 | 90.70 | 5.70 | 14.25 | 3004.48 | 78.7 | 197.9 | 2.51 | 5937.50 | 50.84 | 40.90 | 22.35 |
| PW01_17_S_15 | 52.0 | 116.5 | 2.0 | 3.0 | 82.40 | 7.00 | 15.75 | 2343.14 | 93.0 | 230.1 | 2.47 | 3854.17 | 60.84 | 39.60 | 23.40 |
| PW01_17_S_22 | 52.0 | 116.5 | 1.0 | 2.0 | 84.90 | 6.70 | 12.75 | 2743.85 | 102.0 | 213.2 | 2.09 | 5104.17 | 54.70 | 41.15 | 23.00 |
| PW01_17_S_23 | 52.5 | 109.0 | 1.0 | 2.0 | 67.00 | 5.80 | 13.50 | 2930.02 | 89.9 | 196.4 | 2.18 | 4687.50 | 62.50 | 40.50 | 22.95 |
| PW01_17_S_25 | 51.0 | 117.5 | 1.0 | 2.0 | 76.50 | 7.50 | 19.00 | 3047.28 | 94.9 | 237.8 | 2.50 | 5833.33 | 52.57 | 40.00 | 23.35 |
| PW01_17_S_31 | 50.5 | 113.5 | 1.0 | 1.0 | 81.30 | 6.30 | 12.50 | 2684.48 | 84.9 | 201.1 | 2.40 | 5416.67 | 49.56 | 39.55 | 23.35 |
| PW01_17_S_32 | 50.5 | 114.0 | 1.0 | 2.0 | 93.20 | 5.90 | 18.75 | 3062.27 | 87.8 | 205.3 | 2.34 | 6666.67 | 45.88 | 39.60 | 23.05 |
| PW01_17_S_33 | 51.0 | 117.0 | 1.0 | 2.0 | 79.50 | 7.40 | 13.75 | 2833.31 | 98.5 | 256.9 | 2.61 | 5208.33 | 59.91 | 40.15 | 23.00 |
| PW01_17_S_34 | 52.0 | 109.0 | 1.0 | 1.5 | 77.70 | 6.00 | 15.75 | 2833.71 | 79.8 | 195.7 | 2.45 | 6145.83 | 46.18 | 40.10 | 23.25 |
| PW01_18_S_13_1 | 41.5 | 110.5 | 2.0 | 1.5 | 67.00 | 6.10 | 16.75 | 2643.50 | 92.9 | 194.3 | 2.10 | 5208.33 | 50.53 | 39.50 | 24.55 |
| PW01_18_S_13_2 | 40.5 | 109.5 | 1.0 | 1.0 | 62.10 | 3.80 | 14.75 | 1820.00 | 62.9 | 126.0 | 2.01 | 3750.00 | 49.24 | 38.10 | 23.70 |
| PW02_17_S_31 | 53.5 | 112.0 | 1.0 | 2.0 | 76.00 | 6.10 | 16.25 | 2907.76 | 88.1 | 181.9 | 2.06 | 5625.00 | 51.70 | 41.05 | 23.45 |
| PW02_17_S_35 | 53.5 | 105.0 | 1.0 | 3.0 | 70.20 | 6.80 | 15.50 | 2748.80 | 108.6 | 248.3 | 2.27 | 5312.50 | 52.53 | 41.20 | 23.20 |
| PW02_18_S_15 | 41.5 | 100.0 | 2.0 | 1.5 | 64.50 | 5.70 | 11.25 | 1568.03 | 75.8 | 149.0 | 1.95 | 3541.67 | 44.93 | 40.50 | 22.80 |
| PW02_18_S_21 | 42.0 | 101.0 | 1.0 | 2.0 | 59.30 | 6.30 | 12.50 | 1855.28 | 83.5 | 142.5 | 1.71 | 3750.00 | 50.03 | 40.30 | 22.55 |
| PW02_18_S_22 | 41.0 | 97.5 | 2.5 | 1.0 | 64.50 | 5.60 | 15.50 | 1835.80 | 72.0 | 130.1 | 1.80 | 3645.83 | 50.12 | 41.00 | 22.50 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW02_18_S_23 | 41.5 | 99.0 | 2.5 | 2.0 | 67.80 | 5.40 | 13.75 | 1629.15 | 60.1 | 121.8 | 2.03 | 3750.00 | 43.45 | 40.60 | 22.40 |
| PW02_18_S_24 | 40.5 | 98.5 | 2.5 | 1.0 | 60.90 | 6.70 | 13.00 | 1811.26 | 89.9 | 165.1 | 1.82 | 3750.00 | 50.54 | 40.00 | 22.75 |
| PW02_18_S_25 | 40.0 | 95.5 | 3.0 | 1.0 | 65.30 | 5.60 | 16.50 | 1861.46 | 76.6 | 125.1 | 1.64 | 3854.17 | 48.24 | 41.45 | 22.00 |
| PW03_17_S_21 | 53.0 | 125.5 | 2.0 | 2.5 | 86.10 | 5.40 | 15.75 | 2672.30 | 77.2 | 190.4 | 2.47 | 6354.17 | 42.11 | 41.15 | 21.85 |
| PW04_17_S_11 | 48.0 | 122.5 | 1.0 | 1.0 | 74.20 | 6.40 | 19.25 | 3291.17 | 91.4 | 227.1 | 2.48 | 6354.17 | 51.82 | 40.20 | 23.15 |
| PW04_17_S_12 | 50.5 | 119.5 | 1.0 | 2.0 | 90.70 | 6.30 | 16.00 | 2753.50 | 80.2 | 176.6 | 2.20 | 5625.00 | 48.95 | 37.95 | 23.25 |
| PW04_17_S_13 | 52.5 | 121.0 | 1.0 | 2.0 | 75.90 | 5.90 | 15.75 | 2911.37 | 94.0 | 204.2 | 2.17 | 6458.33 | 45.08 | 39.30 | 23.90 |
| PW04_17_S_14 | 50.0 | 122.0 | 1.0 | 2.5 | 68.30 | 5.20 | 11.75 | 2744.97 | 86.9 | 196.8 | 2.27 | 6041.67 | 45.44 | 39.90 | 23.95 |
| PW04_17_S_23 | 59.5 | 114.5 | 1.0 | 3.0 | 66.50 | 5.60 | 12.75 | 2560.62 | 80.9 | 180.4 | 2.23 | 5104.17 | 50.18 | 39.90 | 22.20 |
| PW04_17_S_31 | 59.5 | 114.0 | 2.5 | 2.0 | 60.30 | 4.60 | 13.25 | 2230.69 | 78.9 | 165.6 | 2.10 | 4375.00 | 50.99 | 40.95 | 22.75 |
| PW04_17_S_32 | 59.0 | 117.5 | 1.0 | 3.0 | 58.40 | 5.60 | 15.75 | 2710.03 | 93.2 | 229.0 | 2.46 | 5937.50 | 45.46 | 42.95 | 20.25 |
| PW04_17_S_33 | 59.5 | 119.0 | 1.5 | 2.5 | 64.50 | 4.90 | 16.75 | 2837.96 | 93.0 | 210.6 | 2.27 | 5104.17 | 55.55 | 41.60 | 21.30 |
| PW04_17_S_35 | 60.5 | 120.0 | 1.0 | 2.5 | 71.10 | 4.80 | 19.00 | 3018.22 | 76.8 | 191.6 | 2.50 | 6354.17 | 47.50 | 42.10 | 20.90 |
| PW04_18_S_25 | 41.5 | 106.5 | 2.0 | 2.0 | 73.70 | 5.00 | 13.75 | 2801.61 | 63.8 | 131.7 | 2.06 | 5000.00 | 56.00 | 41.00 | 24.20 |
| PW04_18_S_32 | 39.0 | 103.0 | 3.5 | 3.5 | 63.90 | 5.00 | 11.00 | 1895.19 | 75.4 | 161.1 | 2.14 | 3750.00 | 51.12 | 41.30 | 23.30 |
| PW04_18_S_33 | 39.5 | 96.0 | 1.0 | 3.5 | 63.00 | 5.20 | 13.75 | 1970.85 | 81.9 | 169.3 | 2.06 | 3750.00 | 52.56 | 41.95 | 22.85 |
| PW04_18_S_34 | 39.0 | 110.0 | 1.0 | 3.0 | 66.50 | 5.20 | 13.75 | 2184.27 | 88.1 | 180.3 | 2.04 | 4895.83 | 44.60 | 41.30 | 23.35 |
| PW04_18_S_35 | 39.5 | 104.0 | 1.0 | 4.0 | 66.00 | 4.80 | 14.25 | 1967.80 | 72.7 | 162.5 | 2.24 | 3854.17 | 50.99 | 41.10 | 23.45 |
| PW04_18_S_52 | 42.5 | 113.5 | 1.0 | 3.0 | 67.40 | 5.90 | 15.00 | 2478.58 | 90.0 | 190.4 | 2.12 | 4270.83 | 58.07 | 40.90 | 24.45 |
| PW05_17_S_11 | 59.5 | 115.0 | 2.5 | 3.0 | 71.40 | 5.40 | 9.00 | 2020.21 | 87.6 | 206.5 | 2.35 | 4166.67 | 48.89 | 41.75 | 20.75 |
| PW05_17_S_12 | 52.0 | 111.5 | 3.5 | 4.0 | 73.80 | 5.90 | 14.00 | 2124.29 | 82.7 | 164.6 | 1.99 | 5625.00 | 37.72 | 41.60 | 23.25 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW05_17_S_13 | 60.5 | 113.5 | 2.0 | 3.0 | 70.80 | 5.80 | 17.25 | 2528.46 | 97.1 | 215.6 | 2.22 | 4583.33 | 55.38 | 42.05 | 20.80 |
| PW05_17_S_21 | 50.5 | 116.0 | 2.5 | 3.0 | 70.60 | 6.30 | 12.00 | 2358.77 | 72.0 | 165.5 | 2.29 | 5104.17 | 46.07 | 41.45 | 23.20 |
| PW05_18_S_21 | 38.0 | 100.0 | 1.0 | 2.0 | 61.50 | 5.00 | 14.50 | 1861.43 | 81.7 | 174.9 | 2.15 | 3750.00 | 49.36 | 41.80 | 23.10 |
| PW05_18_S_51 | 39.0 | 89.0 | 3.0 | 4.0 | 61.40 | 5.10 | 13.00 | 1587.67 | 63.5 | 148.8 | 2.36 | 3333.33 | 47.40 | 41.95 | 22.75 |
| PW05_18_S_52 | 39.0 | 95.0 | 1.0 | 4.0 | 63.30 | 5.50 | 13.25 | 1758.03 | 74.8 | 148.1 | 1.98 | 3645.83 | 48.01 | 41.70 | 22.95 |
| PW05_18_S_53 | 39.5 | 96.0 | 1.0 | 2.5 | 63.70 | 5.70 | 14.50 | 2416.25 | 81.6 | 185.2 | 2.29 | 4270.83 | 56.44 | 41.55 | 23.10 |
| PW06_18_S_11 | 35.5 | 105.0 | 1.0 | 1.0 | 43.00 | 6.30 | 9.25 | 1472.59 | 50.2 | 112.5 | 2.24 | 3125.00 | 47.13 | 40.35 | 22.65 |
| PW06_18_S_13 | 35.0 | 103.5 | 1.0 | 2.0 | 27.00 | 4.10 | 16.75 | 1989.40 | 41.6 | 88.0 | 2.11 | 3125.00 | 64.34 | 40.45 | 22.70 |
| PW06_18_S_14 | 34.5 | 103.0 | 1.0 | 1.0 | 31.50 | 3.20 | 14.25 | 1648.19 | 37.6 | 75.1 | 1.99 | 3125.00 | 53.11 | 41.35 | 22.10 |
| PW06_18_S_15 | 35.5 | 105.5 | 1.0 | 1.5 | 36.10 | 4.80 | 15.00 | 1944.19 | 47.2 | 105.0 | 2.25 | 3125.00 | 62.15 | 40.35 | 22.75 |
| PW06_18_S_31 | 35.5 | 104.5 | 2.5 | 2.0 | 32.90 | 5.40 | 12.75 | 1583.56 | 55.9 | 110.5 | 1.97 | 3020.83 | 52.36 | 41.00 | 22.35 |
| PW06_18_S_34 | 35.0 | 108.5 | 1.0 | 2.0 | 42.10 | 5.40 | 13.00 | 1666.65 | 51.1 | 102.3 | 2.00 | 3229.17 | 51.17 | 40.65 | 22.55 |
| PW06_18_S_35 | 37.0 | 120.5 | 3.5 | 2.5 | 49.40 | 5.30 | 13.00 | 1167.81 | 56.4 | 154.0 | 2.73 | 2291.67 | 51.19 | 40.75 | 22.35 |
| PW07_17_S_11 | 50.5 | 108.0 | 1.0 | 3.0 | 63.50 | 6.50 | 18.50 | 2753.49 | 85.6 | 166.3 | 1.94 | 6041.67 | 45.64 | 41.50 | 23.30 |
| PW07_17_S_21 | 52.5 | 110.0 | 1.0 | 3.0 | 66.30 | 8.20 | 18.25 | 2622.21 | 133.0 | 243.3 | 1.83 | 4895.83 | 53.71 | 41.20 | 23.35 |
| PW07_18_S_33 | 39.0 | 106.5 | 1.0 | 3.0 | 63.00 | 5.50 | 12.75 | 1540.33 | 74.7 | 167.8 | 2.27 | 3229.17 | 47.91 | 41.55 | 22.90 |
| PW07_18_S_55 | 42.0 | 98.5 | 1.5 | 2.0 | 57.90 | 4.40 | 12.50 | 1460.50 | 77.1 | 130.8 | 1.69 | 3229.17 | 45.31 | 40.35 | 23.05 |
| PW08_17_S_11 | 60.0 | 115.0 | 2.5 | 2.5 | 67.40 | 6.40 | 11.75 | 2125.20 | 98.6 | 224.5 | 2.27 | 4270.83 | 49.75 | 42.10 | 20.30 |
| PW08_17_S_12 | 52.5 | 110.5 | 1.0 | 4.0 | 58.50 | 6.30 | 15.50 | 2251.77 | 88.3 | 184.1 | 2.09 | 5312.50 | 42.53 | 41.65 | 23.20 |
| PW08_17_S_21 | 59.5 | 117.0 | 1.5 | 3.0 | 55.60 | 5.40 | 18.50 | 2304.04 | 96.7 | 220.2 | 2.28 | 5208.33 | 44.26 | 41.80 | 21.30 |
| PW08_17_S_23 | 50.5 | 115.5 | 1.0 | 2.0 | 75.00 | 4.70 | 15.00 | 2304.26 | 67.1 | 135.0 | 2.01 | 4687.50 | 49.38 | 41.40 | 23.60 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW08_17_S_31 | 50.0 | 118.0 | 2.0 | 2.0 | 87.50 | 5.40 | 15.75 | 2415.87 | 73.2 | 165.6 | 2.26 | 4375.00 | 55.22 | 40.45 | 23.00 |
| PW09_17_S_11 | 52.0 | 124.0 | 1.5 | 2.5 | 75.40 | 5.90 | 15.00 | 2351.98 | 74.5 | 171.3 | 2.30 | 5000.00 | 47.32 | 41.30 | 22.25 |
| PW09_17_S_21 | 52.0 | 107.5 | 1.0 | 2.0 | 68.80 | 6.40 | 14.25 | 2710.83 | 88.5 | 183.3 | 2.07 | 5000.00 | 54.22 | 41.85 | 22.95 |
| PW09_17_S_31 | 52.5 | 119.5 | 1.0 | 2.0 | 74.70 | 4.30 | 10.50 | 2158.24 | 63.9 | 130.3 | 2.03 | 4270.83 | 50.65 | 41.40 | 22.25 |
| PW09_18_S_11 | 42.0 | 107.5 | 1.0 | 1.0 | 37.10 | 4.00 | 10.25 | 1424.29 | 41.8 | 103.7 | 2.48 | 2812.50 | 50.58 | 41.70 | 22.95 |
| PW09_18_S_12 | 41.0 | 107.5 | 1.0 | 1.5 | 70.20 | 5.80 | 17.50 | 2842.07 | 78.9 | 187.7 | 2.38 | 5416.67 | 52.73 | 41.10 | 22.50 |
| PW09_18_S_13 | 43.0 | 107.5 | 1.0 | 1.0 | 62.60 | 5.00 | 16.25 | 2143.68 | 94.4 | 226.0 | 2.39 | 4166.67 | 51.52 | 41.15 | 22.35 |
| PW09_18_S_15_1 | 43.5 | 107.5 | 2.5 | 2.0 | 69.60 | 7.70 | 16.75 | 2205.71 | 106.0 | 268.5 | 2.55 | 4583.33 | 48.32 | 40.50 | 23.90 |
| PW09_18_S_15_2 | 43.5 | 106.5 | 1.0 | 1.5 | 80.80 | 5.80 | 17.25 | 3593.62 | 66.6 | 136.4 | 2.05 | 6875.00 | 52.24 | 41.40 | 23.15 |
| PW09_18_S_23 | 40.5 | 104.0 | 2.5 | 4.0 | 72.40 | 5.40 | 14.75 | 2043.33 | 68.0 | 131.7 | 1.91 | 3750.00 | 55.18 | 41.05 | 23.20 |
| PW09_18_S_23_1 | 42.5 | 106.0 | 2.5 | 2.5 | 75.30 | 6.60 | 17.00 | 2246.72 | 85.7 | 155.6 | 1.82 | 4687.50 | 47.95 | 40.40 | 22.60 |
| PW09_18_S_23_2 | 43.5 | 106.0 | 1.0 | 3.0 | 62.60 | 5.60 | 18.25 | 2178.67 | 73.0 | 128.8 | 1.77 | 4479.17 | 48.65 | 40.70 | 22.90 |
| PW09_18_S_25_1 | 40.0 | 107.5 | 1.0 | 1.0 | 41.90 | 4.90 | 20.00 | 2274.26 | 46.0 | 112.3 | 2.44 | 4479.17 | 50.69 | 43.25 | 21.60 |
| PW09_18_S_44_1 | 40.5 | 113.0 | 1.0 | 2.0 | 52.40 | 4.30 | 17.75 | 2511.60 | 45.9 | 111.7 | 2.44 | 4895.83 | 51.47 | 41.20 | 23.50 |
| PW09_18_S_44_2 | 41.5 | 108.0 | 1.0 | 2.5 | 52.20 | 5.70 | 15.50 | 2299.18 | 60.6 | 144.7 | 2.40 | 4479.17 | 51.29 | 41.20 | 23.55 |
| PW10_17_S_11 | 58.0 | 109.5 | 1.0 | 3.0 | 68.70 | 5.10 | 13.25 | 1992.76 | 71.9 | 162.2 | 2.26 | 4270.83 | 46.68 | 41.45 | 21.45 |
| PW10_17_S_21 | 53.0 | 112.0 | 1.0 | 4.0 | 65.70 | 6.40 | 18.75 | 2441.49 | 85.9 | 161.8 | 1.88 | 5937.50 | 41.34 | 41.55 | 23.25 |
| PW10_18_S_11 | 39.5 | 102.5 | 2.5 | 3.0 | 57.90 | 5.00 | 13.75 | 1646.79 | 84.4 | 150.7 | 1.78 | 3229.17 | 51.02 | 41.30 | 23.30 |
| PW10_18_S_22 | 36.0 | 108.0 | 1.0 | 2.0 | 29.40 | 4.10 | 9.50 | 1584.38 | 43.7 | 83.4 | 1.91 | 2916.67 | 54.30 | 40.20 | 23.05 |
| PW10_18_S_25 | 34.5 | 101.5 | 2.5 | 1.0 | 43.10 | 4.90 | 10.50 | 1242.72 | 63.0 | 127.0 | 2.01 | 1979.17 | 62.84 | 40.65 | 22.80 |
| PW11_17_S_11 | 59.5 | 119.5 | 1.0 | 2.0 | 61.80 | 4.30 | 17.75 | 2687.37 | 83.1 | 196.5 | 2.42 | 5416.67 | 49.62 | 41.90 | 21.55 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW11_17_S_12 | 60.0 | 116.5 | 2.5 | 3.0 | 65.40 | 5.20 | 16.00 | 2486.32 | 83.7 | 194.8 | 2.33 | 4583.33 | 54.25 | 42.20 | 21.00 |
| PW11_17_S_21 | 60.0 | 113.0 | 2.0 | 2.0 | 66.80 | 4.80 | 12.25 | 2331.09 | 75.5 | 167.3 | 2.21 | 5729.17 | 40.80 | 41.80 | 21.10 |
| PW11_17_S_31 | 59.5 | 106.5 | 1.5 | 2.0 | 63.30 | 5.90 | 15.50 | 2822.94 | 94.2 | 234.2 | 2.49 | 5625.00 | 50.33 | 42.30 | 20.75 |
| PW11_18_S_21 | 41.0 | 108.5 | 2.5 | 1.5 | 67.40 | 6.50 | 15.25 | 1566.68 | 83.8 | 214.9 | 2.57 | 3229.17 | 48.36 | 39.60 | 24.80 |
| PW11_18_S_23 | 40.0 | 106.0 | 1.0 | 2.5 | 64.00 | 5.30 | 13.50 | 1806.32 | 65.3 | 129.9 | 1.98 | 3645.83 | 53.37 | 42.80 | 22.85 |
| PW11_18_S_25 | 41.0 | 108.5 | 2.0 | 3.0 | 71.20 | 5.00 | 14.25 | 1980.63 | 78.0 | 154.8 | 1.99 | 4166.67 | 47.54 | 41.40 | 23.05 |
| PW11_18_S_33_1 | 41.0 | 101.5 | 3.0 | 2.0 | 64.00 | 5.60 | 14.00 | 1918.11 | 69.9 | 141.7 | 2.03 | 4062.50 | 47.20 | 38.10 | 24.30 |
| PW11_18_S_51 | 42.5 | 104.0 | 1.5 | 2.0 | 56.70 | 6.60 | 11.00 | 1697.12 | 118.1 | 230.8 | 1.97 | 3125.00 | 54.08 | 39.65 | 23.80 |
| PW12_17_S_11 | 48.0 | 117.5 | 1.0 | 3.0 | 70.40 | 5.30 | 12.25 | 2126.39 | 83.2 | 177.7 | 2.14 | 4062.50 | 52.50 | 41.25 | 21.75 |
| PW12_17_S_21 | 60.0 | 117.5 | 1.0 | 3.0 | 66.80 | 4.70 | 15.25 | 2612.64 | 90.1 | 185.6 | 2.09 | 5520.83 | 47.38 | 41.85 | 21.05 |
| PW13_17_S_11 | 59.5 | 114.0 | 3.0 | 2.5 | 67.10 | 7.00 | 16.50 | 2384.71 | 136.9 | 308.8 | 2.25 | 7395.83 | 32.28 | 41.30 | 21.40 |
| PW13_17_S_21 | 59.5 | 113.0 | 1.0 | 2.5 | 62.70 | 5.30 | 18.75 | 3067.80 | 88.4 | 206.5 | 2.34 | 5729.17 | 53.57 | 41.85 | 22.10 |
| PW13_17_S_22 | 52.5 | 114.5 | 1.0 | 3.0 | 64.40 | 5.60 | 13.25 | 2486.51 | 71.6 | 159.5 | 2.22 | 6145.83 | 40.50 | 42.35 | 22.45 |
| PW13_17_S_31 | 60.5 | 118.0 | 1.0 | 2.0 | 65.70 | 5.10 | 17.00 | 2750.68 | 82.1 | 193.0 | 2.36 | 5625.00 | 48.83 | 41.50 | 21.50 |
| PW13_18_S_21 | 38.0 | 101.5 | 2.5 | 4.0 | 61.70 | 4.50 | 10.00 | 1736.72 | 66.4 | 131.3 | 1.97 | 4791.67 | 37.43 | 40.70 | 23.70 |
| PW14_17_S_11 | 60.0 | 114.0 | 2.0 | 2.0 | 77.70 | 5.40 | 14.00 | 2401.33 | 88.6 | 190.1 | 2.14 | 4583.33 | 52.40 | 41.65 | 21.30 |
| PW14_17_S_21 | 52.5 | 111.5 | 1.0 | 2.0 | 64.10 | 6.00 | 15.75 | 2416.07 | 85.1 | 169.6 | 1.99 | 5729.17 | 43.31 | 41.45 | 23.20 |
| PW14_17_S_31 | 53.0 | 113.5 | 1.0 | 3.0 | 73.00 | 6.40 | 15.50 | 2455.10 | 114.5 | 234.5 | 2.04 | 5416.67 | 45.35 | 41.10 | 23.40 |
| PW14_18_S_12_1 | 37.0 | 109.0 | 1.0 | 3.0 | 67.70 | 5.40 | 16.75 | 2293.87 | 85.0 | 178.7 | 2.10 | 4583.33 | 49.87 | 40.80 | 23.35 |
| PW14_18_S_12_2 | 39.0 | 110.0 | 1.0 | 2.0 | 72.10 | 5.60 | 17.75 | 2375.77 | 76.2 | 156.0 | 2.05 | 5625.00 | 43.09 | 41.05 | 23.40 |
| PW14_18_S_13 | 41.0 | 117.0 | 2.5 | 2.0 | 62.40 | 4.90 | 9.25 | 1720.77 | 76.6 | 161.3 | 2.10 | 3541.67 | 48.83 | 40.80 | 23.05 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW14_18_S_15_1 | 38.5 | 107.5 | 1.0 | 2.0 | 65.90 | 5.50 | 14.75 | 2560.15 | 76.3 | 169.7 | 2.25 | 4895.83 | 52.28 | 41.15 | 23.10 |
| PW14_18_S_15_2 | 38.0 | 110.0 | 3.0 | 2.0 | 66.10 | 5.10 | 15.25 | 2005.01 | 77.8 | 158.1 | 2.04 | 4270.83 | 47.02 | 39.10 | 24.05 |
| PW14_18_S_21 | 41.5 | 108.5 | 1.0 | 3.0 | 71.70 | 5.10 | 15.50 | 2647.82 | 75.8 | 160.8 | 2.12 | 5416.67 | 48.89 | 41.15 | 23.55 |
| PW14_18_S_22 | 41.5 | 108.5 | 1.0 | 4.0 | 69.30 | 5.70 | 15.75 | 2283.53 | 65.3 | 128.0 | 1.96 | 5104.17 | 44.81 | 40.35 | 24.40 |
| PW14_18_S_44 | 41.5 | 111.5 | 1.0 | 2.5 | 75.80 | 6.30 | 16.00 | 2617.92 | 83.6 | 167.7 | 2.01 | 5208.33 | 50.40 | 41.40 | 24.05 |
| PW14_18_S_45 | 41.5 | 105.0 | 1.0 | 2.0 | 67.00 | 5.60 | 15.25 | 2626.70 | 68.3 | 118.8 | 1.77 | 4791.67 | 55.43 | 41.10 | 24.15 |
| PW15_17_S_11 | 59.5 | 116.0 | 2.0 | 3.0 | 62.60 | 5.20 | 14.75 | 2441.89 | 84.8 | 194.5 | 2.29 | 3958.33 | 61.93 | 41.95 | 21.25 |
| PW15_17_S_21 | 50.5 | 119.0 | 1.0 | 4.0 | 68.90 | 7.10 | 14.00 | 2486.00 | 105.9 | 213.9 | 2.02 | 4166.67 | 60.07 | 40.00 | 24.15 |
| PW15_17_S_31 | 53.0 | 113.0 | 3.0 | 4.0 | 72.50 | 6.40 | 12.75 | 2088.83 | 81.4 | 154.6 | 1.90 | 4166.67 | 50.05 | 40.45 | 24.10 |
| PW16_18_S_12 | 42.0 | 109.5 | 1.0 | 3.0 | 68.50 | 6.30 | 15.75 | 2242.67 | 79.9 | 157.9 | 1.98 | 4479.17 | 50.31 | 41.10 | 24.55 |
| PW16_18_S_14 | 42.0 | 108.5 | 1.0 | 3.0 | 65.40 | 6.00 | 16.00 | 2358.43 | 87.9 | 173.4 | 1.97 | 5000.00 | 47.17 | 41.80 | 24.00 |
| PW16_18_S_15 | 42.5 | 107.5 | 1.5 | 2.0 | 75.90 | 6.50 | 14.75 | 2456.76 | 93.1 | 135.4 | 1.46 | 4375.00 | 56.15 | 41.10 | 24.60 |
| PW16_18_S_21 | 42.5 | 106.0 | 1.0 | 2.5 | 69.80 | 6.00 | 15.25 | 2417.72 | 78.0 | 161.5 | 2.07 | 4583.33 | 52.76 | 40.95 | 24.60 |
| PW16_18_S_22 | 42.0 | 109.5 | 1.0 | 3.0 | 72.10 | 6.20 | 15.75 | 2409.29 | 78.9 | 161.1 | 2.03 | 4895.83 | 49.25 | 40.95 | 24.70 |
| PW16_18_S_23 | 42.0 | 110.5 | 1.5 | 2.0 | 68.30 | 5.70 | 15.00 | 2189.06 | 70.7 | 150.7 | 2.13 | 4270.83 | 51.17 | 40.35 | 24.95 |
| PW16_18_S_24 | 41.5 | 109.0 | 1.5 | 3.0 | 66.30 | 5.40 | 15.00 | 2460.02 | 84.9 | 164.8 | 1.94 | 5833.33 | 42.21 | 41.35 | 24.20 |
| PW16_18_S_25 | 42.0 | 104.5 | 1.0 | 2.0 | 62.80 | 6.20 | 15.50 | 2367.68 | 79.1 | 179.0 | 2.26 | 4166.67 | 59.34 | 41.30 | 24.30 |
| PW16_18_S_31 | 43.0 | 108.0 | 1.0 | 2.0 | 68.50 | 6.20 | 15.75 | 2798.69 | 85.8 | 192.1 | 2.24 | 5520.83 | 50.84 | 41.55 | 24.50 |
| PW16_18_S_35_2 | 40.0 | 104.5 | 1.0 | 1.0 | 73.00 | 6.70 | 16.75 | 2832.71 | 118.9 | 243.1 | 2.04 | 5625.00 | 50.29 | 39.90 | 24.00 |
| PW16_18_S_41 | 39.5 | 96.5 | 1.0 | 4.0 | 57.80 | 5.20 | 14.00 | 2121.14 | 69.7 | 144.3 | 2.04 | 3750.00 | 56.56 | 41.65 | 22.90 |
| PW16_18_S_42 | 39.0 | 98.5 | 1.0 | 3.0 | 63.30 | 6.40 | 10.50 | 1876.66 | 82.1 | 148.9 | 1.81 | 4166.67 | 45.72 | 41.00 | 23.45 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW16_18_S_43 | 39.5 | 98.0 | 1.5 | 3.5 | 65.40 | 5.40 | 15.00 | 1930.08 | 81.7 | 105.5 | 1.30 | 4166.67 | 46.32 | 41.55 | 22.90 |
| PW16_18_S_44 | 40.5 | 96.0 | 2.0 | 3.0 | 69.40 | 5.60 | 14.25 | 1895.69 | 78.2 | 173.9 | 2.22 | 3750.00 | 50.55 | 40.95 | 23.25 |
| PW16_18_S_45 | 39.0 | 96.5 | 3.0 | 3.0 | 57.00 | 5.60 | 11.75 | 1528.83 | 72.9 | 156.0 | 2.13 | 3229.17 | 47.44 | 40.90 | 23.55 |
| PW16_18_S_51_1 | 41.0 | 110.5 | 1.0 | 4.0 | 76.30 | 6.60 | 14.50 | 2371.76 | 89.3 | 203.6 | 2.30 | 6145.83 | 38.55 | 40.80 | 23.75 |
| PW16_18_S_52_1 | 40.0 | 110.5 | 1.0 | 3.5 | 75.30 | 6.50 | 14.25 | 2291.99 | 75.2 | 147.3 | 1.95 | 4166.67 | 55.55 | 42.05 | 22.90 |
| PW16_18_S_53 | 42.5 | 109.0 | 1.0 | 4.0 | 71.80 | 6.00 | 15.25 | 2149.68 | 65.4 | 140.9 | 2.15 | 4375.00 | 49.25 | 41.90 | 24.00 |
| PW17_18_S_13 | 37.5 | 100.5 | 1.0 | 3.0 | 60.80 | 5.00 | 13.75 | 1468.74 | 57.8 | 122.4 | 2.11 | 3229.17 | 45.59 | 40.40 | 23.75 |
| PW17_18_S_14 | 36.0 | 78.5 | 1.0 | 3.5 | 53.10 | 4.00 | 13.00 | 2174.16 | 67.8 | 146.9 | 2.17 | 4166.67 | 52.18 | 42.15 | 22.20 |
| PW17_18_S_41 | 38.0 | 98.5 | 1.0 | 4.0 | 54.00 | 5.30 | 13.00 | 1641.27 | 57.1 | 117.8 | 2.07 | 3541.67 | 46.47 | 41.75 | 23.05 |
| PW17_18_S_43 | 39.5 | 96.0 | 1.0 | 4.0 | 65.30 | 5.00 | 14.25 | 1849.05 | 67.0 | 129.4 | 1.93 | 4062.50 | 45.52 | 42.30 | 22.45 |
| PW17_18_S_44 | 39.0 | 105.5 | 1.0 | 3.0 | 60.40 | 4.90 | 15.75 | 1665.48 | 69.5 | 153.8 | 2.21 | 4687.50 | 35.59 | 42.25 | 22.70 |
| PW19_18_S_15 | 38.5 | 98.0 | 1.0 | 2.0 | 57.70 | 4.70 | 14.00 | 1830.31 | 70.1 | 139.1 | 1.98 | 3645.83 | 50.21 | 41.95 | 22.65 |
| PW19_18_S_25 | 41.0 | 103.5 | 3.5 | 2.5 | 92.60 | 5.90 | 14.75 | 1915.04 | 94.6 | 197.6 | 2.08 | 3854.17 | 49.48 | 40.50 | 23.60 |
| PW20_18_S_21 | 36.0 | 105.0 | 1.0 | 1.0 | 34.10 | 4.90 | 17.25 | 1830.08 | 48.8 | 102.4 | 2.10 | 2604.17 | 70.20 | 40.55 | 22.55 |
| PW20_18_S_31 | 39.0 | 108.5 | 1.0 | 2.0 | 44.50 | 6.50 | 16.75 | 1700.12 | 73.2 | 148.4 | 2.04 | 3437.50 | 49.26 | 42.30 | 21.70 |
| PW20_18_S_44 | 36.0 | 109.0 | 1.0 | 1.5 | 45.60 | 4.30 | 19.25 | 1851.22 | 74.9 | 129.0 | 1.72 | 2708.33 | 68.57 | 40.90 | 22.70 |
| PW21_18_S_22 | 52.5 | 123.0 | 1.0 | 2.0 | 74.40 | 5.40 | 12.25 | 2516.61 | 82.9 | 169.9 | 2.06 | 4687.50 | 53.74 | 41.25 | 21.70 |
| PW21_18_S_23_1 | 51.5 | 120.5 | 1.0 | 1.5 | 67.40 | 5.60 | 20.75 | 3519.17 | 79.9 | 175.2 | 2.19 | 6562.50 | 53.65 | 41.70 | 23.05 |
| PW21_18_S_23_2 | 46.5 | 103.5 | 1.0 | 2.5 | 60.80 | 5.20 | 14.75 | 2629.15 | 82.2 | 195.2 | 2.37 | 5937.50 | 44.29 | 41.35 | 23.15 |
| PW21_18_S_24_1 | 42.5 | 102.5 | 1.0 | 3.0 | 59.80 | 6.60 | 14.75 | 2115.60 | 84.3 | 173.1 | 2.05 | 5520.83 | 38.35 | 40.75 | 22.50 |
| PW21_18_S_24_2 | 46.5 | 116.0 | 1.0 | 2.0 | 68.80 | 4.30 | 15.75 | 2814.08 | 71.8 | 148.8 | 2.07 | 5416.67 | 51.92 | 41.20 | 22.65 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PW21_18_S_25_2 | 51.0 | 120.5 | 2.5 | 2.0 | 71.30 | 4.50 | 14.50 | 2149.06 | 55.4 | 129.1 | 2.32 | 4791.67 | 44.99 | 41.80 | 21.20 |
| PW21_18_S_31 | 36.0 | 106.5 | 1.0 | 1.5 | 37.90 | 4.60 | 14.25 | 2154.91 | 47.6 | 105.5 | 2.22 | 2916.67 | 73.89 | 40.70 | 22.55 |
| PW21_18_S_33 | 37.5 | 104.0 | 1.0 | 2.0 | 35.30 | 4.10 | 17.50 | 2073.40 | 54.2 | 104.2 | 1.93 | 4062.50 | 51.05 | 39.80 | 23.10 |
| SC_Signal | 44.5 | 125.5 | 1.0 | 2.0 | 85.50 | 4.50 | 18.25 | 3186.77 | 76.3 | 165.9 | 2.18 | 5937.50 | 53.64 | 37.55 | 22.15 |
| SCS_1 | 42.5 | 109.0 | 1.0 | 1.5 | 68.30 | 5.60 | 14.25 | 2586.41 | 67.6 | 140.3 | 2.08 | 5416.67 | 47.75 | 38.30 | 24.50 |
| Tana Beles | 49.0 | 116.0 | 1.0 | 2.0 | 73.80 | 5.1 | 13.25 | 2731.00 | 68.8 | 146.6 | 2.13 | 6145.83 | 44.49 | 40.20 | 21.65 |
| Mean | 45.66 | 109.05 | 1.45 | 2.43 | 65.35 | 5.59 | 14.79 | 2274.64 | 78.56 | 167.49 | 2.13 | 4611.11 | 50.13 | 41 | 22.91 |
| CV | 2.72 | 3.16 | 25.36 | 19.03 | 11.43 | 16.41 | 9.32 | 11.04 | 8.46 | 12.33 | 9.73 | 11.08 | 12.09 | 1.92 | 2.03 |
| LSD | 2.46 | 6.81 | 0.73 | 0.91 | 14.78 | 1.81 | 2.73 | 496.62 | 13.15 | 40.86 | 0.41 | 1010.91 | 12.00 | 1.55 | 0.92 |

Appendix table 4. List of experimental materials Studied at PARC

| S.NO | Genotypes | Source | Year of Crossing | Pedigree | S.NO | Genotypes | Source | Year of Crossing | Pedigree |
|---|---|---|---|---|---|---|---|---|---|
| 1 | PW01_17_S_12 | PARC | 2017 | Belessa-95 x Korme | 76 | PW10_17_S_11 | PARC | 2017 | Wogayen x Pawe-3 |
| 2 | PW01_17_S_13 | PARC | 2017 | Belessa-95 x Korme | 77 | PW10_17_S_21 | PARC | 2017 | Wogayen x Pawe-3 |
| 3 | PW01_17_S_14 | PARC | 2017 | Belessa-95 x Korme | 78 | PW10_18_S_11 | PARC | 2018 | Gozale x Williams |
| 4 | PW01_17_S_15 | PARC | 2017 | Belessa-95 x Korme | 79 | PW10_18_S_22 | PARC | 2018 | Gozale x Williams |
| 5 | PW01_17_S_22 | PARC | 2017 | Belessa-95 x Korme | 80 | PW10_18_S_25 | PARC | 2018 | Gozale x Williams |
| 6 | PW01_17_S_23 | PARC | 2017 | Belessa-95 x Korme | 81 | PW11_17_S_11 | PARC | 2017 | Wogayen x Tgx-1887-18F |
| 7 | PW01_17_S_25 | PARC | 2017 | Belessa-95 x Korme | 82 | PW11_17_S_12 | PARC | 2017 | Wogayen x Tgx-1887-18F |
| 8 | PW01_17_S_31 | PARC | 2017 | Belessa-95 x Korme | 83 | PW11_17_S_21 | PARC | 2017 | Wogayen x Tgx-1887-18F |
| 9 | PW01_17_S_32 | PARC | 2017 | Belessa-95 x Korme | 84 | PW11_17_S_31 | PARC | 2017 | Wogayen x Tgx-1887-18F |
| 10 | PW01_17_S_33 | PARC | 2017 | Belessa-95 x Korme | 85 | PW11_18_S_21 | PARC | 2018 | Gozale x Neyala |
| 11 | PW01_17_S_34 | PARC | 2017 | Belessa-95 x Korme | 86 | PW11_18_S_23 | PARC | 2018 | Gozale x Neyala |
| 12 | PW01_18_S_13_1 | PARC | 2018 | Awassa-95 X Gozale | 87 | PW11_18_S_25 | PARC | 2018 | Gozale x Neyala |
| 13 | PW01_18_S_13_2 | PARC | 2018 | Awassa-95 X Gozale | 88 | PW11_18_S_33_1 | PARC | 2018 | Gozale x Neyala |

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| 14 | PW02_17_S_31 | PARC | 2017 | Belessa-95 x Wogayen | 89 | PW11_18_S_51 | PARC | 2018 | Gozale x Neyala |
| 15 | PW02_17_S_35 | PARC | 2017 | Belessa-95 x Wogayen | 90 | PW12_17_S_11 | PARC | 2017 | Wogayen x Tgx-198711F |
| 16 | PW02_18_S_15 | PARC | 2018 | Awassa-95 x Protona | 91 | PW12_17_S_21 | PARC | 2017 | Wogayen x Tgx-198711F |
| 17 | PW02_18_S_21 | PARC | 2018 | Awassa-95 x Protona | 92 | PW13_17_S_11 | PARC | 2017 | Pawe-3 x Tgx-1887-18F |
| 18 | PW02_18_S_22 | PARC | 2018 | Awassa-95 x Protona | 93 | PW13_17_S_21 | PARC | 2017 | Pawe-3 x Tgx-1887-18F |
| 19 | PW02_18_S_23 | PARC | 2018 | Awassa-95 x Protona | 94 | PW13_17_S_22 | PARC | 2017 | Pawe-3 x Tgx-1887-18F |
| 20 | PW02_18_S_24 | PARC | 2018 | Awassa-95 x Protona | 95 | PW13_17_S_31 | PARC | 2017 | Pawe-3 x Tgx-1887-18F |
| 21 | PW02_18_S_25 | PARC | 2018 | Awassa-95 x Protona | 96 | PW13_18_S_21 | PARC | 2018 | Protona x Hawassa-04 |
| 22 | PW03_17_S_21 | PARC | 2017 | Belessa-95 x Pawe-3 | 97 | PW14_17_S_11 | PARC | 2017 | Pawe-3 x Tgx-198711F |
| 23 | PW04_17_S_11 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 98 | PW14_17_S_21 | PARC | 2017 | Pawe-3 x Tgx-198711F |
| 24 | PW04_17_S_12 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 99 | PW14_17_S_31 | PARC | 2017 | Pawe-3 x Tgx-198711F |
| 25 | PW04_17_S_13 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 100 | PW14_18_S_12_1 | PARC | 2018 | Protona x Williams |
| 26 | PW04_17_S_14 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 101 | PW14_18_S_12_2 | PARC | 2018 | Protona x Williams |
| 27 | PW04_17_S_23 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 102 | PW14_18_S_13 | PARC | 2018 | Protona x Williams |
| 28 | PW04_17_S_31 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 103 | PW14_18_S_15_1 | PARC | 2018 | Protona x Williams |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 29 | PW04_17_S_32 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 104 | PW14_18_S_15_2 | PARC | 2018 | Protona x Williams |
| 30 | PW04_17_S_33 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 105 | PW14_18_S_21 | PARC | 2018 | Protona x Williams |
| 31 | PW04_17_S_35 | PARC | 2017 | Belessa-95 xTgx-1887-18F | 106 | PW14_18_S_22 | PARC | 2018 | Protona x Williams |
| 32 | PW04_18_S_25 | PARC | 2018 | Awassa-95 x Hawassa-04 | 107 | PW14_18_S_44 | PARC | 2018 | Protona x Williams |
| 33 | PW04_18_S_32 | PARC | 2018 | Awassa-95 x Hawassa-04 | 108 | PW14_18_S_45 | PARC | 2018 | Protona x Williams |
| 34 | PW04_18_S_33 | PARC | 2018 | Awassa-95 x Hawassa-04 | 109 | PW15_17_S_11 | PARC | 2017 | Tgx-1887-18F x Tgx-198711F |
| 35 | PW04_18_S_34 | PARC | 2018 | Awassa-95 x Hawassa-04 | 110 | PW15_17_S_21 | PARC | 2017 | Tgx-1887-18F x Tgx-198711F |
| 36 | PW04_18_S_35 | PARC | 2018 | Awassa-95 x Hawassa-04 | 111 | PW15_17_S_31 | PARC | 2017 | Tgx-1887-18F x Tgx-198711F |
| 37 | PW04_18_S_52 | PARC | 2018 | Awassa-95 x Hawassa-04 | 112 | PW16_18_S_12 | PARC | 2018 | SCS1 x Hawassa-04 |
| 38 | PW05_17_S_11 | PARC | 2017 | Belessa-95 x Tgx-198711F | 113 | PW16_18_S_14 | PARC | 2018 | SCS1 x Hawassa-04 |
| 39 | PW05_17_S_12 | PARC | 2017 | Belessa-95 x Tgx-198711F | 114 | PW16_18_S_15 | PARC | 2018 | SCS1 x Hawassa-04 |
| 40 | PW05_17_S_13 | PARC | 2017 | Belessa-95 x Tgx-198711F | 115 | PW16_18_S_21 | PARC | 2018 | SCS1 x Hawassa-04 |
| 41 | PW05_17_S_21 | PARC | 2017 | Belessa-95 x Tgx-198711F | 116 | PW16_18_S_22 | PARC | 2018 | SCS1 x Hawassa-04 |
| 42 | PW05_18_S_21 | PARC | 2018 | Awassa-95 x Williams | 117 | PW16_18_S_23 | PARC | 2018 | SCS1 x Hawassa-04 |
| 43 | PW05_18_S_51 | PARC | 2018 | Awassa-95 x Williams | 118 | PW16_18_S_24 | PARC | 2018 | SCS1 x Hawassa-04 |

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| 44 | PW05_18_S_52 | PARC | 2018 | Awassa-95 x Williams | 119 | PW16_18_S_25 | PARC | 2018 | SCS1 x Hawassa-04 |
| 45 | PW05_18_S_53 | PARC | 2018 | Awassa-95 x Williams | 120 | PW16_18_S_31 | PARC | 2018 | SCS1 x Hawassa-04 |
| 46 | PW06_18_S_11 | PARC | 2018 | Awassa-95 x Neyala | 121 | PW16_18_S_35_2 | PARC | 2018 | SCS1 x Hawassa-04 |
| 47 | PW06_18_S_13 | PARC | 2018 | Awassa-95 x Neyala | 122 | PW16_18_S_41 | PARC | 2018 | SCS1 x Hawassa-04 |
| 48 | PW06_18_S_14 | PARC | 2018 | Awassa-95 x Neyala | 123 | PW16_18_S_42 | PARC | 2018 | SCS1 x Hawassa-04 |
| 49 | PW06_18_S_15 | PARC | 2018 | Awassa-95 x Neyala | 124 | PW16_18_S_43 | PARC | 2018 | SCS1 x Hawassa-04 |
| 50 | PW06_18_S_31 | PARC | 2018 | Awassa-95 x Neyala | 125 | PW16_18_S_44 | PARC | 2018 | SCS1 x Hawassa-04 |
| 51 | PW06_18_S_34 | PARC | 2018 | Awassa-95 x Neyala | 126 | PW16_18_S_45 | PARC | 2018 | SCS1 x Hawassa-04 |
| 52 | PW06_18_S_35 | PARC | 2018 | Awassa-95 x Neyala | 127 | PW16_18_S_51_1 | PARC | 2018 | SCS1 x Hawassa-04 |
| 53 | PW07_17_S_11 | PARC | 2017 | Korme x Pawe-3 | 128 | PW16_18_S_52_1 | PARC | 2018 | SCS1 x Hawassa-04 |
| 54 | PW07_17_S_21 | PARC | 2017 | Korme x Pawe-3 | 129 | PW16_18_S_53 | PARC | 2018 | SCS1 x Hawassa-04 |
| 55 | PW07_18_S_33 | PARC | 2018 | Gozale x Protona | 130 | PW17_18_S_13 | PARC | 2018 | SCS1 x Williams |
| 56 | PW07_18_S_55 | PARC | 2018 | Gozale x Protona | 131 | PW17_18_S_14 | PARC | 2018 | SCS1 x Williams |
| 57 | PW08_17_S_11 | PARC | 2017 | Korme x Tgx-1887-18F | 132 | PW17_18_S_41 | PARC | 2018 | SCS1 x Williams |
| 58 | PW08_17_S_12 | PARC | 2017 | Korme x Tgx-1887-18F | 133 | PW17_18_S_43 | PARC | 2018 | SCS1 x Williams |

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| 59 | PW08_17_S_21 | PARC | 2017 | Korme x Tgx-1887-18F | 134 | PW17_18_S_44 | PARC | 2018 | SCS1 x Williams |
| 60 | PW08_17_S_23 | PARC | 2017 | Korme x Tgx-1887-18F | 135 | PW19_18_S_15 | PARC | 2018 | Hawassa-04 x Williams |
| 61 | PW08_17_S_31 | PARC | 2017 | Korme x Tgx-1887-18F | 136 | PW19_18_S_25 | PARC | 2018 | Hawassa-04 x Williams |
| 62 | PW09_17_S_11 | PARC | 2017 | Korme x Tgx-198711F | 137 | PW20_18_S_21 | PARC | 2018 | Hawassa-04 x Neyala |
| 63 | PW09_17_S_21 | PARC | 2017 | Korme x Tgx-198711F | 138 | PW20_18_S_31 | PARC | 2018 | Hawassa-04 x Neyala |
| 64 | PW09_17_S_31 | PARC | 2017 | Korme x Tgx-198711F | 139 | PW20_18_S_44 | PARC | 2018 | Hawassa-04 x Neyala |
| 65 | PW09_18_S_11 | PARC | 2018 | Gozale x Hawassa-04 | 140 | PW21_18_S_22 | PARC | 2018 | Williams x Neyala |
| 66 | PW09_18_S_12 | PARC | 2018 | Gozale x Hawassa-04 | 141 | PW21_18_S_23_1 | PARC | 2018 | Williams x Neyala |
| 67 | PW09_18_S_13 | PARC | 2018 | Gozale x Hawassa-04 | 142 | PW21_18_S_23_2 | PARC | 2018 | Williams x Neyala |
| 68 | PW09_18_S_15_1 | PARC | 2018 | Gozale x Hawassa-04 | 143 | PW21_18_S_24_1 | PARC | 2018 | Williams x Neyala |
| 69 | PW09_18_S_15_2 | PARC | 2018 | Gozale x Hawassa-04 | 144 | PW21_18_S_24_2 | PARC | 2018 | Williams x Neyala |
| 70 | PW09_18_S_23 | PARC | 2018 | Gozale x Hawassa-04 | 145 | PW21_18_S_25_2 | PARC | 2018 | Williams x Neyala |
| 71 | PW09_18_S_23_1 | PARC | 2018 | Gozale x Hawassa-04 | 146 | PW21_18_S_31 | PARC | 2018 | Williams x Neyala |
| 72 | PW09_18_S_23_2 | PARC | 2018 | Gozale x Hawassa-04 | 147 | PW21_18_S_33 | PARC | 2018 | Williams x Neyala |
| 73 | PW09_18_S_25_1 | PARC | 2018 | Gozale x Hawassa-04 | 148 | SC_Signal | PARC |  | Registered variety |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| 74 | PW09_18_S_44_1 | PARC | 2018 | Gozale x Hawassa-04 | 149 | SCS_1 | PARC | Released variety |
| 75 | PW09_18_S_44_2 | PARC | 2018 | Gozale x Hawassa-04 | 150 | Tana Beles | PARC | Released variety |

# BIOGRAPHICAL SKETCH

I, the author of this MSc thesis, Anbesaw Gate, was born in 06/03/1999 in Fendika, Awe Zone of Amhara Regional State. I attended elementary and secondary school in Alukurand and Fendika, respectively. Then I joined Oda Bultum University in October 2018 and graduated with a Bachelor of Science degree in Plant Science in January 28, 2021 G.C. I was then employed at Oda Bultum University in 2021 G.C. as a graduate assistant lecturer I in the department of Plant Science. Then I was promoted from graduate assistant I to graduate assistant II in 2022. In October 2023, I joined the school of postgraduate studies at Bahir Dar University to pursue my Master of Science degree in Plant Breeding.