



CHARACTERIZATION AND GENETIC DIVERSITY STUDY OF
SOYBEAN (*Glycine max* (L.) Merrill) ACCESSIONS FROM
REPUBLIC OF BENIN BASED ON AGRO-MORPHOLOGY
AND QUALITY TRAITS

MSc. THESIS

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JIMMA, ETHIOPIA

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BENIN BASED ON AGRO-MORPHOLOGY AND QUALITY TRAITS

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MSc. Thesis

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DEDICATION

I dedicated this thesis to my beloved parents; father Kadu Hasan and mother Gebi Dheko for their prayers, support, encouragement, patience and set a foundation for my education in my life.

STATEMENT OF THE AUTHOR

I declare and confirm that this Thesis is my work and that all sources of materials used for this Thesis have been duly acknowledged. This Thesis has been submitted in partial fulfillment of the requirements for MSc. degree in Horticulture at the Jimma University, College of Agriculture and Veterinary Medicine and is deposited at the University Library to be made available to users under rules of the Library. I solemnly declare that this Thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

The author was born from Mr. Kadu Hasan and Mrs. Gebi Dheko on 14 January 1992 at Adaba district, West Arsi Zone of Oromia Region State, Ethiopia. He attended his primary education at Hunte State and Meribo Chata elementary school from 2000 to 2007 and secondary education at Adaba secondary and preparatory school from 2008 to 2011.

After the completion of his preparatory School, he joined Ambo University in 2012 and graduated with a BSc Degree in Horticulture in 2014. After graduation, the author was employed at West Arsi zone Agricultural Office as Agricultural extension expert, and after serving for a period of two years, he joined Ethiopian Biodiversity Institute Jimma Botanical Garden as a junior researcher, and had served as junior and assistant researcher positions for two years until he joined the School of Graduate Studies at Jimma University College of Agriculture and Veterinary Medicine to pursue Master of Science Degree in Agriculture (Horticulture).

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ABBREVIATIONS AND ACRONYMS

ANOVA	Analysis of Variance
AOAC	Association of Official Analytical Chemists
IITA	International Institute of Tropical Agriculture
ISRA	Institute of Senegal Research Agriculture
MAEP	Ministry of Agriculture, Livestock and Fisheries
OECD	Organization for Economic Co-operation and Development
RAPD	Random Amplified Polymorphic DNA
SSA	Sub-Saharan Africa
DMRT	Duncan's Multiple Range Test
PCA	Principal Component Analysis
UPGMA	Unweighted Pair-Group Method with Arithmetic Average
SAS	Statistical Analysis System
IPGRI	International Plant Genetic Resource Institute
FAO	Food and Agriculture Organization
GAM	Genetic Advance as Percent of Mean
GCV	Genotypic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
IBPGR	International Board for Plant Genetic Resources
JUCAVM	Jimma University College of Agriculture and Veterinary Medicine

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Characterization and Genetic diversity study of Soybean (*Glycine max* (L.) Accessions from Republic of Benin based on agro-morphology and quality traits.

ABSTRACT

Soybean (*Glycine max* (L.) Merr.) is a vital nutritious oilseed crops that play a crucial role in feeding and supporting the world's expanding population. However, in Benin, its productivity falls below the global average due to narrow genetic base, limited improved cultivars, biotic and abiotic stress. To enhancing production and productivity this study was conducted to characterize and assess the extent of genetic diversity and characters association using agro-morphology and quality traits for soybean accessions collected from Republic of Benin. A total of 64 soybean accessions were evaluated for quantitative and quality traits in 8x8 simple lattice designs with two replications during 2022 main season. The result of Shannon-wiener diversity index showed that there was a significant variability among accessions. The results of analysis of variance showed significant to highly significant ($P \leq 0.05$ and $P \leq 0.01$) differences for most of studied traits, except pod width and number of seed per pod. Oil and protein content ranged from 12.50% to 24.49% and 27.32% to 42.21% respectively. Estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variation value ranged from 4.85 to 46.22% and 5.99 to 52.28%, respectively. Heritability in broad sense (H^2) and genetic advance as percent mean (GAM) value ranged between 25.67% to 84.23% and 6.57 to 84.30%, respectively. Estimates of GCV, PCV, H^2 and GAM were high for number of pod per plant, number of seed per plant, shoot dry weight, root dry weight and seed yield. Seed yield had positive and significant genotypic and phenotypic correlation coefficients with days to maturity, plant height, Pod per plant, number of seed per plant and biological yield. Path coefficient analysis showed that number of pods per plant, biological yield and harvest index had high positive direct effects on seed yield at genotypic and phenotypic levels. This indicates the direct selection for these traits are important for grain yield improvement in soybean breeding programs. The first four principal components had accounted for 74.8% of the total variation. The first PCA alone had largest contribution of 40%, and PCA2, PCA3 and PCA4 contributed 14%, 12.9%, and 7.9%, respectively. Cluster analysis had showed the existence of five divergent groups and the maximum squared distance between cluster-I and III ($D^2=209.73$), while the minimum inter-cluster distance was observed between cluster-III and V ($D^2=74.99$). Based on mean values, SO-NDA-81 (3.92t/h) and SO-TAN-19 (3.22t/h) had shown to be high yielding accessions, while SO-OUE-39 (0.33t/h) had shown low yielding. In conclusion this study showed the presence of genetic variability among accessions, and indicates that there is an opportunity to use for selection and to improve specific traits using distant parents. Moreover, further molecular characterization is suggested to supplement morphological characterization.

Keywords: Accessions, Cluster, Correlation, Heritability, GCV, PCV, Soybean, Variability

1. INTRODUCTION

Soybean [*Glycine max* (L) Merrill; $2n = 40$] is an annual self-pollinated crops that belongs to the genus *Glycine* and family *Leguminosae* (Angele *et al.*, 2018). It is a native of eastern Asia, originally growing wild in China, Manchuria, Korea and Japan, and now worldwide grown (Hymowitz and Shurtleff, 2005). It is the most important oilseed crop that ranks the first compared to other oilseed crops, and it produces more protein and oil (roughly 40% protein and 20% oil content) (Wijewardana, 2018; Angele *et al.*, 2018).

Soybean is a key source of protein, carbohydrates, vegetable oils, vitamins and minerals for human consumption and production of livestock feed. Soybeans seeds account for around 56% of global oilseed production. It contains around 40% protein with all essential amino acids and 20% oil as compared to other legume crops (Wilson, 2008). Soybean can be used as grain soybean and vegetable soybean; both are rich in protein, oil, and other nutritious constituents, and also improve soil fertility by converting atmospheric nitrogen from the soil for its own use. Grain soybean is primarily used for manufacturing oil and protein products, whereas vegetable soybean is consumed mainly as a vegetable or snack. A wide range of vegetable soybean have been cultivated and there is an increased consumption of vegetable soybean in south-East Asian countries (Sonkamble *et al.*, 2020).

Globally, over 130 million hectares of soybean have been cultivated, with the total soybean production was 372.7 metric tons with a global productivity of 2.87 t/ha grain per year (FAOSTAT, 2021). Brazil, USA, Argentina, China, and India are the world's largest soybean producers with more than 90% of global soybean production (FAOSTAT, 2021). Soybean was first introduced to Africa in the early 19th century, through Southern Africa (Ngeze and Mse, 2000). South Africa is the top producer of soybean among the Sub-Saharan African countries, followed by Nigeria, Zambia, and Uganda (Khojely *et al.*, 2018; USDA, 2022).

Soybean introduced to Benin since around 1939 (Laura *et al.*, 2018), and the country became the second largest producer of soybean next to Nigeria, in West Africa. Following its introduction, soybean has been grown as an important source of vegetable protein for humans, which can be used as a substitute for meat, eggs and milks in the reduction of malnutrition, especially in rural areas (Loko *et al.*, 2022). The farmer's interest of soybean cultivation has increased in the country for its exceptional nutritional values (Wendland and Sills, 2008). In the country, the area under soybean production was estimated at 232,951 ha

with an annual production of 291,278.98 tons with a productivity of 1.25 tons/ha (FAOSTAT, 2021). The average national yield of soybean (1.25 tons/ha) in Benin was lower than the global yield 2.87 tons/ha (FAOSTAT, 2021). This limitation for soybean production may become for low genetic improvement due to narrow genetic base (low yield cultivars), limited improved cultivars, susceptibility to pests and diseases, adverse environmental conditions and poor agronomic activities (Khojely *et al.*, 2018). The local adaptation of repeatedly use closely related resources has narrowed the genetic base of the crops in which increase its vulnerability to changes in biotic and abiotic stresses (Ssendege *et al.*, 2015; Bisen *et al.*, 2015), and this situation became leads to cause of significant yield losses and to rampant malnutrition related disorders (Singh, 2010).

The genetic enhancement of crops is largely dependent on available genetic variability, but there hasn't been much research on soybean genetic variability in Benin, resulting in soybean output restrictions. Loko *et al.* (2022) studied on 35 Soybean local varieties were recorded with 7 types classified based on morphological seed features. Diversity in the germplasms is a very important precondition for hybridization program. Ramesh *et al.* (2020) suggested that evaluation of genetic diversity would promote the effective use of genetic variations within the breeding program. To improve the effectiveness of crop, it is essential to obtain the information on genetic diversity and relationships among breeding materials for a plant breeder. Previous research has explored the significance of phenotypic characterization in estimating diversity in soybean, Dayaman *et al.* (2009) using 52 morphological and agronomic characters found variability for the traits studied in soybean. Other study involving phenotypic characterization of 139 soybean genotypes (Iqbal *et al.*, 2008) revealed significant differences among all the assessed traits. The assessment of genetic diversity is important not only for crop improvement but also its essential for efficient management and conservation of germplasm resources (Tahir and Karim, 2011).

Researchers are striving to satisfy the need for abundant and inexpensive food to meet the challenge of feeding the growing population from a degrading area of land and conservation to reduce genetic erosion (Minnesota Agri-growth Council, 2009). Genetic diversity is essential to identify the sources of genes for a particular trait from the existing germplasms and to sort out parental lines with complementary features that can enhance breeding progress (Arslanoglu *et al.*, 2011). The development of high yielding and resistance varieties will depend on the presence and magnitude of the genetic variability available in a population

(Karnwal and Singh, 2009). Therefore, precise information on the nature and degree of genetic diversity helps the plant breeder in choosing desirable traits and diverse parents for purposeful hybridization for the crop improvement.

The success or failure of crop improvement largely depends on the amount of genetic diversity present in the breeding materials, and available information's are basis for a successful improvement. But, in Benin studies on soybean were mainly limited to adaptation and performance evaluation. Equally, there is a research information gap on genetic variability of soybean in the country. Therefore, this study was designed to characterize and assess the genetic diversity of soybean accessions based on agro-morphological and quality traits.

1.1. Objectives of the study

1.1.1. General Objective

To characterize and assess the genetic diversity of soybean accessions from the Republic of Benin based on agro-morphology and quality traits.

1.1.2. Specific Objectives

- To estimate variability and genetic divergence of soybean accessions collected from Benin Republic based on agro-morphological and quality traits.
- To characterize and determine the association of yield, yield related and quality traits of soybean accessions.

2. LITERATURE REVIEW

2.1. Origin and distribution of soybean

Soybean was originated in the north and central China and the first domestication has been traced to the eastern half of the North China. Primarily, soybean was called the Chinese soybean or Manchurian bean (Morse, 1950). Although, in 1948, Ricker and Morse coined the botanical name to the domesticated soybean wild types as *Glycine max* (L.) Merrill, which originated from *G. soja*. The subgenus *Soja* (Moench) and its wild annual progenitors, which have around 26 wild perennial species, have been separated from the genus *Glycine* (Hymowitz and Shurtleff, 2005).

In 1765, soybean was introduced to the United States by Samuel Bowen for use as a green forage crop and primarily, appeared to be well adapted to Pennsylvania soil. The first reference of soybeans that had been tested in a scientific agricultural school in the United States was in 1879, at the Rutgers Agricultural College in New Jersey. Soybeans introduced to Europe were about 1908, and the soybean attracted world-wide attention and Europeans had been aware of soybeans as early as 1712 through the writing of a German botanist (Bertheau and Daviso, 2011). It is believed that some soybean seed may have been sent from China by missionaries as early as 1740 and planted in France.

Soybean was first introduced to Africa in the early 19th century, through Southern Africa (Ngeze and Mse, 2000) and is now widespread across the continent. However, it might have been introduced at an earlier date in East Africa, since that region had long traded with the Chinese. The same report indicates that soybean has been under cultivation in Tanzania in 1907 and Malawi in 1909. Soybeans introduced to Benin since around 1939 (Laura *et al.*, 2018), and its production is low compared to other countries and continent.

The modern soybean arose after domestication by natural and conventional crossings as well as through genetically modified cultivars. Today, soybean is well adapted and commercially cultivated in all climatic zones and in all populated continents (Wijewardana, 2018).

2.2. Description and botany of soybean

Soybean (*Glycine max* (L.) Merrill) like that of legume crops peas, beans, lentils and peanuts, belongs to the large botanical family *Leguminosae*, in the subfamily *Papilionidae*, and is well adapted to many soil types and climatic conditions. The genus *Glycine*, consists of two

subgenera, *Soja* and *Glycine*, and Subgenus *soja* includes *Glycine max* and its annual wild relative *Glycine soja* which are native to eastern Asia, throughout China, Japan, Korea and part of Russia (Chen *et al.*, 2015).

The crop was well adapted in the tropical, sub-tropical and temperate climates. The plant breeders have been argued that within the soybean species, there are varieties which react differently to photoperiod, and classified them as long day, short day and day neutral plants. Soybean as being typically a short day plant, physiologically adapted to temperate climatic conditions. But, some have been adapted to the hot, humid, tropical climate. This affects the extent of vegetative growth, flower induction, production of viable pollen, and length of flowering, pod filling and maturity characteristics (Singh *et al.*, 2007).

The soybean plant grows up to 61 to 91 cm in height, the leaves are trifoliate and the flowers are usually purple or yellow. It can bear as many as 100 to 150 pods containing yellow seeds. The pods usually contain two to three seeds per pod but some pods rarely have one seed especially the low yielding cultivars. Soybean growth is designated by several vegetative and reproductive growth stages (Fehr *et al.*, 1971). The plant is covered with very soft tiny brown hairs. The growth of the plant from seed germination to seed maturity takes about sixteen weeks.

Soybean plants can be grouped according to their growth habits into basically two main types, determinate and indeterminate. The determinant varieties will flower at a definite period of the year, mainly when the days begin to shorten. The latter usually complete their vegetative growth prior to flowering with a group of flowers (raceme) at the tip where the stem ends. Indeterminate varieties will continue to flower and put on fruit until the weather dictates that it is time to curtail plant growth, they continue to increase in length for some time after the beginning of flowering (Nyerovwo, 2011).

Soybean maturity (flowering and ripening) usually takes about 90 to 100 days after planting date depending on the type of variety. Early cultivars can mature after about 75 days whereas it can take up to 200 days or more for the late varieties to mature. Soybean maturity varies for different cultivars and is determined by the photoperiod, which is the length of day and night (Nyerovwo, 2011).

Morphological characters of soybean, the height of the plant can vary and the pod, stem, and leaf are usually covered with fine brown or gray hairs. The leaves of soybean are trifoliate, having three to four leaflets per leaf, and the leaflets are 6-15 cm (2.4-5.9 in) long and 2-7 cm (0.79-2.8 in) broad. The leaves of soybeans are fall before the seeds are mature. The inconspicuous, self-fertile flowers are developed in the axil of the leaf and are white, pink or purple. The pod is a hairy one that grows in clusters of three to five; each pod is 3-8 cm long (1-3 in) and usually contains two to four (rarely more) seeds with 5-11 mm in diameter. Soybeans occur in various sizes, and in different seed coat colors, including black, brown, blue, yellow, green, and mottled (Sandar, 2012).

2.3. Soybean production

Global soybean production is more than twice as much compared to that of all the other grain legumes. Soybean production and consumption are both increasing around the worldwide, as its production provides a significant contribution to the economic structure, and it has a prominent place as the world's most important seed legume, which contributes 25 per cent to the global vegetable oil production, about two thirds of the world's protein concentrate for livestock feeding and is a valuable ingredient in feeds for poultry and fish. In the first two decades of the twenty-first century, global soybean production was estimated to be at 351 million tons (Wijewardana, 2018).

The United States, Argentina, Brazil, China, and India are the world's largest soybean producers and represent more than 90% of global soybean production (FAO, 2017). With a production volume of 120.52 million metric tons in 2018/2019, the United States was the world's biggest soybean producer. However, with a production level of 126 million metric tons in 2020/21, Brazil has surpassed the United States as the world's biggest soybean producer (Engelbrecht *et al.*, 2020).

Soybean growing area and production have been expanded dramatically and its cultivation is gaining popularity in Africa. Because of its importance's; in addition to human nutrition, animal and fish feeding, it has a strong ability to absorb atmospheric N₂ into forms that plants can utilize, the crop is both affordable and agronomical beneficial. Soybean is a very useful legume crop in improving the soil as most important agronomic characteristics that capability to take atmospheric nitrogen and fix or convert it a usable form by the soybeans themselves and other plants (Ahmed *et al.*, 2010). Nitrogen fixation in soybean is brought about by a

mutualistic relationship between the soybean roots and *Bradyrhizobium japonicum* bacterium which forms nodules (swellings) in the roots. The bacterium supports the plant in fixing or converting atmospheric nitrogen into a form that is more usable by the plant (Ahmed *et al.*, 2010).

In the African continent Nigeria, Uganda, Zimbabwe and South Africa are the main soybean cultivating countries (Chianu *et al.*, 2008). The total soybean produced in Africa during the season 2008/2009, Nigeria contributed 39 %, South Africa 35 %, Uganda 14 %, Zimbabwe 6 %, Egypt and Zambia being the least soybean producing countries contributing 3 % each. In Sub-Saharan Africa (SSA), soybean planting area has expanded rapidly from 20,000 hectares in the early 1970s to 1,500,000 ha in 2016. This rise has been the driving force behind SSA's 177-fold increase in soybean production, from 13,000 tons in the early 1970s to 2,300,000 tons in 2016. In 2016, South Africa was the top producer of soybeans in Sub-Saharan Africa, followed by Nigeria, Zambia, and Uganda. Other SSA nations with significant commercial soybean expansion include Zimbabwe, Malawi, Ghana, Sudan, Ethiopia, and Benin (Khojely *et al.*, 2018). Soybean production can also be affected by high temperature, low yielding varieties, poor seed quality, weed competition, uneven rain distribution, soil pH, insects, diseases, weeds as well as nutrient availability in the soil.

Benin has become the one of soybeans producer country in the West Africa, and the introduction of soybeans is since in 1939 (Laura *et al.*, 2018). In the country, soybean is grown everywhere but southern and central regions are the main production areas of the country. In the country, soybeans are grown alternately with other food crops to fix nitrogen in the soil and improve soil fertility, seem today as one of the speculations that are increasingly as a cash crop to replace cotton and also grown as its usefulness in reducing malnutrition, especially in rural areas (Loko *et al.*, 2022). Accordingly, soybean production interest among the farmers in the country has increased as a result of its highly nutritious crop with high economic value (Wendland and Sills, 2008). In the period between 2008–2015 at the country, soybean production increased from 31,111 to 139,909 tons, this was mainly achieved total increasing of area under soybean from 37,042 ha in 2008 to 152,138 ha in 2015 (Khojely *et al.*, 2018). In 2021 the area under soybean production was estimated at 232,951 ha with an annual production of 291,278.98 tons with a productivity of 1.25 tons/ha (FAOSTAT, 2021). The average national yield of soybean (1.25 tons/ha) was lower than the global yield 2.8tons/ha (FAOSTAT, 2021). But, the country's average soybean production

yield decline due to several biotic and abiotic factors includes lack of improved cultivars, disease and pests, fertilizer limitation, moisture stress and poor agronomic practices (Singh, 2010). The cause for lower yields of soybean was also attributed to poor-performing cultivars due to mentioned factors (Khojely *et al.*, 2018).

2.4. Importance of soybean

Soybean can be categorized as vegetable soybean; which is harvested at the reproductive stages when the seeds have developed to fill 80% - 90% of the pod, and grain soybean; which is harvested at reproductive stage when the pod has reached full maturity; and both are rich in protein, oil, and other nutritious constituents (Sonkamble *et al.*, 2020). Grain soybean is primarily used for manufacturing oil and protein products whereas vegetable soybean is consumed mainly as a vegetable or snack. Vegetable soybean is good source of vitamin A, carbohydrates, protein and iron and is more nutritious than vegetable green peas. Vegetable soybeans are also used in the preparation of innovative products such as green milk, green tofu and green noodles. A wide range of vegetable soybean varieties have been cultivated and there is an increased consumption of vegetable soybean in south-East Asian countries (Sonkamble *et al.*, 2020). Its cultural practices are identical with ordinary soybean except that the green pods are harvested at the mature green stage when the pods almost filled (Fehr *et al.*, 1971), and Japan is one of the most importer countries of vegetable green soybean.

Soybean production is regarded as the most important protein source compared with crops like wheat and maize, and it's used for drinks (Joyner *et al.*, 2010), food and animal feed all over the world, and also has very high oil and protein contents which are important seed quality components in the economy. Since the crop is important for uses, demand for soybean production has increased globally.

Soybean has the potential of providing an inexpensive source of protein both for human consumption and animal feed preparation. Soybean is usually grown for its seed protein and oil. For protein sources, it can be used in different ways, such as soy milk, soy meat, snaps, tofu, etc. For oil source, some products have been produced from soybean oil, such as cooking oil, margarine, cosmetics, biodiesel, etc. Besides these products, it can also be used as soy ink. It is more superior to petroleum based inks because it is not toxic, renewable and easily cleans up. Soybean like all other legumes also improves soil fertility by converting atmospheric nitrogen from the soil for its own use, which also benefits subsequent crops in

rotation. It reduces the amount of nitrogen fertilizer that farmers have to purchase to apply to their fields to improve productivity. In West Africa, soybean has become a major source of high quality and cheap protein for the poor and rural households (Abbey *et al.*, 2001).

Some studies have shown that soybeans contain several compounds such as isoflavones, which play a key role in reducing the risk of heart disease, breast cancer, and osteoporosis. In addition, soybeans are used in traditional Oriental medicine to treat many ailments, such as high blood pressure and stomach cancer (Moța *et al.*, 2007).

2.5. Soybean genetic diversity

Soybeans *Glycine max* (L.) [Merr.] and *Glycine soja* (Seib. et Zucc.) are the annuals and the two species of the subgenus Soja. *Glycine max* is the cultivated soybean while *Glycine soja* is the wild annual progenitor found naturally in China, Japan, Korea, Russia and Taiwan (Hymowitz and Shurtleff, 2005). Both the cultivated soybean *G. max* and its annual wild progenitor, *G. soja*, are cross compatible and have $2n=2x=40$ chromosomes. Random amplified polymorphic DNA (RAPD) study data by Chen and Nelson (2004) found that *G. soja* was more diverse than that of *G. max*. *G. soja* has been found to be a potential good source of resistance to diseases and pests. Dong *et al.* (2001) used 43 isoenzyme loci to investigate polymorphism in 72 wild soybean (*G. soja*) accessions from Japan and the Republic of Korea, finding that the average genetic variation among the accessions was 67.4 percent. (Dong *et al.*, 2004) used 15 enzymes to investigate genetic diversity in 400 cultivars of *G. max*, and more than 100 accessions of *G. soja* from several geographical distributions, and found that morphological traits and simple sequence repeat (SSR) markers have a clear geographic effect on genetic structure.

Genetic diversity plays a major role in crop improvement for identification of distinctive accessions vital for the curators of gene banks. Through genetic diversity and breeding for tolerant varieties to diverse biotic and abiotic factors, understanding the crop diversity as well as production limiting factor and tackles is required to meet farmer's interest to the crops. In any diversity studies, morphological characterization is recommended as the first step to be taken before in depth molecular and biochemical analyses are employed (Bello *et al.*, 2011).

Genetic variability is the numbers of genetic characteristics in the genetic makeup of species. Plant breeders attempt to make their genetic material broader in several programs such as landraces exploration, hybridization, artificial mutation, and germplasm introduction from

other countries. Variability refers to the occurrence of variances among individuals as a result of differences in their genetic makeup and/or their upbringing (Harris and Manlove, 2013).

Soybean was first introduced to Africa in the early 19th century, through Southern Africa (Ngeze and Mse, 2000) and is now widespread across the continent. Zimbabwe, Zambia, Nigeria, Cote d'Ivoire, Malawi, Benin, Uganda, Cameroon, and Kenya have released the most soybean varieties, accounting for 80 percent of total releases in SSA (Khojely *et al.*, 2018). Between 1970 and 2011, 195 soybean varieties were released in, among the 195 releases in SSA, 119, 71, and 5 varieties were released by private breeders, IITA, and national research programs, respectively (Alene and Mwalughali, 2012).

About 35 soybeans local varieties were studied by Loko *et al.* (2022), 7 types are classified based on morphological seed features. This diversity is found to be very low compared to other country like China that is area of origin of soybeans. This happened is due to loss of soybean diversity in the study area remains significant and conservation method like in situ and ex situ of the existing diversity should be important to maintain the genotypes.

Alene and Mwalughali (2012) carried survey on the adoption of improved soybean varieties and varietal catalogues from participating countries indicate that in total, over 100 IITA varieties were released in more than 15 countries with Nigeria, Cote d'Ivoire, Benin and Ghana having the highest number of genotypes. In the last few decades, the International Institute of Tropical Agriculture (IITA) and the Institute of Senegal Research Agriculture (ISRA) have released about ten soybean varieties with high yields and resistance to disease and insects as a result of introduction and selection breeding, and that being grown in various part of the country.

2.6. Shannon-wiener diversity index (H') for qualitative traits

Qualitative characters have played an important role in the classification of crop genotypes due to their steady inheritance over generations. These characters have proved their reliability for characterization of genotypes and are the important determination that they are fewer influenced by fluctuations in environmental circumstances (Tripathi and Khare, 2016). The Shannon procedure was used to compute the genetic diversity index (Shannon index) of soybean genotypes of qualitative traits. Each section's Shannon index value was very divergent from the others. Shannon diversity index (H') of qualitative traits was used to estimate the frequency distribution of the diversity index. The phenotypic dissimilarity index,

genotypes that diverged from others can be used as parents in upcoming breeding program through hybridization for the investigation of qualitative traits (Sharma *et al.*, 2023) studied on 60 soybean genotypes had recorded 14 genotypes were ovate, 30 rounded ovate, 8 with lanceolate and 8 with triangular for leaf shape; flower colour were seen with 43 genotypes white and 17 purple; and found the highest value of (1.525) Shannon diversity index (H') for the characteristic of helium color's that indicates this traits more divergent of all traits.

2.7. Genetic Variability Components

Estimating the extent of genetic variability and genetic parameters are the most important factors that determining the genetic potential of the crop for future improvement. Genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV), heritability (H^2) and genetic advance (GA), Principal component analysis, Cluster analysis, Correlation and Path Coefficient Analysis are important estimators of genetic variability.

2.7.1. Genotypic and phenotypic coefficient of variation

Estimation of type and amount of genetic variability associated with the target traits is very important. Determination of the type of genetic variability may help in the formulation of a comprehensive breeding program regarding the further improvement of the target trait. The components of variability include phenotypic variation, genotypic variation, and environmental variation.

Phenotype variation has both heritable and non-heritable components. The value of progeny obtained from a selected plant is largely depending upon the relative contributions by the heritable and non-heritable components to its phenotype. Individual plants in a mixed population will vary in yield, height, hardiness, and other characteristics of a quantitative nature. If two plants are selected at random from a mixed population, they differ in yield. This difference may be due to hereditary differences in the plants, difference in the environments in which the plants were grown, or a combination of both (Poehlman and Sleper, 1995).

Variation is the occurrence of differences among individuals is due to the differences in their genetic composition and/ or the environmental in which they grow (Allard, 1960). Progress in plant breeding depends on variability, because superior genotypes obviously cannot be selected from homogenous populations, but homogeneity is desirable in the final product. Success in improving adaptation requires that the population under selection be genetically

variable. In beginning a breeding program with any crop, information on the nature and magnitude of genetic variation within the genotypes for traits of agronomic importance greatly helps in formulating a sound crop breeding program and in efforts to bred better varieties (Dudley and Moll, 1969).

Phenotypic variability is the visible variation present in a character in a population; it includes both genotypic and environmental components of variation and, as a result, its magnitude differs under different environmental conditions. Genotypic variation is the component of variation, which is due to the genotypic differences among individuals within a population, and is the main concern of plant breeding.

High phenotypic and genotypic variability (PCV and GCV) have been reported for plant height, branch per plant, pod per plant, seed per plant, days to flowering, days to maturity, grain yield, harvest index and yield per plot, 100-seed weight, oil and protein content (Mahbub *et al.*, 2016; Wanderi *et al.*, 2013). On the other hand, moderate value of variability (PCV and GCV) has been reported for pods per plant, seed per plant, seed per pod and harvest index, branch per plant and grain yield per plant in soybean (Wanderi *et al.*, 2013).

2.7.2. Genetic parameters of traits

Heritability refers to the extent to which the variability for a quantitative character is transmitted to the progeny. Heritability of a trait is essential in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Akinwale *et al.*, 2011). The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960).

Heritability also indicates the efficiency in which selection of genotypes could be based on phenotypic performance. Most effective yield component breeding to increase grain yield could be achieved, if the component traits are highly heritable and positively correlated with grain yield. However, it is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations. Several studies have been conducted so far in soybean to determine the magnitude of heritable portion of the total variations.

High broad sense heritability has been reported for days to flowering, pod per plant, days to maturity, plant height, pod length and seed per pod, 100-seed weight, branches per plant (Aditya *et al.*, 2011; Akram *et al.*, 2016; Desissa, 2017; Mahbub *et al.*, 2016). High heritability was reported for protein and oil content (Aditya *et al.*, 2011). (Desissa, 2017) has been reported moderate broad sense heritability for harvest index and days to flowering; and also low broad sense heritability was reported for seed per pod, pod length and branches per plant.

Genetic advance under selection indicates measure of the difference between the mean genotypic values of the selected population over the mean genotypic value of the original population for a given character (Allard, 1960). Genetic advance refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at given selection intensity. Since high heritability does not mean indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties. Genetic advance gives clear image and precise view of segregating generations for possible selection. Higher estimates of heritability together with better genetic advance confirms the scope of selection in developing desirable crop with desirable characteristics (Ali *et al.*, 2002).

High heritability coupled with genetic gain has been reported for plant height, pod per plant, pod per plant, seed per plant, pod length and biological yield in soybean (Aditya *et al.*, 2011; Akram *et al.*, 2016; Desissa, 2017; Wanderi *et al.*, 2013). And also high heritability coupled with moderate genetic gain for 100-seed weight, days to flowering and maturity and branches per plant (Akram *et al.*, 2016) and high heritability and low genetic gain for pod length (Wanderi *et al.*, 2013) have been reported for soybean.

2.7.3. Association among traits

Correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of relationship between two or more variables. Correlation coefficient analysis measures the common relationship among various plant characters and determines the component characters on which selection can be based on for the genetic improvement in yield. Correlation studies provide better understanding of yield components which helps the plant breeder during selection (Johnson *et al.*, 1955; Robertson, 1959). The correlation coefficient, r ranges from -1 to 1. If r is -1, there is 100% correlation between two variables,

but both vary in opposite direction (negative correlation). On the other hand, if r is +1, it implies perfect correlation (100%) where both traits vary in the same direction (positive correlation). Phenotypic and genotypic correlations are regularly used in plant breeding.

2.7.3.1. Phenotypic correlation coefficients

Phenotypic correlations involve both genetic and environmental effects; both measure the extent to which the same genes or closely linked genes cause co variation in two different characters. Phenotypic correlations measure the extent to which the two observed characters are linearly related. It is determined from measurements of the two characters in a number of individuals in the populations (Falconer and Mackay, 1996). Phenotypic correlations, also known as correlations of phenotypic (r_p) values, are associations between two traits that may be seen immediately. Correlation between yield and other traits is helpful in selection of superior plant types. Yield is resulting from multiple interactions between many yield-contributing traits. The degree of relatedness between important plant traits is an index that can be used to predict yield responses in relation to changes associated with a particular trait. Iqbal *et al.* (2010) reported significant and positive correlation between grain yield and day to maturity and number of branches per plant. In contrast, non-significant and negative correlations showed in grain yield with days to first flowering, days to 50% flowering, days to maturity, plant height and the number of seeds per pod (Akram *et al.*, 2016).

2.7.3.2. Genotypic correlation coefficients

Genotypic correlation is inherent or heritable association between two variables. Genotypic correlation (r_g) may be either due to pleiotropic action of genes or due to linkage or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to manifold effects of a gene (Falconer, 1989). More significant genotypic association between the different pairs of characters than the phenotypic correlation means that there is strong association between those characters genetically, but the phenotypic value is lessened by the significant interaction of environment. Aditya *et al.* (2011) reported that grain yield per plant showed highly significant and positive genetic correlation with, number of primary branches per plant, number of pods per plant and harvest index. It has been reported that seed yield per plant has been positively correlated with branches per plant, pod length, seed per plant, pod per plant, 100-seed weight, days to flowering, days to maturity and plant height (Jain *et al.*, 2015; Mahbub *et al.*, 2016).

2.7.4. 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 (Singh and Chaudhary, 1977). As correlation coefficients alone are insufficient to interpret cause and effects relationships among traits associated with yield. Yield is interrelated and influenced by many traits, in which correlation studies do not give a complete picture of the associations. Path correlation coefficients allows by partitioning the phenotypic value into direct and indirect effects which in return offers information on the actual contribution of independent variables with respect to a dependent variable.

Akram *et al.* (2016) indicated that a maximum positive direct effect on seed yield by the number of seeds per plant, number of pods per plant, number of branches per plant, 100- seed weight and pod length. Jain *et al.* (2015) indicated that biological yield, number of pods per plant and 100-seed weight were the characters influencing seed yield directly. Chlorophyll content, days to pod initiation, number of branches per plant, number of pods per plant and 100-seed weight employed positive direct effects (Malek *et al.*, 2014). Another study shows that number of pods per plant, days to maturity and harvest index had positive direct effect on seed yield per plot, whereas number of branches per plant and plant height employed positive and significant indirect effect on seed yield per plot through number of pod per plant and plant height (Aditya *et al.*, 2011).

2.7.5. Multivariate analysis

2.7.5.1. Clustering and genetic divergence analysis

Cluster analysis is a multivariate technique with a primary purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptions are mathematically gathered into the same cluster. The resulting clusters of individuals that exhibit high internal (within cluster) homogeneity and high external (between clusters) heterogeneity. Then, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart (Hair, 1995). Hierarchical cluster analysis has been suggested for classifying entries of germplasm collections based on degree of similarity and dissimilarity through their associations by constructing a dendrogram. The important aspect in cluster analysis is determining the optimal number of clusters or number of acceptable clusters; this involves determining where to cut a dendrogram to find the true or natural groups. The method of X^2 -test were used to

performed for genetic distances (D^2) between clusters to identify the diversity. Mohammadi and Prasanna (2003) was evaluated 49 soybean genotypes for 13 morphological trait, the result indicates that, soybean genotypes have classified into five clusters, which shows moderately divergent.

2.7.5.2. Principal component analysis

The principal component analysis (PCA) was calculated to reduce the dimensionality of a data set consisting of a large number of interrelated variables though retaining as much as possible of the variation present in the data set. It was performed using the correlation matrix to express the patterns of variation among accession based on the mean of quantitative characters that helps to identify characters that load the most in explaining the observed variation. This is accomplished by transforming to a new set of variables, the principal components (PCs), which are uncorrelated, and which are ordered so that the first few retain most of the variation present in all of the original variables.

Principal component analysis elucidates the contribution of the most important traits that account for the total genetic variability. Principal component analysis (PCA) has several uses such as the study of genetic divergence between genotypes which permits the identification and selection of the most promising genotypes for cultivation and improvement. Several study suggested that first principal component (PC) scores as input variables for the clustering process. Ghiday and Sentayehu (2015) reported that the analyses of principal component in 49 soybean germplasm classified in to five principal components, the major contributing characters for the diversity in the first principal components analyses are number of pods per plant, biological yield, seed yield per plot and seed yield per plant. Sileshi *et al.* (2019) used PCA to determine the variability of soybean from different geographical regions of which the first four principal components together accounted for 70.28 % of the total variance.

3. MATERIALS AND METHODS

3.1. Description of the study area

The field trial was conducted at the experimental site of Laboratory of Genetics, Horticulture and Seed Sciences (GBioS), University of Abomey-Calavi (UCA), Republic of Benin. The place is found in the latitudes 6.4130° N and longitudes 2.3450° E with the altitudes 54 m.a.s.l. Most of the territory of the municipality of Abomey-Calavi is occupied by tropical ferruginous soils and sandy soils. The area has average annual temperature and rainfall of 26.5 °C and 1342 mm, respectively.

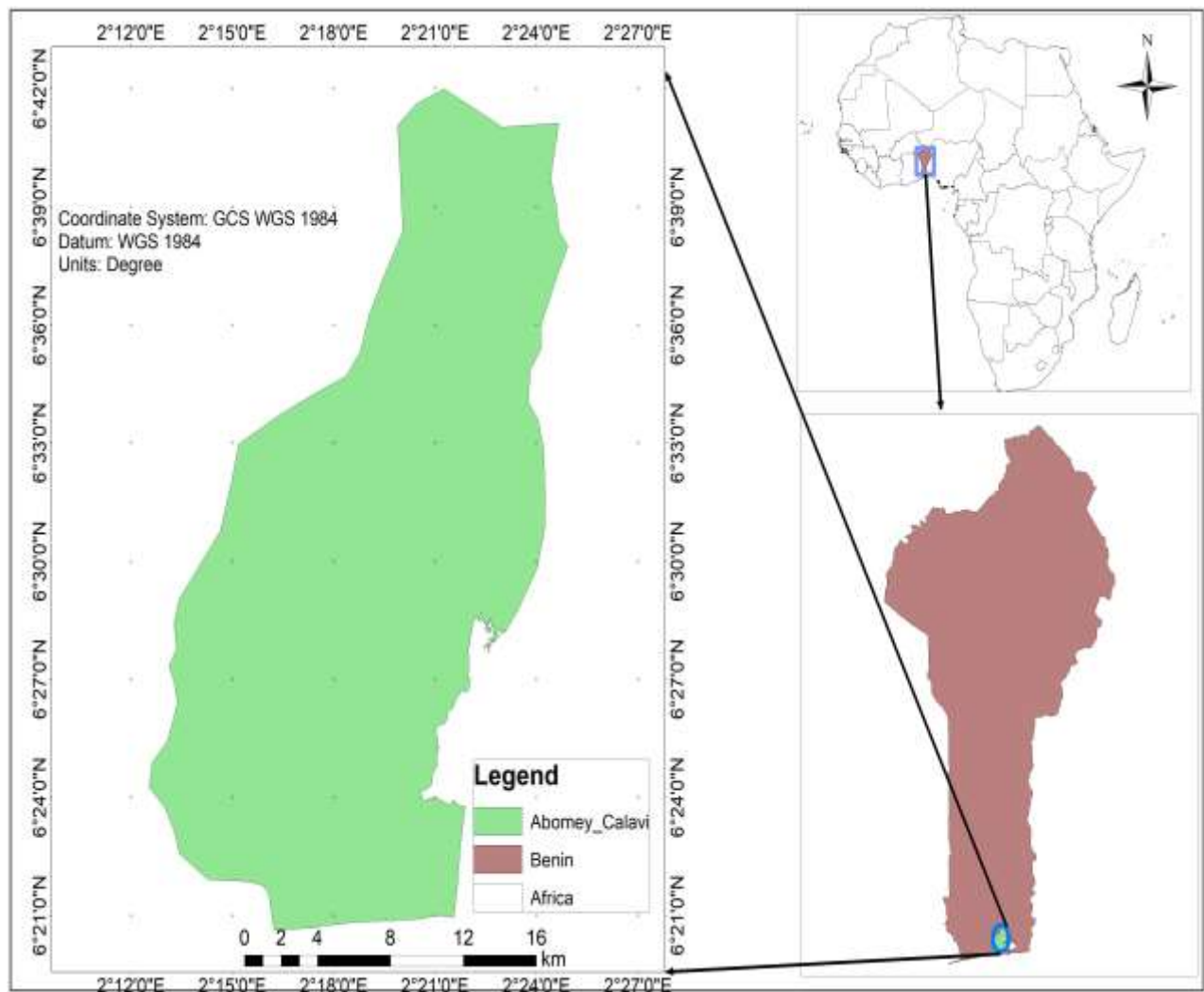


Figure 1: Map of experimental study area at the University of Abomey-Calavi, Benin.

3.2. Experimental materials

A total of 64 soybean accessions that were collected from fourteen (14) different municipality of Benin were used for the study (Table 1).

Table 1: The list of collected soybean accessions to be used in the study

S/N	Accessions	Collection		S/N	Accessions	Collection	
		Area in Benin	Year			Area in Benin	Year
1	SO-BAN-101	Banikoara	2022	33	SO-GLA-50	Glazoue	2022
2	SO-BAN-102	Banikoara	2022	34	SO-GLA-51	Glazoue	2022
3	SO-BAN-109	Banikoara	2022	35	SO-KAN-119	Kandi	2022
4	SO-BAN-111	Banikoara	2022	36	SO-KAN-125	Kandi	2022
5	SO-BAN-115	Banikoara	2022	37	SO-KAN-126	Kandi	2022
6	SO-BOH-119	Bohicom	2022	38	SO-KAN-128	Kandi	2022
7	SO-BOH-125	Bohicom	2022	39	SO-KAN-130	Kandi	2022
8	SO-BOU-42	Boukoumbe	2022	40	SO-NDA-63	N'dali	2022
9	SO-BOU-45	Boukoumbe	2022	41	SO-NDA-66	N'dali	2022
10	SO-BOU-46	Boukoumbe	2022	42	SO-NDA-67	N'dali	2022
11	SO-BOU-47	Boukoumbe	2022	43	SO-NDA-70	N'dali	2022
12	SO-BOU-56	Boukoumbe	2022	44	SO-NDA-81	N'dali	2022
13	SO-COB-25	Cobly	2022	45	SO-NIK-84	NIKKI	2022
14	SO-COB-27	Cobly	2022	46	SO-NIK-87	NIKKI	2022
15	SO-COB-32	Cobly	2022	47	SO-NIK-95	NIKKI	2022
16	SO-COB-35	Cobly	2022	48	SO-NIK-98	NIKKI	2022
17	SO-COB-40	Cobly	2022	49	SO-NIK-100	NIKKI	2022
18	SO-DAS-01	Dassa-zoume	2022	50	SO-OUA-82	Ouake	2022
19	SO-DAS-02	Dassa-zoume	2022	51	SO-OUA-84	Ouake	2022
20	SO-DAS-03	Dassa-zoume	2022	52	SO-OUA-85	Ouake	2022
21	SO-DAS-04	Dassa-zoume	2022	53	SO-OUA-93	Ouake	2022
22	SO-DAS-05	Dassa-zoume	2022	54	SO-OUA-94	Ouake	2022
23	SO-DJI-110	Djidja	2022	55	SO-OUE-21	Ouisse	2022
24	SO-DJI-114	Djidja	2022	56	SO-OUE-23	Ouisse	2022
25	SO-DJI-95	Djidja	2022	57	SO-OUE-36	Ouisse	2022
26	SO-DJI-96	Djidja	2022	58	SO-OUE-39	Ouisse	2022
27	SO-DJO-65	Djoungou	2022	59	SO-OUE-41	Ouisse	2022
28	SO-DJO-70	Djoungou	2022	60	SO-TAN-05	Tanguieta	2022
29	SO-DJO-75	Djoungou	2022	61	SO-TAN-09	Tanguieta	2022
30	SO-GLA-04	Glazoue	2022	62	SO-TAN-10	Tanguieta	2022
31	SO-GLA-48	Glazoue	2022	63	SO-TAN-15	Tanguieta	2022
32	SO-GLA-49	Glazoue	2022	64	SO-TAN-17	Tanguieta	2022

3.3. Experimental design

The experiment was laid out in 8x8 simple lattice design with two replications was used. Single plot measuring $2 \times 4 = 8\text{m}^2$ with inter row spacing of 0.5 m and intra row spacing of 0.2 m was used. The spacing between two plot rows within the same block was 0.5 m and the spacing between blocks and replications was 1 m and 2 m, respectively. Each accession was

planted in one plot in each replication with each plot containing 10 plants per row. The layout and randomization were done as per the standard procedure set by Cochran and Cox (1957).

3.4. Field management

Land preparation was done in human labor and soybean plants were established by direct seeding on the field. Soybean seeds were sown in a depth of 3 cm with two seeds per hill and thinned to one after emergence (Sandar, 2012). Cultural practices (hoeing, cultivating and weeding) was applied for weed control. All the necessary agronomic practices (Watering, weeding, fertilizer application and biotic factors like disease and insects) was applied (Faki *et al.*, 2021). When the plant grows three fully extended leaves, inorganic fertilizers N, P, K, Mg, and Zn were applied at doses of 14.02, 23.89, 17.82, 11.45, and 4.26 kg ha⁻¹, respectively, as recommended for the south republic of Benin (Faki *et al.*, 2021).

3.5. Data collection

Data were collected based on standard descriptor of international board for plant genetic resources for soybean (IBPGR, 1984). The data were collected on a plot and plant bases, and data of 20 quantitative, 10 qualitative and 2 quality traits was recorded from five randomly selected plants and the mean values of these five plants were calculated.

3.5.1. Qualitative traits data

Qualitative traits data were recorded on a plot basis according to international board for plant genetic resources (IBPGR, 1984) descriptor list for soybean species as follows.

Leaflet shape: was assessed from the ratio of length/width of fully developed terminal leaflet on middle part of main stems as: narrow (lanceolate), intermediate, and broad (ovate).

Pubescence and Pubescence color: Pubescence was observed at fully grown leaf stages and described as: absent or present and Pubescence color was observed and recorded when plants have dried at maturity as: gray, light brown and tawny.

Flower color: was assessed by observing at the time that plant fully flowing as: white, yellow, red and purple according to descriptor for soybean.

Pod color: was recorded when pods had dried and described as: tan, brown and black.

Seed character: this was observed from the seed and described according to the descriptor for soybean. Seed shape as near round, oblong and oval; Seed coat surface luster as shiny, intermediate, dull and heavy blooms; Seed coat color as yellowish white, yellow, green, buff,

reddish brown, grey, imperfect black and black; Seed quality as poor, medium and good; and Hilum color as yellow, buff, brown, green, grey, imperfect black, black and others.

Table 2: Descriptions and scores of qualitative traits of soybean descriptor list

Traits	Character codes
Flower color	1 White 3 Red 2 Yellow 4 Purple
Pubescence	0 Absent 1 Present
Pubescence color	1 Gray 2 Light brown 3 Tawny = brown
Pod color	3 Tan 5 Brown 7 Black
Seed shape	1 Near round 2 Oblong 3 Oval
Leaflet shape	4. Lanceolate 5 Intermediate 7 Ovate
Seed quality	3 Poor 5 Medium 7 Good
Seed coat luster	3 Shiny 7 Dull 5 Intermediate 9 heavy blooms
Seed coat color	1 Yellowish white 5 Reddish brown 2 Yellow 6 Grey 3 Green 7 Imperfect black 4 Buff 8 Black
Hilum color	1 Yellow 5 Grey 2 Buff 6 Imperfect black 3 Brown 7 Black 4 Green 8 Others

3.5.2. Quantitative traits data

Days to 50% flowering (DF) (days): It was recorded by counting the number of days from planting to the flowering of 50% of plants in each plot.

Days to maturity (90%) (DM) (days): The number of days from sowing to the date of 90% of the plants in a plot change the color of their pod from green to lemon yellow was recorded.

Plant height (PH) (cm): The height of the plants from the ground surface to the tip of the main stem was measured in centimeters at the final harvest from 5 selected plants and the averaged to be record for statistical analysis.

Leaf width (LW) (cm) and Length of leaf (LL)(cm): Measured by using ruler (cm) from 5 randomly selected plants on randomly selected three trifoliate leaf at the bottom, middle and top part of the main stem and the mean was taken at seed filling stage.

Number of branches per plant (NPB) (count): The total number of primary branches per plant was counted at harvest and the average of 5 plants was calculated and recorded.

Number of nodes (ND) (count): The total number of nodes per plant on main stem of randomly selected five plants was counted and the average was taken from each plot.

Chlorophyll contents (CC) ($\mu\text{mol m}^{-2}$): chlorophyll concentration from five randomly selected plant on three mature leaves / fully grown leaf from the third position on the top of the plant was recorded by hand-held chlorophyll meters typically provide a relative indication of chlorophyll in the plant leaves (Kashiwagi *et al.*, 2006). The patented Apogee model MC-100 chlorophyll concentration meter measures were used, and the average was taken.

Number of pod per plant (NPP) (count): On individual plant basis, number of pods per plant was recorded from five randomly selected plants from each plot and the average was taken.

Pod length (PL) (mm): Average length of pods was measured at physiological maturity on five randomly selected plants from five randomly taken pods per plant and the average was taken.

Pod width (PW) (mm): Average diameter of pod was taken at physiological maturity on 5 randomly selected plants and five randomly taken pods per plant are measured by using caliper.

Number of seed per pod (NSpD) (count): On well-matured, dried and normal size pods selected from each of the 5 randomly selected plants for recording number of seeds per pods. The seeds from each pod was separated manually and counted on an individual pod basis and the average was calculated to express a number of seeds per pod.

Number of seed per plant (NSpP) (count): It was recorded by counting from the sampled plants and average will be recorded.

Shoot dry weight (SDW) (gm): the total above ground part of 5 randomly selected plants dried for 72 hours at 70°C and weight was measured by using sensitive balance in gram. Shoot dry weight was computed by the sum of stem and leaf dry weight.

Taproot lengths (RL) (cm): Tap root length was measured from the soil surface up to the tip of the tap root from 5 randomly selected plants per plot by using ruler and the average of 5 plants was taken at harvesting.

Root dry weight (RDW) (gm): the total of the 5 randomly selected plant roots were dried for 72 hours at 70°C and the dry weight was measured by using sensitive balance in gram and the average of 5 plants was taken.

Biological yield (BY) (gm): The above ground parts of the plants was oven dried for 72 hours at 70°C and average of the 5 sampled plants was recorded to get the biological yield per plant in grams. Total biomass was calculated by the sum of stem, leaf, and pod dry weight.

Harvest index (HI) (%) = Grain yield / Biological yield × 100. Sampled plant was cut to count number of pod, threshed individually by hand and final grain traits were recorded. Biological yield was measured by weighing the dried total above ground plant biomass (straw + grain). Harvest index (HI) was calculated from grain yield dry weight divided by total biomass.

Hundred seed weight (HSW) (g): was recorded by counting hundred seeds randomly from a bulk of shelled seeds and weighed using a sensitive balance.

Seed yield (YD) (kg ha⁻¹): It was obtained from five randomly taken plants per plot and adjusted to standard moisture content (12%), and weight was measured by analytical balance and converted to hectare in kg.

3.5.3. Quality traits data

The biochemical contents of the seeds (oil and protein) were determined at Jimma University College of Agriculture and Veterinary Medicine, at the Postharvest laboratory.

Oil content (%): oil content was determined in according to the Soxhlet method (AOAC, 1980) extraction apparatus. About the 2 gm of sample powder was placed in cellulose acetate capsules and the solvent hexane was used to extract the oil.

Protein content (%): Protein was determined by Kjeldahl procedure as per the AOAC (Association of Official Analytical Chemists) methods (1990). About the 1 gm of sample powder, and the digestion was done in 15 ml of sulfuric acid with the catalyst was copper sulfate (0.2 g) and potassium sulfate (7 g). The method was used 40% NaOH to produce an alkaline distillation environment and 4% boric acid solution to collect the distilled ammonia. The titrations were performed with the standardized 0.1 N hydrochloric acid, and the indicator was used to identify the end point of the titration by methyl red and methylene blue. Protein content was calculated by determining the nitrogen content, using a nitrogen conversion factor of 6.25.

3.6. Data analysis

3.6.1. Analysis of qualitative traits

The Shannon-wiener diversity index (H') was calculated using Microsoft Excel 2016. The index used as a measure of the phenotypic diversity of each qualitative trait is determined as follows:

$$H' = - \sum_{i=1}^s p_i \ln p_i$$

Where: S is the number of phenotypic classes for a trait,
 p_i is the proportion of genotypes in the i^{th} class,
 $\ln$ = natural logarithm.

3.6.2. Analysis of variance

All the data collected for each quantitative trait was subjected to analysis of variance (ANOVA) for simple lattice design using R software version 4.1.3. The mean separation was done following the significance of mean squares using least significant difference (LSD) at $P < 0.05$. The analysis of variance was computed considering the general linear model as follows:

$$Y_{ijk} = \mu + r_i + G_j + b(r)_{ik} + e_{ijk};$$

Where; Y_{ijk} = Yield, μ = grand mean, r_i = effect of the i^{th} replication, G_j = effect of the j^{th} genotype, $b(r)_{ik}$ = effect of the i^{th} block in k^{th} replication, e_{ijk} = error effects. The traits were further subjected to the analysis of variance, phenotypic and genotypic coefficients of variations, heritability and genetic advance were calculated.

Table 3: Schematic representation of analysis of variance (ANOVA) table of lattice design

Source of variation	DF	Sum of squares (SS)	Mean square	Computed F
Replication	$r - 1$	SSR	MSR	$\frac{MSR}{MSE}$
Treatment (unadj.)	$k^2 - 1$	SST (unadj.)	MST (unadj.)	$\frac{MST_{unadj.}}{MSE}$
Blocks within replication (adj.)	$r(k-1)$	SSB (adj.)	MSB (adj.)	$\frac{MSB_{adj.}}{MSE}$
Intra-block error	$(k-1)(rk-k-1)$	SSE	MSE	
Total	$rk^2 - 1$	SST		

r = number of replications, k^2 = number of treatments, k = number of plots in a block, SS = sum square, MS = mean square, t = number of genotypes, MSe = mean squares for error.

3.6.3. Phenotypic and genotypic coefficients of variation

The phenotypic (σ^2_p) and genotypic (σ^2_g) variances and the corresponding phenotypic (PCV) and genotypic (GCV) coefficients of variation for each trait were estimated. The genotypic

and phenotypic variance was estimated according to the method suggested by (Burton and DeVane, 1953) considering mean square expectations from the analysis of variance as follows in equation 1 and 2.

Genotypic variance

$$\sigma^2_g = \frac{(K+1)}{rk} (Msg - Mse) \quad \text{or} \quad \sigma^2_g = \frac{Msg - Mse}{r} \dots\dots\dots \text{(Equation 1)}$$

Where; σ^2_g = genotypic variance, Msg = genotype/treatment mean square, Mse = error mean square, r = number of replications, k= number of plots with in block

Phenotypic variance

$$\sigma^2_p = \sigma^2_g + \sigma^2_e \dots\dots\dots \text{(Equation 2)}$$

Where; σ^2_p = phenotypic variance, σ^2_g = genotypic variance and σ^2_e = environmental variance = error mean square.

$$PCV = \left[\frac{\sqrt{\sigma^2_p}}{\bar{X}} \right] * 100 \qquad GCV = \left[\frac{\sqrt{\sigma^2_g}}{\bar{X}} \right] * 100$$

Where; PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, X = Population mean of the character. PCV and GCV values were categorized as low, moderate, and high values as indicated by Deshmukh *et al.* (1986) as; Low = 0 - 10%, Moderate = 10 – 20% and High = >20%.

3.6.4. Heritability and genetic advance

Broad-sense heritability values were estimated using the formula: $H^2 = (\sigma^2_g / \sigma^2_p) \times 100$ where; H^2 = heritability in a broad sense, σ^2_p = phenotypic variance, σ^2_g = Genotypic variance. The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.* (1949) as: Low = 0 - 30%, Moderate = 30 – 60%, and High = > 60%.

Expected genetic advance

Genetic advance (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al.* (1955) as: $GA = K \times \sqrt{\sigma^2_p} \times H^2$; Where, GA = Genetic advance, $\sqrt{\sigma^2_p}$ = Phenotypic variance on mean basis; H^2 = Heritability in the broad sense and K = the standardized selection differential at 5% selection intensity (K = 2.063).

Genetic advance as percent of mean (GAM)

Genetic advance as percent of mean were estimated as follows: $GAM = \frac{GA}{\bar{X}} * 100$

Where, GAM = genetic advance as percent of mean, GA = genetic advance and $\bar{X}$ = population mean of the character being evaluated. The genetic advance as percent of mean were categorized as low, moderate and high as suggested by Johnson *et al.* (1955) as: Low = 0 - 10%, Moderate = 10 – 20, and High = >20

3.6.5. Phenotypic and Genotypic correlation coefficient analysis

Phenotypic (rp) and genotypic (rg) correlations between two traits were estimated using the formula suggested by Johnson *et al.* (1955).

$$r_{pxy} = \frac{P_{cov\ xy}}{\sqrt{(V_{px}.V_{py})}} \quad r_{gxy} = \frac{G_{cov\ xy}}{\sqrt{(V_{gx}.V_{gy})}}$$

Where, r_{pxy} = phenotypic correlation coefficient between character x and y, $P_{cov\ xy}$ = Phenotypic covariance between variables x and y, $G_{cov\ xy}$ = Genotypic covariance between variables x and y, V_{px} = Phenotypic variance of variable x, V_{gx} = Genotypic variance of variable x, V_{py} = Phenotypic variance of variable y, V_{gy} = Genotypic variance of variable y.

The coefficient of correlation at genotypic levels was tested for their significant by the formula designated by Robertson, 1959 as: $t = r_{gxy} / SE_{rgxy}$. The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significant. Where, n is number of genotypes. $SE_{rgxy} = \sqrt{(1-r^2_{gxy})/(2h^2_x.h^2_y)}$; Where, h^2_x = heritability of trait x; h^2_y = heritability of trait y, SE_{rgxy} = standard error of genotypic correlation coefficient between character x and y.

The calculated phenotypic correlation value was tested for its significant using t-test: $t = r_{ph} / SE(r_{ph})$ Where, r_{ph} = Phenotypic correlation; $SE(r_{ph})$ = Standard error of phenotypic correlation was obtained using the following formula; $SE(r_{ph}) = \sqrt{(1-r^2_{ph})/(n-2)}$ Where, n is the number of genotypes tested, r_{ph} is phenotypic correlation coefficient.

3.6.6. Path coefficient analysis

Based on genotypic and phenotypic correlations, path coefficient analysis which refers to the estimation of direct and indirect effects of the seed yield attributing characters (independent character) on seed yield (dependent character) were calculated based on the method used by (Dewey and Lu, 1959) as follows:

$r_{ij} = p_{ij} + \sum r_{ik}p_{kj}$; Where, r_{ij} = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic and phenotypic correlation coefficients.

p_{ij} = direct effects of the independent character (i) on the dependent variable (j) as measured by the path coefficients, and $\sum r_{ik}p_{kj}$ = Summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, were computed using the formula: $\sqrt{1 - R^2}$; Where: $R^2 = \sum p_{ij}r_{ij}$ Where, R^2 is the residual factor, P_{ij} is the direct effect on yield by i^{th} trait, and r_{ij} is the correlation of yield with the i^{th} trait of variables.

3.6.7. Clustering and genetic divergence analysis

Hierarchical clustering using the units of Euclidean distance was performed to test for linkage between soybean accessions, and the optimal number of clusters was obtained using wss (within cluster sum squares) method using R software version 4.1.3. The dendrogram was built based on hierarchical classification with Euclidian distance as a measure of dissimilarity. The distance matrix from phenotype traits was used to construct dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of dendrogram. Genetic distances D^2 between clusters were calculated by χ^2 -test.

3.6.8. Principal component analysis

Principal component analysis (PCA) was computed to find out the characters, which accounted more to the total variation. The biplot analysis and its graphical output were then used to understand and interpret the relationship and association between the soybean genotypes and the observed quantitative trait. The data were standardized to mean zero and variance of one before computing principal component analysis to avoid bias due to the differences in measurement scales. The principal component based on the correlation matrix was calculated in using R version 4.1.3.

4. RESULTS AND DISCUSSION

4.1. Qualitative traits analysis

4.1.1. Shannon diversity index for qualitative traits

The results of Shannon-wiener diversity index had showed the presence of diversity in the tested soybean accessions based on 10 qualitative traits (table 4). According to Eticha *et al.* (2005), Shannon diversity indexes are categorized as high (>0.67), intermediate (0.34 to 0.66) and low (0.01 - 0.33). Accordingly, there is highest diversity for pod color (1.37), followed by leaf shape (0.93), hilum color (0.87), seed quality (0.80), pubescence color (0.69) and seed luster (0.69) and seed shape (0.68) indicates there was a diversity in the germplasm. Whereas flower color (0.23) and seed coat color (0.27) had showed low diversity indexes; while there was no diversity for the trait pubescence absent or present (0). High diversity was reported by Yechalew (2018) on 8 out of 11 qualitative characters, which includes pod color, hilum color, seed quality, pubescence density, leaf shape, seed luster, seed shape and flower color, out of 36 soybean genotypes, and no diversity on pubescence present or absent. Dong *et al.* (2001) reported that the Shannon diversity index of flower color, pubescence color, hilum color, leaf shape, and seed color was 0.49, 0.55, 1.45, 2.41 and 1.89 respectively from soybean genotypes.

4.1.2. Frequency distribution in the qualitative traits of tested soybean accessions

The accessions grouped into two different flower color categories, viz., white and purple. Out of the 64 tested soybean accessions, majority of the accessions (93.75%) had purple and 6.25% of accessions had white flower color (table 4 and appendix table 3). The accessions showed two different pubescence colors which are tawny and gray, about 53.13% accessions had gray and 46.88% accessions had tawny pubescence color. Pubescence absent or present had 100% present that influences seed yield in soybean by modifying the microclimatic condition of canopy. Hence, such diversity is very important for soybean improvement program. Out of the total 64 accessions, 38 had ovate leaflet shape, 18 had intermediate leaflet shape, while 8 had Lanceolate leaflet shape. Leaf is the main organ of the plant and the diversity of its shape has important, that influenced the yield and yield related components in soybean. Hence, leaf shape is one important trait that needs to be considered in improving the yield of soybean.

Brown and tan pod colors accounted for 48.44% and 14.06%, respectively, while black accounted 9.38%, and each of dark brown and light brown pod colors accounted for 20.31%

and 7.81%, respectively, out of the total germplasm. Out of the 64 soybean accessions, about majority that is 60 had yellow seed coat color, while three of the accessions (SO-BAN-101, SO-COB-27 and SO-TAN-10) had imperfect black, and one accession that is SO-COB-40 had black seed coat color. Out of the 64 tested soybean accessions, about more than half 34 had shiny seed luster, while 30 had Intermediate seed luster. Out of total tested soybean germplasms, majority of accessions about 71.88% had brown hilum color, 17.19% had imperfect black hilum color, 7.81% had yellow hilum color; while buff and black hilum color accounted for 1.56% in equal proportion. Out of the total tested accessions, 36 had good seed quality, 26 had medium seed quality; while two accessions (SO-COB-40 and SO-TAN-10) had poor seed quality. More than half about 57.81% of the accessions had oval seed shape; while 42.19% of the accessions had round seed shape. Sharma *et al.* (2023) studied on 60 soybean genotypes and reported 14 genotypes were ovate, 30 rounded ovate, 8 lanceolate and 8 triangular for leaf shape; flower colour were seen with 43 genotypes white and 17 purple.

Table 4: Frequency distribution and Shannon-wiener diversity index of qualitative traits of tested soybean accessions

Traits	Variation	No. of genotypes	Frequency %	Shannon index (H')
Flower color	White	4	6.25	0.23
	Purple	60	93.75	
Pubescence	Present	64	100.00	0.00
	Absent	0	0.00	
Pubescence color	Gray	34	53.13	0.69
	Tawny	30	46.88	
Pod color	Brown	31	48.44	1.37
	Tan	9	14.06	
	Black	6	9.38	
	Light brown	5	7.81	
	Dark brown	13	20.31	
Seed shape	Oval	37	57.81	0.68
	Round	27	42.19	
Leaf shape	Ovate	38	59.38	0.93
	Intermediate	18	28.13	
	Lanceolate	8	12.50	
Seed quality	Good	36	56.25	0.80
	Medium	26	40.63	
	Poor	2	3.13	
Seed luster	Shiny	34	53.13	0.69
	Intermediate	30	46.88	

Seed coat color	Imperfect black	3	4.69	0.27
	Black	1	1.56	
	Yellow	60	93.75	
Hilum color	Imperfect black	11	17.19	0.87
	Brown	46	71.88	
	Buff	1	1.56	
	Yellow	5	7.81	
	Black	1	1.56	

4.2. Analysis of variance

4.2.1. Quantitative traits analysis

The results of analysis of variance (ANOVA) was showed the presence of highly significant ($P \leq 0.01$) differences among the evaluated soybean accessions for most of studied traits including days to 50% flowering, days to maturity, plant height, leaf length, chlorophyll contents, number of pod per plant, number of seed per plant, pod length, shoot dry weight, taproot lengths, root dry weight, biological yield, 100-seeds weight, harvest index, yield, oil and protein content (Table 5). Whereas some of the traits had showed significant ($P \leq 0.05$) differences for leaf width, number of primary branches and number of nodes per plant, and except pod width and number of seed per pod had showed non-significant differences. (Aditya *et al.*, 2011; Asmamaw *et al.*, 2020; Masreshaw *et al.*, 2022; Yechalew, 2018) studies results were found significant to highly significant difference values for various soybean genotypes.

The presence of significant variations among accessions indicated the existence of considerable genetic variation in the experimental materials.

Table 5: Mean square from analysis of variance for 22 Agro-morphological traits of 64 Soybean accessions evaluated in Benin during the 2022/23 main cropping season

Traits	Mean squares				LSD (5%)	CV (%)	P value
	Rep. (df=1)	Blocks within Rep. (Adj.) (df=14)	Accessions (Unadj.) (df=63)	Intra-block Error (df=49)			
Days to 50% flowering (days)	4.883	5.231	36.320**	3.110	3.54	3.3	<0.01
Days to maturity (days)	0.281	73.710	99.681**	20.771	9.17	3.5	<0.01
Plant height (cm)	253.688	284.172	183.332**	86.854	18.75	20.4	<0.01
Leaf Length (cm)	0.077	3.320	3.055**	1.366	2.35	12.9	<0.01
Leaf Width (cm)	6.377	1.181	0.888*	0.485	1.40	15.3	<0.05
Number of primary branches (count)	12.998	3.776	2.477*	1.415	2.39	30.2	<0.05
Number of nodes per plant (count)	17.843	15.776	7.669*	4.537	4.29	22.7	<0.05
Chlorophyll contents ($\mu\text{mol m}^{-2}$)	917.69	2721.04	2125.78**	547.20	47.06	5.8	<0.01
Number of pod per plant (count)	369.27	191.47	1134.88**	127.76	22.74	21.4	<0.01
Pod length (mm)	1.672	9.559	16.194**	8.378	5.82	8.3	<0.01
Pod width (mm)	2.109	0.627	0.951 ^{ns}	0.740	1.73	13.9	0.182
Number of seed per pod (count)	0.001	0.050	0.0285 ^{ns}	0.023	0.30	7.3	0.206
Number of seed per plant (count)	1620.2	1085.4	4713.1**	627.5	50.40	23	<0.01
Shoot dry weight (g)	24.186	32.125	76.036**	9.319	6.14	24.4	<0.01
Taproot lengths (cm)	18.415	124.528	77.030**	39.269	12.61	27.4	<0.01
Root dry weight (g)	0.223	0.912	4.295**	0.512	1.44	23.6	<0.01
Biological Yield (g)	625.08	476.02	554.51**	177.56	26.81	32.2	<0.01
100-seeds weight (g)	23.71	4.866	9.593**	3.266	3.64	11.6	<0.01
Harvest index (%)	8.031	112.287	224.321**	102.155	20.34	24.7	<0.01
Yield (Kg)	1.431	0.317	1.108**	0.185	0.86	26.1	<0.01
Protein (%)	4.068	6.283	36.680**	3.927	3.99	5.9	<0.01
Oil (%)	0.228	0.868	23.082**	2.664	3.28	9.4	<0.01

*significant at $P \leq 0.05$, ** highly significant at $P \leq 0.01$ level of significant and ns = nonsignificant. Rep= replication, Adj. = adjusted, Unadj. = unadjusted, CV (%) = coefficient of variation in percent and LSD (5%) = least significant difference at $P < 0.05$. Number in parenthesis in each source of variation, df = represents degree of freedom.

4.2.2. Performances of soybean accessions based on agro-morphology and quality traits

Based on the means of 64 soybean accessions the wide ranges between the minimum and maximum mean values were observed for each trait (appendix table 1 and 2). Days to 50% flowering of the accession SO-TAN-09 showed the earliest flowering (41.77 days); while SO-NDA-81 showed the latest flowering (67.79 days) with the mean value of (53.60 days). Days to maturity ranged from 113.19 to 145.48 days for the accessions SO-BOU-56 and SO-NDA-81 with mean value of 129.53 days, respectively. Similar result has been reported by (Aditya *et al.*, 2011; Yechalew *et al.*, 2019). Masreshaw *et al.* (2022) reported that days to flowering ranged from (26.75 to 66.75), and days to maturity ranged from (115.50 to 130.75). The differences in days to maturity and flowering was indicates that the genotypes early flower do not necessarily mature early because some genotypes take more time for reproductive stage while other genotypes need longer time for days to maturity and take less time for the vegetative stage.

The maximum plant height was recorded from the accession SO-NDA-66 (65.79cm), while the minimum from SO-OUA-82 (27.41cm) with a mean value of 45.70cm. Masreshaw *et al.* (2021) reported a range of 28.56-74.05cm plant height in various soybean genotypes. Wide variation in plant height of different germplasm might be due to the genetic characters of the different germplasm (Govindarao, 2010). The maximum number of nodes was observed for the accession SO-COB-27 (14.73), while the minimum for SO-OUE-21 (4.31) with the mean value of 9.37. Number of branches per plant ranged from 1.58 for SO-GLA-49 to 7.01 for SO-COB-27 accessions. Similar result has been reported by (Yechalew, 2018) for number of nodes from 7.9 to 12.9, number of branches 1.07 to 3.91, leaf width 2.94 to 8.8cm and leaf length 5.3 to 12.65cm, respectively. Number of branch ranged from 2.90 to 5.30 reported by (Masreshaw *et al.*, 2022).

The highest number of pod per plant was recorded on the accession SO-NDA-81 (129.66), while the lowest on SO-OUE-39 (10.72) with mean value of 52.75. Similar results were reported by (Sandar, 2012) that number pods per plant ranged from (1 to 182); (Masreshaw *et al.*, 2021) reported the range from (24.3 to 42.27); Malik *et al.* (2011) observed the range in number of pods per plant (26 to 130), and indicated a high level of diversity among the accessions for these traits. Seeds per plant ranged from 21.09 for accession SO-NDA-66 to 258.89 for SO-NDA-81 with mean value of 108.68. Masreshaw *et al.* (2021) reported number

of seed per plant 22.89-66.04 in soybean. Pod length ranged from 28.6mm for accession SO-DAS-01 to 41.53mm for SO-BOU-46 with mean value of 34.99mm.

The range of taproot length was from 10.72cm for the accession SO-OUA-82 to 36.79cm for SO-NDA-81 with mean value of 22.88cm. Root dry weight per plant ranged from 0.69g for accession SO-NIK-87 to 7.66g for SO-DJI-114 with mean value of 3.03g; and shoot dry weight was ranged from 1.5g for accession SO-OUE-21 to 27.58g for SO-NIK-84 with mean value of 12.50g. Similar results reported by (Yechalew, 2018) for taproot length and root dry weight.

Biomass per plant ranged from 11.3g for accession SO-TAN-09 to 81.99g for SO-NIK-84 with mean value of 41.35g. Hundred-seed weight ranged from 10.73g for accession SO-DAS-01 to 22.26g for SO-BAN-102 with mean value of 15.55g; and harvest index ranged from 13.33% for accession SO-OUE-39 to 70.25% for SO-OUA-94 with mean value of 40.91%. (Sandar, 2012) reported harvest index ranged from (4.8 to 90.8%); Malik *et al.* (2011) observed that 100-seed weight ranged (4.2 to 21.5 g); Masreshaw *et al.* (2022) reported hundred seed weight ranged (8.78-17.53gm); and biomass per plant ranged from 12.9 to 31.4g.

Govindarao (2010) were grouped yield of soybean genotypes into three categories as low yielding (< 1,100 kg/ha), medium yielding (1,100-1,400 kg/ha), and high yielding (>1,400 kg/ha). The accession, SO-NDA-81 produced the highest yield (3.92ton/ha) followed by SO-TAN-19, SO-OUA-94, and SO-GLA-50 that produced high yield (3.22ton/ha), (2.97ton/ha), and (2.92ton/ha), respectively; while the accession SO-OUE-39 produced the lowest yield (0.33ton/ha). Similar results for yield ranged from (4,944.5 to 84.9 kg/ha) were reported by (Sandar, 2012) in soybean.

In the present study, the range for oil content was from 12.50% in accession SO-DJI-110 to 24.49% in SO-GLA-50 with a mean value of 17.43%. SO-OUA-94, SO-BAN-111, SO-KAN-126, SO-NDA-81 and SO-DAS-05 are the accessions that had shown 20 % oil content. Similar variability for oil content was also reported by Huskey *et al.* (1990) and Yechalew (2018). The soybean germplasm collection from Department of Agriculture of United States of America, reported that oil content ranged from 8.1%- 27.9% (Wilson, 2004).

The highest protein content was recorded in SO-DAS-04 (42.21%) and the lowest in SO-GLA-49 (27.32%) with mean protein content of 33.58%. Soybean accessions that produced 40% protein contents were SO-TAN-10, SO-BAN-102 and SO-DJO-70. The protein content was similar to the reports from other authors *i.e.*, Huskey *et al.* (1990) who reported the range from 27.31 to 41.35%.

4.3. Estimates of genetic variability components

4.3.1. Phenotypic and genotypic coefficient of variation

This study revealed that phenotypic variance (σ^2_p) and phenotypic coefficient variation (PCV) were generally higher than that of their corresponding genotypic variance (σ^2_g) and genotypic coefficient of variation (GCV), respectively, for all the traits evaluated, and indicating the expression of these characters was influenced by environment (Table 6). The (PCV) value ranged from 5.99 to 52.28 and genotypic coefficient of variation (GCV) value ranged from 4.85 to 46.22, which showed a wide range of estimates for all the characters evaluated.

According to Deshmukh *et al.* (1986), the GCV and PCV values were categorized as low (<10%), moderate (10 to 20%) and high (>20%). Based on this category, high PCV and GCV values were found for number of pod per plant, number of seed per plant, shoot dry weight, root dry weight, biological yield and seed yield, and the difference between them was small. The result showed that the variability among genotypes for these characters was mainly due to genetic effects than that of environment. The extent of the environmental influence on any character is indicated by the magnitude of the differences between PCV and GCV. The lesser difference between GCV and PCV which implies less influence of environmental factors for the phenotypic expression of traits and selection on the basis of phenotype expression might leads to improvement.

High PCV and moderate GCV values were found for plant height, number of branches, number of nodes, root length, and harvest index, and the difference was large. This suggests that these characters were influenced by the environment, and the genetic factor has less influence on these characters. Large differences reflect high environmental influence, while small differences reveal high genetic influence (Aditya *et al.*, 2011). Therefore, the selection of such characters needs to be done very carefully. The current finding is in agreement with (Masreshaw *et al.*, 2021) and (Yechalew, 2018) who reported high GCV and PCV for

number of pod, number of seed per plant and plant height, number of branches and biological yield. Medium PCV and GCV values were recorded for leaf length, 100-seeds weight and protein contents; and high PCV and moderate GCV values were recorded for oil contents.

Low PCV and GCV values were computed for phenology traits (days to 50% flowering and maturity), and chlorophyll contents. Low estimate of GCV coupled with moderate PCV for leaf width and pod length. Low GCV and PCV indicating the existence of limited variability in the genotypes evaluated for the traits showing low genetic variability (Singh *et al.*, 2017). Genetic parameters like PCV and GCV determines the effectiveness of selection for a particular trait.

According to (Burton and DeVane, 1953) suggested that the estimates of genetic coefficient of variance together with high heritability and genetic advance would give the best picture of the amount of advance to be expected from selection. As GCV provides information on the genetic variability present in quantitative characters in the base population, but it is not possible to determine the amount of variation that was heritable, only from the genotypic coefficient of variance.

4.3.2. Broad sense heritability

Estimates of broad sense heritability ranged from 25.67% for number of nodes per plant to 84.23% for days to 50% flowering (Table 6). Robinson *et al.* (1949) generally classified the values of heritability estimates as low (0- 30%), moderate (30-60%) and high (>60%). Based on this classification, high heritability values were recorded for days to 50% flowering (84.23%), days to maturity (65.51%), number of pod per plant (79.76%), number of seed per plant (76.50%), shoot dry weight (78.16%), root dry weight (78.71%), seed yield (71.40%), protein content (80.66%) and oil content (79.31%). Moderate value of heritability estimates were recorded for plant height, leaf length, chlorophyll contents, pod length, root length, biological yield, 100-seeds weight and harvest index. Similar results were reported by (Aditya *et al.*, 2011). Low value of heritability estimates were observed for leaf width, number of branches and number of nodes.

For a trait with high heritability indicating the predominance of genotypic component of the inheritance of the traits creates an opportunity for breeders that result in improvement for these characters, selection for such characters could be fairly easy on the basis of phenotypic performance. This is because there would be a close correspondence between the genotype

and the phenotype due to the relative small contribution of the environment to the phenotype. For characters with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of environment.

4.3.3. Genetic advance and genetic advance as percent of mean

According to Johnson *et al.* (1955) suggested that, heritability alone does not provide information on the genetic progress for an effective selection of the best individual; but heritability in coupled with genetic advance would give a more reliable index of selection, and categorize the range of genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high ($\geq 20\%$). Based on this category the highest genetic advance as percent of mean (GAM) values were observed for number of pod per plant, number of seed per plant, shoot dry weight, root length, root dry weight, biological yield, harvest index, seed yield and biochemical contents (oil and protein).

High heritability estimates accompanied by the high genetic advance as percent of mean is usually more helpful in predicting increase under selection than heritability estimates alone (Johnson *et al.*, 1955). In this study, high heritability is coupled with high genetic advance as percent of mean was observed for number of pod per plant, number of seed per plant, shoot dry weight, root dry weight, seed yield and biochemical contents (oil and protein), and indicates that better genetic gain could be achieved through selection. Similar results were reported by (Reni *et al.*, 2013; Yechalew *et al.*, 2019)). This showed that the heritability of these characters is due to additive gene effects and selection might be effective for these characters, and the trait can be improved through direct selection more easily than other traits.

High heritability with a moderate GAM was observed for days to 50% flowering; and moderate heritability with high GAM was observed for root length, biomass per plant and harvest index. Medium heritability with medium GAM was obtained for plant height, leaf length, chlorophyll contents, and hundred seed weight. Medium heritability with low GAM was exhibited by pod length; and high heritability and low GAM values were obtained for days to maturity. The present findings are in-agreement with the results reported by (Ramteke *et al.*, 2010 and Aditya *et al.*, 2011). The combined high GCV, high heritability and high GAM were recorded for number of pod per plant, number of seed per plant, shoot dry weight, root dry weight and seed yield. This trait can be improved through direct selection more easily than other traits.

Table 6: Means, ranges, phenotypic and genetic variability, heritability, genetic advance and genetic gains estimates for soybean traits in 2022/2023 main cropping season

Traits	Mean	Min	Max	σ^2_g	σ^2_p	PCV%	GCV%	H ² (%)	GA	GAM (%)
Days to 50% flowering (days)	53.60	41.77	67.79	16.60	19.71	8.28	7.60	84.23	7.72	14.39
Days to maturity (days)	129.53	113.19	145.48	39.45	60.23	5.99	4.85	65.51	10.49	8.10
Plant height (cm)	45.70	27.41	65.79	48.24	135.09	25.43	15.19	35.71	8.56	18.73
Leaf Length (cm)	9.04	6.33	12.23	0.84	2.21	16.45	10.17	38.19	1.17	12.96
Leaf Width (cm)	4.55	2.99	6.82	0.20	0.69	18.19	9.86	29.40	0.50	11.03
Number of branches primry (count)	3.94	1.58	7.01	0.53	1.95	35.44	18.51	27.28	0.78	19.95
Number of nodes per plant (count)	9.37	4.31	14.73	1.57	6.10	26.36	13.36	25.67	1.31	13.96
Chlorophyll contents ($\mu\text{mol m}^{-2}$)	400.24	342.15	474.36	789.29	1336.49	9.13	7.02	59.06	44.54	11.13
Number of pod per plant (count)	52.75	10.72	129.66	503.56	631.32	47.63	42.54	79.76	41.34	78.38
Pod length (mm)	34.99	28.6	41.53	3.91	12.28	10.02	5.65	31.81	2.30	6.57
Number of seed per plant (count)	108.68	21.09	258.89	2042.8	2670.3	47.54	41.58	76.50	81.55	75.04
Shoot dry weight (g)	12.50	1.5	27.58	33.36	42.68	52.28	46.22	78.16	10.53	84.30
Taproot length (cm)	22.88	10.72	36.79	18.88	58.15	33.32	18.98	32.47	5.11	22.32
Root dry weight (g)	3.03	0.69	7.66	1.89	2.40	51.08	45.32	78.71	2.52	82.95
Biological Yield (g)	41.35	11.3	81.99	188.47	366.04	46.26	33.19	51.49	20.32	49.15
100-seeds weight (g)	15.55	10.73	22.26	3.16	6.43	16.31	11.44	49.20	2.57	16.55
Harvest index (%)	40.91	13.33	70.25	61.08	163.24	31.23	19.11	37.42	9.86	24.11
Yield (Kg)	1.64	0.33	3.92	0.46	0.65	48.86	41.28	71.40	1.18	71.97
Protein (%)	33.58	27.32	42.21	16.38	20.30	13.42	12.05	80.66	7.50	22.33
Oil (%)	17.43	12.5	24.49	10.21	12.87	20.58	18.33	79.31	5.87	33.67

σ^2_g and σ^2_p = genotypic and phenotypic variance, respectively, GCV (%) and PCV (%), genotypic and phenotypic coefficient of variation, respectively.

H² =heritability in broad sense, GA and GAM (%) =genetic advance and genetic advance as percent of mean, respectively.

4.4. Correlation Analysis

The genotypic correlation coefficients were higher than the phenotypic correlation coefficients indicating that the observed relationships among the various traits were due to genetic effects. This suggests that the genotypes have a stronger genetic relationship with the traits in enquiry than environmental factors. Phenotypic correlation (r_p) measures the extent to which the two observed characters are linearly related, while genotypic correlation (r_g) measures the extent to which degree the same genes or closely linked genes cause co-variation (simultaneous variations) in two different characters (Singh and Chaudhary, 1977). Estimation of genotypic and phenotypic correlation coefficients had exhibited significant at ($P \leq 0.05$) to highly significant at ($P \leq 0.01$) correlation for most of studied traits within the characters and with yield is presented in table 7.

4.4.1. Phenotypic and Genotypic correlations among yield related trait

Days to 50% flowering was correlated positively and significant ($P \leq 0.05$) with days to maturity, number of pod per plant and number of seed per plant; while negatively and significantly correlated with chlorophyll content and 100-seeds weight at both phenotypic and genetic levels. Days to 50% flowering showed negative and significant associations with leaf width, number of primary branches and number of nodes at genotypic levels. Similar results were reported in which days to 50% flowering correlated positively and significantly with days to maturity and number of pod per plant (Masreshaw *et al.*, 2022; Yechalew, 2018).

Days to maturity was correlated positively and significant ($P \leq 0.05$) with plant height, leaf length, leaf width, number of nodes, root length, shoot dry weight, root dry weight, number of pod per plant, number of seed per plant, biological yield and oil content at both phenotypic and genotypic levels. Similar results were reported by Asmamaw *et al.* (2020) and Sandar (2012), who indicated that a positive correlation between traits allow the selection of genotypes simultaneously for the correlated traits.

Plant height showed positive and significant correlation ($P \leq 0.05$) with leaf length, number of primary branches, number of nodes, root length, shoot dry weight, root dry weight, number of pod per plant, number of seed per plant, 100-seeds weight, biological yield and oil content at both phenotypic and genotypic levels. Similar results were reported by Painkra *et al.* (2018)

that plant height showed a highly significant and positive association with pod length, number of nodes and number of pods per plant.

Number of primary branches had significant and positive correlation with number of nodes, root length, shoot dry weight, and root dry weight, number of pod per plant, pod length, number of seed per plant, biological yield and oil content at both levels, while it was a significant and negative correlated with protein content and chlorophyll content at genotypic level. Root length had significant and positive correlation with shoot dry weight, root dry weight, number of pod per plant, number of seed per plant, biological yield and oil content at both phenotypic and genotypic levels. Shoot dry weight had significant and positive correlation with root dry weight, number of pod per plant, pod length, number of seed per plant, 100-seeds weight, biological yield and oil content. Root dry weight was significant and positive correlation with number of pod per plant, number of seed per plant, 100-seeds weight, biological yield and oil content at both phenotypic and genotypic levels. Similar results were reported by (Yechalew, 2018).

Number of pod per plant had significant and positive correlation with pod length, number of seed per plant, biological yield, harvest index and oil content at both phenotypic and genotypic levels. Pod length was significant and positive correlation with number of seed per plant, 100-seeds weight, biological yield, harvest index and protein content at both phenotypic and genotypic levels. Number of seed per plant was significant and positive correlation with biological yield, harvest index and oil content at both phenotypic and genotypic levels. Biological yield was significant and positive correlation with oil content at both phenotypic and genotypic levels; but it was significant positive correlation with harvest index at genotypic levels. There was non-significant negative correlation between protein and oil content at both phenotypic and genotypic levels.

Similar results reported by Aditya *et al.* (2011); Asmamaw *et al.* (2020), and Mahbub *et al.* (2016) that significant and positive association among yield related traits and that would indicate an increase in the value of one of these traits would increase the value of another trait. Generally, positive and significant associations of pairs of characters at phenotypic and genotypic level justify the possibility of simultaneous response to selection. But, negative correlations make difficult the simultaneous improvement of those traits.

4.4.2. Phenotypic and Genotypic correlation of seed yield with yield related traits

Genotypic correlation revealed that seed yield had positive and highly significant ($P \leq 0.01$) association with number of pod per plant ($r=0.97^{**}$), number of seed per plant ($r=0.96^{**}$), biological yield ($r=0.87^{**}$), oil content ($r=0.81^{**}$), harvest index ($r=0.79^{**}$), number of nodes ($r=0.68^{**}$), leaf width ($r=0.66^{**}$), root length ($r=0.63^{**}$), number of primary branches ($r=0.59^{**}$), pod length ($r=0.56^{**}$), root dry weight ($r=0.55^{**}$), leaf length ($r=0.52^{**}$), plant height ($r=0.46^{**}$), shoot dry weight ($r=0.39^{**}$) and days to maturity ($r=0.39^{**}$) (Table 7). This result is in agreement with Aditya *et al.* (2011) and Asmamaw *et al.* (2020) reported that days to flowering showed non-significant genotypic correlation with grain yield. In agreement to this result, positive and significant association of days to maturity and number of primary branches with seed yield has been reported by Iqbal *et al.* (2010); Aditya *et al.* (2011). The result indicates that extended days to maturity resulted in increased yielding potential the crop through increasing the biomass with plant height. In general, genotypes that displayed longer time to mature gave greater grain yield ha^{-1} than genotypes that took shorter time to mature. The difference could be attributed to the effective translocation and utilization of photosynthetic assimilates in late maturing genotypes having long grain filling period.

Phenotypic correlation showed that seed yield had positive and highly significant ($P \leq 0.01$) association with most of studied traits that are number of seed per plant ($r=0.95^{**}$), number of pod per plant ($r=0.94^{**}$), biomass ($r=0.79^{**}$), oil content ($r=0.57^{**}$), number of primary branches ($r=0.54^{**}$), plant height ($r=0.51^{**}$), root dry weight ($r=0.52^{**}$), leaf length ($r=0.51^{**}$), harvest index ($r=0.41^{**}$), number of nodes ($r=0.47^{**}$), leaf width ($r=0.49^{**}$), shoot dry weight ($r=0.48^{**}$), root length ($r=0.44^{**}$), pod length ($r=0.38^{**}$), days to maturity ($r=0.37^{**}$), 100-seeds weight ($r=0.34^{**}$), chlorophyll content ($r=0.23^{**}$) and day to flowering ($r=0.19^{*}$) (Table 7). The present investigation also in-agreement with the results of Sunil *et al.* (2011) reported that plant height had positive and significant association with yield.

A positive correlation between plant height and seed yield, indicating that increase in plant height will increase the soybean seed yield. This is due to the reason that soybean flowers and pods appear along the stem of the plant, therefore the higher the appearance of a plant, the more likely it is to produce the pods. Similar result reported by (Keep, 2013) that chlorophyll content has been found to have a significant positive correlation with seed yield. Jain *et al.* (2015); Aditya *et al.* (2011) and Mahbub *et al.* (2016) reported that number of pods and biomass had showed positive and significant associations with seed yield at both level, and

suggested increase in biomass might be attributed to increased light interception and assimilates production; which latter on translocate to the sink in this case to the seed.

Oil content had showed significant positive correlation with seed yield at both phenotypic and genotypic levels; but seed yield was negative and non-significant correlated with protein content at genotypic levels. Therefore, selection for higher oil could result in lower protein content of the seed. The selection for these traits should depend on the value of the genotype either for protein or oil content; hence increase or decrease of both traits simultaneously would be difficult. Similar results were reported by Thapa *et al.* (2019) that there was non-significant negative correlation between protein content and grain yield. A positive and significant correlation between desirable traits is favorable, because it helps in simultaneous improvement of both the characters. On the other hand, negative correlation will hinder the simultaneous expression of both characters with high values.

Table 7: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient of 20 yield and yield related traits on 64 soybean accessions

Traits	50% DF	90% DM	PH	LL	LW	NPB	ND	CC	RL	SDW	RDW
50% DF		0.73**	-0.24	-0.01	-0.31*	-0.48**	-0.67**	-0.55**	-0.05	-0.06	0.02
90%DM	0.60**		0.43**	0.42**	0.29*	0.15	0.39**	-0.62**	0.46**	0.38**	0.42**
PH	-0.07	0.42**		0.52**	0.15	0.81**	0.96**	-0.90**	0.29*	0.76**	0.89**
LL	0.02	0.42**	0.77**		0.28*	0.25*	0.35**	-0.84**	0.71**	0.57**	0.90**
LW	-0.11	0.28**	0.66**	0.71**		-0.17	0.22	-0.43**	0.24	0.51**	0.71**
NPB	-0.16	0.21*	0.82**	0.67**	0.56**		0.97**	-0.92**	0.28*	0.69**	0.98**
ND	-0.14	0.27**	0.83**	0.72**	0.57**	0.87**		-0.94**	0.12	0.93**	0.87**
CC	-0.25**	-0.09	0.18*	0.21*	0.36**	0.22*	0.23*		-0.76**	-0.17	-0.15
RL	0.02	0.42**	0.60**	0.57**	0.39**	0.46**	0.53**	0.14		0.62**	0.89**
SDW	-0.02	0.38**	0.61**	0.53**	0.45**	0.52**	0.54**	0.16	0.52**		0.62**
RDW	0.004	0.36**	0.62**	0.66**	0.49**	0.51**	0.57**	0.09	0.53**	0.63**	
NPP	0.30**	0.37**	0.43**	0.44**	0.33**	0.47**	0.39**	0.09	0.39**	0.35**	0.43**
PL	-0.08	0.06	0.23**	0.21*	0.31**	0.21*	0.19*	0.23**	0.14	0.21*	0.17
NSP	0.27**	0.35**	0.44**	0.45**	0.35**	0.47**	0.42**	0.14	0.41**	0.37**	0.44**
HSW	-0.21*	0.11	0.39**	0.33**	0.55**	0.31**	0.31**	0.33**	0.27**	0.44**	0.34**
BY	0.15	0.46**	0.67**	0.69**	0.54**	0.66**	0.63**	0.20*	0.54**	0.74**	0.67**
HI	0.07	-0.09	-0.17*	-0.19*	-0.05	-0.11	-0.18*	0.13	-0.06	-0.28**	-0.18*
PC	-0.13	-0.1	-0.003	-0.07	0.12	-0.07	-0.12	0.13	-0.11	0.18 *	-0.02
OC	0.15	0.30 **	0.20 *	0.27 **	0.25 **	0.20 *	0.17	0.08	0.18 *	0.29 **	0.33 **
YD	0.19*	0.37**	0.51**	0.51**	0.49**	0.54**	0.47**	0.23**	0.44**	0.48**	0.52**

Table 7 (continued)

Traits	NPP	PL	NSP	HSW	BY	HI	PC	OC	YD
50% DF	0.34**	-0.11	0.31*	-0.39**	0.2	0.01	-0.16	0.21	0.22
90%DM	0.43**	0.05	0.41**	-0.02	0.61**	-0.22	-0.12	0.48 **	0.39**
PH	0.49**	0.22	0.48**	0.31*	0.66**	-0.02	-0.03	0.62 **	0.46**
LL	0.54**	0.36**	0.55**	0.24	0.71**	0.11	-0.09	0.59 **	0.52**
LW	0.45**	0.79**	0.49**	0.87**	0.58**	0.41**	0.40 **	0.72 **	0.66**
NPB	0.64**	0.41**	0.69**	0.22	0.66**	0.32**	-0.28 *	0.83 **	0.59**
ND	0.71**	0.24	0.73**	0.55**	0.93**	-0.04	-0.69 **	0.81 **	0.68**
CC	-0.06	0.60**	0.02	0.44**	-0.38**	0.84**	0.25 *	0.14	0.11
RL	0.63**	-0.07	0.62**	0.12	0.81**	0.14	-0.36 **	0.71 **	0.63**
SDW	0.29*	0.30*	0.29*	0.46**	0.78**	-0.26*	0.24	0.46 **	0.39**
RDW	0.46**	0.32*	0.48**	0.35**	0.82**	-0.06	0.002	0.45 **	0.55**
NPP		0.34**	0.90**	-0.098	0.81**	0.82**	-0.18	0.76 **	0.97**
PL	0.24**		0.39**	0.86**	0.52**	0.44**	0.67 **	0.32 **	0.56**
NSP	0.98**	0.31**		-0.079	0.83**	0.81**	-0.18	0.76 **	0.96**
HSW	0.03	0.53**	0.08		0.36**	-0.15	0.67 **	0.15	0.16
BY	0.73**	0.29**	0.73**	0.33**		0.47**	0.06	0.84 **	0.87**
HI	0.39**	0.19*	0.41**	0.12	-0.18*		-0.13	0.41 **	0.79**
PC	-0.16	0.32 **	-0.13	0.46 **	-0.03	0.01		-0.13	-0.001
OC	0.57 **	0.16	0.56 **	0.09	0.41 **	0.25 **	-0.11		0.81**
YD	0.94**	0.38**	0.95**	0.34**	0.79**	0.41**	0.003	0.57 **	

Where; *significant at ($P \leq 0.05$), **highly significant at ($P \leq 0.01$) and ns = nonsignificant. DF = days to 50% flowering (days), DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), CC = chlorophyll content ($\mu\text{mol m}^{-2}$), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), HSW = hundred seed weight (g), YD = yield per ha (Kg), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%) and OC=oil content (%).

4.5. Path coefficient analysis

4.5.1. Genotypic path coefficient analysis

The genotypic direct and indirect effects of traits on grain yield are presented in Table 8, and majority of the traits exerted positive direct effect on grain yield. Lenka and Mishra (1973) rated the direct and indirect effects into negligible (0.00-0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-1.00) and very high (>1.00).

According to this rating, number of pods per plant (0.567), biological yield (0.565) and harvest index (0.34) had showed positive and high direct effect on grain yield and indicates the simultaneous selection of the traits may improve genetic gain on grain yield in soybean breeding. Whereas protein content (0.211) exerted positive moderate direct effects, and oil content (0.145) and root dry weight (0.113) had showed low positive direct effect. Number of nodes (0.018), day to maturity (0.028), leaf length (0.04) and leaf width (0.019) had negligible positive direct effects on grain yield. These results of positive direct effect on seed yield are in agreement with the reports of (Masreshaw *et al.*, 2022).

However, number of seed per plant (-0.313) had showed high negative direct effect on seed yield; while pod length (-0.203) and plant height (-0.208) had showed moderate negative direct effect on seed yield. Root length (-0.169) and shoot dry weight (-0.111) had showed low negative direct effect, and number of primary branch per plant (-0.001) had exerted negative negligible direct effect on seed yield. If the trait has positive correlation and the direct effect of the trait is negative or negligible, the positive correlation of the trait is because of the indirect effects through other traits. In such situation, the indirect causal factors/traits are to be considered simultaneously for selection (Singh and Chaudhary, 1977). Hence, indirect selection for these traits should be effective for seed yield improvement.

The maximum positive direct effect was observed for number of pods per plant (0.567) on seed yield, and it was assisted by other traits of indirect effects. In addition, pods per plant exerted high positive indirect effect on seed yield via number of seed per plant, biological yield, harvest index, oil content, root length, number of nodes and number of primary branch per plant. Whereas, root dry weight, plant height, day to maturity, leaf length and leaf width had exerted moderate positive indirect effect on seed yield. Pods per plant exerted low positive indirect effect on seed yield via shoot dry weight and pod length. These results of

positive direct effect on seed yield are in agreement with the reports of (Masreshaw *et al.*, 2022; Asmamaw *et al.*, 2020).

The second maximum positive direct effect was observed for biological yield (0.565) on seed yield. Biological yield exerted high positive indirect effect on seed yield via number of seed per plant, number of pod, biological yield, harvest index, oil content, root length, number of nodes and primary branch per plant, plant height and oil content, while biological yield had exerted low positive indirect effect on seed yield via protein content.

The third maximum positive direct effect was observed on harvest index (0.34) on seed yield. Harvest index had exerted moderate positive indirect effect on seed yield via number of pods per plant and number of seed per plant, and also had exerted low positive indirect effect on seed yield via leaf width, number of primary branch, biological yield, pod length and oil content.

Positive direct effect of most traits on seed yield indicated true relationship between traits and should be given prior attention in practicing selection aimed at the improvement of seed yield, since the major of them influence on grain yield. Therefore, from the result of this study the high consideration should be given for number of pods per plant, biological yield and harvest index had indicating the importance of these traits in improving yield of the crop through selection.

The residual effect in the present genotypic path study was 0.287, indicating that 71.3% of the variability in the grain yield was contributed by traits considered in the path analysis. The remaining 28.7% is explained by other traits not considered in this study. The residual effect was small which indicates that the characters under consideration were appropriate for the study of yield determination in soybean. The residual effect in path analysis determines how best the component (independent) variables account for the variability of the dependent variable, yield (Singh and Chaudhary, 1977).

Table 8: Genotypic direct effect path (bold) and indirect effect (off diagonal) of various characters on seed yield

Traits	DM	PH	LL	LW	NPB	ND	RL	SDW	RDW
DM	<u>0.028</u>	-0.089	0.017	0.006	0.000	0.031	-0.077	-0.042	0.047
PH	0.012	<u>-0.208</u>	0.021	0.003	-0.001	0.078	-0.05	-0.084	0.101
LL	0.011	-0.109	<u>0.04</u>	0.005	0.000	0.028	-0.12	-0.064	0.102
LW	0.008	-0.031	0.011	<u>0.019</u>	0.000	0.018	-0.041	-0.057	0.079
NPB	0.004	-0.167	0.01	-0.003	<u>-0.001</u>	0.104	-0.048	-0.077	0.111
ND	0.027	-0.201	0.014	0.004	-0.001	<u>0.081</u>	-0.020	-0.103	0.111
RL	0.013	-0.061	0.028	0.005	0.000	0.009	<u>-0.169</u>	-0.069	0.1
SDW	0.011	-0.158	0.023	0.01	-0.001	0.098	-0.105	<u>-0.111</u>	0.069
RDW	0.011	-0.186	0.036	0.013	-0.001	0.015	-0.151	-0.068	<u>0.113</u>
NPP	0.012	-0.102	0.021	0.009	-0.001	0.057	-0.107	-0.032	0.051
PL	0.001	-0.046	0.014	0.015	-0.001	0.019	0.012	-0.034	0.036
NSP	0.011	-0.101	0.022	0.009	-0.001	0.058	-0.106	-0.033	0.054
BY	0.017	-0.138	0.028	0.017	-0.001	0.08	-0.137	-0.086	0.097
HI	-0.006	0.005	0.004	0.008	0.000	-0.003	-0.024	0.028	-0.007
PC	-0.003	0.006	-0.004	0.008	0.000	-0.056	0.061	-0.027	0.000
OC	0.013	-0.13	0.024	0.014	-0.001	0.081	-0.12	-0.05	0.051

Where; DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%) and OC=oil content (%), rg = Genotypic correlation coefficient.

Table 8 (continued)

Traits	NPP	PL	NSP	BY	HI	PC	OC	rg
DM	0.227	-0.01	-0.129	0.417	-0.073	-0.026	0.069	0.396
PH	0.259	-0.045	-0.152	0.451	-0.008	-0.007	0.091	0.461
LL	0.285	-0.074	-0.172	0.48	0.036	-0.019	0.086	0.515
LW	0.24	-0.161	-0.155	0.398	0.139	0.085	0.105	0.657
NPB	0.337	-0.083	-0.216	0.45	0.109	-0.059	0.121	0.591
ND	0.497	-0.049	-0.216	0.564	-0.044	-0.147	0.144	0.661
RL	0.332	0.015	-0.195	0.55	0.049	-0.076	0.103	0.634
SDW	0.154	-0.061	-0.092	0.531	-0.087	0.051	0.066	0.398
RDW	0.242	-0.064	-0.149	0.559	-0.021	0.00	0.066	0.55
NPP	<u>0.567</u>	-0.068	-0.303	0.532	0.278	-0.057	0.111	0.968
PL	0.179	<u>-0.203</u>	-0.122	0.359	0.151	0.141	0.047	0.568
NSP	0.539	-0.079	<u>-0.313</u>	0.559	0.274	-0.038	0.111	0.966
BY	0.449	-0.101	-0.26	<u>0.565</u>	0.191	0.022	0.122	0.865
HI	0.433	-0.09	-0.252	0.322	<u>0.34</u>	-0.028	0.059	0.789
PC	-0.093	-0.135	0.056	0.039	-0.046	<u>0.211</u>	-0.018	-0.001
OC	0.402	-0.065	-0.239	0.563	0.148	-0.027	<u>0.145</u>	0.809

Where; DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%) and OC=oil content (%), rg = Genotypic correlation coefficient.

4.5.2. Phenotypic direct and indirect effect of various characters on seed yield

The results of path analysis at phenotypic level are presented in Table 9. According to the rating reported by Lenka and Mishra (1973), number of pods per plant (0.526) had high positive direct effect on seed yield followed by biological yield (0.236) which exerted positive moderate direct effect on seed yield. Hundred seeds weight (0.197), number of seed per plant (0.181) and harvest index (0.134) had low direct effect on seed yield. Leaf width, number of primary branches, number of nodes, chlorophyll content, root length, root dry weight, oil and protein content had positive and negligible direct effects on seed yield. On the other hand, days to 50% flowering, day to maturity, leaf length, plant height, shoot dry weight and pod length had exerted negative and negligible direct effects on seed yield. These results of positive direct effect on seed yield are in agreement with the result reported by (Masreshaw *et al.*, 2022; Asmamaw *et al.*, 2020).

In addition, pods per plant exerted high positive indirect effect on seed yield via number of seed per plant, biological yield and oil content. It had also exerted moderate and positive indirect effect on seed yield through plant height, leaf length, primary branches, and number of nodes, root length, root dry weight and harvest index; and had also exerted low positive indirect effect on seed yield through days to 50% flowering and maturity, leaf width, shoot dry weight and pod length.

High consideration should be given for the traits with highest positive direct effect on seed yield. In this study, the results of phenotypic path coefficient analysis showed that number of pods per plant followed by biological yield and number of seed per plant could be used as selection criteria for high grain yield in soybean accessions. Besides positive and highly significant correlation of these traits with seed yield, the traits had high, moderate and low positive direct effect. If the correlation coefficient between causal factor and the effect is almost equal to its direct effect, the correlation explains the true relationship and the direct selection through these traits will be effective (Singh and Chaudhary, 1977).

The residual effect from phenotypic path analysis was 0.121, indicating that all the traits included in the study explained high percentage of variation (87.9%) in seed yield in soybean and other factors not included in the study can explain 12.1%.

Table 9: Phenotypic direct effect path (bold) and indirect effect (off diagonal) of various characters on seed yield

Traits	50% DF	90% DM	PH	LL	LW	NPB	ND	CC	RL	SDW	RDW
50% DF	-0.001	-0.002	0.003	-0.001	-0.007	-0.002	-0.002	-0.004	0.000	0.001	0.000
90%DM	-0.001	-0.003	-0.016	-0.026	0.018	0.003	0.004	-0.001	0.000	-0.009	0.016
PH	0.000	-0.001	-0.039	-0.048	0.043	0.012	0.013	0.003	0.000	-0.015	0.027
LL	-0.000	-0.001	-0.030	-0.062	0.047	0.009	0.012	0.003	0.000	-0.013	0.029
LW	0.000	-0.001	-0.026	-0.045	0.065	0.008	0.009	0.005	0.000	-0.011	0.022
NPB	0.000	-0.001	-0.032	-0.042	0.037	0.014	0.014	0.003	0.000	-0.013	0.023
ND	0.000	-0.001	-0.032	-0.045	0.037	0.012	0.016	0.003	0.000	-0.013	0.025
CC	0.000	0.000	-0.007	-0.013	0.024	0.003	0.004	0.015	0.000	-0.004	0.004
RL	-0.000	-0.001	-0.023	-0.036	0.026	0.007	0.009	0.002	0.001	-0.013	0.023
SDW	0.000	-0.001	-0.024	-0.033	0.030	0.007	0.009	0.002	0.000	-0.024	0.028
RDW	-0.000	-0.001	-0.024	-0.041	0.032	0.007	0.009	0.001	0.000	-0.015	0.044
NPP	-0.000	-0.001	-0.017	-0.028	0.022	0.007	0.006	0.001	0.000	-0.009	0.019
PL	0.000	-0.000	-0.009	-0.013	0.020	0.003	0.003	0.003	0.000	-0.005	0.008
NSP	-0.000	-0.001	-0.017	-0.028	0.023	0.007	0.007	0.002	0.000	-0.009	0.019
HSW	0.000	-0.000	-0.015	-0.021	0.036	0.004	0.005	0.005	0.000	-0.011	0.015
BY	-0.000	-0.001	-0.026	-0.043	0.035	0.009	0.010	0.003	0.000	-0.018	0.029
HI	-0.000	0.000	0.007	0.012	-0.003	-0.002	-0.003	0.002	-0.000	0.007	-0.008
PC	0.000	0.000	0.000	0.004	0.008	-0.001	-0.002	0.002	-0.000	-0.004	-0.001
OC	-0.000	-0.001	-0.008	-0.017	0.016	0.003	0.003	0.001	0.000	-0.007	0.015

Where; DF = days to 50% flowering (days), DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), CC = chlorophyll content ($\mu\text{mol m}^{-2}$), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), HSW = hundred seed weight (g), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%) and OC=oil content (%), rp = phenotype correlation coefficient.

Table 9 (continued)

Traits	NPP	PL	NSP	HSW	BY	HI	PC	OC	rp
50% DF	0.160	0.002	0.048	-0.042	0.035	0.010	-0.004	0.003	0.198
90%DM	0.198	-0.001	0.063	0.022	0.109	-0.013	-0.003	0.007	0.366
PH	0.225	-0.006	0.079	0.077	0.158	-0.023	-0.000	0.005	0.509
LL	0.235	-0.006	0.081	0.065	0.163	-0.025	-0.002	0.006	0.510
LW	0.173	-0.008	0.063	0.108	0.127	-0.006	0.003	0.006	0.492
NPB	0.246	-0.006	0.086	0.061	0.155	-0.015	-0.002	0.004	0.532
ND	0.208	-0.005	0.075	0.061	0.148	-0.024	-0.003	0.004	0.466
CC	0.051	-0.006	0.025	0.065	0.048	0.018	0.003	0.002	0.232
RL	0.206	-0.004	0.074	0.053	0.128	-0.008	-0.003	0.004	0.445
SDW	0.187	-0.006	0.067	0.086	0.175	-0.038	0.005	0.007	0.476
RDW	0.225	-0.005	0.079	0.067	0.159	-0.025	-0.000	0.008	0.522
NPP	<u>0.526</u>	-0.006	0.178	0.006	0.172	0.052	-0.004	0.013	0.937
PL	0.125	<u>-0.027</u>	0.056	0.105	0.071	0.026	0.009	0.004	0.379
NSP	0.519	-0.008	<u>0.181</u>	0.016	0.173	0.054	-0.004	0.013	0.947
HSW	0.017	-0.014	0.015	<u>0.197</u>	0.077	0.016	0.013	0.002	0.341
BY	0.384	-0.008	0.133	0.064	<u>0.236</u>	-0.024	-0.001	0.009	0.792
HI	0.206	-0.005	0.073	0.023	-0.042	<u>0.134</u>	0.000	0.006	0.406
PC	-0.082	-0.009	-0.024	0.091	-0.008	0.001	<u>0.028</u>	-0.002	0.003
OC	0.300	-0.004	0.102	0.018	0.098	0.034	-0.003	<u>0.023</u>	0.573

Where; DF = days to 50% flowering (days), DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), CC = chlorophyll content ($\mu\text{mol m}^{-2}$), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), HSW = hundred seed weight (g), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%) and OC=oil content (%), rp = phenotype correlation coefficient.

4.6. Multivariate Analysis

4.6.1. Genetic diversity analysis

4.6.1.1. Cluster analysis

Cluster analysis is to group individuals based on the characteristics they possess with similar descriptions are gathered into the same cluster. Based on the plot performed by wss (within cluster sum squares) method, the mean data of 64 soybean accessions tested for the 20 quantitative traits were categorized into five clusters (table 10 and appendix figure 1). The grouping pattern was showed; cluster-I contained highest number of accessions 20 (31.25%), followed by cluster-IV with 18 (28.13%), cluster-III with 10 (15.63%), cluster-II with 9 (14.06%) and cluster-V with 7 (10.94%). In cluster analysis the categorizations within individuals (homogenous) shall be closer and different clusters (heterogeneous) shall be farther apart (Hair, 1995). Regardless of the source of the germplasm, clustering pattern at the cluster level was mainly based on the similarities of the traits. Similar results were reported by Masreshaw *et al.* (2022) studied 100 soybean genotypes and identified five major clusters, and also Yechalew (2018) studied on 36 soybean genotypes and grouped into five distinct groups.

Table 10: Distribution of 64 soybean accessions into five clusters that tested (2022/23)

Clusters	Number of genotypes	Name of Genotypes
Cluster I	20 (31.25%)	SO-BAN-101, SO-BOU-47, SO-BOU-56, SO-COB-32, SO-DAS-01, SO-DAS-03, SO-DAS-05, SO-DJI-110, SO-DJI-95, SO-DJO-70, SO-GLA-49, SO-NIK-87, SO-NIK-98, SO-OUA-82, SO-OUE-21, SO-OUE-36, SO-OUE-39, SO-TAN-05, SO-TAN-09, SO-TAN-10
Cluster II	9 (14.06%)	SO-BAN-102, SO-BAN-115, SO-COB-27, SO-COB-40, SO-DJI-114, SO-DJI-96, SO-KAN-125, SO-NDA-66, SO-TAN-15
Cluster III	10 (15.63%)	SO-BAN-109, SO-DAS-02, SO-GLA-50, SO-KAN-126, SO-NDA-63, SO-NDA-67, SO-OUA-93, SO-OUA-94, SO-OUE-41, SO-TAN-19
Cluster IV	18 (28.13%)	SO-BAN-111, SO-BOH-119, SO-BOU-42, SO-BOU-45, SO-BOU-46, SO-COB-25, SO-DAS-04, SO-DJO-65, SO-DJO-75, SO-GLA-04, SO-GLA-48, SO-KAN-128, SO-NIK-95, SO-OUA-84, SO-OUA-85, SO-OUE-23, SO-NDA-70, SO-NIK-100
Cluster V	7 (10.94%)	SO-BOH-125, SO-COB-35, SO-GLA-51, SO-KAN-119, SO-KAN-130, SO-NDA-81, SO-NIK-84

4.6.1.2. Comparison of cluster means analysis

The accessions in cluster I are characterized by early flowering and maturity, shortest plant height, and lowest in leaf length, leaf width, number of branches, number of nodes, number of pod per plant, pod length, number of seed per plant, shoot dry weight, root length, root dry weight, biomass per plant and low yield. The accessions in cluster II are characterized by lowest oil contents and harvest index, and the tallest plant height, highest number of branches and number of nodes. The accessions in cluster III exhibited the highest mean estimate for leaf width, longest pod length, high in shoot dry weight and 100-seed weight, high in root dry weight, highest in biomass, high in harvest index, and the higher in yield and oil contents. The accessions in cluster IV exhibited the highest mean estimate for chlorophyll contents and high in protein content. While accessions in cluster V are also characterized by lowest chlorophyll contents, late flowering and maturity, and highest number of pods per plant and number of seed per plant and the longest in root length (Table 11). The result indicates that the accessions in cluster V could be used for crossing, if the aim is to develop with high number of pods per plant, number of seed per plant, as well as for late flowering and maturity. While the accessions in cluster III could be also used for the purpose of crossing, if the aim is for the high in yield and oil contents; and the accessions in cluster II could be also used for the tallest in plant height. The accessions in cluster I could be also used for the purpose of crossing, if the aim is to develop early flowering and maturity and for shortest plant height; and accessions in cluster IV could be also used for high in protein content. Malek *et al.* (2014) reported that some of the clusters constructed by soybean genotypes showed higher mean values for desirable traits including seed yield and yield parameters.

Table 11: Cluster mean values for 20 traits of 64 soybean accessions that tested during 2022/23 cropping season in Benin Republic

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to 50% flowering	50.30	53.72	52.54	53.45	60.04
Days to maturity	125.86	130.57	130.95	128.24	139.96
Plant height	36.18	55.90	50.40	45.49	53.64
Leaf Length	8.07	10.07	9.65	8.75	10.32
Leaf Width	4.09	4.73	5.30	4.49	4.77
Number of branches	2.84	5.18	4.68	3.81	4.74
Number of nodes	7.47	11.65	10.61	9.03	10.96
Chlorophyll contents	386.62	382.72	416.54	427.14	369.23
Number of pod per plant	33.80	46.15	77.31	49.34	89.06
Pod length	33.45	34.41	36.97	36.46	33.58

Number of seed per plant	68.05	94.75	160.99	104.38	179.04
Shoot dry weight	8.00	15.95	16.66	12.54	14.82
Taproot length	20.59	25.96	25.38	20.66	27.61
Root dry weight	2.15	4.01	4.18	2.56	3.90
Biological Yield	23.95	48.45	59.59	40.85	57.21
100-seeds weight	14.55	15.71	17.22	16.42	13.57
Harvest index	40.37	30.03	47.40	41.86	44.68
Yield	1.01	1.40	2.64	1.61	2.45
Protein	33.56	32.27	33.29	35.75	30.13
Oil	15.40	15.14	22.44	16.28	22.00

4.6.1.3. Genetic divergence analysis

The values of pair wise complete inter-cluster divergence (D^2) for 64 soybean accessions in five clusters based on agro-morphological traits are presented in Table 12. The inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider diversity among the accessions, and showed the significant difference at ($P < 0.01$). The values of intra-cluster degree of diversity for the accessions in each cluster were a little heterogeneous, and indicated homogeneous nature among the clusters.

The maximum inter-cluster distance was found between cluster one and three ($D^2 = 209.73$); followed by cluster one and five ($D^2 = 184.42$), cluster one and two ($D^2 = 153.19$) and cluster two and five ($D^2 = 140.66$). The shortest squared distance was found between cluster-III and V ($D^2 = 74.99$); followed by cluster-II and IV ($D^2 = 83.54$) and cluster-I and IV ($D^2 = 91.97$). This investigation revealed that the accessions included in the study were genetically more divergent. The highest value of inter-cluster distance indicated that the accessions belonging to these cluster were more divergent.

The minimum inter-cluster distances were found between cluster-III and V, indicating that the accessions in these clusters were not genetically diverse or there was little genetic diversity between these clusters, and this suggests that crossing of accessions from these clusters might not give higher heterotic value the progeny.

Maximum genetic recombination is expected from the parents selected from divergent cluster groups. Therefore, maximum recombination and segregation of progenies is expected from crosses involving parents selected from cluster-I and III, followed by cluster-I and V. However, the breeder must specify his/her objectives in order to make best use of the characters where the characters are divergent depending on the wanted purpose.

Table 12: Pair-wise generalized square distance (D^2) inter and intra (bold) cluster among five clusters constructed from 64 soybean accessions based on agro-morphological traits

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	(8.53)	153.19**	209.73**	91.97**	184.42**
Cluster II		(9.32)	107.95**	83.54**	140.66**
Cluster III			(7.44)	101.60**	74.99**
Cluster IV				(6.35)	124.77**
Cluster V					(7.68)

*significant at $P \leq 0.05$ ($X^2 = 30.14$) and ** highly significant at $P \leq 0.01$ ($X^2 = 36.19$)

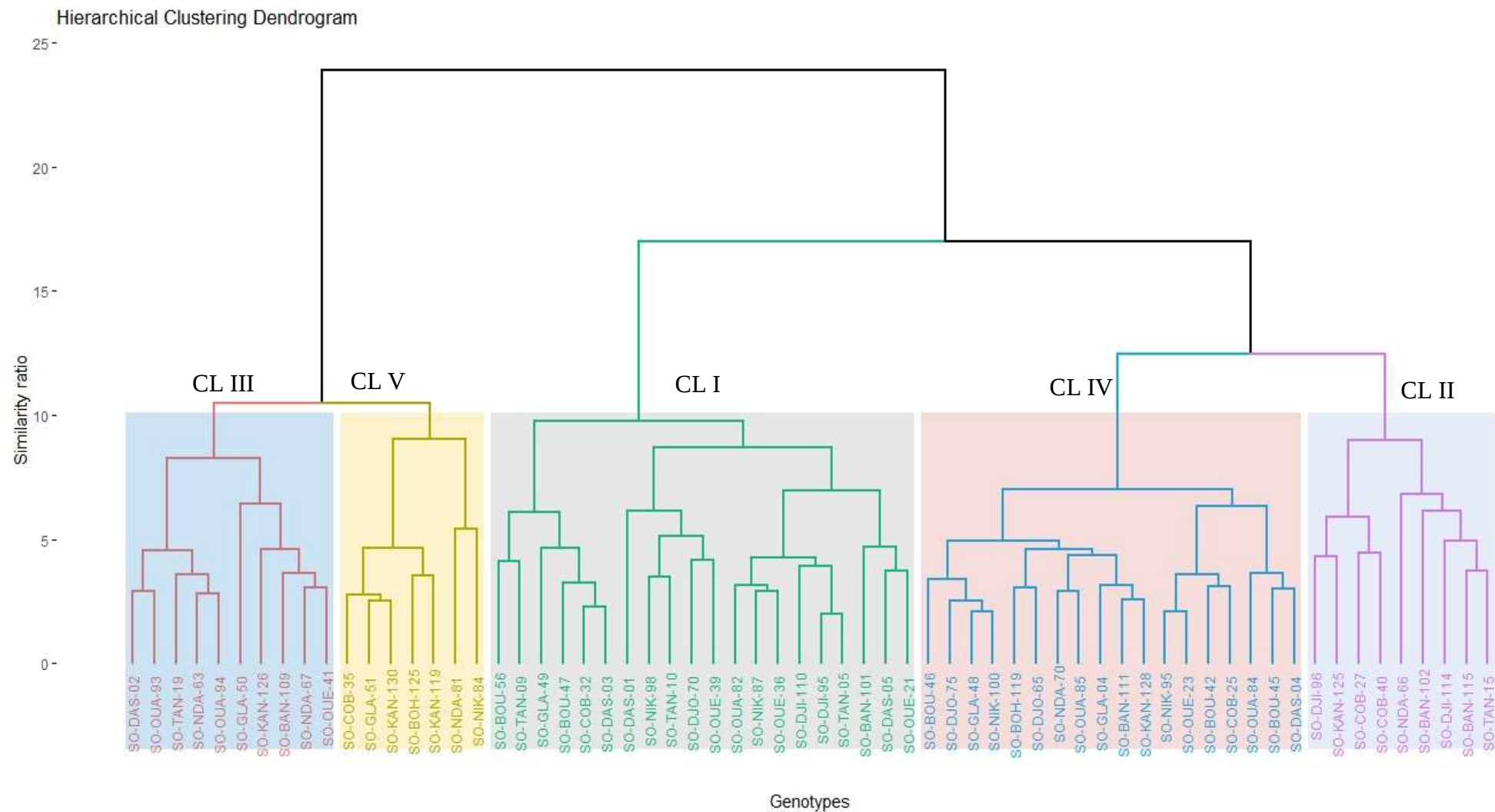


Figure 2: Dendrogram for 64 soybean accessions using 20 quantitative traits during the 2022/23 main season

4.6.2. Principal component analysis

Principal component analyses (PCA) are one of multivariate analyses that give clear information about certain traits and the accessions for an indication to the breeding programs. It helps to reduce complex data in to simplified structure; the eigen values are often used to determine how many factors to retain. If the characteristic value is lower than one, it explains that the explanatory power of principal components is lower.

In the present study, the principal components analysis revealed that four principal components with eigen-values greater than one (Eigen value >1) and the first four principal components explained 74.8% of the total variation among the traits in 64 soybean accessions (Table 13). Out of these total principal components, PCA1 record the highest variation 40% followed by second PCA which account 14%, the third PCA 12.9%, and 7.9% for the fourth PCA. Similar result was reported by (Yechalew, 2018) who found the first five principal components (PCA1, PCA2, PCA3, PCA4 and PCA5) with values of 37.1%, 19.2%, 7.9%, 6.3% and 4.6%, respectively, contributed more to the total of 75.3% variation. Masreshaw *et al.* (2022) reported the first, second, third and fourth principal components with values of 39.31%, 13.82%, 10.26% and 9.23% that accounted about 72.62 % of the total variation. (Yechalew *et al.*, 2019) studies indicated that the first four principal components explains 82% of the total variation amongst 36 tested soybean genotypes for 14 morphological traits, out of the total principal components, PC1 (42%), PC2 (22%), PC3 and PC4 accounts 11% and 7 % respectively.

The first principal component (PCA1) which accounts the highest variation was mostly related with traits biomass yield per plant, seed yield, plant height, leaf length, number of pod per plant and number of seed per pod, number of primary branches and number of nodes had relatively higher contribution to PCA1. This indicated that these traits had more contribution to the total diversity and they were responsible for the differentiation of the clusters. In PCA2, 100-seed weight, days to 50% flowering, number of pod per plant and harvest index had more contribution; while chlorophyll content, harvest index and pod length had relatively more contribution in the PCA3. In PCA4, days to 50% flowering and date of maturity had relatively more contribution.

Chahal and Gosal (2002) concluded that characters with the largest absolute values closer to one within the first principal component influence the clustering more than those with lower absolute values closer to zero.

Table 13: Eigen values, the percent of variance and cumulative variance, obtained from PCA for 20 traits among 64 soybean accessions

Traits	PCA1	PCA2	PCA3	PCA4
DF	0.051	-0.367	0.166	0.456
LL	0.282	0.106	0.145	-0.028
LW	0.238	0.208	-0.105	0.026
CC	0.023	0.136	-0.351	-0.242
DM	0.179	-0.173	0.245	0.432
PH	0.282	0.163	0.179	-0.091
NPB	0.270	0.141	0.104	-0.298
ND	0.264	0.158	0.190	-0.267
RL	0.230	0.009	0.173	-0.067
RDW	0.259	0.115	0.084	0.047
PL	0.129	0.152	-0.398	0.208
SDW	0.241	0.202	0.070	0.190
BY	0.326	-0.019	0.018	0.109
NPP	0.272	-0.331	-0.146	-0.056
NSP	0.276	-0.312	-0.166	-0.072
HSW	0.124	0.392	-0.279	0.220
HI	0.034	-0.312	-0.437	-0.199
YD	0.295	-0.211	-0.236	0.004
PC	-0.031	0.270	-0.300	0.427
OC	0.226	-0.194	-0.118	0.025
Eigenvalue	7.999	2.797	2.576	1.580
Variance (%)	39.997	13.984	12.880	7.901
Cumulative variance %	39.997	53.980	66.860	74.761

Where; DF = days to 50% flowering (days), DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), CC = chlorophyll content ($\mu\text{mol m}^{-2}$), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), HSW = hundred seed weight (g), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%), OC=oil content (%) and YD = yield per ha (Kg).

Biplot analysis was carried out based on the first two PCAs (Figure 3). The accessions and the quantitative traits were shown on a biplot to clearly visualize their associations and differences. Out of the entire variations, the first and the second PCA explained (54%) of the total variations among the accessions, and displaying that number of pod per plant, number of

seed per plant, seed yield, biological yield, plant height, leaf length and number of primary branches were considered as the most discriminating traits. Characters with lower absolute values closer to zero have less influence than largest absolute values within the principal components.

The accessions that were positioned on the right top quadrant were closely associated and characterized by highest plant height, leaf length, number of primary branches, and number of nodes, shoot dry weight and root dry weight. The accessions demarcated on the bottom right quadrant were associated with high seed yield, high number of pod per plant, high number of seed per plant and biomass yield. The accessions concentrated around the origin had similar genetic characteristics, while the accessions that were found far from the origin are considered as unrelated accessions (Gerrano *et al.*, 2017). Therefore, selection of these accessions as potential parents would result in successful hybridization to develop heterotic groups in the soybean breeding program (Figure 3).

5. SUMMARY AND CONCLUSIONS

Soybean is the most important oilseed crop that grown worldwide for multi-purposes. A total of 64 soybean accessions were assessed to estimate the magnitude of genetic diversity and the association of characters using agro-morphological and biochemical traits in the main cropping seasons of the year 2022 at Laboratory of Genetics, Horticulture and Seed Sciences (GBioS), University of Abomey-Calavi (UCA), in 8 x 8 simple lattice designs.

The analysis of variance revealed that the presence of significant differences among the tested soybean accessions for most of quantitative traits, and the qualitative traits had also showed the existence of diversity in the tested materials. Phenotypic variance (σ^2_p) and phenotypic coefficient variation (PCV) were generally higher than genotypic variance (σ^2_g) and genotypic coefficient of variation (GCV), respectively, for all the traits, and indicating the expression of these characters was influenced by environment. High heritability values were recorded for days to 50% flowering, days to maturity, pod per plant, seed per plant; shoot dry weight, root dry weight, seed yield, oil and protein content. High heritability along with high GAM were exhibited by pod per plant, seed per plant, shoot dry weight, root dry weight, seed yield and oil and protein content, and this indicates that the heritability of these characters is due to additive gene effects and selection might be effective for these characters. Generally, estimates of GCV, PCV, H^2 and GAM were high for pod per plant, seed per plant, shoot dry weight, root dry weight and seed yield, and these traits can be improved through direct selection more easily than other traits.

The genotypic correlation coefficients were higher than the phenotypic correlation coefficients indicating that the observed relationships among the various traits were due to genetic causes. The grain yield had significant and positive association with most of the traits at both genotypic and phenotypic levels. Seed yield had positive and significant correlations with days to maturity, plant height, leaf length, leaf width, number of nodes, number of branch, pod per plant, pod length, seed per plant, biological yield, harvest index, shoot dry weight, root dry weight, root length and oil content at both genotypic and phenotypic levels. Path coefficient analysis indicated that pods per plant, biological yield and harvest index had positive direct effects on seed yield at both genotypic and phenotypic levels.

The first four principal components had accounted for 74.8% of the total variation, and the first PCA alone had largest contribution of 40%, and PCA2, PCA3 and PCA4 contributed

14%, 12.9%, and 7.9%, respectively. Cluster analysis of quantitative characters showed the existence of five divergent groups and the maximum inter-cluster distance was found between cluster-I and III followed by cluster-I and V and cluster-I and III. While, the shortest distance was found between cluster-III and V, indicating that the accessions in these clusters were not genetically diverse or there was little genetic diversity between these clusters. Based on the results, the maximum genetic recombination and segregation of the progenies is expected from crosses made between parents selected from cluster-I and III followed by cluster-I and V and cluster-I and III.

The results of this investigation can be concluded that there is adequate genetic variability for most of quantitative characters evaluated among the soybean accessions, and indicates that there is an opportunity to use for direct selection and to improve specific traits using distant parents. Based on the mean values the accessions SO-NDA-81 (3.92t/h), SO-TAN-19 (3.22t/h), SO-OUA-94 (2.97t/h), and SO-GLA-50 (2.92t/h) had shown to be high yielding and these accessions could be advanced for further trials.

Furthermore, the materials in this study were evaluated for one season on a single location and it needs to be checked in a different location at different seasons to identify the genetic variation and validate the current results. Moreover, further molecular characterization is suggested to supplement morphological characterization to perceive the genetic diversity and for more appropriate information.

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7. APPENDIXES

Appendix Table 1: Mean values of 64 Soybean accessions tested during the 2022/23 main cropping season

Accessions	50% DF	LL	LW	CC	DM	PH	NPB	ND	RL	RDW
SO-BAN-101	51.27 ^{m-u}	7.02 ^{nop}	3.66 ^{h-l}	381.21 ^{j-v}	125.21 ^{k-t}	38.99 ^{g-o}	2.76 ^{e-l}	6.42 ⁱ⁻ⁿ	22.95 ^{b-k}	2.37 ^{i-r}
SO-BAN-102	54.66 ^{f-m}	11.11 ^{a-d}	6.25 ^{ab}	393.05 ^{g-v}	139.88 ^{a-e}	62.44 ^{abc}	5.10 ^{a-e}	11.46 ^{a-f}	27.43 ^{a-i}	3.30 ^{e-m}
SO-BAN-109	56.15 ^{d-i}	9.91 ^{a-l}	5.31 ^{b-f}	410.75 ^{d-q}	136.07 ^{a-i}	59.68 ^{a-e}	4.55 ^{a-i}	10.94 ^{a-i}	24.98 ^{a-j}	3.68 ^{d-j}
SO-BAN-111	53.35 ^{i-s}	8.78 ^{d-o}	4.86 ^{b-k}	432.68 ^{a-i}	127.13 ^{h-s}	42.08 ^{d-o}	4.78 ^{a-h}	8.85 ^{c-n}	15.86 ^{g-k}	2.27 ^{i-r}
SO-BAN-115	53.11 ^{i-s}	10.76 ^{a-f}	5.54 ^{a-e}	372.24 ^{n-v}	130.51 ^{e-p}	61.53 ^{a-d}	5.64 ^{a-d}	12.20 ^{abc}	29.17 ^{a-g}	3.34 ^{e-l}
SO-BOH-119	57.69 ^{def}	8.26 ^{g-p}	4.25 ^{c-l}	413.64 ^{c-p}	122.27 ^{o-v}	41.19 ^{e-o}	2.36 ^{h-l}	8.46 ^{c-n}	14.19 ^{h-k}	2.19 ^{j-s}
SO-BOH-125	63.41 ^b	8.63 ^{e-p}	4.59 ^{c-k}	391.58 ^{h-v}	144.61 ^{ab}	46.83 ^{a-o}	4.25 ^{b-k}	11.19 ^{a-h}	30.49 ^{a-e}	3.67 ^{d-j}
SO-BOU-42	55.21 ^{e-k}	9.77 ^{a-m}	4.43 ^{c-l}	464.00 ^{abc}	129.53 ^{f-r}	49.01 ^{a-m}	4.59 ^{a-h}	10.54 ^{a-k}	23.63 ^{a-k}	1.52 ^{p-s}
SO-BOU-45	56.35 ^{d-i}	8.20 ^{h-p}	4.61 ^{c-k}	403.56 ^{f-s}	130.74 ^{e-o}	40.49 ^{e-o}	3.24 ^{d-l}	7.32 ^{d-n}	18.03 ^{e-k}	1.56 ^{o-s}
SO-BOU-46	51.62 ^{k-u}	8.87 ^{d-o}	5.21 ^{b-f}	443.18 ^{a-g}	120.55 ^{q-v}	45.73 ^{a-o}	4.43 ^{b-j}	10.37 ^{a-l}	18.96 ^{d-k}	2.49 ^{h-r}
SO-BOU-47	52.87 ^{i-s}	9.33 ^{c-n}	4.67 ^{c-k}	427.18 ^{a-j}	131.82 ^{d-o}	46.75 ^{a-o}	3.67 ^{c-l}	9.83 ^{b-m}	36.33 ^{ab}	4.28 ^{c-f}
SO-BOU-56	50.42 ^{p-u}	8.44 ^{f-p}	3.97 ^{f-l}	371.54 ^{n-v}	113.19 ^v	41.49 ^{d-o}	4.08 ^{b-l}	9.40 ^{b-m}	30.08 ^{a-e}	3.08 ^{e-n}
SO-COB-25	50.18 ^{q-u}	8.45 ^{f-p}	4.47 ^{c-l}	473.96 ^a	128.81 ^{g-r}	51.83 ^{a-k}	5.11 ^{a-e}	11.27 ^{a-g}	25.32 ^{a-j}	1.80 ^{m-s}
SO-COB-27	48.42 ^u	9.19 ^{c-o}	3.94 ^{f-l}	381.66 ^{i-v}	123.47 ^{n-u}	49.99 ^{a-m}	7.01 ^a	14.73 ^a	26.69 ^{a-i}	4.36 ^{cde}
SO-COB-32	53.95 ^{g-p}	8.70 ^{d-p}	4.86 ^{b-k}	392.61 ^{g-v}	128.92 ^{g-r}	44.75 ^{c-o}	3.99 ^{b-l}	9.15 ^{b-m}	26.90 ^{a-i}	3.23 ^{e-m}
SO-COB-35	56.35 ^{d-i}	9.22 ^{c-n}	4.99 ^{b-i}	380.52 ^{j-v}	135.09 ^{b-k}	45.32 ^{b-o}	4.13 ^{b-l}	10.61 ^{a-j}	26.95 ^{a-i}	3.05 ^{e-o}
SO-COB-40	48.85 ^{tu}	9.39 ^{c-n}	3.42 ^{kl}	373.89 ^{l-v}	117.89 ^{s-v}	52.11 ^{a-k}	5.91 ^{abc}	11.49 ^{a-e}	20.76 ^{d-k}	1.93 ^{l-s}
SO-DAS-01	64.35 ^{ab}	6.33 ^p	2.99 ^l	385.72 ^{i-v}	134.20 ^{c-m}	27.52 ^{no}	1.69 ^{kl}	6.03 ^{j-n}	15.41 ^{h-k}	1.28 ^{rs}
SO-DAS-02	48.42 ^u	8.25 ^{f-p}	5.30 ^{b-f}	415.41 ^{b-o}	126.53 ^{i-t}	49.13 ^{a-m}	4.30 ^{b-j}	8.77 ^{c-n}	23.54 ^{b-k}	2.63 ^{h-r}
SO-DAS-03	55.07 ^{e-l}	9.29 ^{c-n}	4.82 ^{b-k}	411.33 ^{d-q}	131.81 ^{d-o}	47.62 ^{a-n}	4.12 ^{b-l}	8.19 ^{c-n}	27.27 ^{a-i}	1.69 ^{n-s}
SO-DAS-04	52.79 ^{i-s}	7.32 ^{m-p}	4.57 ^{c-k}	409.95 ^{d-r}	125.58 ^{k-t}	42.42 ^{d-o}	3.41 ^{c-l}	7.27 ^{c-n}	22.08 ^{c-k}	3.77 ^{d-i}
SO-DAS-05	51.85 ^{j-u}	8.47 ^{f-p}	4.54 ^{c-k}	364.18 ^{o-v}	125.43 ^{k-t}	39.38 ^{f-o}	3.04 ^{e-l}	6.59 ^{h-n}	22.16 ^{c-k}	2.68 ^{g-r}
SO-DJI-110	53.15 ^{i-s}	7.44 ^{l-p}	3.61 ^{h-l}	358.80 ^{r-v}	121.06 ^{p-v}	37.26 ^{g-o}	4.13 ^{b-l}	10.55 ^{a-j}	13.34 ^{ijk}	1.49 ^{p-s}
SO-DJI-114	48.87 ^{tu}	11.60 ^{abc}	4.87 ^{b-k}	423.43 ^{a-l}	126.23 ^{i-t}	51.64 ^{a-k}	5.10 ^{a-e}	12.04 ^{abc}	25.75 ^{a-j}	7.66 ^a
SO-DJI-95	49.97 ^{r-u}	7.59 ^{k-p}	3.76 ^{g-l}	408.74 ^{d-r}	119.77 ^{r-v}	34.48 ^{j-o}	3.13 ^{d-l}	6.71 ^{g-n}	24.15 ^{a-k}	1.88 ^{l-s}
SO-DJI-96	52.89 ^{i-s}	10.92 ^{a-e}	3.57 ^{i-l}	347.42 ^{uv}	132.54 ^{d-n}	55.89 ^{a-i}	4.00 ^{b-l}	8.99 ^{c-m}	31.82 ^{a-d}	5.57 ^{bc}
SO-DJO-65	51.91 ^{j-u}	8.94 ^{d-o}	4.98 ^{b-i}	450.22 ^{a-f}	126.18 ^{j-t}	43.44 ^{c-o}	3.43 ^{c-l}	8.49 ^{c-n}	18.88 ^{d-k}	1.38 ^{qrs}
SO-DJO-70	58.50 ^{cde}	9.29 ^{c-n}	4.08 ^{e-l}	355.15 ^{s-v}	135.94 ^{a-i}	35.43 ^{j-o}	2.39 ^{h-l}	6.89 ^{e-n}	23.57 ^{b-k}	1.83 ^{m-s}
SO-DJO-75	56.13 ^{d-i}	8.42 ^{f-p}	4.20 ^{c-l}	420.22 ^{b-n}	131.12 ^{d-o}	43.75 ^{c-o}	3.32 ^{d-l}	8.01 ^{c-n}	25.28 ^{a-j}	2.49 ^{h-r}

SO-GLA-04	51.42 ^{l-u}	8.11 ^{h-p}	4.09 ^{d-l}	396.58 ^{g-u}	128.27 ^{h-r}	45.55 ^{a-o}	4.32 ^{b-j}	8.78 ^{c-n}	20.74 ^{d-k}	2.63 ^{h-r}
SO-GLA-48	50.50 ^{p-u}	8.86 ^{d-o}	4.02 ^{f-l}	451.12 ^{a-f}	126.72 ^{h-s}	45.90 ^{a-o}	3.34 ^{d-l}	8.88 ^{c-n}	23.36 ^{b-k}	3.11 ^{e-n}
SO-GLA-49	50.55 ^{o-u}	10.15 ^{a-i}	4.85 ^{b-k}	418.18 ^{b-n}	126.03 ^{j-t}	30.28 ^{l-o}	1.58 ^l	7.16 ^{e-n}	25.53 ^{a-j}	1.87 ^{l-s}
SO-GLA-50	48.54 ^u	11.05 ^{a-e}	6.82 ^a	443.14 ^{a-g}	129.32 ^{f-r}	56.38 ^{a-h}	6.47 ^{ab}	13.64 ^{ab}	26.22 ^{a-i}	7.27 ^a
SO-GLA-51	55.03 ^{e-l}	9.86 ^{a-l}	4.81 ^{b-k}	398.27 ^{g-t}	134.23 ^{c-m}	53.77 ^{a-k}	5.09 ^{a-f}	10.78 ^{a-i}	21.23 ^{d-k}	3.10 ^{e-n}
SO-KAN-119	61.97 ^{bc}	10.47 ^{a-h}	4.28 ^{c-l}	346.99 ^v	139.93 ^{a-e}	48.96 ^{a-m}	4.46 ^{b-i}	10.37 ^{a-l}	22.77 ^{b-k}	3.50 ^{e-j}
SO-KAN-125	49.71 ^{stu}	8.67 ^{e-p}	4.20 ^{c-l}	375.58 ^{k-v}	140.72 ^{a-d}	50.32 ^{a-l}	4.54 ^{a-i}	9.73 ^{b-m}	27.26 ^{a-i}	1.31 ^{rs}
SO-KAN-126	57.63 ^{d-g}	9.78 ^{a-m}	5.65 ^{abc}	371.73 ^{n-v}	133.83 ^{d-m}	45.41 ^{b-o}	4.37 ^{b-j}	10.03 ^{b-m}	20.35 ^{d-k}	3.27 ^{e-m}
SO-KAN-128	51.82 ^{j-u}	8.87 ^{d-o}	4.59 ^{c-k}	417.91 ^{b-n}	124.52 ^{m-t}	52.22 ^{a-k}	4.34 ^{b-j}	9.98 ^{b-m}	19.05 ^{d-k}	2.54 ^{h-r}
SO-KAN-130	56.10 ^{d-i}	9.86 ^{a-l}	4.61 ^{c-k}	350.77 ^{tuw}	136.40 ^{a-h}	59.53 ^{a-f}	4.89 ^{a-h}	10.14 ^{a-m}	19.64 ^{d-k}	3.68 ^{d-j}
SO-NDA-63	50.49 ^{p-u}	9.31 ^{c-n}	4.91 ^{b-k}	458.31 ^{a-d}	127.37 ^{h-s}	47.16 ^{a-o}	4.43 ^{b-j}	10.67 ^{a-j}	21.85 ^{d-k}	3.07 ^{e-o}
SO-NDA-66	50.85 ^{n-u}	8.86 ^{d-o}	5.20 ^{b-g}	342.15 ^v	133.51 ^{d-m}	65.79 ^a	5.03 ^{a-g}	12.38 ^{abc}	15.11 ^{h-k}	5.11 ^{bcd}
SO-NDA-67	54.55 ^{f-n}	9.483 ^{b-n}	4.08 ^{e-l}	384.93 ^{i-v}	131.39 ^{d-o}	51.99 ^{a-k}	4.73 ^{a-h}	11.29 ^{a-g}	31.61 ^{a-d}	5.62 ^{bc}
SO-NDA-70	58.39 ^{cde}	8.21 ^{g-p}	4.24 ^{c-l}	373.53 ^{m-v}	134.25 ^{c-l}	44.48 ^{c-o}	3.77 ^{c-l}	9.05 ^{b-m}	19.79 ^{d-k}	2.88 ^{f-q}
SO-NDA-81	67.79 ^a	12.23 ^a	5.29 ^{b-f}	345.48 ^v	145.48 ^a	56.49 ^{a-g}	4.70 ^{a-h}	11.18 ^{a-h}	36.79 ^a	6.17 ^{ab}
SO-NIK-100	50.37 ^{p-u}	8.73 ^{d-p}	4.156 ^{c-l}	424.74 ^{a-k}	126.90 ^{h-s}	42.31 ^{d-o}	3.48 ^{c-l}	8.36 ^{c-n}	18.80 ^{d-k}	3.55 ^{e-j}
SO-NIK-84	59.65 ^{cd}	11.94 ^{ab}	4.80 ^{b-k}	370.99 ^{n-v}	144.00 ^{abc}	64.57 ^{ab}	5.64 ^{a-d}	12.46 ^{abc}	35.43 ^{abc}	4.16 ^{c-g}
SO-NIK-87	54.20 ^{f-o}	7.44 ^{l-p}	3.84 ^{f-l}	387.64 ^{h-v}	124.83 ^{l-t}	29.99 ^{mno}	2.04 ^{i-l}	5.79 ^{lmn}	14.54 ^{h-k}	0.69 ^s
SO-NIK-95	50.82 ^{o-u}	9.78 ^{a-m}	4.44 ^{c-l}	465.04 ^{ab}	124.95 ^{l-t}	43.85 ^{c-o}	3.49 ^{c-l}	9.41 ^{b-m}	20.23 ^{d-k}	3.54 ^{e-j}
SO-NIK-98	54.65 ^{f-m}	7.64 ^{j-p}	3.92 ^{f-l}	406.27 ^{e-s}	125.24 ^{k-t}	34.24 ^{k-o}	1.87 ^{jkl}	5.92 ^{k-n}	12.13 ^{jk}	2.31 ^{i-r}
SO-OUA-82	57.82 ^{def}	6.70 ^{op}	3.47 ^{jkl}	403.87 ^{f-s}	132.58 ^{d-n}	27.41 ^o	2.54 ^{f-l}	5.65 ^{mn}	10.72 ^k	2.18 ^{j-s}
SO-OUA-84	53.89 ^{h-q}	9.36 ^{c-n}	4.84 ^{b-k}	393.43 ^{g-v}	138.77 ^{a-f}	50.52 ^{a-l}	3.05 ^{e-l}	8.56 ^{c-n}	25.53 ^{a-j}	3.31 ^{e-m}
SO-OUA-85	55.45 ^{e-j}	9.63 ^{b-m}	4.36 ^{c-l}	380.34 ^{j-v}	135.70 ^{a-j}	50.77 ^{a-k}	3.81 ^{c-l}	9.18 ^{b-m}	22.46 ^{c-k}	2.17 ^{j-s}
SO-OUA-93	49.75 ^{stu}	10.01 ^{a-k}	5.59 ^{abc}	421.82 ^{b-m}	128.22 ^{h-r}	54.59 ^{a-j}	4.72 ^{a-h}	10.27 ^{a-m}	19.23 ^{d-k}	3.90 ^{d-h}
SO-OUA-94	52.25 ^{j-t}	9.17 ^{c-o}	5.07 ^{b-h}	457.01 ^{a-e}	126.64 ^{i-s}	40.77 ^{e-o}	3.98 ^{b-l}	8.69 ^{c-n}	27.29 ^{a-i}	2.87 ^{f-q}
SO-OUE-21	50.87 ^{n-u}	7.33 ^{m-p}	3.85 ^{f-l}	370.88 ^{n-v}	124.92 ^{l-t}	27.46 ^o	1.86 ^{jkl}	4.31 ⁿ	13.61 ^{ijk}	2.58 ^{h-r}
SO-OUE-23	54.26 ^{f-o}	9.03 ^{d-o}	4.49 ^{c-k}	474.36 ^a	126.33 ^{i-t}	43.33 ^{c-o}	4.22 ^{b-k}	9.77 ^{b-m}	19.76 ^{d-k}	2.93 ^{e-p}
SO-OUE-36	57.17 ^{d-h}	8.10 ^{h-p}	4.00 ^{f-l}	371.70 ^{n-v}	131.58 ^{d-o}	34.87 ^{j-o}	2.48 ^{g-l}	8.16 ^{c-n}	16.02 ^{g-k}	1.48 ^{p-s}
SO-OUE-39	57.29 ^{d-h}	7.09 ^{nop}	4.05 ^{e-l}	374.01 ^{km-v}	133.29 ^{d-m}	33.67 ^{k-o}	2.05 ^{i-l}	9.35 ^{b-m}	19.99 ^{d-k}	1.95 ^{k-s}
SO-OUE-41	53.97 ^{g-p}	10.64 ^{a-g}	5.27 ^{b-f}	388.24 ^{h-v}	138.12 ^{a-g}	48.93 ^{a-m}	4.33 ^{b-j}	11.04 ^{a-i}	27.24 ^{a-i}	6.30 ^{ab}
SO-TAN-05	51.42 ^{l-u}	7.70 ^{l-p}	3.86 ^{f-l}	418.38 ^{b-n}	120.66 ^{p-v}	36.14 ^{h-o}	2.86 ^{e-l}	7.23 ^{c-n}	16.33 ^{f-k}	1.87 ^{l-s}
SO-TAN-09	41.77 ^v	9.06 ^{d-o}	4.57 ^{c-k}	363.94 ^{p-v}	114.07 ^{uv}	40.15 ^{e-o}	3.04 ^{e-l}	9.24 ^{b-m}	22.68 ^{c-k}	1.85 ^{l-s}
SO-TAN-10	48.95 ^{tu}	8.20 ^{h-p}	4.37 ^{c-l}	361.16 ^{q-v}	116.61 ^{tuw}	35.74 ^{i-o}	3.48 ^{c-l}	6.82 ^{f-n}	18.03 ^{e-k}	2.32 ^{i-r}

SO-TAN-15	49.08 ^{tu}	10.13 ^{a-j}	5.59 ^{a-d}	435.04 ^{a-h}	130.38 ^{e-q}	53.39 ^{a-k}	4.29 ^{b-j}	11.84 ^{a-d}	29.66 ^{a-f}	3.49 ^{e-k}
SO-TAN-19	53.67 ^{h-r}	8.94 ^{d-o}	4.95 ^{b-j}	414.04 ^{b-p}	132.01 ^{d-o}	49.94 ^{a-m}	4.89 ^{a-h}	10.76 ^{a-i}	31.46 ^{a-e}	3.15 ^{e-n}
Mean	53.6	9.04	4.55	400.24	129.53	45.7	3.94	9.37	22.88	3.03
CV (%)	3.30	12.90	15.30	5.80	3.50	20.40	30.20	22.70	27.40	23.60
Minimum	41.77	6.33	2.99	342.15	113.19	27.41	1.58	4.31	10.72	0.69
Maximum	67.79	12.23	6.82	474.36	145.48	65.79	7.01	14.73	36.79	7.66
LSD (5%)	3.54	2.35	1.40	47.06	9.17	18.75	2.39	4.29	12.61	1.44

Appendix Table 1 Continued.

Accessions	PL	SDW	BY	NPP	NSP	HSW	HI	YD	PC	OC
SO-BAN-101	37.99 ^{a-g}	24.35 ^{a-d}	30.99 ^{h-q}	55.67 ^{h-s}	108.62 ^{h-t}	17.11 ^{b-k}	56.71 ^{ab}	1.92 ^{d-o}	41.34 ^{ab}	19.13 ^{i-m}
SO-BAN-102	39.95 ^{a-d}	23.25 ^{a-e}	59.83 ^{a-g}	31.68 ^{t-D}	65.56 ^{r-z}	22.26 ^a	24.39 ^{l-p}	1.38 ^{k-u}	40.50 ^{a-d}	14.69 ^{s-AB}
SO-BAN-109	34.34 ^{d-o}	13.53 ^{h-t}	60.76 ^{a-g}	63.14 ^{f-p}	128.77 ^{e-m}	17.01 ^{b-k}	42.48 ^{b-m}	2.21 ^{c-k}	35.45 ^{f-n}	21.85 ^{c-h}
SO-BAN-111	35.26 ^{c-m}	9.96 ^{o-z}	41.61 ^{e-p}	63.16 ^{f-p}	136.65 ^{e-k}	15.30 ^{d-o}	50.81 ^{a-g}	1.97 ^{d-n}	32.67 ^{k-t}	20.83 ^{e-i}
SO-BAN-115	36.04 ^{a-k}	11.08 ^{l-x}	40.06 ^{f-q}	55.41 ^{h-s}	117.92 ^{f-q}	14.56 ^{f-p}	42.64 ^{b-m}	1.62 ^{h-s}	28.04 ^{v-y}	15.62 ^{p-w}
SO-BOH-119	34.98 ^{c-n}	7.33 ^{t-AB}	32.63 ^{g-q}	67.75 ^{e-n}	136.39 ^{e-k}	13.68 ^{j-q}	52.86 ^{a-e}	1.86 ^{d-q}	33.52 ^{h-q}	13.48 ^{w-AB}
SO-BOH-125	33.80 ^{e-o}	11.49 ^{k-x}	43.98 ^{d-o}	81.21 ^{d-g}	161.82 ^{c-g}	13.72 ^{j-q}	56.54 ^{ab}	2.28 ^{c-j}	31.95 ^{l-w}	23.66 ^{abc}
SO-BOU-42	37.27 ^{a-i}	7.32 ^{t-AB}	39.24 ^{f-q}	42.96 ^{o-A}	101.80 ^{i-v}	15.76 ^{b-n}	38.77 ^{b-n}	1.37 ^{k-u}	37.66 ^{b-h}	17.83 ^{k-p}
SO-BOU-45	34.14 ^{d-o}	18.68 ^{c-i}	36.33 ^{f-q}	34.25 ^{s-C}	74.05 ^{o-y}	18.14 ^{b-f}	36.44 ^{b-o}	1.22 ^{m-w}	37.27 ^{b-i}	14.21 ^{t-AB}
SO-BOU-46	41.53 ^a	10.60 ^{m-y}	42.17 ^{d-p}	56.37 ^{h-s}	130.12 ^{e-l}	17.17 ^{b-j}	49.67 ^{b-i}	1.98 ^{d-n}	35.46 ^{f-n}	15.46 ^{q-x}
SO-BOU-47	33.29 ^{f-o}	13.75 ^{h-t}	32.78 ^{g-q}	47.03 ^{m-y}	90.69 ^{j-x}	14.52 ^{f-p}	42.50 ^{b-m}	1.35 ^{k-u}	27.76 ^{xy}	14.44 ^{t-AB}
SO-BOU-56	30.11 ^{l-o}	8.21 ^{r-A}	30.42 ^{h-q}	37.90 ^{q-A}	77.17 ^{m-y}	15.98 ^{b-n}	45.24 ^{b-k}	1.24 ^{l-v}	30.26 ^{p-y}	13.95 ^{t-AB}
SO-COB-25	35.59 ^{c-m}	13.37 ^{h-u}	34.33 ^{g-q}	29.69 ^{w-D}	67.40 ^{q-z}	16.46 ^{b-m}	33.14 ^{e-p}	0.98 ^{p-x}	31.04 ^{o-y}	14.33 ^{t-AB}
SO-COB-27	34.99 ^{c-n}	21.57 ^{a-g}	57.19 ^{a-i}	57.69 ^{g-r}	125.45 ^{e-o}	14.98 ^{e-o}	31.29 ^{f-p}	1.73 ^{e-r}	31.85 ^{m-w}	12.77 ^{AB}
SO-COB-32	31.22 ^{j-o}	9.52 ^{p-A}	34.40 ^{g-q}	42.76 ^{o-A}	88.14 ^{k-x}	14.48 ^{f-q}	39.91 ^{b-n}	1.27 ^{l-v}	28.56 ^{t-y}	15.70 ^{p-w}
SO-COB-35	29.30 ^{no}	12.95 ^{i-u}	45.72 ^{c-n}	78.54 ^{d-h}	158.09 ^{d-h}	13.34 ^{k-q}	45.13 ^{b-k}	2.13 ^{c-l}	27.81 ^{wxy}	19.89 ^{g-l}
SO-COB-40	31.42 ^{i-o}	12.84 ^{i-v}	38.82 ^{f-q}	64.14 ^{e-o}	128.94 ^{e-l}	11.57 ^{opq}	38.87 ^{b-n}	1.47 ^{i-t}	28.92 ^{r-y}	18.34 ^{j-o}
SO-DAS-01	28.60 ^o	3.30 ^{AB}	18.81 ^{n-q}	23.86 ^{y-D}	49.96 ^{v-z}	10.73 ^q	35.41 ^{c-o}	0.57 ^{u-x}	27.48 ^y	14.06 ^{t-AB}
SO-DAS-02	39.24 ^{a-e}	11.93 ^{j-w}	50.82 ^{c-k}	80.53 ^{d-g}	173.90 ^{b-e}	16.21 ^{b-n}	48.29 ^{b-j}	2.64 ^{b-e}	38.55 ^{a-f}	22.29 ^{a-h}
SO-DAS-03	31.94 ^{h-o}	5.76 ^{w-AB}	21.81 ^{l-q}	29.97 ^{v-D}	57.70 ^{t-z}	15.61 ^{c-n}	41.17 ^{b-m}	0.89 ^{r-x}	32.15 ^{l-v}	15.22 ^{r-z}
SO-DAS-04	35.01 ^{c-n}	18.40 ^{d-j}	53.08 ^{b-j}	51.66 ^{j-w}	100.47 ^{i-v}	18.36 ^{b-e}	35.45 ^{c-o}	1.87 ^{d-p}	42.21 ^a	14.87 ^{s-A}
SO-DAS-05	34.37 ^{d-o}	5.43 ^{w-AB}	29.82 ^{i-q}	59.80 ^{g-q}	116.89 ^{f-r}	16.61 ^{b-l}	50.85 ^{a-g}	1.97 ^{d-n}	37.33 ^{b-i}	20.07 ^{f-k}
SO-DJI-110	33.89 ^{e-o}	4.38 ^{y-AB}	22.76 ^{k-q}	30.55 ^{u-D}	63.48 ^{s-z}	14.60 ^{e-p}	44.20 ^{b-l}	0.91 ^{r-x}	34.94 ^{f-o}	12.50 ^B

SO-DJI-114	36.58 ^{a-k}	17.71 ^{e-l}	61.26 ^{a-g}	47.33 ^{m-y}	103.22 ^{i-u}	17.84 ^{b-g}	28.83 ^{j-p}	1.67 ^{g-r}	35.68 ^{f-n}	15.59 ^{p-x}
SO-DJI-95	37.20 ^{a-j}	5.44 ^{w-AB}	24.59 ^{j-q}	39.03 ^{q-A}	89.03 ^{k-x}	15.09 ^{e-o}	45.97 ^{b-k}	1.19 ^{n-x}	31.72 ^{n-x}	14.53 ^{s-AB}
SO-DJI-96	32.53 ^{f-o}	16.78 ^{e-n}	58.63 ^{a-h}	53.93 ^{i-u}	106.57 ^{h-u}	13.71 ^{j-q}	24.19 ^{l-p}	1.46 ^{i-u}	28.39 ^{u-y}	16.22 ^{o-v}
SO-DJO-65	32.35 ^{g-o}	7.23 ^{t-AB}	38.98 ^{f-q}	53.26 ^{i-v}	107.27 ^{h-u}	15.14 ^{e-o}	50.46 ^{a-g}	1.74 ^{e-r}	36.58 ^{d-k}	13.14 ^{y-AB}
SO-DJO-70	33.85 ^{e-o}	7.60 ^{t-AB}	26.29 ^{j-q}	21.68 ^{A-D}	42.65 ^{xyz}	15.56 ^{c-n}	26.71 ^{k-p}	0.74 ^{s-x}	40.49 ^{a-d}	13.49 ^{u-AB}
SO-DJO-75	40.12 ^{abc}	9.86 ^{o-z}	36.83 ^{f-q}	45.42 ^{m-z}	106.93 ^{h-u}	17.00 ^{b-k}	44.03 ^{b-l}	1.58 ^{h-t}	37.96 ^{b-g}	17.33 ^{m-r}
SO-GLA-04	36.20 ^{a-k}	11.69 ^{k-w}	42.49 ^{d-p}	44.71 ^{n-A}	83.28 ^{l-x}	15.89 ^{b-n}	35.52 ^{c-o}	1.40 ^{j-u}	33.08 ^{j-r}	21.91 ^{b-h}
SO-GLA-48	38.01 ^{a-g}	7.76 ^{s-AB}	36.29 ^{f-q}	51.48 ^{j-w}	120.30 ^{f-q}	16.02 ^{b-n}	47.66 ^{b-j}	1.69 ^{f-r}	32.93 ^{j-s}	15.40 ^{q-y}
SO-GLA-49	34.13 ^{d-o}	6.81 ^{u-AB}	18.82 ^{n-q}	27.64 ^{x-D}	55.68 ^{u-z}	13.07 ^{l-q}	38.30 ^{b-n}	0.72 ^{t-x}	27.32 ^y	14.74 ^{s-AB}
SO-GLA-50	38.27 ^{a-f}	25.43 ^{ab}	73.74 ^{abc}	76.15 ^{d-i}	166.68 ^{b-f}	19.01 ^{abc}	38.31 ^{b-n}	2.92 ^{bc}	37.00 ^{c-j}	24.49 ^a
SO-GLA-51	33.48 ^{e-o}	8.73 ^{q-A}	46.68 ^{c-n}	73.49 ^{d-j}	148.68 ^{d-i}	15.03 ^{e-o}	48.30 ^{b-j}	2.22 ^{c-k}	29.03 ^{r-y}	22.51 ^{a-g}
SO-KAN-119	35.12 ^{c-n}	11.94 ^{i-w}	55.06 ^{a-i}	104.89 ^{bc}	214.55 ^{abc}	11.14 ^{pq}	45.47 ^{b-k}	2.37 ^{b-i}	29.47 ^{q-y}	23.25 ^{a-d}
SO-KAN-125	30.74 ^{k-o}	15.11 ^{g-q}	56.57 ^{a-i}	44.96 ^{n-A}	87.50 ^{k-x}	12.69 ^{n-q}	20.52 ^{nop}	1.17 ^{n-x}	27.34 ^y	16.74 ^{n-s}
SO-KAN-126	41.47 ^{ab}	18.57 ^{c-j}	69.70 ^{a-d}	60.47 ^{f-q}	122.07 ^{e-p}	19.49 ^{ab}	34.67 ^{d-o}	2.35 ^{b-i}	36.05 ^{e-l}	20.40 ^{f-j}
SO-KAN-128	34.86 ^{c-n}	12.77 ^{i-v}	45.27 ^{d-n}	59.83 ^{g-q}	119.01 ^{f-q}	17.82 ^{b-g}	47.17 ^{b-k}	2.10 ^{c-m}	35.75 ^{e-n}	16.31 ^{o-t}
SO-KAN-130	31.36 ^{j-o}	14.69 ^{h-r}	46.22 ^{c-n}	69.02 ^{e-m}	136.97 ^{e-k}	13.03 ^{l-q}	41.43 ^{b-m}	1.79 ^{e-q}	28.22 ^{v-y}	21.01 ^{d-i}
SO-NDA-63	34.59 ^{c-n}	11.00 ^{m-y}	48.78 ^{c-m}	83.69 ^{c-f}	168.77 ^{b-f}	15.20 ^{d-o}	55.68 ^{abc}	2.59 ^{b-f}	28.84 ^{s-y}	23.12 ^{a-e}
SO-NDA-66	33.47 ^{e-o}	11.05 ^{m-x}	21.81 ^{l-q}	11.54 ^{CD}	21.09 ^z	15.80 ^{b-n}	17.45 ^{op}	0.34 ^{wx}	34.21 ^{g-p}	13.14 ^{x-AB}
SO-NDA-67	35.05 ^{c-n}	22.23 ^{a-f}	56.15 ^{a-i}	63.87 ^{e-o}	128.19 ^{e-n}	17.54 ^{b-i}	39.14 ^{b-n}	2.22 ^{c-k}	32.41 ^{l-u}	22.57 ^{a-f}
SO-NDA-70	36.38 ^{a-k}	10.76 ^{m-y}	48.93 ^{c-l}	71.46 ^{d-k}	141.76 ^{e-j}	13.85 ^{i-q}	43.93 ^{b-l}	1.97 ^{d-n}	30.70 ^{p-y}	12.78 ^{AB}
SO-NDA-81	36.47 ^{a-k}	16.36 ^{f-o}	80.81 ^{ab}	129.66 ^a	258.89 ^a	15.04 ^{e-o}	45.85 ^{b-k}	3.92 ^a	35.95 ^{e-m}	20.35 ^{f-j}
SO-NIK-100	40.21 ^{abc}	10.16 ^{n-z}	37.02 ^{f-q}	54.40 ^{i-t}	111.60 ^{g-s}	15.77 ^{b-n}	46.69 ^{b-k}	1.71 ^{f-r}	38.67 ^{a-f}	14.54 ^{s-AB}
SO-NIK-84	35.52 ^{c-m}	27.58 ^a	81.99 ^a	86.58 ^{b-e}	174.29 ^{b-e}	13.69 ^{j-q}	30.07 ^{h-p}	2.41 ^{b-h}	28.48 ^{u-y}	23.33 ^{abc}
SO-NIK-87	32.67 ^{f-o}	3.58 ^{zAB}	14.15 ^{pq}	23.74 ^{y-D}	44.44 ^{w-z}	15.42 ^{c-n}	52.02 ^{a-e}	0.73 ^{s-x}	30.65 ^{p-y}	15.36 ^{r-y}
SO-NIK-95	35.65 ^{b-m}	16.02 ^{f-p}	38.55 ^{f-q}	45.29 ^{n-A}	95.46 ^{j-x}	16.90 ^{b-k}	38.42 ^{b-n}	1.52 ^{h-t}	36.61 ^{d-k}	18.81 ⁱ⁻ⁿ
SO-NIK-98	29.83 ^{mno}	16.99 ^{e-m}	26.29 ^{j-q}	31.65 ^{t-D}	62.36 ^{s-z}	11.62 ^{opq}	29.41 ^{i-p}	0.75 ^{s-x}	37.37 ^{b-i}	15.86 ^{p-v}
SO-OUA-82	34.85 ^{c-n}	5.09 ^{x-AB}	26.89 ^{j-q}	48.69 ^{k-x}	93.19 ^{j-x}	14.22 ^{g-q}	51.98 ^{a-e}	1.36 ^{k-u}	34.27 ^{g-p}	13.05 ^{zAB}
SO-OUA-84	36.40 ^{a-k}	25.19 ^{abc}	52.46 ^{b-j}	39.64 ^{p-A}	85.65 ^{k-x}	18.35 ^{b-e}	30.36 ^{g-p}	1.48 ^{i-t}	39.91 ^{a-e}	17.71 ^{l-q}
SO-OUA-85	36.64 ^{a-k}	10.90 ^{m-y}	36.95 ^{f-q}	47.97 ^{l-x}	99.46 ^{i-v}	16.18 ^{b-n}	43.83 ^{b-l}	1.51 ^{h-t}	35.89 ^{e-m}	15.00 ^{s-A}
SO-OUA-93	36.62 ^{a-k}	16.77 ^{e-n}	44.45 ^{d-n}	75.06 ^{d-i}	148.75 ^{d-i}	17.90 ^{b-g}	55.11 ^{a-d}	2.57 ^{b-g}	35.13 ^{f-o}	22.95 ^{a-e}
SO-OUA-94	37.66 ^{a-h}	14.42 ^{h-r}	57.66 ^{a-i}	92.23 ^{bcd}	198.64 ^{bcd}	15.94 ^{b-n}	70.25 ^a	2.97 ^{bc}	27.39 ^y	20.85 ^{e-i}
SO-OUE-21	37.88 ^{a-g}	1.54 ^B	15.29 ^{opq}	42.12 ^{o-A}	80.19 ^{l-x}	15.45 ^{c-n}	53.64 ^{a-e}	1.26 ^{l-v}	41.08 ^{abc}	19.65 ^{h-l}
SO-OUE-23	35.69 ^{a-m}	17.80 ^{d-k}	42.07 ^{d-p}	28.79 ^{w-D}	61.27 ^{s-z}	17.69 ^{b-h}	28.35 ^{j-p}	1.02 ^{o-x}	35.61 ^{f-n}	19.09 ⁱ⁻ⁿ
SO-OUE-36	34.67 ^{c-n}	7.01 ^{u-AB}	27.25 ^{j-q}	32.94 ^{s-D}	70.52 ^{p-z}	13.96 ^{h-q}	39.54 ^{b-n}	0.95 ^{q-x}	33.33 ^{i-q}	15.01 ^{r-A}

SO-OUE-39	31.54 ^{i-o}	8.18 ^{r-AB}	21.95 ^{l-q}	10.72 ^D	24.32 ^{yz}	13.61 ^{j-q}	13.33 ^p	0.33 ^x	29.04 ^{r-y}	16.24 ^{o-u}
SO-OUE-41	36.52 ^{a-k}	19.89 ^{b-h}	69.37 ^{a-e}	71.02 ^{d-l}	157.04 ^{d-h}	18.97 ^{a-d}	38.49 ^{b-n}	2.71 ^{bcd}	28.57 ^{t-y}	24.31 ^{ab}
SO-TAN-05	36.38 ^{a-k}	5.41 ^{w-AB}	20.97 ^{m-q}	35.53 ^{r-B}	75.69 ^{n-y}	13.95 ^{h-q}	38.24 ^{b-n}	0.97 ^{p-x}	28.72 ^{t-y}	15.54 ^{q-x}
SO-TAN-09	32.76 ^{f-o}	6.19 ^{v-AB}	11.30 ^q	11.96 ^{BCD}	25.55 ^{yz}	16.61 ^{b-l}	40.06 ^{b-n}	0.43 ^{vwxy}	36.61 ^{d-k}	14.34 ^{t-AB}
SO-TAN-10	31.86 ^{h-o}	11.48 ^{k-x}	23.37 ^{k-q}	22.69 ^{z-D}	44.69 ^{w-z}	12.71 ^{m-q}	22.11 ^{m-p}	0.58 ^{u-x}	40.86 ^{abc}	15.21 ^{r-z}
SO-TAN-15	33.95 ^{e-o}	14.18 ^{h-s}	41.87 ^{d-p}	48.69 ^{k-x}	96.50 ^{i-w}	18.02 ^{b-f}	42.09 ^{b-m}	1.77 ^{e-r}	35.53 ^{f-n}	13.14 ^{x-AB}
SO-TAN-19	35.97 ^{a-l}	12.79 ^{i-v}	64.45 ^{a-f}	106.91 ^{ab}	217.11 ^{ab}	14.89 ^{e-o}	51.59 ^{a-f}	3.22 ^{ab}	33.49 ^{i-q}	21.58 ^{c-h}
Mean	34.99	12.5	41.35	52.75	108.68	15.55	40.91	1.64	33.58	17.43
CV (%)	8.30	24.40	32.20	21.40	23	11.60	24.70	26.10	5.90	9.40
Minimum	28.6	1.5	11.3	10.72	21.09	10.73	13.33	0.33	27.32	12.5
Maximum	41.53	27.58	81.99	129.66	258.89	22.26	70.25	3.92	42.21	24.49
LSD (5%)	5.82	6.14	26.81	22.74	50.40	3.64	20.34	0.86	3.99	3.28

Where; DF = days to 50% flowering (days), DM = days to maturity (days), PH = plant height (cm), LL = leaf length (cm), LW = leaf width (cm), CC = chlorophyll content ($\mu\text{mol m}^{-2}$), ND = number of nodes per plant (count), NPB = number of primary branch per plant (count), NPP = Number of pod per plant (count), PL = pod length (mm), NSP= Number of seed per plant (count), BY = biological yield (g), HI = harvest index (%), HSW = hundred seed weight (g), SDW = shoot dry weight (g), RDW = root dry weight (g), RL = taproot length (cm), PC=protein content (%) and OC=oil content (%), YD = yield per ha (Kg), CV (%) = coefficient of variation in percent and LSD (5%) = least significant difference at $P<0.05$. Means with similar letter (s) with in column had nonsignificant difference at $P<0.05$.

Appendix Table 2: Ranges and means of 20 agro-morphological traits of 64 Soybean accessions tested during the 2022/23 main cropping season

Traits	Range				Mean
	Minimum	Accession	Maximum	Accession	
Days to 50% flowering	41.77	SO-TAN-09	67.79	SO-NDA-81	53.60
Days to maturity	113.19	SO-BOU-56	145.48	SO-NDA-81	129.53
Plant height	27.41	SO-OUA-82	65.79	SO-NDA-66	45.70
Leaf Length	6.33	SO-DAS-01	12.23	SO-NDA-81	9.04
Leaf Width	2.99	SO-DAS-01	6.82	SO-GLA-50	4.55
Number of primary branches	1.58	SO-GLA-49	7.01	SO-COB-27	3.94
Number of nodes	4.31	SO-OUE-21	14.73	SO-COB-27	9.37
Chlorophyll contents	342.15	SO-NDA-66	474.36	SO-OUE-23	400.24
Number of pod per plant	10.72	SO-OUE-39	129.66	SO-NDA-81	52.75
Pod length	28.6	SO-DAS-01	41.53	SO-BOU-46	34.99
Number of seed per plant	21.09	SO-NDA-66	258.89	SO-NDA-81	108.68
Shoot dry weight	1.5	SO-OUE-21	27.58	SO-NIK-84	12.50
Taproot lengths	10.72	SO-OUA-82	36.79	SO-NDA-81	22.88
Root dry weight	0.69	SO-NIK-87	7.66	SO-DJI-114	3.03
Biological Yield	11.3	SO-TAN-09	81.99	SO-NIK-84	41.35
100-seeds weight	10.73	SO-DAS-01	22.26	SO-BAN-102	15.55
Harvest index	13.33	SO-OUE-39	70.25	SO-OUA-94	40.91
Yield	0.33	SO-OUE-39	3.92	SO-NDA-81	1.64
Protein	27.32	SO-GLA-49	42.21	SO-DAS-04	33.58
Oil	12.50	SO-DJI-110	24.49	SO-GLA-50	17.43

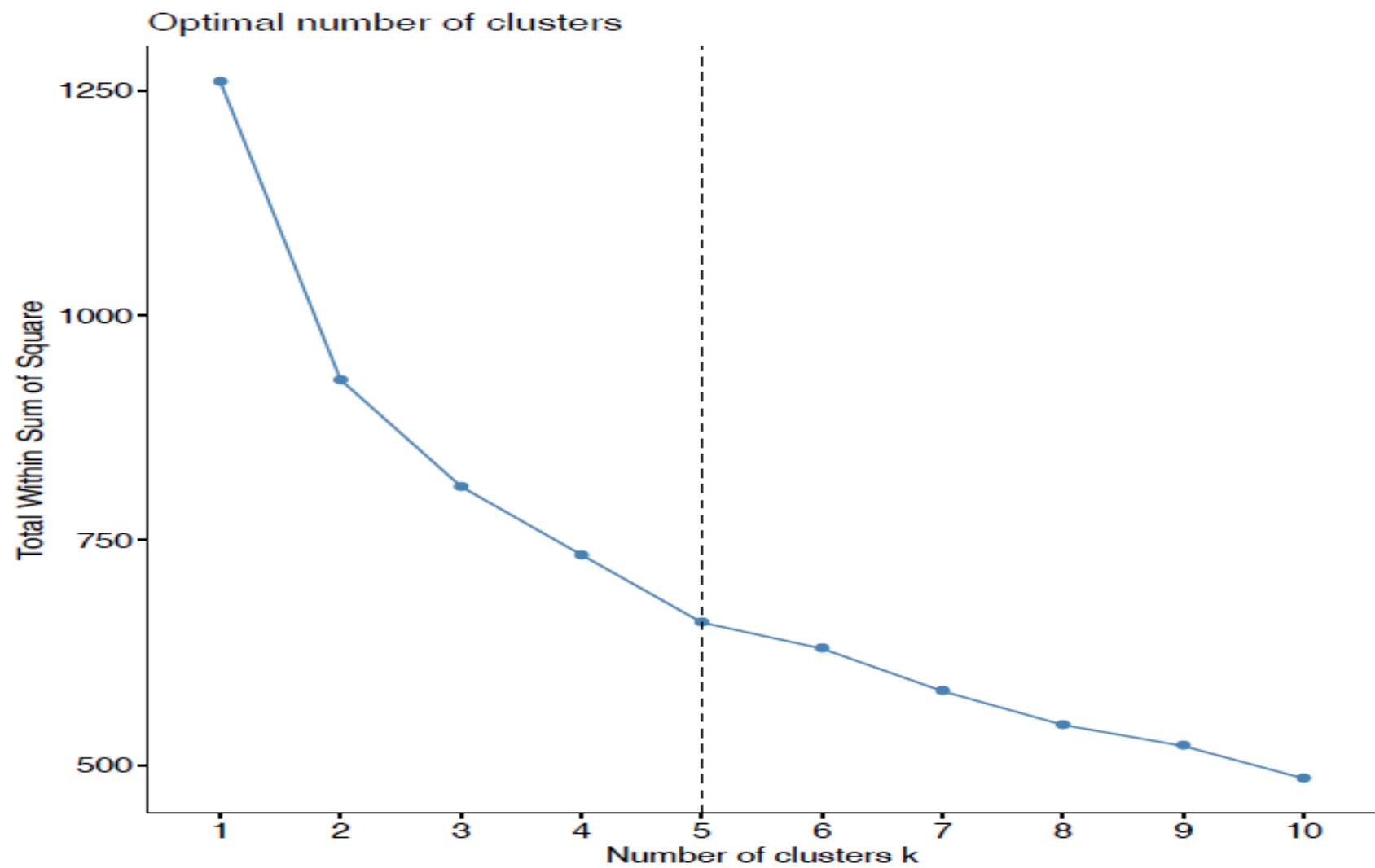
Appendix Table 3: The descriptions of qualitative traits of 64 tested soybean accessions according to (IBPGR, 1984) descriptor

Genotypes	FC	Pb/PA	PbC	PdC	SS	LS	SQ	SL	SCC	HC
SO-BAN-101	Purple	Present	Gray	Black	Oval	Intermediate	Good	Shiny	Impft black	Impft black
SO-BAN-102	Purple	Present	Gray	Tan	Round	Ovate	Good	Shiny	Yellow	Brown
SO-BAN-109	Purple	Present	Tawny	Brown	Round	Ovate	Good	Intermediate	Yellow	Brown
SO-BAN-111	Purple	Present	Gray	Tan	Oval	Ovate	Good	Intermediate	Yellow	Brown
SO-BAN-115	Purple	Present	Gray	Dark brown	Oval	Intermediate	Medium	Intermediate	Yellow	Brown
SO-BOH-119	Purple	Present	Gray	Brown	Oval	Intermediate	Medium	Intermediate	Yellow	Impft black
SO-BOH-125	Purple	Present	Tawny	Brown	Oval	Ovate	Medium	Intermediate	Yellow	Impft black
SO-BOU-42	Purple	Present	Tawny	Brown	Oval	Ovate	Medium	Shiny	Yellow	Brown
SO-BOU-45	Purple	Present	Gray	Dark brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-BOU-46	Purple	Present	Gray	Tan	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-BOU-47	Purple	Present	Tawny	Tan	Round	Ovate	Medium	Shiny	Yellow	Brown
SO-BOU-56	Purple	Present	Tawny	Brown	Oval	Lanceolate	Good	Shiny	Yellow	Brown
SO-COB-25	Purple	Present	Gray	Dark brown	Oval	Intermediate	Good	Shiny	Yellow	Brown
SO-COB-27	Purple	Present	Gray	Black	Oval	Lanceolate	Good	Shiny	Impft black	Impft black
SO-COB-32	White	Present	Tawny	Light brown	Round	Ovate	Medium	Intermediate	Yellow	Buff

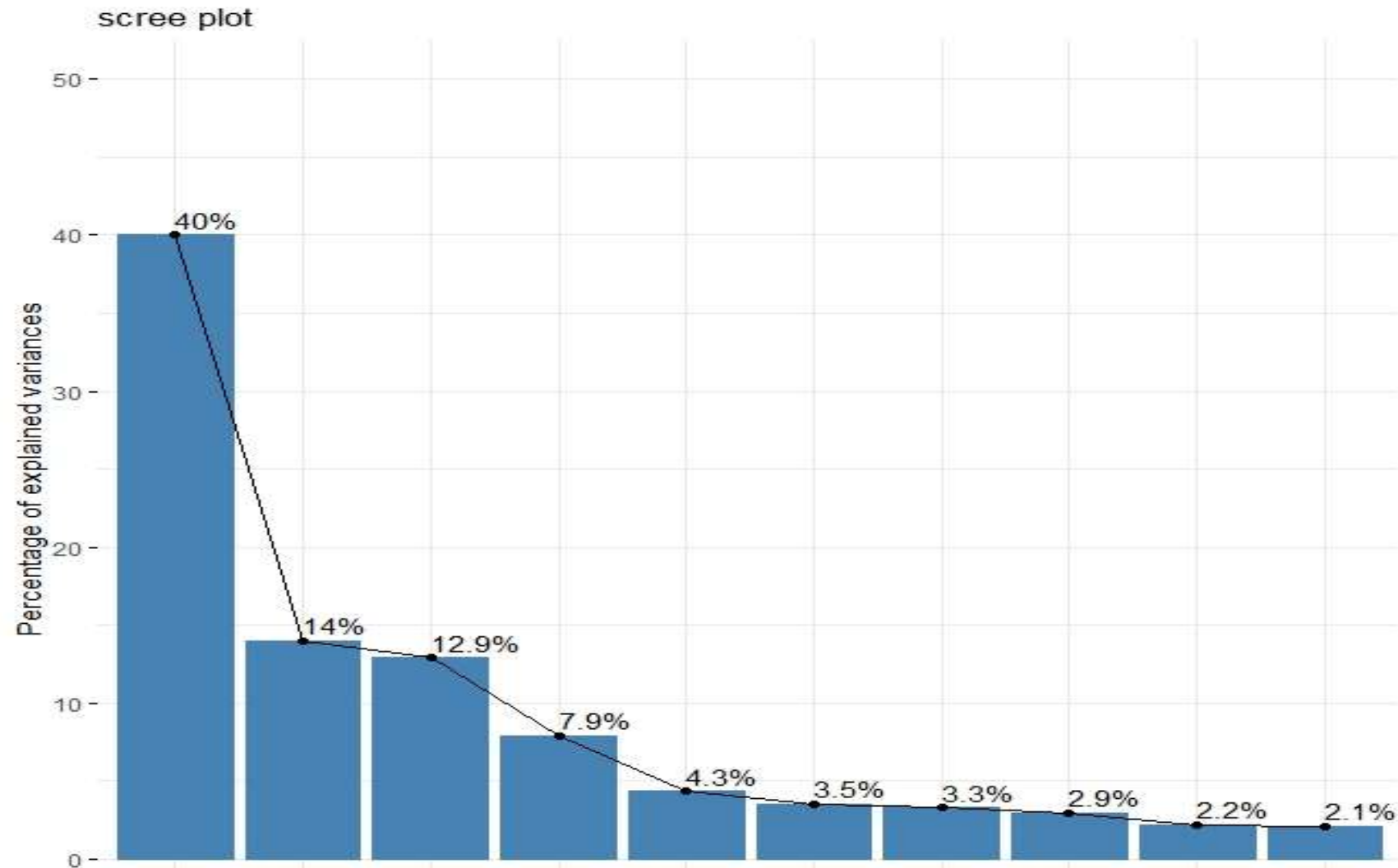
SO-COB-35	Purple	Present	Tawny	Brown	Oval	Intermediate	Medium	Shiny	Yellow	Yellow
SO-COB-40	Purple	Present	Gray	Black	Round	Lanceolate	Poor	Intermediate	Black	Black
SO-DAS-01	Purple	Present	Gray	Brown	Oval	Ovate	Medium	Intermediate	Yellow	Brown
SO-DAS-02	Purple	Present	Gray	Dark brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-DAS-03	Purple	Present	Tawny	Light brown	Round	Ovate	Good	Shiny	Yellow	Brown
SO-DAS-04	Purple	Present	Tawny	Brown	Round	Ovate	Good	Shiny	Yellow	Brown
SO-DAS-05	Purple	Present	Gray	Brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-DJI-110	Purple	Present	Gray	Brown	Oval	Intermediate	Good	Shiny	Yellow	Brown
SO-DJI-114	Purple	Present	Tawny	Dark brown	Round	Lanceolate	Good	Shiny	Yellow	Brown
SO-DJI-95	Purple	Present	Tawny	Tan	Oval	Lanceolate	Good	Intermediate	Yellow	Impft black
SO-DJI-96	Purple	Present	Tawny	Brown	Oval	Ovate	Medium	Intermediate	Yellow	Impft black
SO-DJO-65	Purple	Present	Tawny	Brown	Round	Ovate	Medium	Intermediate	Yellow	Brown
SO-DJO-70	Purple	Present	Tawny	Brown	Oval	Intermediate	Good	Intermediate	Yellow	Brown
SO-DJO-75	Purple	Present	Gray	Light brown	Round	Ovate	Good	Intermediate	Yellow	Brown
SO-GLA-04	Purple	Present	Gray	Dark brown	Oval	Intermediate	Good	Shiny	Yellow	Brown
SO-GLA-48	Purple	Present	Tawny	Dark brown	Oval	Lanceolate	Medium	Shiny	Yellow	Brown
SO-GLA-49	Purple	Present	Gray	Brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-GLA-50	Purple	Present	Tawny	Brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-GLA-51	Purple	Present	Tawny	Brown	Round	Ovate	Good	Shiny	Yellow	Brown
SO-KAN-119	Purple	Present	Gray	Brown	Round	Lanceolate	Medium	Shiny	Yellow	Brown
SO-KAN-125	Purple	Present	Tawny	Brown	Oval	Intermediate	Good	Intermediate	Yellow	Yellow
SO-KAN-126	Purple	Present	Tawny	Brown	Oval	Ovate	Good	Shiny	Yellow	Yellow
SO-KAN-128	Purple	Present	Tawny	Brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-KAN-130	Purple	Present	Gray	Tan	Round	Ovate	Medium	Intermediate	Yellow	Brown
SO-NDA-63	Purple	Present	Tawny	Brown	Oval	Ovate	Medium	Intermediate	Yellow	Brown
SO-NDA-66	Purple	Present	Gray	Dark brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-NDA-67	Purple	Present	Tawny	Dark brown	Oval	Ovate	Good	Intermediate	Yellow	Brown
SO-NDA-70	Purple	Present	Gray	Dark brown	Oval	Ovate	Medium	Intermediate	Yellow	Brown
SO-NDA-81	Purple	Present	Tawny	Brown	Oval	Intermediate	Medium	Intermediate	Yellow	Brown
SO-NIK-100	Purple	Present	Gray	Dark brown	Round	Intermediate	Good	Shiny	Yellow	Brown
SO-NIK-84	Purple	Present	Tawny	Brown	Round	Ovate	Medium	Intermediate	Yellow	Brown
SO-NIK-87	Purple	Present	Gray	Tan	Round	Ovate	Medium	Intermediate	Yellow	Brown
SO-NIK-95	Purple	Present	Tawny	Light brown	Round	Ovate	Good	Intermediate	Yellow	Brown
SO-NIK-98	Purple	Present	Gray	Brown	Oval	Intermediate	Medium	Intermediate	Yellow	Brown
SO-OUA-82	Purple	Present	Tawny	Brown	Oval	Intermediate	Medium	Intermediate	Yellow	Impft black
SO-OUA-84	White	Present	Gray	Light brown	Round	Intermediate	Good	Intermediate	Yellow	Impft black

SO-OUA-85	White	Present	Gray	Brown	Round	Ovate	Good	Shiny	Yellow	Impft black
SO-OUA-93	Purple	Present	Gray	Dark brown	Round	Ovate	Good	Shiny	Yellow	Brown
SO-OUA-94	Purple	Present	Tawny	Brown	Oval	Ovate	Medium	Shiny	Yellow	Brown
SO-OUE-21	Purple	Present	Gray	Brown	Oval	Intermediate	Medium	Intermediate	Yellow	Yellow
SO-OUE-23	Purple	Present	Gray	Tan	Oval	Lanceolate	Good	Intermediate	Yellow	Brown
SO-OUE-36	Purple	Present	Gray	Black	Round	Intermediate	Medium	Shiny	Yellow	Brown
SO-OUE-39	Purple	Present	Tawny	Brown	Round	Ovate	Medium	Shiny	Yellow	Brown
SO-OUE-41	White	Present	Tawny	Brown	Round	Ovate	Medium	Intermediate	Yellow	Impft black
SO-TAN-05	Purple	Present	Tawny	Tan	Round	Ovate	Medium	Intermediate	Yellow	Brown
SO-TAN-09	Purple	Present	Gray	Black	Round	Intermediate	Good	Shiny	Yellow	Yellow
SO-TAN-10	Purple	Present	Gray	Black	Round	Intermediate	Poor	Intermediate	Impft black	Impft black
SO-TAN-15	Purple	Present	Gray	Brown	Oval	Ovate	Good	Shiny	Yellow	Brown
SO-TAN-19	Purple	Present	Gray	Dark brown	Round	Ovate	Good	Shiny	Yellow	Brown

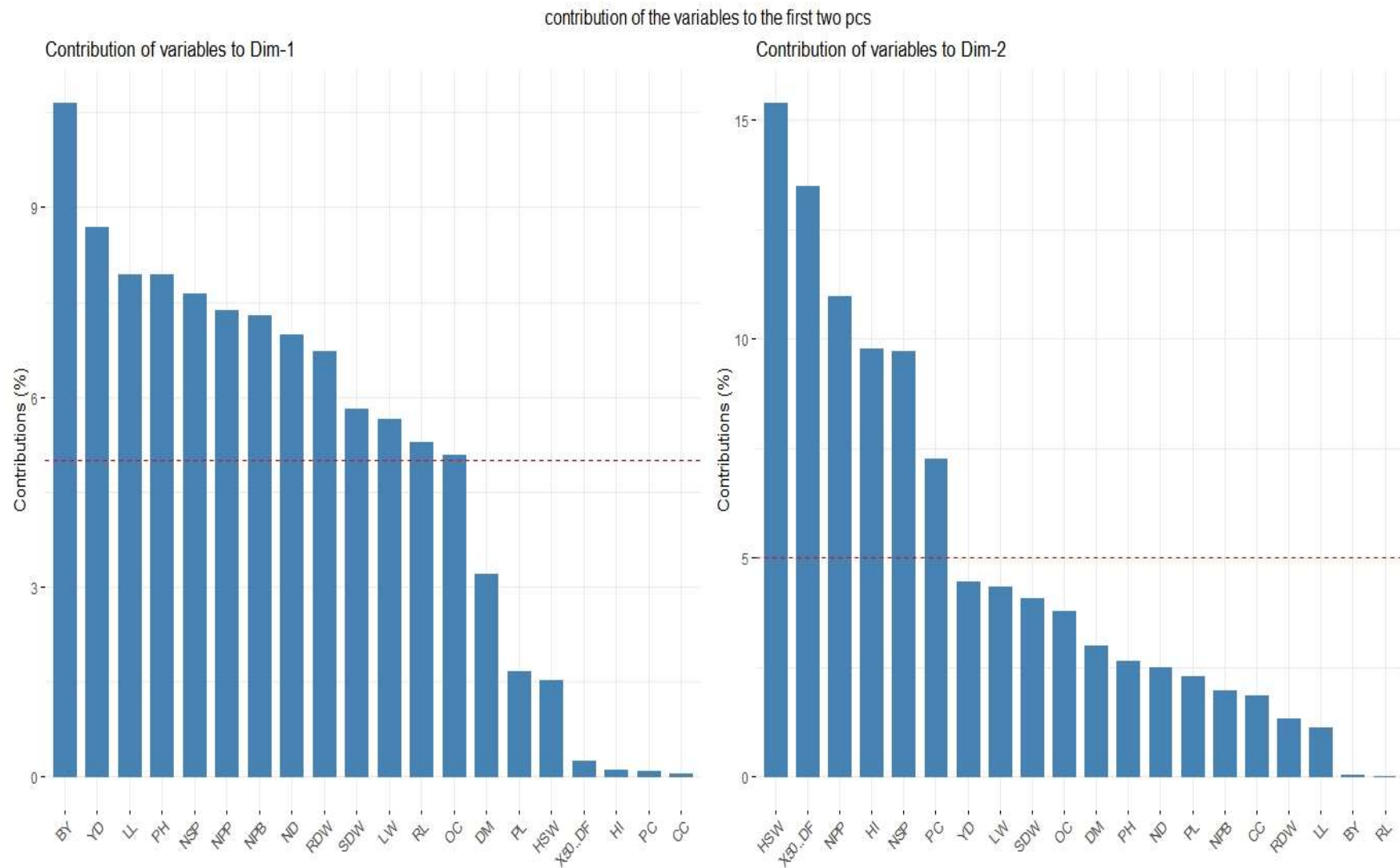
Where; FC = flower color; P/PA = pubescence absent or present; PC = pubescence color; LS = leaf shape; PDC = pod color; SCC = seed coat color; SL = seed luster; HC = hilum color; SQ = seed quality; SS = seed shape



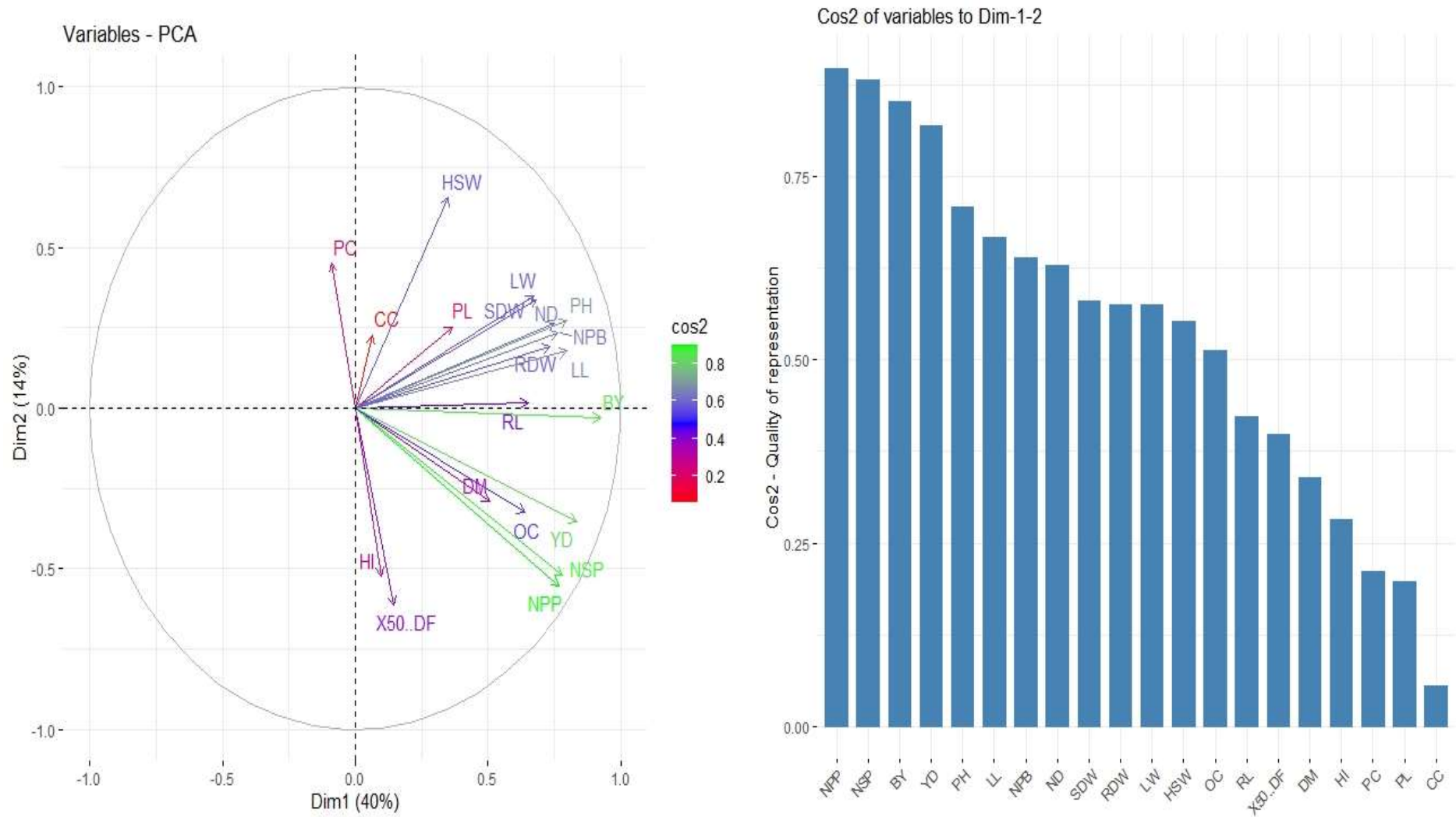
Appendix Figure 1: Plot for optimum number of clusters



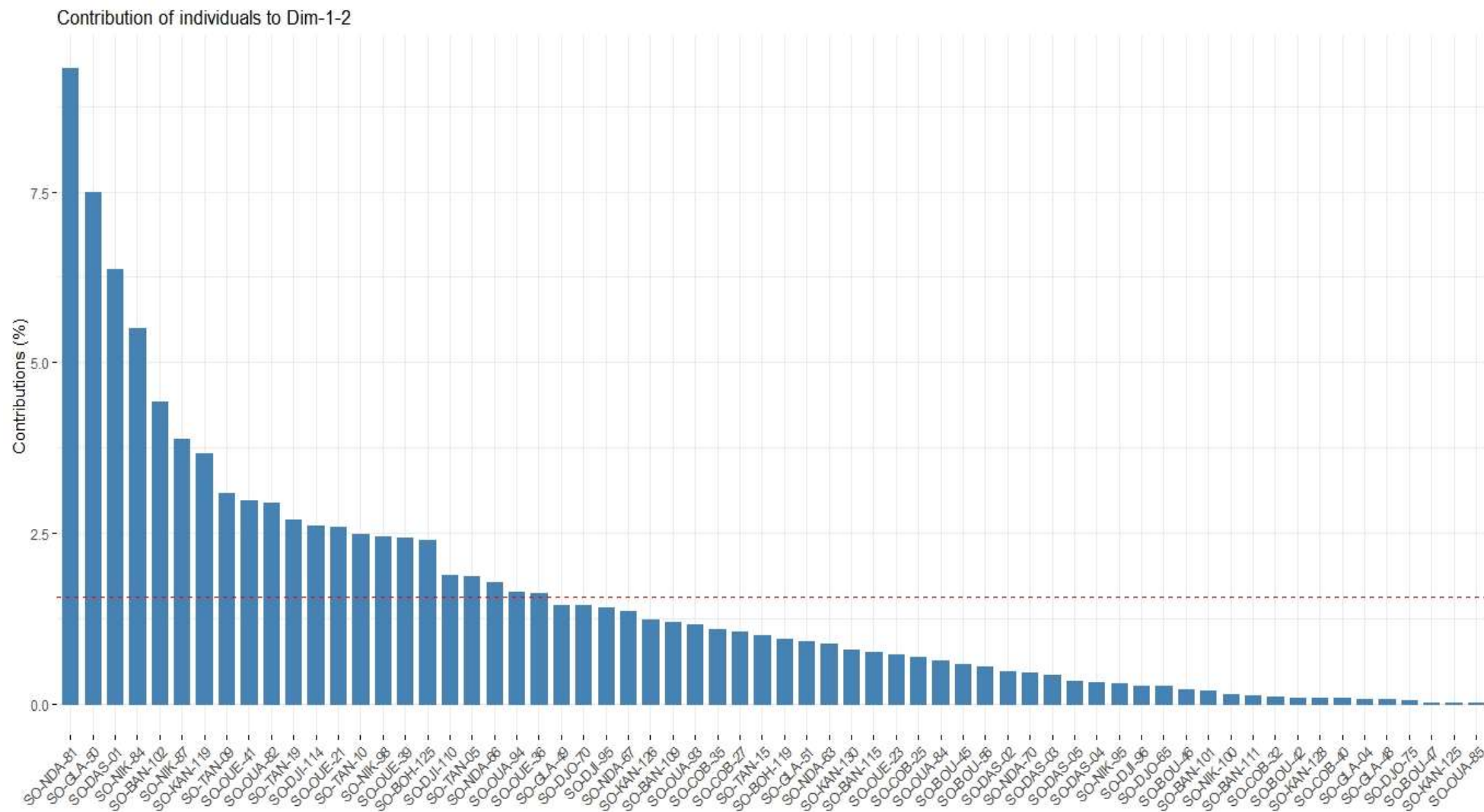
Appendix Figure 2: PCA Scree plot of variances explained by variables



Appendix Figure 3: Contribution of variables to the first two dimensions.



Appendix Figure 4: Contribution of individual variables to the 1st two dimensions



Appendix Figure 5: Contribution of individual genotypes to the 1st two dimensions