GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN SOYBEAN (*Glycine max* L. Merrill) GENOTYPES

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GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN SOYBEAN (Glycine Max L. Merrill) GENOTYPES

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BY

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APPROVAL SHEET

As Thesis Research advisor, I hereby certify that I have read and evaluated this thesis prepared, under my guidance, by **Besufekad Enideg**, entitled **Genetic Variability and Character Association in Soybean (*Glycine Max* L. Merrill) Genotypes**. I recommend that it be submitted as fulfilling the thesis requirement.

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DEDICATION

To my mother ETALEMAHU GIZAW to whom I shall remain indebted.

STATEMENT OF THE AUTHOR

First, I declare that this thesis is my original work and that all sources of materials used for this thesis have been dully acknowledged. This thesis has been submitted in partial fulfillment of the requirements for M. Sc. degree in Plant Breeding at the Jimma University and is deposited at the university Library to be made available to borrowers under rules of the library. I solemnly declare that this thesis is not submitted to any other institutions anywhere for award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

The author was born on July 22, 1985 in Addis Ababa, Ethiopia. He attended his primary school at Elay Elementary school from 1993 to 1998, and RasGobena elementary school from 1999 to 2000, and secondary high school at Gambella Senior Secondary School from 2001 to 2004.

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ABBREVIATIONS

AVRDC	Asian Vegetable Research Development Center
CSA	Central Statistical Agency
ECV	Environmental Coefficient of Variation
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agriculture Organization of the united nation
FAOSTAT	Food and Agriculture Organization Statistics
GA	Genetic Advance
GAM	Genetic Advance as Percent of the Mean
GCV	Genetic Coefficient of Variation
H^2	Broad Sense Heritability
JARC	Jimma Agricultural Research Center
MASL	Meter Above Sea Level
MoARD	Ministry of Agriculture and Rural Development
NGO	Non-Governmental Organization
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variance
SB-RVT	Soybean Regional Variety Trial
SAS	Statistical Analysis System
USDA	United States Department of Agriculture

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ABSTRACT

Information on the extent and pattern of genetic variability, interrelationship among different agronomic characters and knowledge of diversity are essential to design breeding strategies in the available germplasm of soybean and helps to identify elite genotypes that will be incorporated into soybean crop improvement programs to address the growing demand of the crop in Ethiopia. Forty-nine soybean (Glycine max (L.) Merrill) genotypes were tested in 7x7 simple lattice design at Jimma and Assosa with the objectives of estimating genetic variability and associations among characters, and to estimate genetic divergence and, thereby, to cluster the test genotypes into genetically divergent classes. Analysis of variance revealed that there was statistically significant difference among the forty nine genotypes for most of the traits studied except root volume and root dry weight at Jimma. The relatively wide range of the mean values for most of the characters indicated the existence of variations among the tested genotypes. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was recorded for grain yield, biomass yield, pod number per plant, plant height, total nodules per plant, effective nodules per plant, and harvest index at both locations. The highest heritability value was recorded for grain yield at both locations. High heritability, coupled with high expected genetic advance as percent of mean, was observed for grain yield, harvest index, biomass yield, total nodules per plant, effective nodules per plant and pod number per plant across both locations. This indicates that the characters can be improved through selection. Days to 50% flowering, days to pod setting and days to maturity showed negative and significant genotypic and phenotypic association with grain yield at Jimma. Grain yield was negatively and significantly correlated with biomass yield, pod number per plant and hundred seed weight both at genotypic and phenotypic levels at Assosa. Genotypic path analysis revealed that effective nodules per plant and pod number per plant at Jimma and Assosa, respectively exerted the highest positive direct effect. The D^2 analysis grouped the 49 soybean genotypes into five and three distinct clusters at Jimma and Assosa, respectively. The principal component analysis revealed that 6 and 5 principal components at Jimma and Assosa, respectively have accounted for 79.90% and 73.81% of the total variation, respectively.

1. INTRODUCTION

Soybean *Glycine max* (L.) Merrill] (2n= 14) belongs to the family *Leguminacae*, subfamily *Papilionoideae*, tribe *phaseolae*, and genus *Glycine*. It is reported to be originated in Asia, probably in north eastern China about 2500 B.C. (Poehlman and Sleeper, 1995). Since then, it has spread to different countries in the world and become an established component of world agriculture.

It is the world's leading source of oil and protein. It has the highest protein content (40%) of all food crops and is second only to groundnut in terms of oil content (20%) among food legumes (Norman *et al*., 1995; Soy Stats 2008; Poehlman and Sleeper, 1995). The meal is also rich in minerals, particularly calcium, phosphorus and iron (Ogoke*et al.,* 2003).

The majority of the soybean crop is processed into oil and meal. Oil extracted from soybeans is made into shortening, margarine, cooking oil, and salad dressings. Soybeans account for 80 percent or more of the edible fats and oils consumed in the United States. Soy oil is also used in industrial paint, varnishes, caulking compounds, linoleum, printing inks, and other products. Development efforts in recent years have resulted in several soy oil-based lubricant and fuel products that replace non-renewable petroleum products (Gibson and Benson, 2005).

Since soybean is a leguminous crop, it fixes its own nitrogen in association with *Bradyrhizobiurnjaponicum.* If soybeans have not been grown on the field or it has been many years since soybeans were raised, an inoculant should be applied at planting to establish the bacteria in the soil (Hoeft*et al.,* 2000).

The soybean is a day length sensitive crop. Length of daylight is the principal factor that affects the amount of vegetative growth before flowering begins. The ideal situation is that the plants grow to a reasonable size (2-3 feet) before they bloom. Large plants tend to bear a large number of seeds. Thus, seed yield potential per plant is closely related to the day length requirement of the variety and to the season of planting. It is recommended, therefore, that in the preliminary stages of developing soybean as a crop in a new region, several varieties be

tried as well as several planting dates, and that careful notes be taken including planting date, date of flowering, harvest date, and number of seeds per plant (Gibson and Benson, 2005).

Soybean is a hot weather crop suitable for year-round growth in most parts of the tropics. Temperatures of at least 15^0 c are needed to germinate the seed and mean temperatures of 20-25 ^{0}c to grow the crop. Soybeans need at least moderate soil moisture in order to germinate and for seedlings to become established, but need dry weather for the production of dry seed. Soybeans suffer if the soil is waterlogged.

In 2007, the total cultivated area of soybean in the world was 90.19 million hectares and the total production was 220.5 million tons (FAO, 2009).United States of America is the leading soybean producer and exporter with annual production of 70 million metric tonnes in 2007.The second largest producer and exporter Brazil produced 61.0 million metric tonnes in the same year. Argentina, China and India produced 47, 14.3 and 9.3 million metric tons respectively in the year 2007 (USDA, 2008).

In 2005, the U.S. was the number one soybean consumer in the world with a total amount of 51 million tones followed by Brazil 32 million tones, Argentina 31 million tones and China 25 million tons (USDA, 2008). In 2007/08 a total of 236.8 million tons of soybean was produced worldwide (FAO, 2008).

Twenty-one African countries now produce soybean. Nigeria has the highest 6-year (2000-05) average production of 486,000 tons on an area of 553,260 hectares, followed by South Africa with 205,270 tons from 122,870 hectares, and Uganda with 155,500 tons from 139,500 hectares (IITA 2008).

In Ethiopia, soybean is grown over wider agro-ecologies especially in low to mid altitude areas (1300 to 1700 masl) that have moderate annual rainfall (500-1500mm) (Gurmu*et al*,. 2009). The area covered under soybean is 6,236 hectares and the total production of the crop in the country is 78,989 quintals. The productivity of the crop is 12.67 quintals per hectare

(CSA, 2008) which is very low as compared to the productivity of the crop in the world (FAO, 2009). This is attributed to lack of improved varieties, biotic factors such as diseases and insect pests, and abiotic factors.

Diseases such as rust, red leaf blotch, frog-eye leaf spot, bacterial pustule, bacterial blight, and soybean mosaic virus are problems to be resolved in soybean. Soybean rust (*Phakopsorapachyrhizi*) particularly is the most destructive foliar disease of soybean in recent times, and can cause 50–60% yield loss. It is a major disease worldwide. Among insect pests, pod sucking and defoliating insects are major constraints (IITA, 2009).

Lack of varieties tolerant to midseason moisture stress and high yielding varieties tolerant to low phosphorus are among the abiotic constraints. Research on seed quality such as protein, oil, carbohydrate, and anti-nutritional factors is lacking. Moreover, lack of emphasis on using molecular markers as aid to conventional breeding is also worth mentioning (IITA, 2009).

Much effort has been made to improve soybean productivity in Ethiopia since conception of soybean breeding in the country (Asfaw*et al.* 2003). As a result some varieties have been released. For further improvement of the crop the knowledge of variability and association of yield and its related traits is essential. Therefore this research project was conducted with the following objectives:

- To estimate the extent of phenotypic and genotypic variability, heritability and the genetic advance expected under selection.

- To estimate association among yield and yield related traits.

- To estimate the genetic distance between the clusters

2. LITERATURE REVIEW

2.1. Taxonomy, Evolution and Distribution

2.1.1. Taxonomy

Soybean belongs to the family Fabaceae (Leguminosae), subfamily Papilionoideae, tribe Phaseoleae and genus Glycine. Linnaeus (1737), listed eight Glycine species, all of which were subsequently moved to other genera with the exception of *G. javanica*, which remained as the lectotype in the genus until 1766 (Hitchcock and Green, 1947). Soybean has been known under various names, including *G. hispida*, *G. soja* and *G. max*. Kelsey and Dayton (1942), considered *G. soja* to be the approved botanical name, but the name G. max, proposed by Merrill (1917), is widely accepted as the valid designation.

According to recent taxonomical classification, soybean belongs to the genus *Glycine*, which has two subgenera: *Soja* and *Glycine*. Cultivated soybean (*G. max*) and its wild annual relative *G. soja* belong to the subgenus *Soja*. The subgenus *Glycine* contains 16 wild perennial species, mostly found in Australia. All of these species generally carry 2n = 40 chromosomes, except for *G. hirticaulis, G. tabacina* and *G. tomentella* (Vaughan and Hymowitz, 1983; Brown *et al.,* 1987; Hymowitz*et al.,* 1997). Some of these wild perennial species also have polyploidcytotypes. Glycine is believed to be an ancient polyploid having × = 10; however, plants with 2n = 40 behave cytologically like diploids. The annual Glycine is derived from the perennial forms.

The subgenus *Soja* is most diverse in the eastern half of north China, whereas maximum diversity for the subgenus *Glycine* occurs in Australia. The wild perennial Glycine species found outside of Australia were taken to other neighboring regions by migratory birds via long distance dispersal (Hymowitz*et al.*, 1997).

2.1.2. Evolution

The genus *Glycine* is thought to be of ancient polyploid origin due to the high chromosome number of the majority of the species (*n* = 20) compared to closely related genera (mostly *n* = 10 or 11, one with *n* = 14; Goldblatt, 1981). Additional lines of evidence exist, including cytogenetic studies in haploid *G. max* (Crane *et al*., 1982), supporting this hypothesis of polyploidy origin. Schuelter*et al*. (2004), found that the *Glycine* genome has gone through two major rounds of duplication, the first estimated at 41.6 million years ago and another at 14.5 million years ago. Van *et al*. (2008), looked at evolutionary events, revealing that the recent divergence of two soybean homologous regions occurred at 60 and 12 million years ago, respectively. Clarindo*et al*. (2007) found that the karyograms support soybean's tetraploid nature (4× = 40), specifically for the presence of chromosomes with identical morphology, and suggested that chromosome rearrangements may have occurred during the speciation of *G. max*.

The genus *Glycine* Willd.is divided into two subgenera, *Glycine* (perennials) and *Soja*(Moench) F.J. Herm. (annuals). The perennial species are extremely diverse in morphology, cytology and genome composition. They grow in very diverse climatic and soil conditions and have a wide geographic distribution. The species have been screened for many physiological and biochemical traits as well as for sources of resistance to economic pathogens. Some perennial *Glycine* species are sources of resistance to soybean cyst nematode and a source of lack of Bowman-Birk protease inhibitor (Hymowitz, 2004).

2.1.3. Distribution

Soybean is believed to be of Chinese origin, having been derived from a slender, twig-like plant known as *G. ussuriensis.* Nagata (1960), suggested that the species originated in China proper, probably in the north and central regions. Piper and Morse (1923), considered that the wild form *G. ussuriensis* was known to occur in China, Manchuria and Korea and stated that soybean is native of eastern Asia. According to Hymowitz (1970), *G. ussuriensis* grows wild in Korea, Taiwan and Japan throughout the Yangtze valley, the northern provinces of China and the adjacent areas of the former USSR. Based on cytogenetic evidence, Hymowitz (1970) concluded that *G. max* and *G. ussuriensis* are the same species and also stated that historical

and geographical evidence points to the eastern half of northern China as the area where soybean was first domesticated around the 11th century BC. Nagata (1960) suggested that the cultivated form of soybean was introduced into Korea from China and then disseminated to Japan between 200 BC and the third century AD. Shipments of soybeans and soybean products were made to Europe around 1908 and soybean attracted worldwide attention. Aiton (1814) indicated that soybean was first brought to England in 1790 and cultivated at the Royal Botanic Gardens, Kew, in that year.

Hymowitz and Barnard (1991) made a detailed account of early introductions in the USA and mentioned that during the first two decades, new soybean accessions were introduced from India and China into the USA by plant explorers.

Soybean was introduced to neighboring countries (Japan, India, Nepal, Russia) from China around the first century AD. It appears that missionaries may have been the first to bring soybean to Europe early in the 18th century. Soybean was first introduced to the USA in 1765 (Hymowitz and Harlan, 1983) and was then spread to Canada and Latin America. Soybean production began only recently in Africa, during the second half of the 20th century. Soybeans were taken to Brazil and Argentina in 1822 and 1862, respectively (Larreche and Brenta, 1999).

2.1.4. Centres of diversity

Thousands of soybean landraces with great genetic diversity have been selected and preserved by Chinese farmers during a long history of cultivation. The Yellow River region of China is generally considered as the centre of origin of soybean, based on the existence of a great number of wild soybeans and the earliest record of soybean in China (Hymowitz and Kaizuma, 1981). Wild soybean (*G. sojaSieb.* and*Zucc*.) is widely distributed in nearly all provinces of China, Korea, Japan and parts of Russia (Hymowitz and Singh, 1987). Based on tremendous diversity in cultivated and wild soybean, China has collected 23,000 accessions of *G. max*. In addition, 5300 accessions of *G. soja* have been conserved in a gene bank for long-term storage.

Thirteen wild perennial species of soybean collected by USDA explorers are indigenous to Australia (Hymowitz and Bernard, 1991). All carry 2n = 40 chromosomes. *G. tabacina* (Labill.)Benth., with 2n = 40 or 80 chromosomes, has been found in Australia, Taiwan, the South Pacific Islands and the islands of the west central Pacific. All accessions of *G. tabacina* collected outside of Australia are tetraploid (2n = 80) and, even including Australia, the tetraploid predominates over the diploid form (Singh *et al.*, 1987, 1989; Hymowitz and Bernard, 1991), demonstrating that the complexes of *G. tabacina* and *G. tomentella* evolved through alloploidy in Australia. This clearly indicates that the wild perennial species of soybean have invaded Australia and associated areas, and the wild annual *G. soja* has invaded central and northern Asia. Since *G. soja* is the wild ancestor of soybean (Hymowitz and Newell, 1981) and all morphological and genetic variability exist in China in the form of landraces and primitive cultivars, this indicates that China is the centre of diversity.

2.2 Genetic Variability

Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1960; Falconer and Mackay, 1996). If the character expression of two individuals could be measured in the environment identical for both, differences in the expression would result from genetic control and hence such variation is called genetic variation (Welsh, 1981; Falconer and Mackay, 1996).

Developing crop cultivars with high seed and oil yield and with desirable nutritional and feed quality has been the principal aim of soybean breeding programs worldwide. The strategy of crop improvement of any trait comprises the collection or generation of highly ranking variant types of populations and the progressive reduction of them by selection (Ashley, 1999).
The presence of variation in the germplasm for the trait of interest is, therefore, very important. Information on the nature and magnitude of genetic variability present in a crop species is thus important for developing effective crop improvement program (Singh *et al.*, 1980; Welsh, 1981).

Genetic variability, which is due to the genetic differences among individuals within a population, is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations (Welsh, 1990; Sharma, 1998). In addition, estimation of the magnitude of variation within germplasm collections for important plant attributes will enable breeders to exploit genetic diversity more efficiently (Jahufer and Gawler, 2000).

Effective selection is dependent on the existence of genetic variability. The characterization of this variability in a population is pertinent since genetic diversity within population and within species determines the rates of adaptive evolution and the extent of response in crop improvement.

As in other major crops, genetic diversity of soybean commercially grown cultivars has been decreasing at an alarming rate. The narrowness of North American (Gizlice*et al.,* 1994; Sneller, 1994) as well as Brazilian (Vello*et al.,* 1984) soybean germplasm has been well documented by pedigree analyses. Gizlice*et al.* (1994) determined that only 35 ancestors contributed more than 95 % of all alleles and only five lines account for more than 55 % of the genetic background of public cultivars in North America. Similarly, Gai*et al.* (1998) and Wang *et al.*,(2008), reported that 651 soybean cultivars released from 1923 to 1995 in China could be traced back to only 308 ancestors or about 1.5% of the germplasm resources available in China.

According to Poehlman (1979) and Welsh (1981), dissimilarity will always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success in a crop improvement program. Frey (1981) indicated that the extent of the genetic variability in a specific breeding population depends on the germplasm included in it. Hence, genetic variability is of immense importance to plant breeders because it can be transmitted to the progeny and the proper management of the diversity can produce permanent gain in the performance of the plant (Welsh, 1981).

Oya*et al.* (2004) in the study for drought tolerance characteristics of 11 Brazilian soybean cultivars, wide range of variability was observed on the basis of seed yield among all the cultivars studied. The report also indicated that in cultivars with higher drought tolerance crop growth rate during the drought stress period was higher than in other drought susceptible cultivars.

Hufstetler*et al.,* (2007) studied genetic variability in 23 cultivars of soybean for the three physiological traits that may affect performance of soybean when soil water availability is limiting viz. water use efficiency (WUE), regulation of whole plant water use in response to soil water content, and leaf epidermal conductance (ge) when stomata are closed. They reported significant variation (P<.001) among the genotypes for the three traits that determine drought tolerance ability of the soybean crop. Significant differences were found among genotypes for minimum ge values (P <.001) across leaf positions, but there was no difference in ge on the basis of leaf position (upper vs. lower), and no genotype by leaf position interactions were present.

Tahir*et al.* (2009), conducted a research to evaluate the effect of rhizobium inoculation and NP fertilization on growth, yield and nodulation of soybean genotypes the result revealed a wide range of variability among the rhizobium inoculation levels and treatment combinations of NP fertilizer levels and demonstrated significant increase of grain yield and nodulation compared to the un-inoculated genotypes.

Asfaw*et al.* (2009) conducted a research on 11 soybean genotypes in 12 environments on matching varieties onto soybean production environments in Ethiopia and reported grain yield was significantly affected by environments (E), genotypes (G) and genotype x environment interaction (GEI). In the study of variability for quantitative characters in soybean genotypes, Jagdish*et al*. (2000), Jain and Ramgiry (2000), Basavaraja (2002), Bangar*et al.(*2003) and Yadav (2006) investigated wide range of morphological variability.

2.3 Heritability

Heritabilitycanbedefined,inbroadsense,astheproportionofthegenotypicvariabilitytothetotalvariance(Allard,1960).Itreferstotheportionofphenotypicallyexpressed variation,withinagivenenvironmentanditmeasuresthedegreetowhichatraitcanbe modified byselection(Christianson andLewis, 1982). According toFalconerandMackay(1996),heritabilityinnarrowsenseisdefinedas "theratioofadditivegeneticvariancetophenotypicvariance".Sincebroadsenseheritabilitydoesnot giveaclear pictureoftransmissibilityofvariationfromgenerationtogeneration(becausethegenetic variationincludesthefixableandnon-fixabledominanceandepistaticvariation),itsutilization islimited inplant improvementprogram.

Incontrast,estimateofheritabilityinanarrowsensecangiveclearerpicturethanthatofbroadsense(FalconerandMackay, 1996). Estimationofheritabilityasaratioofgenotypic tophenotypicvariancemayvarygreatly dependingup on theunitforwhichvarianceisconsidered(Johnson*etal.*,1955a).

It is obvious that difference due to environment may tend to obscure genotypic variations. The greater the proportion of the total variability that is due to the environment the more difficult it will be to select for inherited differences. On the other hand, if environmental variability is small in relation to heritable differences, selection will be efficient because the characters to be selected will be transmitted to its progeny (Briggs and Knowles, 1987).
If genetic variation in a progeny is large in relation to the environmental variation the heritability will be high or if genetic variation is small in relation to the environmental variation, then heritability will be low (Mittal and Sethi., 2004).

Heritabilityvaluebyitselfcannotprovidethe amount of genetic progress that wouldresult from selectionof the best individuals (Johnson*etal.*,1955a).However,geneticprogressexpectedfromselectionincreaseswithanincreaseingenotypicvariance.Therefore,theutilityofestimateofheritabilityis increasedwhentheyareusedin conjunctionwiththeselectiondifferentialleadingto concomitant estimateof genetic advance expected from selection.

Scully *et al.*(1991) found the heritability of phenological traits (days to flowering and days to maturity) greater than 0.93. The biomass, harvest index and yield had heritabilities of 0.90 to 0.93. The extremely high heritabilities for these traits were attributed to the large genetic diversity among the 112 genotypes. They also noted highly positive genetic, phenotypic and environmental correlations between yield and biomass yield. The genotypic correlations between yield and Phenological traits (days to flowering and days to maturity) ranged from 0.30 to 0.42, with lower phenotypic correlations. Harvest index had the lowest correlation with seed yield at the phenotypic and genotypic level.

High heritability was reported by Aditya*et al,* (2011), for three characters viz, days to 50 per cent flowering, number of primary branches per plant and 100 seed weight (91%) in 31 soybean genotypes.

2.4 Genetic Advance under Selection

Improvement in the mean genetic value of the selected plants over the base population is usually termed as genetic advance under selection. It measures the difference between genotypic values of generation obtained from the selected population over the mean value of the population. Genetic advance under selection is a genotypic value which depends on three things (Allard, 1960). These are genetic variability, heritability or masking effect of non-genetic variability on the genetic variability and the selection intensity applied.

Genetic advance with conjunction to heritability can provide the estimate of expected gain for a particular character (Johnson *et al.*, 1955a). The product of heritability, phenotypic standard deviation and selection differential can estimate it. Burton and Devane (1953) indicated that the genotypic coefficient of variation together with heritability estimate also gives the best picture of expected advances from selection.

Aditya*et al*, (2011), reported high heritability coupled with high expected genetic advance in 31 soybean genotypes for number of pods per plant and dry matter weight per plant.

Genetic progress would increase with increase in the variance. Therefore, the utility of estimates of heritability is increased when they are used in conjunction with the selection differential, the amount that the mean of the selected lines exceeds the mean of the entire group (Johnson *etal*., 1955a). According to Burton and DeVane (1953), genetic advance tell us the estimate of the expected gain for a particular character through selection. Shivakumar (2008), in the study for genetic variability and character association in 64 soybean genotypes reported high heritability coupled with high genetic advance as percent of mean for grain yield and pod number per plant.

2.5. Correlation Coefficients

The various characteristics of crop plants are generally interrelated or correlated. Such correlations can be either negative or positive. In plant breeding and genetic studies, correlated characters are of prime importance because genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes brought about by a natural or artificial selection (Singh, 1993; Falconer and Mackay, 1996; Sharma, 1998).
The relative influence of various traits and their degree of associations can be estimated statistically by correlation (Dewey and Lu, 1959). Determination of relationships of characters can help to identify traits of economic importance.

Generally, three types of correlations are discussed in quantitative genetics and these are phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlations (rp).
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 of the populations. Genetic correlation (rg) is the associations of breeding values (i.e., additive genetic variance) of the two characters.

Studies on genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters in breeding program (Johansson et al., 1955b). Correlations between different characters of crop plants may arise either from genotypic or environmental factors. Environmental correlations arise from the effect of overall environmental factors that vary at different environments. Correlations due to genetic causes are mainly pleiotropic effects of genes and linkage (a phenomenon of genes inherited together) between genes affecting different characters.

Pleiotropy is the property of a gene, which affects two or more characters; as a result it causes simultaneous variations in the two characters when the genes are segregating (Singh, 1993; Falconer and Mackay, 1996).

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. Characters that are not easily measured or which are largely influenced by the environment have low heritability ratio; hence, there is a need to examine the relationships among various characters. Knowledge of the correlations that exist between important characters may facilitate the interpretations of the results that are already obtained, and provides the basis for planning more efficient breeding program. However, as the number of independent variables influencing a particular dependent variable increases, a certain amount of interdependence is expected. Therefore, correlation may be insufficient to explain the associations in a manner that will enable one to decide on either a direct or an indirect selection strategy (Bhatt, 1970).

Correlation coefficients may range in value from -1 to +1. Phenotypic correlations can normally be estimated with a high degree of accuracy. Estimates of genetic correlations however, usually have high standard errors because of difficulties to avoid the directional effects of confounding factors (i.e. dominance and epistatic genetic effects) on additive genetic correlation estimates (Lynch and Walsh, 1998 in Amsal 2001). In addition, genetic

correlations are strongly influenced by gene frequencies, and, therefore, may differ markedly in different populations (Falconer and Mackay 1996).

Estimate of correlations and significance test was previously discussed by several workers (Robertson 1959; Singh and Chaudhary 1977; Sharma, 1998). Depending on the sign genetic correlations between two characters can either facilitate or impede selection progress. Correlation value (r = 1) implies perfect (100%) correlation, where both traits vary hand in hand, r = -1 means there is 100 % correlation between two characters, but they vary in opposite direction, and r = 0 carries the implication that there is no correlation at all between the two characters (Falconer and Mackay 1996; Sharma 1998).

Correlated characters are important for three basic reasons. First, in connection with the genetic causes of correlation through the pleiotropic action of genes.Second, in connection with the changes brought about by selection. And third, in connection with the effect of natural selection on the relationship of metric character with its fitness, which is the primary agent, that determines the genetic properties of that character in a natural population (Falconer and Makey, 1996).

Inadequate knowledge of interrelationships among various traits and the practice of unilateral selection for agronomic traits frequently end up with less than optimum result in plant breeding (Bhatt, 1973). The practical utility of selecting for a given character as a means of improving another depends on the extent to which improvement in major characters is facilitated by selection for the indicators. Such improvement depends not only on the genotypic correlation but also phenotypic correlation (Johnson *et al.*, 1955b).

For selection based on yield component to be effective in increasing yield, Sidwell*et al.* (1976) stated that the components should fulfill the following: they should be highly heritable, the component should be genotypically independent or genotypic correlation among the component should be positive and the component should be physiologically related in a positive manner.

Character association studies provide reliable information on the nature, extent and directions of selection (Kumar and Chauhan, 1979). The knowledge of genetic correlations between different yield attributes becomes of paramount importance when the breeder is confronted with problem of introducing a quantitatively inherited character into some agronomically superior cultivars from wild or uneconomic genotypes (Saraf and Hedge, 1984). Seed yield is a polygenically controlled complex character and is dependent on a number of component traits that are also quantitatively inherited. Selection on seed yield per se is often less effective, making it imperative to go for indirect selection through component traits (Singh, 1983).

Vasic*et al*. (1997) found correlations of plant height and productive height with yield, which were established, via the number of pods per plant and the number of seeds per plant. These results give a clear indication that the yield components are mutually very closely associated. Thus, they concluded that productivity was more dependent on the number of pods per plant than on the number of seeds per pod because the latter characteristic was quite stable in the climatic region. The authors exhibited a positive direct correlation between seed size and yield, which was masked by the negative correlation between seed size and the number of pods per plant. 100-seed weight is positively and strongly correlated with seed length and seed height (Zeven*et al*., 1999) but negatively correlated with number of pods per plant (Nienhuis and Singh, 1986). Seed length is positively correlated with pod length and seed height (Zeven*et al*., 1999). They also found positive correlations between pod length and number of seeds/pod, 100-seed weight, seed length and seed height.

2.6. Path Coefficient Analysis

Although correlation estimates are helpful in determining the components of complex trait such as yield, they do not provide an exact picture of the relative importance of direct and indirect influences of each of the component characteristics of this trait. Path coefficient analysis, which is simply a standardized partial regression coefficient partition the correlation in to direct and indirect effect. The use of this method requires cause and effect relationship among the variables, and the experimenter must assign direction in the casual system based up on priori grounds of experimental evidence (Dewey and Lu, 1959**).**

Singh *et al.* (1985), conducted path coefficient study in pea for ten quantitative traits. They concluded number of pods per plant, number of seeds per pod, 100-seed weight and harvest index are the main yield components affecting yield directly. High indirect effects were contributed by number of branches, plant height and flowering via number of pods per plant; by pod length via 100-seed weight and by maturity via both the component traits. Protein content had negligible effect on seed yield.

Arshad*et al.* (2006), in the study of character correlation and path coefficient in soybean found days to maturity, branches, pod length, pods and 100 seed weight had positive direct effects on grain yield. High indirect effect was also exhibited via pod length by most of the traits hence these characters may be given more emphasis while selecting high yielding soybean lines. Basavaraja (2002), in the study of soybean induced mutagenesis found hundred seed weight exerted positive direct effect on grain yield.
In parameters selection for yield improvement in French bean, Babar *et al*. (2002), identified positive and significant direct effect of days to flowering onseed yield while they found negative direct effects by days to maturity andplant height.

Shivakumar (2008) conducted a research on correlation and path coefficient analysis of some quantitative traits in 40 genotypes of soybean and the result revealed that biological yield and harvest index were major characters influencing seed yield directly and indirectly. The results indicated that biological yield is responsible for manipulation of seed yield in soybean. Basavaraja (2002), Sultana *et al*. (2005) and Gaikwad*et al*. (2007) reported direct effect of pod length on seed yield in soybean genotypes.

2.7. Genetic Divergence

Genetic divergence is the statistical distance between the genotypes. It is determined by using cluster analysis, which assigns genotypes into different groups (Singh and Chaudhary, 1999).

Selection, direct or indirect, can be effective on heritable variability that already exists in a population. Variability can also be created artificially through hybridization technique by crossing genetically distant parents (Arunchalam*et al*., 1984). The effectiveness, however, depends on the genetic divergence among the lines being crossed. The greater the divergence, the greater are the chances of developing superior yielding genotypes. Mahalanobis's D^2 analysis provides a means of grouping the genotypes based upon their genetic divergence (Mahalanobis, 1936). Thus, the estimation of divergence among the lines is of paramount importance.

Crossing of genotypes belonging to the same cluster would not be expected to yield desirable recombinants. Consequently, a crossing program might be formulated in such a way that parents belong to different clusters. The more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining higher amount of heterotic expression of F1's and broad spectrum of variability in segregating populations (Norden, 1980; Rao*et al.*, 1981). The use of D^2 statistic (Mahalanobis, 1936) is one of the most important biometrical techniques for estimating genetic divergences present in a population.

Clustering using D^2(genetic distance) matrix is useful for analyzing the divergence of the population to identify genotypic variability. The D^2statistics measures the forces of differentiation at intra- and inter-cluster levels and determines the relative contribution of each component trait to the total divergence (Sharma, 1998). Clusters separated by the largest D^2(genetic distance) show the maximum divergence, while the genotypes in the same clusters or groups are less divergent (Singh and Chaudhary, 1977). In selecting genotypes from the already chosen groups, other important characteristics such as disease resistance, earliness, quality or even performance of particular characters should be also considered, and selecting one genotype from each group and testing them by different statistical analysis could prove to be fruitful.

Jaylal (1994) carried out genetic divergence study in forty genotypes of soybean using MahalanobisD^2statistics. The Wilk's test revealed highly significant differences (D^2= 242.31) for all the characters, and he grouped the forty genotypes into 9 and 7 clusters respectively,

based on physiological and yield attributes. The analysis for estimating the contribution of characters to the divergence indicated carotene content and total chlorophyll in the case of physiological and pods/cluster, branches/plant and seed yield/plant in the case of yield attributes contributed maximum to the total genetic divergence.

Sarma and Roy (1994) classified 42 early maturing pigeon pea genotypes on the basis of D^2analysis. The analysis of variance revealed significant differences among the 42 genotypes for allthe characters under study, indicating considerable variation among the genotypes. The D^2valuesranged from 11.5 to 2658.6, reflecting wide diversity among the genotypes. Based on thesevalues, they grouped the 42 genotypes into eight clusters. Cluster means for branches/plantpods/plant, harvest index and yield/plant were conspicuous and contributing more to the totalgenetic divergence, which was also reflected by their high coefficient of variation.

Information on the extent of genetic diversity amongst the breeding materials is very important in the crosses between groups with maximum genetic divergence which would be more responsive for improvement since they are likely to produce desirable recombination and segregation in their progenies after hybridization (Norden, 1980; Reddy *et al*., 1988).

Barelli*et al.,* (2005) used 35 landraces of common bean from Brazil to study the divergence among them. They evaluated traits like, number of days to emergence, number of days to flowering, height of the insertion of the first pod, longitudinal length of the pods, total number of pods/plant, number of total seeds/plant, number of seeds/pod and seed weight. The genetic distance measurements using generalized MahalanobisD^2demonstrated greater dissimilarity between genotypes from Mesoamerica and Andean gene pools. Cluster analysis grouped the genotypes into nine clusters; with the most similar cultivars grouped in cluster I. cluster I to V contained landraces from Mesoamerican origin, whereas groups from VII to IX only possess Andean origin.

2.8. Principal Component Analysis

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). PCA can be used to drive a two dimensional scatter plot of individuals, such that the geometrical distance among individuals in the plot reflect the genetic distances among them with minimal distortion. Aggregates of individuals in such a plot will reveal sets of genetically similar individuals (Warburton and Crossa, 2000).

Although, it is easy to make analysis in a multivariable case, inference pertaining to their results is not an easy task. In cluster analysis, there are many distance measures and methods based on these measures. Depending on either distance measure or selected method, the results of cluster analysis could be different and this can lead the researcher in to an uncertainty. That is why, in recent years, in cluster analysis principal component analysis is mostly used. By this way, on the one hand, the number of variables is reduced; on the other hand, the correlation pattern between variables, which is negatively affecting the multi variable analysis methods, can be removed (Bensmail*et al.*, 1997).

The first step in PCA is to calculate Eigen values, which define the amount of total variation that is displayed on the PC axis. The first PC summarizes most of the variability present in the original data relative to all remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on (Jollife, 1986).

3. MATERIALS AND METHODS

3.1 The Experimental Sites

The experiment was conducted at two locations, namely Jimma Agricultural Research Center (JARC) and Assosa Agricultural Research Center (AARC). Jimma Agricultural Research Center is located at 7^0 40'9"N latitude and $36^0$47'6"E longitude at elevation of 1753 m. a. s. l. in south western part of Ethiopia, 365 km away from the capital Addis Ababa. It is categorized under tepid to cool sub-humid (H2) sub agro-ecology zone of the country. The average annual rainfall is 1559 mm. The maximum and minimum temperatures are 26.2^0C and 11.3^0C, respectively. The major soil types of the area are chromic Nitosols and Cambisols in the uplands, whereas Fluvisol is the dominant soil type in the bottom land and almost all soil types have pH less than 5 (EIAR, 2008).

Assossa Agricultural Research Center is located at latitude $10^0$03'12'' N and longtiude: 34^0,59'48''E at elevation of 1950 m. a. s. l. in western part of Ethiopia, 656 km away from the capital Addis Ababa. And it is categorized under Hot to warm moist lowland plain, Tepid to cool humid, sub humid lowland plain, Tepid to cool sub humid mountain. The area receives mean annual rainfall of about 950 mm. Maximum and minimum temperatures of the site are 34.4^0C and 9^0C, respectively. The major soil type of the area is Nitosol with pH of 5.8 (EIAR, 2008).

3.2 Experimental Materials

In this study 49 soybean genotypes (Table 1) were obtained from different sets of soybean variety trial conducted by soybean Breeding Section of Jimma Agricultural Research Center (JARC); that were introduced from Asian Vegetable Research Center (AVRDC) and Mozambique. In addition, released varieties of soybean and collections from Ethiopia were also included in this study.

Table1.Listofsoybean genotypesusedinthis study

No.	Genotype	Origin/source	Source trial	Source of seed
1	SR-4-3	Awassa-IITA	SB-RVT	JARC
2	TGX1895-33F	PAWE-IITA	SB-RVT (MS)	JARC
3	H4	IIAM-Mozambique	SB-RVT	JARC
4	H1	IIAM-Mozambique	SB-RVT	JARC
5	TGX-297-6E1	Awassa-IITA	JM-Seed increase 2007	JARC
6	AGS-7-1	Awassa-IITA	SB-RVT	JARC
7	Crawford	Jimma-IITA	JM-Seed increase 2007	JARC
8	AGS-234	Awassa-IITA	JM-Seed increase 2007	JARC
9	H14	IIAM-Mozambique	SB-RVT	JARC
10	HS-82-2136	PAWE-IITA	SB-RVT	JARC
11	Protana 2	Awassa-IITA	JM-Seed increase 2007	JARC
12	Bossier-2	Awassa-IITA	JM-Seed increase 2007	JARC
13	Essex-1	Awassa-IITA	JM-Seed increase 2007	JARC
14	PR-149-81-EP7	PAWE-IITA	SB-RVT (LS)	JARC
15	IAC-6	IIAM-Mozambique	SB-RVT	JARC
16	Assosa local check-1	AARC-Ethiopia	JM-Seed increase 2007	JARC
17	Clark-63K	JARC-Ethiopia	JM-seed increase 2007	JARC
18	PR-41-(339)	PAWE-IITA	SB-RVT (LS)	JARC
19	TGX-1895-49-F	Awassa-IITA	JM-Seed increase 2007	JARC
20	Davis	PAWE-IITA	SB-RVT (MS)	JARC
21	SR-4-1	Awassa-IITA	JM-Seed increase 2007	JARC
22	IAC-11	IIAM-Mozambique	SB-RVT (MS)	JARC

Table 1 continued

No.	Genotype	Origin/source	Source trial	Source of seed
23	PR-143(14)	PAWE-IITA	SB-RVT (MS)	JARC
24	H18	IIAM-Mozambique	SB-RVT	JARC
25	H2	IIAM-Mozambique	SB-RVT	JARC
26	PR-160-6	PAWE-IITA	SB-RVT (LS)	JARC
27	JSL-1	JARC-Ethiopia	SB-RVT	JARC
28	G9945	SCAU- China	SB-RVT	JARC
29	Hardee-1	Awassa-IITA	JM-Seed increase 2007	JARC
30	H3	IIAM-Mozambique	SB-RVT	JARC
31	IAC-73-5115	PAWE-IITA	SB-RVT (LS)	JARC
32	H12	IIAM-Mozambique	SB-RVT	JARC
33	AGS-214	Awassa-IITA	SB-RVT	JARC
34	AGS-3-1	Awassa-IITA	JM-Seed increase 2007	JARC
35	F81-7636-4	Awassa-IITA	JM-Seed increase 2007	JARC
36	G00391	SCAU- China	SB-RVT	JARC
37	G03705	SCAU- China	SB-RVT	JARC
38	G01853	SCAU- China	SB-RVT	JARC
39	H10	IIAM-Mozambique	SB-RVT	JARC
40	V1-1	Awassa-IITA	JM-Seed increase 2007	JARC
41	AGS-299-2	Awassa-IITA	JM-Seed increase 2007	JARC
42	AGS-115-1	Awassa-IITA	JM-Seed increase 2007	JARC
43	PR-145-2	PAWE-IITA	SB-RVT (LS)	JARC
44	FB1-7636	PAWE-IITA	SB-RVT (MS)	JARC
45	F82-7629-2	Awassa-IITA	JM-Seed increase 2007	JARC
46	G00386	SCAU-China	SB-RVT	JARC
47	AGS-3	Awassa-IITA	SB-RVT (MS)	JARC
48	G00141	SCAU- China	SB-RVT	JARC
49	H5	IIAM-Mozambique	SB-RVT	JARC

3.3 Experimental Design, Management and Season

The trials were established in the field on the main cropping season of 2010. The experiments were laid out in 7 X 7 simple lattice design with two replications. The plot size was three rows of 4m length with 0.6m row spacing i.e. 4m x 3 x 0.6m = 4.8m^2. Planting was done by hand on June 10 at Jimma and June 13 at Assosa. Seed rate was 25kg/ha. Rhizobia bacteria were incorporated in to the soil based on the standard recommendation per hectare basis to increase Nitrogen fixing process by the genotypes to be studied. All experimental factors were applied uniformly to the entire plot.

3.4. Data Collected

3.4.1. On plot basis

The data recording for each trait were carried out as follows. Five sample plants were used for all the characters under study.

1. **Days to 50% flowering:** Number of days from emergence to the day on which 50 per cent of the plants on a plot produced flowers.
2. **Days to 50% pod setting**: Number of days from emergence to the day on which 50 per cent of the plants on a plot set pods.
3. **Days to maturity:** Number of days from sowing to the stage when 95 % of the plants in a plot have changed the color of their pods from green to yellow.
4. **Hundred seed weight (g):** Weight in grams of 100 seeds at harvesting.
5. **Grain yield per hectare (kg):** plot yield converted to hectare yield by using the formula Grain yield (kg/ha)= (plot yield (kg) x 10,000)/plot size in square meters.

3.4.2. On plant basis

1. **Biological yield per plant (g):** Recorded by weighing the total above ground yield harvested from the sample plants at the time of harvest.

2. **Harvest Index:** To estimate the harvest index, average seed yield was divided by the average biological yield.

$$\text{Harvest index} = \frac{\text{Seed yield per plant (g)}}{\text{total biological yield per plant (g)}}$$

3. **Root to biomass ratio:** Average root dry weight was divided by the average above ground biomass dry weight and expressed in percentage.
4. **Root volume**: Was recorded for sampled plants using volume displacement technique.
5. **Pods per plant:** Total number of pods for sampled plants were counted and recorded.
6. **Root dry weight (g):** Was estimated after drying the roots of the sampled plants in an oven for 24 hours at 70 degree Celsius till constant weight is achieved.
7. **Pod length (cm):**Exterior distance of fully matured pod from the pod apex to the peduncle was measured in centimeters from five sample plants.
8. **Plant height (cm):** The height of the plant from the ground surface to the tip of the main guide was recorded in centimeters at harvesting period.
9. **Total nodules per plant:** The total number nodules produced for sampled plants were counted and recorded.
10. **Effective nodules per plant:** Nodules that have pink color which is an indication of fixed atmospheric nitrogen to the plant roots were counted and recorded.

3.5. Data Analyses

3.5.1 Analysis of variance

The data were subjected to statistical analysis of variance as per the simple lattice design for each character by the GLM and ANOVA procedures of SAS (SAS, version 9.2).

Efficiency of the simple lattice design relative to RCBD was checked and in most of the response variables the lattice was found to be more efficient than that of the RCBD. In addition, test of homogeneity of error variance was done using F-test and the result demonstrated heterogeneous error

variance for most of the characters; therefore, the results of the two locations were interpreted and discussed separately. LSD was used to separate the means. Skeleton of ANOVA for simple lattice is given below (Table 2).

Table 2.Skeleton of Analysis of variance (ANOVA) for simple lattice design

Sources of variation	Df	SS	MS	F-Value	Pr>F
Replication (unadjusted)	r-1				
Genotype (adjusted)	(k^2-1)		MSg		
Intra-block(error)	(k-1) (rk-k-1)		MSe		
Block (adjusted)	r(k-1)		MSb		
Total	$(r) (k^2) -1$				

Where- r and k are number of replications and blocks respectively.

3.5.2. Estimation of genetic parameters

In order to identify and ascertain the genetic variability among genotypes, for the characters under study and to confirm the presence of environmental effect on various characters, different genetic parameters were estimated by adopting the following formulas.

3.5.2.1. Estimation of variance components

Genotypic and phenotypic variances and coefficients of variation were estimated based on the formula suggested by Burton and Devane (1953).

Genotypic variance $\delta^2 g = \frac{Msg - Mse}{r}$

Where, r = number replication, MSg = mean square due to genotypes MSe = mean square of error (Environmental variance)

Phenotypic variation $\delta^2 P = \delta^2 g + Mse$

Where, σ^2g = genotypic variance, σ^2p= phenotypic variance

Genotypic coefficient of variation $GCV = \frac{\sqrt{\delta^2 g}}{\bar{X}} * 100$

Phenotypic coefficient of variation $PCV = \frac{\sqrt{\delta^2 P}}{\bar{X}} * 100$

Where, $\bar{X}$ the grand mean of a character.

3.5.2.2. Broad- sense heritability

Broad-sense heritability (h^2) for all traits was calculated using the method suggested by Falconer (1989).

$$H = \frac{\sigma^2 g}{\sigma^2 P} \times 100$$

Where, H^2 = heritability (in the broad sense)

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

3.5.2.3. Genetic advance

The method described by Johnson *et al.* (1955) was followed to compute expected genetic advance (GA).

$$GA = K * \sigma_p * H$$

Where, k is a constant, which at a selection intensity of 5% is about 2.06;

σ_p is the phenotypic standard deviation on mean basis;

h^2 is broad sense heritability;

and x is the grand mean of the trait under consideration.

Genetic advance as percent of mean was computed to compare the extent of predicted advance of different traits under selection using the following formula:

$$GAM = \frac{GA}{\bar{X}} * 100$$

Where, GAM = Genetic advance as percent of mean

GA = genetic advance

$\bar{X}$ = grand mean of the trait under consideration

3.5.3. Association of characters

3.5.3.1. Estimation of correlation coefficients

Phenotypic correlation, the observable correlation between variables, which is the sum of genotypic and environmental effects was calculated from variance covariance components using the formula of Miller *et al.* (1958) as follows

Phenotypic correlationis given by $rp = \frac{Pcovx.y}{\sqrt{\sigma^2 px.\sigma^2 py}}$

Genotypic correlationis also given by $rg = \frac{gcovx.y}{\sqrt{\sigma^2 gx.\sigma^2 gy}}$

Where $r_g$and r_p= genotypic correlation and phenotypic correlation, respectively. Pcovx.yand g covx.yare phenotypic and genotypic, co-variances between variables x and y, respectively; δ^2pxand δ^2gxare phenotypic and genotypic, variances for variable x; and δ^2pyand δ^2gyare phenotypic and genotypic variances for the variable y, respectively.

The significances of the correlation coefficients were tested using 'r' tabulated value at n-2 degrees of freedom, at 5% and 1% probability levels, where, n= number of treatments (genotypes).

3.5.3.2. Path coefficient analysis

Based on genotypic correlation, path coefficient which refers to the direct and indirect effects of the yield attributing traits (independent character) on grain yield (dependent character) was estimated with the method described by Dewey and Lu (1959) as follows:

$$rij = Pij + \sum rik.Pkj$$

Where, rij = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficient.

Pij = direct effects of the independent character (i) on the dependent character (j) as measured by the genotypic path coefficients, and $\sum$rikpkj = 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 was estimated as given in Dewey and Lu (1959).

$$1 = p^2r + \sum p_{iy} \cdot r_{iy}$$

Where, p^2r is the residual effect

p_{iy} is the direct effect of yield by i^{th} trait, and

r_{iy} is the correlation of yield with the i^{th} trait.

3.5.4. Cluster analysis

Clustering of genotypes in to different groups was carried out by average linkage method. The appropriate number of clusters was determined from the values of Pseudo F and Pseudo T^2 statistics using the procedures of SAS computer software version 9.2 facilities so as to group sets of genotypes in to homogenous clusters (SAS 2008).

3.5.4.1. Genetic divergence analysis

Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistic (Mahalanobis, 1936) by using SAS software program. Squared distances (D^2) for each pair of genotype combinations were computed using the following formula:

$D^2ij = (Xi- Xj)\ S^{-1}\ (Xi – Xj)$

Where, D^2ij = total generalized distance between class i and j,

Xi and Xj = the difference in mean vectors of i^{th} and j^{th} genotypes, and

S^{-1} = the inverse of pooled variance covariance matrix.

3.5.4.2. Principal component (PC) analysis

Principal component analysis (PCA) was used to find out the characters, which accounted more to the total variation (Wiley, 1981). The data were standardized to mean of zero and variance of one before computing principal component analysis. Principal component analysis was performed using correlation matrix by employing the procedure prin comp corr of SAS

software version 9.2 (SAS Institute, 2001) in order to examine the relationships among 15 quantitative traits that are correlated among each other by converting in to uncorrelated traits called principal components (PC).

4. RESULTS AND DISCUSSION

Results on variability assessment, associations among yield and yield related characters and genetic divergence are presented and discussed hereunder.

4.1. Analysis of Variance

The result of analysis of variance (ANOVA) of 15 quantitative characters for the 49 genotypes tested at Jimma and Assosa are presented in Tables 3 and 4, respectively. Mean square of all the characters studied at Jimma showed highly significant difference ($P< 0.01$), except for root volume and root dry weight. At Assosa, all the characters showed highly significant difference ($P<0.01$) among the tested genotypes indicating the presence of adequate variability that can be exploited through selection. Highly significant difference between the genotypes is in agreement with the finding of Ojo (2003), where highly significant differences were observed for all the characters studied in 18 soybean genotypes.Combined analysis was done for pod length, root dry weight, root to biomass ratio and hundred seed weight (Appendix 3).

4.2. Mean, Range and Estimates of Genetic Parameters

4.2.1. Mean and range

Range and mean values of the 15 characters are shown in Tables 5 and 6 for Jimma and Assosa, respectively. The mean performance of the 49 genotypes for 15 traits is presented in Appendix Tables III and IV for Jimma and Assosa, respectively. The 49 soybean genotypes showed wide range of variability for all characters; except pod length and root dry weight at both locations (Table 5 and 6).

At Jimma, the highest grain yield (3868 kg/ha) was recorded from TGX-297-6E-1 followed by G01892 (3735kg/ha) which were higher than the grand mean of the genotypes studied (2160.00 kg/ha). While low yield (795 kg/ha) was obtained from the genotype PR-160-6.
At Jimma, about 57.14 per cent of the genotypes gave above the grand mean of grain yield.
If the breeding objective is to improve seed yield, genotypes with high yield in this study need further work.

At Assosa, the highest grain yield (2134 kg/ha) was recorded from the genotype TGX-1895-33F and the lowest yield (444 kg/ha) was obtained from G00386. The grand mean of grain yield at Assosa was 885.76 kg/ha. Earlier days to flowering, days to pod setting and days to maturity was observed at Assosa as compared to Jimma with mean values of (37.00), (65.50) and (94.50) days for the genotypes F81-7636-4, FB1-7636 and H2, respectively. 46.93 per cent of the genotypes gave above the grand mean of grain yield at Assosa.

The characters such as plant height, pod number per plant, total nodules per plant, effective nodules per plant, biomass yield, root dry weight and harvest index showed relatively higher values at Jimma as compared to those recorded at Assosa with mean of 76.79cm, 46.44, 31.53, 18.29, 32.99g, 8.02g, and 38.12, respectively. The genotype G01853 had scored the highest plant height (118.17cm) at Jimma. Therefore, when breeding for higher plant height this genotype should be considered. PR-160-6 scored the highest pod number per plant (79.00) at Jimma indicating it could be the preferable genotype in breeding for high number of pods per plant.

Characters such as root to biomass ratio, root volume, pod length and hundred seed weight showed relatively higher values at Assosa compared to those at Jimma with mean values of 25.50%, 4.96, 4.49cm and 13.68g, respectively. The genotypes such as H18, Promoveria and IAC-6 scored the highest values of root to biomass ratio (32.29%), root volume (12.50cm^3) and hundred seed weight (21.50g), respectively at Assosa. Therefore, if the breeding objective is to improve the above traits the respective genotypes should be given due attention.

Table 3. Analysis of variance for 15 characters in 49 soybean genotypes tested at Jimma (2010/2011)

Source of variance	Mean squares						
	Replication	Treatments	Blocks within replications	Error		R^2	Efficiency relative to RCBD
				Intra block	RCBD		
Degrees of freedom	1	48	12	36	48		
DF	13.22	94.83**	6.11	7.26	6.97	94.67	96.06
DPS	13.96	95.56**	5.38	5.66	5.59	95.32	98.77
DM	13.97	93.82**	3.82	8.04	6.99	94.04	97.89
PlH	77.23	495.99**	28.75	14.97	18.42	97.18	109.85
PPP	0.82	289.55**	18.11	14.95	15.74	95.67	100.88
PL	0.44	0.52**	0.04	0.05	0.05	92.78	95.16
BY	0.09	136.02**	7.21	11.07	10.11	94.35	91.27
TNPP	58.93	355.25**	3.89	3.42	3.54	99.17	100.39
ENPP	32.00	212.85**	4.07	3.58	3.70	98.59	100.39
RV	11.79	5.59	2.26	4.58	4.00	65.04	87.32
RDW	4.71	0.70	0.43	0.48	0.47	69.58	97.59
RBR	17.67	9.16**	2.89	3.83	3.59	79.13	93.89
HSW	16.32	9.36*	4.08	3.93	3.97	75.65	100.04
HI	223.18	246.96**	36.95	43.31	41.72	88.60	96.32
GY	2140.45	798682.80**	198.26	189.18	191.45	99.98	100.05

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod number per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield

Table 4. Analysis of variance for mean square of the 15 characters of 49 soybean genotypes tested at Assosa (2010/2011)

Mean squares							
Source of variance	Replication	Treatments	Blocks within replications	Error		R^2	Efficiency relative to RCBD
				Intra block	RCBD		
Degrees of freedom	1	48	12	36	48		
DF	0.04	245.85**	0.87	0.95	0.93	99.70	97.82
DPS	0.01	82.80**	0.01	0.58	0.67	99.36	105.46
DM	0.16	135.60**	0.16	0.76	0.72	99.51	95.18
PlH	0.04	198.44**	0.70	1.48	1.29	99.39	86.90
PPP	0.16	35.48**	0.88	0.84	0.85	98.04	100.04
PL	0.04	0.46**	0.05	0.07	0.06	89.23	94.72
BY	0.65	17.40**	2.54	1.82	2.00	92.05	102.59
TNPP	0.04	140.60**	0.52	1.04	0.91	99.43	87.65
ENPP	0.25	49.73**	0.42	1.25	1.04	98.18	83.40
RV	0.16	4.41**	0.30	0.36	0.35	94.44	95.93
RDW	1.02	0.48*	0.29	0.20	0.22	73.76	102.91
RBR	18.87	25.46**	4.63	3.67	3.91	89.13	101.30
HSW	0.09	13.78**	0.77	1.17	1.07	94.08	91.44
HI	1.27	263.42**	1.08	2.08	1.83	99.40	87.95
GY	326.95	153462.34**	823.35	979.09	940.16	99.50	96.02

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod number per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield

Table 5. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as per cent of mean for characters of soybean genotypes studied at Jimma (2010/11)

Characters	Range	Mean ± S.E Mean	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GA (%)
DF	46.00-86.00	64.20±2.55	43.79	7.26	51.05	10.30	11.12	85.77	12.82	19.97
DPS	57.00-97.00	75.62±2.39	44.95	5.66	50.61	8.86	9.40	88.81	13.47	17.81
DM	111.00-148.00	125.74±2.69	42.89	8.04	50.93	5.20	5.67	84.21	13.08	10.40
PlH	37.00-120.00	76.78±4.23	240.51	14.97	255.48	20.20	20.81	94.14	32.04	41.73
PPP	26.00-79.00	46.43±4.00	137.30	14.95	152.25	25.23	26.57	90.18	23.70	51.02
PL	3.00-5.00	4.10±0.22	0.24	0.05	0.29	11.83	13.03	82.45	0.93	22.64
BY	19.00-51.00	32.99±3.22	62.48	11.07	73.55	23.96	26.00	84.94	16.20	49.11
TNPP	13.00-98.00	31.53±1.88	175.92	3.42	179.34	42.07	42.47	98.09	27.72	87.91
ENPP	7.00-66.00	21.18±1.91	104.64	3.58	108.22	48.28	49.10	96.69	21.20	100.06
RDW	2.00-5.00	2.92±0.66	0.11	0.48	0.59	11.35	26.30	18.64	0.31	10.67
RV	4.00-16.00	8.02±2.01	0.37	4.85	5.22	7.58	28.48	7.08	0.87	10.81
RBR	4.34-16.00	8.93±1.96	2.67	3.83	6.50	18.27	28.53	41.03	2.99	33.51
HSW	8.00-22.00	12.35±1.97	2.72	3.93	6.65	13.35	20.88	40.86	2.28	18.46
HI	16.80-72.63	38.21±6.38	101.82	43.31	145.14	26.41	31.53	70.15	18.65	48.80
GY	795.00-3868.00	2160.12±14.09	399246.81	189.18	399436.00	29.25	29.26	84.45	1428.4	66.14

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield. S.E. Mean= Standard error of the mean, σ^2g= Genotypic variance, σ^2e = Environmental variance, σ^2p= Phenotypic variance, H^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, GA= Genetic advance, GA (%) = Genetic advance as per cent of mean.

Table 6. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as per cent of mean for characters of soybean genotypes studied at Assosa 2010/11

Characters	Range	Mean ± S.E Mean	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GA (%)
DF	36.00-75.00	50.06±0.95	245.38	0.95	246.33	31.29	31.35	89.99	23.62	47.18
DPS	65.00-103.00	72.60±0.80	82.51	0.58	83.09	12.51	12.56	99.30	13.63	18.77
DM	94.00-120.00	111.10±0.87	135.22	0.76	135.98	10.47	10.50	99.44	16.97	15.28
PlH	20.00-62.00	35.27±1.18	197.7	1.48	199.18	39.87	40.02	99.26	20.62	58.48
PPP	9.00-28.00	15.98±0.91	35.06	0.84	35.90	37.05	37.49	97.66	8.52	53.29
PL	3.50-5.00	4.49±0.26	0.43	0.07	0.50	14.52	15.67	85.86	0.82	18.24
BY	11.00-31.00	14.12±1.33	16.49	1.82	18.31	28.96	30.52	90.06	3.11	22.20
TNPP	4.00-47.00	15.37±0.99	140.08	1.04	141.12	77.02	77.30	99.26	17.92	116.64
ENPP	2.00-25.00	7.79±1.07	49.11	1.25	50.36	90.00	91.14	97.52	10.42	133.86
RV	3.00-13.00	4.96±0.58	4.23	0.36	4.59	41.47	43.20	92.16	2.96	59.76
RDW	3.00-5.00	3.53±0.47	0.38	0.2	0.58	17.87	22.08	65.52	0.29	8.28
RBR	11.11-33.33	25.50±1.93	23.63	3.67	27.30	19.06	20.49	86.55	5.86	22.98
HSW	8.00-22.00	13.68±1.05	13.20	1.17	14.37	26.55	27.70	91.86	5.13	37.48
HI	16.13-71.07	32.79±1.37	262.38	2.08	264.46	49.39	49.59	81.25	23.86	72.74
GY	444.00-2134.00	885.76±30.51	152972.8	979.09	153951.89	44.16	44.30	82.36	593.49	67.01

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield. S.E. Mean= Standard error of the mean, σ^2g= Genotypic variance, σ^2e = Environmental variance, σ^2p= Phenotypic variance, H^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, GA= Genetic advance, GA (%) = Genetic advance as per cent of mean.

4.2.2. Estimates of genetic parameters

4.2.2.1. Estimates of variance components

Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances and phenotypic (PCV) and genotypic coefficients of variation (GCV) are provided in (Tables 5 and 6) for Jimma and Assosa, respectively.

At Jimma, grain yield, biomass yield, number of pods per plant, plant height, total nodules per plant, effective nodules per plant, days to 50% flowering, days to pod setting, days to maturity and harvest index exhibited high genotypic and phenotypic variances. Phenotypic coefficients of variation (PCV) values ranged from 5.67% for days to maturity to 49.10% for effective nodules per plant, whereas the genotypic coefficients of variation (GCV) ranged from 5.20% for days to maturity to 48.28% for effective nodules per plant. In addition, PCV values were generally higher than their corresponding GCV values for all the characters considered indicating the importance of environment in the expression of these traits.

According to Deshmukh*et al*. (1986), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Based on this delineation, PCV and GCV values were high for grain yield, biomass yield, number of pods per plant, plant height, total nodules per plant, effective nodules per plant, and harvest index. It indicates that selection may be effective based on these characters and there phenotypic expression would be a good indication of genetic potential. This result is in harmony with the findings of Jagdish*et al.* (2000), Patel *et al.* (1998), Singh *et al.* (2000), Dixit (2002), and Jains and Ramgiry (2000), where high genotypic and phenotypic coefficients of variation for grain yield, biomass yield, number of pods per plant, plant height, and harvest index in soybean genotypes were reported. The PCV and GCV values were medium for pod length, and days to 50% flowering. The low PCV and GCV values were obtained for days to pod setting and days to maturity indicating lack of adequate variability for these traits which hinders the breeding work for the improvement of

these traits. A low genotypic and phenotypic coefficient of variation for days to maturity is in agreement with the reports of Ramana*et al.* (2000) and Agarwal*et al.* (2001).

In contrary to the present study Veenakumari (1994), NirmalaKumari and Balasubramanian (1993), and Raman *et al.* (2000) reported high genotypic and phenotypic coefficients of variation for days to pod setting and days to maturity in soybean genotypes. The high GCV values of these characters suggest that the possibility of improving these trait through selection.

At Assosa, grain yield, days to 50% flowering, pod number per plant, plant height, total nodules per plant, effective nodule per plant, harvest index, biomass yield, root volume and hundred seed weight have exhibited high genotypic and phenotypic variances. Phenotypic coefficient of variation (PCV) values ranged from 10.50% for days to maturity to 91.14% for effective nodules per plant; whereas the genotypic coefficient of variation (GCV) ranged from 10.47% for days to maturity to 90.00% for effective nodules per plant. High PCV and GCV values were recorded for grain yield, days to flowering, biomass yield, number of pods per plant, hundred seed weight, plant height, root volume, total nodules per plant, effective nodules per plant, and harvest index indicating the availability of adequate variability for these traits which aids in the improvement of the respective characters.

Genotypic coefficients of variation (GCV) and phenotypic coefficient of variation (PCV) values were medium for days to pod setting, days to maturity and pod length. This result is in agreement with the findings of Basavaraja (2002) and Agarwal*et al.* (2001). The present finding is in agreement with the reports of Jain *et al.*(2000), Ramana *et al.* (2000), Patel *et al.* (1998), Singh *et al.* (1996), Singh *et al.*(2000), Bangar*et al.* (2003), and Kausar (2005). Medium GCV values were recorded for days to pod setting, days to maturity and pod length. High PCV values were recorded for root dry weight and root to biomass ratio.

4.2.2.2. Estimation of broad-sense heritability and genetic advance

Heritability estimate for characters under study at Jimma and Assosa are indicated in Table 5 and 6, respectively.

At Jimma, estimates of heritability in broad sense ranged from 7.08% for root volume to 99.95% for grain yield (Table 5). Similarly, root dry weight and grain yield had moderate and high heritability with 65.52% and 99.36% respectively at Assosa. Ojo (2003), Jain and Ramgiry (2000), and Basavaraja (2002) reported high heritability for grain yield in soybean genotypes. According to Singh (2001), heritability values greater than 80% are very high, values from 60-79% are moderately high, values from 40-59% are medium and values less than 40% are low. Accordingly at Jimma, all the characters except root dry weight, root volume, root to biomass ratio and hundred seed weight had high to very high heritability.

At Assosa, all characters except root dry weight (65%), had very high heritability. This indicates that selection will be the best approach to be employed to identify the best soybean genotypes for the traits with high heritability. This is because; there will be a close correspondence between the genotype and the phenotype of the genotypes, due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical, due to the masking effect of the environment. In contrary to the present study Basavaraja (2002) reported low heritability for pod length in soybean genotypes. Low heritability values were recorded for root dry weight and root volume at Jimma. Root dry weight showed moderate heritability at Assosa. The magnitudes of heritability for most of the quantitative characters at both locations were moderate to high, except the low heritability of root dry weight and root volume at Jimma.

At Jimma, genetic advance as percent of mean ranged from 10.48 for days to maturity to 100.06 for effective nodules per plant (Table 5). At this location relatively high genetic

advance as percent of mean was recorded for effective nodules per plant (100.06%), total nodules per plant (87.91%), grain yield (66.14%), pod number per plant (51.02%), biomass yield (49.11%), harvest index (48.80%), plant height (41.73%), root to biomass ratio (33.51%) and pod length (22.64%). Medium genetic advance as percent of mean was recorded for days to 50% flowering (19.97%), hundred seed weight (18.46), days to pod setting (17.81%), root volume (10.81%), root dry weight (10.67%) and days to maturity (10.40%).

At Assosa, genetic advance as percent of mean ranged from 8.28 for root dry weight to 133.86 for effective nodules per plant (Table 6). Within this range, a relatively high genetic advance was observed for effective nodules per plant (133.86%), total number of nodules per plant (116.64%), harvest index (72.74%), grain yield (67.01%), root volume (59.76%), plant height (58.48) and days to 50% flowering (47.58). Low genetic advance as per cent of mean values were observed for root dry weight (8.28), days to maturity (15.28), pod length (18.24%) and days to pod setting (18.77%). This low estimate of genetic advance as a percent of mean arises from low estimate of phenotypic variance and heritability.

According to Johnson *et al*. (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study showed high heritability coupled with high expected genetic advance as per cent of mean for effective nodules per plant, total nodules per plant, pod number per plant and harvest index across both locations. These characters were controlled by additive gene effects and phenotypic selection would likely be effective than other characters measured (Sumati and Muralidharan, 2009).

4.3. Association Studies

4.3.1. Correlation of grain yield with other characters

At Jimma (Table 7) grain yield showed negative and highly significant association both at phenotypic and genotypic levels with days to 50% flowering, days to pod setting and days to maturity. In support of the present finding, Aditya*et al*., (2011), Kole*et al*., (2008), Ramteke*et al.* (2010) and Arshad*et al.,* (2006), reported negative correlation of grain yield with days to 50% flowering and days to maturity in soybean genotypes. This demonstrates that whenever the value of these characters increases, it adversely affects grain yield. This may be related to the fact that when days to maturity increases, the phenology of the crop enters into the dry spell, which in turn leads to decrease in yield. In contrast to the present finding Mukhekar*et al.* (2004), Basavaraja (2002) and Ojwang (2003) reported positive significant association of days to flowering with grain yield in soybean genotypes. Grain yield displayed positive non-significant correlation with pod length, total nodules per plant, effective nodules per plant, root dry weight, root to biomass ratio, hundred seed weight and harvest index at genotypic and phenotypic levels. However, yield had negative non-significant association with plant height pod number per plant and biomass yield at genotypic and phenotypic levels. Moreover, grain yield had negative non-significant association with root volume at genotypic level.

At Assosa, grain yield manifested positive and highly significant association with pod number per plant, biomass yield and hundred seed weight at phenotypic and genotypic level (Table 8). Moreover, grain yield had positive significant association with root dry weight at genotypic level. Therefore, improving one or more of the characters could result in high grain yield in the soybean genotypes. This result is in harmony with the report of Qi Yang and Jinling Wang (2000), Parameshwar (2006), Rajanna*et al.* (2000) and Malik *et al.,* (2006).

Similar to the present study Ojo (2003) and Shivakumar (2008), reported significantly positive correlation of grain yield with pod number per plant in soybean genotypes studied at phenotypic level. Furthermore, grain yield had positive non-significant correlation with days to 50% flowering, days to pod setting, plant height, root volume, harvest index and total

nodules per plant both at genotypic and phenotypic levels. Root dry weight had positive non-significant correlation with grain yield at phenotypic level. Grain yield had negative non-significant correlation with pod length and effective nodules per plant at phenotypic and genotypic levels. This suggests the improvement of characters which had non-significant association with grain yield will not have a sound effect on the improvement of grain yield in the soybean genotypes. Supportive to the previous findings of Kalaimagal (1991), grain yield had negative and significant association with days to maturity both at genotypic and phenotypic level. The negative correlation of grain yield with days to maturity and root to biomass ratio implies the improvement of one character affects the others in the opposite direction making it impractical to improve the characters simultaneously. In contrary to the present study Raman *et al*. (2000) and Bangar*et al*. (2003) reported positive significant correlation of grain yield with days to maturity.

Table 7. Genotypic (above diagonal) and phenotypic correlation coefficients at Jimma (2010/11)

Traits	DF	DPS	DM	PlH	PPP	PL	BY	TNPP	ENPP	RDW	RV	RBR	HSW	HI	GY
DF	-	0.88**	0.63**	0.40**	0.30*	-0.11	0.26	-0.50**	-0.38**	0.28	0.24	-0.19	-0.16	0.20	-0.48**
DPS	0.83**	-	0.74**	0.52**	0.15	-0.16	0.24	-0.57**	-0.44**	0.37*	0.19	-0.17	-0.19	-0.15	-0.55**
DM	0.62**	0.72**	-	0.60**	0.09	-0.18	0.20	-0.44**	-0.32*	0.17	0.16	-0.23	0.03	-0.13	-0.52**
PlH	0.35*	0.50**	0.56**	-	0.08	-0.31*	0.36*	-0.38**	-0.22	0.26	-0.29*	-0.29*	0.03	-0.26	-0.22
PPP	0.24	0.11	0.06	0.07	-	-0.19	0.33*	-0.13	0.03	-0.02	0.30*	-0.40**	-0.22	0.53**	-0.05
PL	-0.10	-0.14	-0.15	-0.27	-0.21	-	0.06	0.15	0.08	0.22	0.19	0.01	0.06	-0.19	0.08
BY	0.22	0.19	0.17	0.31*	0.33*	0.05	-	-0.27	-0.21	0.40**	0.85**	-0.97**	0.30*	-0.45**	-0.10
TNPP	-0.45**	-0.53**	-0.41**	-0.36*	-0.12	0.13	-0.24	-	0.89**	-0.21	-0.24	0.28	0.11	0.19	0.13
ENPP	-0.34*	-0.41**	-0.29*	-0.21	0.02	0.07	-0.19	0.89**	-	-0.17	-0.24	0.21	-0.09	0.17	0.14
RV	0.17	0.17	0.08	0.08	-0.03	0.10	0.28	-0.09	-0.07	-	1.28**	-0.11	-0.05	-0.49**	0.01
RDW	0.17	0.09	0.10	-0.08	0.15	0.10	0.26	-0.09	-0.11	0.28	-	-0.24	-0.42**	-0.59**	0.52**
RBR	-0.12	-0.13	-0.17	-0.25	-0.29*	-0.03	-0.64**	0.20	0.16	0.42**	-0.19	-	-0.32*	0.32*	0.19
HSW	-0.02	-0.08	0.08	0.05	-0.08	-0.06	0.21	0.07	-0.06	0.01	-0.08	-0.19	-	0.04	0.12
HI	0.05	-0.09	-0.05	-0.20	0.46**	-0.21	-0.42**	0.16	0.16	-0.25	-0.17	0.17	0.36*	-	0.12
GY	-0.44**	-0.52**	-0.48**	-0.21	-0.04	0.08	-0.09	0.13	0.14	0.00	-0.22	0.14	0.08	0.11	-

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield.

Table 8. Genotypic (above diagonal) and phenotypic correlation coefficients at Assosa (2010/11)

Traits	DF	DPS	DM	PlH	PPP	PL	BY	TNPP	ENPP	RV	RDW	RBR	HSW	HI	GY
DF		0.62**	0.39**	0.50**	-0.30*	-0.12	0.35*	0.47**	0.40**	0.20	0.09	-0.28	0.14	-0.24	0.06
DPS	0.62**		0.31*	0.31*	-0.20	-0.18	0.13	0.14	0.10	0.05	0.18	-0.16	0.04	-0.20	0.01
DM	0.38**	0.30*		0.37*	-0.53**	-0.14	0.09	0.22	0.22	0.18	-0.44**	-0.25	-0.14	-0.47**	-0.33*
PlH	0.50**	0.30*	0.36*		-0.22	-0.18	0.55**	0.46**	0.36*	0.29*	0.15	-0.42**	0.28	-0.25	0.20
PPP	-0.25	-0.19	-0.51**	-0.22		0.14	-0.14	-0.21	-0.28	-0.07	0.13	0.17	-0.07	0.79**	0.38**
PL	-0.10	-0.15	-0.11	-0.15	0.15		-0.22	-0.05	0.07	-0.40**	-0.30*	-0.06	0.20	0.32*	-0.09
BY	0.26	0.09	0.07	0.41**	-0.09	-0.10		0.56**	0.42**	0.56**	0.32*	-0.80**	0.53**	-0.33*	0.50**
TNPP	0.46**	0.13	0.22	0.45**	-0.21	-0.06	0.42**		0.95**	0.12	-0.16	-0.53**	0.24	-0.28	0.03
ENPP	0.40**	0.09	0.21	0.35*	-0.28	0.03	0.31*	0.94**		0.08	-0.23	-0.44**	0.26	-0.26	-0.08
RV	0.20	0.05	0.17	0.26	-0.05	-0.35*	0.39**	0.11	0.06		0.51**	-0.16	0.20	-0.16	0.12
RDW	0.04	0.08	-0.23	0.09	0.06	-0.17	0.33*	-0.08	-0.11	0.20		0.43**	0.24	-0.08	0.33*
RBR	-0.25	-0.15	-0.23	-0.36*	0.15	-0.09	-0.52**	-0.47**	-0.39**	-0.12	0.43**		-0.39**	0.21	-0.36*
HSW	0.14	0.05	-0.12	0.27	-0.07	0.11	0.35*	0.21	0.23	0.20	0.16	-0.32*		0.29*	0.39**
HI	-0.24	-0.20	-0.46**	-0.24	0.77**	0.27	-0.26	-0.28	-0.26	-0.15	-0.05	0.17	0.30*		0.25
GY	0.06	0.01	-0.33*	0.20	0.37*	-0.08	0.36*	0.03	-0.08	0.11	0.20	-0.31*	0.37**	0.25	

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield.

4.3.1.1. Phenotypic correlation

At Jimma, biomass yield had positive and significant phenotypic correlation with plant height and pod number per plant. However, it had negative significant phenotypic association with harvest index and root to biomass ratio. The positive and significant association of biomass yield with plant height and pod number per plant as indicated in the phenotypic correlation and among each other, indicated that these traits can be improved simultaneously through selection. Days to 50% flowering showed positive and highly significant phenotypic correlation with days to pod setting, days to maturity, and plant height. However it had negative and highly significant phenotypic correlation with total nodules per plant and effective nodules per plant. Ramana*et al.* (2000), Devvart*et al.,* (2005) and Manasa (2008) reported significant positive association of days to 50% flowering with days to maturity in soybean.

Days to pod setting had positive and highly significant phenotypic correlation with days to maturity and plant height. However, it had negative and significant association with total nodules per plant and effective nodules per plant.

Effective nodules per plant had positive and significant phenotypic correlation with total nodules per plant. Pod number per plant showed significantly positive and negative phenotypic association with harvest index and root to biomass ratio, respectively. In contrary to the present finding Mukhekar (2004), Ramana*et al.* (2000) and Devvart*et al.,* (2005) reported positive significant association of pod number per plant with harvest index.

At Assosa, days to maturity showed positive and significant phenotypic correlation with plant height, days to 50% flowering and days to pod setting. However, it had negative and significant association with pod per plant and harvest index. This result is in harmony with the finding of DevVart*et al.,* (2005) where negative association of days to maturity with harvest index is reported. In contrary to the present study Mukhekar (2004) reported negative significant association of days to maturity with plant height in soybean genotypes.

Total nodule per plant correlated positively and significantly with effective nodules per plant, plant height, days to 50% flowering and biomass yield, it had negative and significant association with root to biomass ratio. Days to pod setting had positive and significant association with plant height, days to 50% flowering and days to maturity.

Biomass yield showed positive and significant correlation with total nodules per plant, effective nodules per plant, root volume, root dry weight, hundred seed weight and plant height. While it showed negative and significant association with root to biomass ratio. Kausar (2005) from the study on genetic variability of F3 populations of two crosses involving three diverse parents of soybean reported positive and significant phenotypic correlation of biomass yield with plant height.

Plant height had positive and significant association with effective nodules per plant, days to 50% flowering, biomass yield, while it had negative significant association with root to biomass ratio. This finding is in harmony with the report of Manasa (2008), where positive and significant association of plant height with days to flowering is reported.

Pod number per plant had positive and negative significant association with harvest index and days to maturity, respectively. In contrary to the present study Ramgiry and Raha (1999) reported significantly negative association of number of pods per plant with harvest index at phenotypic level in 64 soybean genotypes studied. Root dry weight had positive and significant association with root to biomass ratio.

4.3.1.2. Genotypic correlation

At Jimma, biomass yield showed positive and significant association with root volume, plant height, pod number per plant, root dry weight and hundred seed weight; whereas, it had negative and significant correlation with harvest index and root to biomass ratio.

Days to 50% flowering showed positive and highly significant correlation with days to pod setting, days to maturity, plant height and pod number per plant. Days to 50% flowering showed negative and significant correlation with total nodules per plant and effective nodules per plant.

Days to pod setting had positive and highly significant correlation with days to maturity, root dry weight and plant height. However, it had negative and significant association with total nodules per plant and effective nodules per plant. Days to maturity had significantly positive correlation with plant height. However, it had negative and significant association with pod number per plant, root dry weight, effective nodules per plant and harvest index.

Plant height had significant and negative correlation with pod length, total nodule per plant and root to biomass ratio. Supportive to the present study Manasa (2008), reported negative and significant association of plant height with pod length in ovate leaflet type of soybean genotypes. Plant height had positive significant correlation with biomass yield.

Effective nodules per plant had positive and significant correlation with total nodules per plant. Pod number per plant had positive and significant correlation with root volume, biomass yield and harvest index. It also showed negatively significant genotypic correlation with root to biomass ratio.

At Assosa, days to maturity showed positive and significant correlation with plant height; while it showed negative and significant correlation with pod number per plant, root dry weight and harvest index. This finding is in contrary to the report of Manasa (2008) where days to maturity had positive and significant association with pod number per plant and harvest index.

Total nodules per plant showed positive and significant correlation with effective nodules per plant, days to 50% flowering and plant height. However, it had negative significant association with root to biomass ratio. Biomass yield had positive and significant association with total nodules per plant, effective nodules per plant, root volume, hundred seed weight, plant height, root dry weight and days to 50% flowering; while it showed negative and significant association with root to biomass ratio and harvest index.

Plant height had positive and significant correlation with days to pod setting, biomass yield, effective nodules per plant and root volume. However, it had negative significant correlation

with root to biomass ratio. Similar to the present study Gadde (2006), reported positive significant genotypic correlation of plant height with days to pod setting in the same crop.

Effective nodules per plant showed positive and significant correlation with biomass yield and total nodules per plant while it showed negative and significant correlation with root to biomass ratio. Pod number per plant showed positive and significant correlation with harvest index. Pod number per plant showed negative significant association with days to 50% flowering and days to maturity. Root to biomass ratio had negative and significant correlation with plant height, biomass yield and hundred seed weight. Root dry weight had positive and significant correlation with biomass yield, root volume and root to biomass ratio.

Generally, positive and significant association of pairs of characters at phenotypic and genotypic levels justified the possibility of correlated response to selection. Furthermore, negative correlations prohibit the simultaneous improvement of those traits.

4.4. Path Coefficient Analysis

Correlation analysis describes merely the mutual relationship between different pairs of characters without providing the nature of the cause and effect relationships of each character. Hence, the phenotypic and genotypic correlations were further analyzed by path coefficient analysis technique to partition the correlation coefficient into direct and indirect effects. This allows separation of the direct influence of each component on grain yield production from the indirect influences caused by the mutual relationships among them. Such analysis leads to identification of important traits useful for indirect selection of complex trait such as grain yield (Dewey and Lu, 1959).

The Genotypic direct and indirect effect of different characters on seed yield is presented in Tables 9 and 10 for Jimma and Assosa, respectively. At Jimma, effective nodules per plant had the highest positive direct effect (0.837). Moreover, the indirect effect via other traits was negative and hence the correlation it had with yield was largely due to the direct effect. This

suggests the correlation showed the true relationship and direct selection through this character will be effective (Singh and Chaudhary, 1979).

The high positive direct effect of hundred seed weight on grain yield was counter balanced by indirect negative effects of root to biomass ratio, total nodules per plant, root dry weight and harvest index and reduced the correlation to 0.120.

Total nodules per plant which had the highest negative direct effect revealed prominent indirect effects via days to maturity, effective nodules per plant, days to 50% flowering, days to pod setting, pod length, biomass yield and root volume.

The third highest positive direct effect of root to biomass ratio was counter balanced by indirect negative effects of total nodules per plant, pod number per plant, harvest index, plant height and root dry weight and reduced the correlation to 0.190.

Direct positive effect of pod length on grain yield was counter balanced by indirect negative effects of days to maturity, plant height, root to biomass ratio, biomass yield, total nodules per plant, and hundred seed weight and reduced the correlations to 0.08.

The second highest negative direct effect of harvest index (-0.459) is counter balanced by the indirect positive effect via pod number per plant, biomass yield, root volume, root to biomass ratio, effective nodules per plant, days to maturity and days to pod setting and reduced the correlation to 0.120.

The indirect negative effect of pod number per plant via days to 50% flowering, days to pod setting, days to maturity, harvest index, biomass yield, pod length, root to biomass ratio and harvest index counter balanced the positive direct effect of pod number per plant on grain yield and reduced the correlations to –0.051. The correlation of pod number per plant with grain yield was negative and path analysis showed that the negative correlation was mainly due to the indirect negative effect of the character.

Even though root volume had direct negative effect (-0.269) on grain yield, it was counter balanced by the indirect positive effect via the characters root dry weight, harvest index, total nodules per plant, pod length and plant height as a result the correlation was changed to 0.011. Path analysis showed the positive correlation of root volume with grain yield was through indirect effects of other characters.

The direct positive effect of plant height (0.290) was counter balanced by indirect negative effects of days to maturity, root to biomass ratio, biomass yield, days to pod setting, effective nodules per plant, days to 50% flowering, pod length, root volume and root dry weight. The negative correlation of this character was mainly due to the indirect negative effect of other characters.

The positive direct effect of root dry weight (0.214) was counter balanced by the negative indirect effect of root volume, hundred seed weight, root to biomass ratio, effective nodules per plant, biomass yield, plant height, days to maturity, days to flowering and days to pod setting and the correlation was changed to -0.520. Path analysis showed that the negative correlation of root dry weight with grain yield was due to the indirect effects of other characters.

The second highest negative direct effect of days to maturity (-0.615) was counter balanced by positive indirect effect of total nodules per plant, plant height, pod number per plant, root dry weight, hundred seed weight and harvest index, which reduced the correlation to -0.52. Path analysis showed that increase in days to maturity will negatively affect grain yield.

Days to 50% flowering, days to pod setting, days to maturity and biomass yield had negative direct effect on grain yield indicating any increase in these characters affects grain yield in the negative direction. Therefore, selecting genotypes having less number of days to flowering, less number of days to pod setting and less number of days to maturity could be used to improve seed yield in soybean genotypes, as a result of their direct effect on yield.

The residual effect (0.252) indicated that characters which are included in the genotypic path analysis explained (74.80%) of the total variation in grain yield which indicates that there may be some more components that are contributing towards seed yield.

Path analysis at Jimma indicated selecting genotypes having high root to biomass ratio, hundred seed weight and effective nodules per plant could be used to improve seed yield in soybean genotypes as a result of their direct effect on grain yield.

Table 9. Path coefficients of direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of 15 traits on grain yield on 49 soybean germplasm tested at Jimma (2010/11).

Traits	DF	DPS	DM	PlH	PPP	PL	BY	TNPP	ENPP	RV	RDW	RBR	HSW	HI	rg
DF	**-0.201**	-0.101	-0.384	0.115	0.177	-0.014	-0.059	0.568	-0.314	-0.074	0.050	-0.119	-0.121	-0.001	-0.48**
DPS	-0.177	**-0.115**	-0.454	0.152	0.089	-0.020	-0.053	0.639	-0.367	-0.100	0.041	-0.111	-0.141	0.071	-0.55**
DM	-0.126	-0.085	**-0.615**	0.175	0.053	-0.023	-0.046	0.501	-0.270	-0.047	0.034	-0.150	0.024	0.058	-0.52**
PlH	-0.080	-0.060	-0.370	**0.290**	0.050	-0.039	-0.081	0.424	-0.183	-0.069	-0.062	-0.188	0.026	0.119	-0.22
PPP	-0.060	-0.017	-0.055	0.024	**0.591**	-0.024	-0.075	0.141	0.022	0.006	0.065	-0.254	-0.165	-0.245	-0.05
PL	0.022	0.018	0.113	-0.089	-0.111	**0.127**	-0.014	-0.165	0.062	-0.059	0.040	0.007	0.043	0.089	0.08
BY	-0.052	-0.027	-0.123	0.104	0.196	0.008	**-0.228**	0.304	-0.173	-0.106	0.183	-0.623	0.230	0.208	-0.10
TNPP	0.101	0.065	0.273	-0.109	-0.074	0.019	0.061	**-1.130**	0.747	0.056	-0.051	0.177	0.081	-0.089	0.13
ENPP	0.076	0.050	0.199	-0.063	0.016	0.009	0.047	-1.008	**0.837**	0.046	-0.052	0.132	-0.072	-0.078	0.14
RV	-0.056	-0.043	-0.107	0.074	-0.012	0.028	-0.090	0.236	-0.143	**-0.269**	0.275	-0.073	-0.036	0.225	0.01
RDW	-0.047	-0.022	-0.097	-0.084	0.179	0.024	-0.194	0.268	-0.202	-0.345	**0.214**	-0.153	-0.323	0.268	-0.52**
RBR	0.037	0.020	0.144	-0.085	-0.234	0.001	0.222	-0.312	0.172	0.030	-0.051	**0.640**	-0.247	-0.148	0.19
HSW	0.032	0.021	-0.019	0.010	-0.128	0.007	-0.069	-0.120	-0.078	0.013	-0.091	-0.207	**0.764**	-0.017	0.12
HI	0.001	0.018	0.078	-0.075	0.315	-0.025	0.103	-0.219	0.142	0.132	-0.125	0.207	0.029	**-0.459**	0.12

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index.

At Assosa (Table 10) pod number per plant had the highest positive direct effect (0.792) on grain yield followed by hundred seed weight (0.546), biomass yield (0.227), days to 50% flowering (0.180) and plant height (0.094). Path analysis showed that the positive and significant correlation of pod number per plant with grain yield was the true relationship. Similar results were reported by Haghi*et al.,* (2011), Gupta (2008) and Arshad*et al,* (2006) on the same crop. In contrary to the present result Iqbal*et al,* (2003) and Agdew and Getnet (2005) reported negative direct effect of pod number per plant on grain yield of soybean genotypes.

The highest negative direct effect of harvest index (-0.536) was counter balanced by the favorable indirect effect of pod number per plant, hundred seed weight, days to maturity and total nodules per plant and the correlation was reduced to 0.250. This finding is in harmony with the report of Agdew and Getnet (2005) and Haghi*et al,* (2011) where harvest index had negative direct effect on soybean yield. In contrary to the present finding Shivakumar (2008) reported positive direct effect of harvest index on grain yield of soybean.

The second highest positive direct effect of hundred seed weight (0.546) was counter balanced by the indirect negative effects of the characters biomass yield, root to biomass ratio, effective nodules per plant, pod number per plant, pod length, plant height, days to pod setting, and days to 50% flowering. Similar results were reported by Agdew and Getnet (2005), Shivakumar (2008) and Arshad*et al,* (2006) in soybean genotypes. Path analysis showed that correlation explained the true relationship of these two characters. In contrary to the present finding Haghi*et al,* (2011) and Gupta (2008) reported negative direct effect of hundred seed weight on grain yield on the same crop.

The third highest positive direct effect of biomass yield (0.227) showed significant positive correlation with grain yield and path analysis showed that the correlation explained the true relationship of the character with grain yield. This result is in harmony with the findings of Showcat and Tyagi (2006) and Shivakumar (2008) where positive direct effect of biomass yield is reported in soybean genotypes.

However, root dry weight, root volume, total nodules per plant and days to pod setting had showed negative direct effect on grain yield. They only contributed to grain yield mainly via their positive indirect effect with other characters.

Days to maturity, pod length, effective nodules per plant and root to biomass ratio had negative direct effect on grain yield. Moreover, their correlation with grain yield is negative which suggested any increase in these characters affects grain yield in the negative direction. Showkat and Tyagi, (2010) reported negative direct effect for days to maturity and pod length in 40 soybean genotypes. The residual effect (0.231) indicated that characters which are included in the genotypic path analysis explained (76.6%) of the total variation in grain yield which indicates that there may be some more components that are contributing towards seed yield.

Path analysis at Assosa indicated selecting genotypes having high number of pods per plant, biomass yield and hundred seed weight could be used to improve seed yield in soybean genotypes as a result of their direct effect on grain yield.

Table 10. Path coefficients of direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of 15 traits on grain yield on 49 soybean germplasm tested at Assosa (2010/11).

Traits	DF	DPS	DM	PlH	PPP	PL	BY	TNPP	ENPP	RV	RDW	RBR	HSW	HI	rg
DF	**0.180**	-0.036	-0.071	0.047	-0.206	0.023	0.080	-0.109	-0.053	-0.037	-0.009	0.037	0.078	0.131	0.06
DPS	0.112	**-0.057**	-0.056	0.029	-0.159	0.035	0.029	-0.032	-0.013	-0.010	-0.017	0.022	0.024	0.106	0.01
DM	0.069	-0.017	**-0.184**	0.034	-0.420	0.028	0.020	-0.052	-0.028	-0.035	0.042	0.033	-0.074	0.252	-0.33*
PlH	0.089	-0.018	-0.067	**0.094**	-0.173	0.036	0.125	-0.108	-0.047	-0.055	-0.015	0.055	0.153	0.132	0.20
PPP	-0.047	0.011	0.098	-0.021	**0.792**	-0.028	-0.031	0.049	0.037	0.013	-0.013	-0.023	-0.036	-0.426	0.38**
PL	-0.021	0.010	0.025	-0.017	0.108	**-0.201**	-0.050	0.013	-0.009	0.078	0.029	0.008	0.108	-0.173	-0.09
BY	0.063	-0.007	-0.016	0.052	-0.107	0.044	**0.227**	-0.132	-0.056	-0.109	-0.031	0.106	0.287	0.178	0.50**
TNPP	0.084	-0.008	-0.041	0.043	-0.167	0.011	0.128	**-0.234**	-0.125	-0.024	0.015	0.070	0.130	0.150	0.03
ENPP	0.072	-0.006	-0.040	0.034	-0.223	-0.014	0.096	-0.221	**-0.132**	-0.015	0.023	0.058	0.144	0.140	-0.08
RV	0.034	-0.003	-0.033	0.027	-0.052	0.081	0.127	-0.028	-0.010	**-0.194**	-0.049	0.021	0.107	0.088	0.12
RDW	0.017	-0.010	0.080	0.014	0.103	0.060	0.072	0.037	0.031	-0.099	**-0.097**	-0.057	0.133	0.041	0.33*
RBR	-0.051	0.009	0.047	-0.039	0.137	0.012	-0.181	0.124	0.058	0.030	-0.041	**-0.132**	-0.215	-0.112	-0.36*
HSW	0.026	-0.003	0.025	0.026	-0.052	-0.040	0.119	-0.056	-0.035	-0.038	-0.024	0.052	**0.546**	-0.154	0.39**
HI	-0.044	0.011	0.087	-0.023	0.631	-0.065	-0.076	0.065	0.034	0.032	0.007	-0.028	0.157	**-0.536**	0.25

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index.Residual effect = 0.296

4.5. Cluster Analysis

Divergence analysis is a technique used to categorize genotypes that are similar into one group and others into a different group. D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups. The genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents.

At Jimma, the genotypes were grouped in to five distinct clusters (Table 11). This indicates the tested soybean genotypes were moderately divergent. The genotypes were distributed in such a way that 21 (42.85%) genotypes were grouped into Cluster I, 14 (28.57%) genotypes into Cluster III, 8 (16.32%) genotypes into Cluster II, 4 (8.16%) genotypes into cluster IV and 2 (4.08%) genotypes into cluster V.

Table 9. The distribution of genotypes into five clusters based on D^2 analysis for 49 soybean genotypes tested at Jimma (2010/11).

Cluster	Number of genotypes	Genotypes included
I	21	IAC-11, H10, G01892, H5, AGS-7-1, G9945, F81-7636-4, JSL1, AGS-3-1, AGS-234, AGS-299-2, PR-145-2, IAC-6, Essex-1, H2, V1-1, H1, Promoveria, H4, SR-4-3, HS-82-2136
II	8	PR-41(339), IAC-73-5115, Assosa local check 1, G03705, TGX-1895-49-F, H18, Protana, PR-160-6
III	14	Lotus, Clark 63k, PR-149-81-EP, G01853, H14, F82-7629-2, G00391, H3, FB1-7636,G00386, Crowford, PR-143-(14), SR-4-1, TGX-1895-33F
IV	4	AGS-3, G00141, Davis, AGS-214
V	2	TGX-297-6E-1, Hardee-1

At Assosa, the genotypes were classified into three clusters (Table 12). Cluster II was the largest cluster with 29 (59.18%)genotypes followed by cluster I which contained 19 genotypes or almost 38.77% of the total population. Cluster III contained only 1 genotype which is 2.04% of the total population.

Table 10. The distribution of genotypes into three clusters based on D^2 analysis for the 49 soybean genotypes tested at Assosa (2010/11).

Cluster	Number of genotypes	Genotypes included
I	19	H10, G00386, Promoveria, IAC-11, H4, Essex, H1, Crowford, PR-41(339), G01892, G00141, AGS-3-1, H14, PR-160-6, G01853, PR-143 (14), F82-7629-2, Clark-63k, V1-1
II	29	AGS-234, AGS-214, HS-82-2136, SR-4-1, H18, PR-149-81-EP7, Davis, FB1-7636, TGX-1895-49-F, G03705, AGS-299-2, H2, H3, H5, TGX-297-6E-1, PR-145-2, JSL-1, G9945, F81-7636-4, Lotus, SR-4-3, Protana, IAC-6, IAC-73-5115, Assosa local check-1, AGS-7-1, AGS-3, Hardee-1, G00391
III	1	TGX-1895-33F

4.5.1 Genetic distance between clusters

The pair wise generalized squared distance (D^2) among clusters is depicted in table 13 and 14 for Jimma and Assosa, respectively.

The χ^2-test for the five clusters at Jimma (Table 13) indicated that there was statistically significant difference among the clusters except between cluster I and III (22.65). The maximum distance was found between cluster II and V (D^2=305.26) followed by cluster III and V (D^2 =179.31), cluster II and cluster IV (D^2 = 162.82), cluster III and IV (D^2 = 90.35), cluster I and V (D^2 =87.13), cluster I and II (D^2 = 77.19) and cluster IV and V (D^2= 60.58).

The χ^2-test for the three clusters at Assosa (Table 14) indicated that there was statistically significant difference among the clusters except cluster I and III (11.85). The highest cluster distance was recorded between cluster I and cluster III (D^2=304.36) followed by cluster I and cluster III (D^2=224.41), which revealed that these clusters were genetically more divergent from each other.

According to Ghaderi*et al*. (1984), increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F2 and F3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors.

Crosses involving parents belonging to most divergent clusters are expected to manifest maximum genetic recombination and variation in genetic architecture (Singh *et al*., 1987). For instance, in the present result (Jimma) crosses involving parents belonging to most divergent clusters, for example clusters V with cluster II, cluster V with cluster III, and cluster IV with cluster II are expected to provide relatively better genetic recombination and combination in their progenies.

However, the selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on specific objectives of hybridization (Singh, 2001; Chahal and Gosal (2002).

Table 11.Mahalanobis distance between groups of soybean genotypes at Jimma

CLUSTERS	I	II	III	IV	V
I	-	77.19**	22.65^{ns}	30.65**	87.13**
II		-	27.17*	162.82**	305.26**
III			-	90.35**	179.31**
IV				-	60.58**
V					-

χ^2= 23.68 and 29.14 at 5%, 1% probability level respectively.

Table 12.Mahalanobis distance between groups of soybean genotypes at Assosa

CLUSTERS	I	II	III
I	-	11.85^{ns}	304.36**
II		-	224.41**
III			-

χ^2= 23.68 and 29.14 at 5%, 1% probability level respectively.

Populations from areas far separated geographically and having complex environment are normally expected to accumulate enormous genetic diversity (Chandel and Joshi, 1983). However, the distribution of strains in different clusters did not follow definite pattern with regard to geographical origins in the present case. Some accessions from different regions were found to be closely related regardless of their geographic origin (source) and the rugged nature of the terrain which could have favored isolation among the genotypes and hence, distinct lines of evolution in each region. This could be realized from the overlapping in clustering pattern among genotypes from different origin. In most of the cases, genotypes from same place of origin fell in to the different clusters and from different places of origin fell in to same cluster. Regarding to genotypes collected from Ethiopia, at Jimma, those

genotypes from Awassa area are distributed in to cluster I (47.36%) and the rest of the genotypes were distributed in to cluster II to cluster V each cluster having 10.52% of the genotypes. Genotypes from Pawe area are also distributed in to different clusters at Jimma. For instance, 40% of the genotypes are in cluster III, 30% in cluster II, 20% in cluster I and 10% in cluster IV. The genotypes from Jimma area are distributed in cluster III and cluster IV each having 66.66% and 33.34%, respectively. The genotype from Assosa area is found in cluster II.

At Assosa, genotypes from Awassa area are distributed in cluster I (27.77%) and in cluster II (72.23%). Genotypes from Pawe area are distributed in to the three clusters 60% in cluster II, 30% in cluster I and the rest 10% in cluster III. The genotypes from Jimma area are distributed in cluster I (66.66%) and in cluster II (33.34%). The genotype from Assosa area is found in cluster II.

Several possible reasons could be given for the genetic similarity among accessions from different regions. There could also be a tendency, particularly among resource poor farmers in marginal areas, of selecting for the same traits of interest like yield stability, resistance to diseases, insects and abiotic calamities and low dependence on the external inputs (de Boef*et al,*. 1996). Although the original sources might vary, the crop might have also been forced to evolve in the same direction by this kind of local breeding for the same targets which may emanate from similar economic, social cultural and ecological reasons in the area.

In this study the results showed that there was moderate diversity in soybean genotypes. Genetic architecture of a population is generally believed to be the result of breeding system, gene flow within and between populations, isolation mechanisms and prolonged selection by various natural and artificial forces (Chandel and Joshi, 1983). Ecological environment is believed to be the major force in crop evolution (Spagnoletti and Qualset, 1987). Therefore this diversity in soybean genotypes could mainly be attributed to diverse agro-climatic conditions of the areas from where they were collected (Harlan, 1969). However, there was no definite relationship between geographic diversity and genetic diversity. It is suggested that

selection of parents for hybridization need not necessarily be based on geographic diversity but genetic diversity must form the base for parental selection.

4.5.2. Cluster mean analysis

At Jimma, mean value of the 15 quantitative characters in each cluster is presented in Table 15. The characteristic feature of each cluster is discussed hereunder. The data obtained from the two locations were checked for homogeneity following F test but they were found to be heterogeneous therefore the results are analyzed and discussed independently.

Cluster I had medium maturity (123.9 days), high pod length (4.27cm) and heavier seed weight (12.75g). Cluster II had late days to flowering (73.00 days), late days to pod setting (84 days), late days to maturity (137 days), highest plant height (92.07), highest pod number per plant (58.50), highest root dry weight (2.90g), lowest number of total nodules per plant (17), and the lowest grain yield (1158.40 kg/ha).

Cluster III had a characteristic feature of highest biomass yield (35.00g), highest root volume (8.93cm^3), shortest plant height (72.66cm), lowest root dry weight (2.64g) and lowest root to biomass ratio (7.97%).

Cluster IV had characteristic feature of highest number of total nodules per plant and effective nodules per plant with 42.38 and 37.50, respectively. Moreover, the cluster also had the highest harvest index (51.41%), highest root to biomass ratio (10.08%), the lowest biomass yield (30.38g) and the shortest pod length of (3.69g).

Cluster V could be characterized by early flowering (55.00 days), early days to pod setting (71.00 days), early maturity (119.65 days), lowest number of pods per plant (39.50), lowest seed weight (11.00g), lowest harvest index (29.44%), lowest root volume (6.25cm^3), lowest number of effective nodules per plant (13.50) and highest grain yield (3795 kg/ha).

Table 13. Cluster mean for 15 characters in soybean tested at Jimma (2010/11)

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to 50% flowering	64.29	73.00**	64.07	62.75	55.00*
Days to pod setting	72.00	83.88**	73.18	71.50	71.00*
Days to maturity	123.90	136.53**	124.44	123.02	119.65*
Plant height	73.91	92.07**	72.66*	75.20	77.89
Pod number per plant	44.55	58.50**	46.07	57.00	39.50*
Pod length	4.27**	3.88	4.11	3.69*	3.85
Biomass yield	32.48	32.50	35.00**	30.38*	31.50
Total nodules per plant	31.10	23.94*	34.29	42.38**	25.50
Effective nodules per plant	16.86	16.25	16.79	37.50**	13.50*
Root volume	7.69	8.06	8.93**	7.38	6.25*
Root dry weight	2.85	2.90**	2.64*	2.88	2.75
Root to biomass ratio	9.40	8.83	7.97*	10.08**	8.89
Hundred seed weight	12.75**	11.88	12.36	12.57	11.00*
Harvest index	38.08	37.07	36.57	51.41**	29.44*
Grain yield	2480.00	1158.40*	1746.40	3115.30	3794.50**

**= highest value and *= lowest value

At Assosa, cluster I had characteristics of early days to 50% flowering (48.60days), early days to pod setting (71.52 days), highest pod length (4.56cm), lowest root dry weight (3.42cm), lowest hundred seed weight (12.92g), lowest number of pods per plant (14.02), shortest plant height (33.18cm) and the lowest grain yield of 630.78kg/ha (Table 16).

Cluster II had early days to maturity (108.87 days), the highest number of pods per plant (17.27), the highest harvest index (36.42%), the lowest number of total nodules per plant (14.68) , effective nodules per plant (7.24) and the lowest root volume (4.81cm^3).

Cluster III is characterized by late flowering (65days), late days to pod setting (73days), and medium maturity (116days). The cluster also had tallest plant height (61.20cm), highest number of total nodules per plant (29.50), highest number of effective nodules per plant (11.00), highest root dry weight (4.50g), highest biomass yield (24.00g), lowest root to biomass ratio (15.71%), highest seed weight (19.50g), lowest harvest index (17.50%) and the highest grain yield of (2130 kg/ha).

Table 14. Cluster mean for 14 characters in soybean tested at Assosa (2010/11)

Traits	Cluster I	Cluster II	Cluster III
Days to 50% flowering	48.60*	50.48	65.50**
Days to 50% pod setting	71.52*	73.27	73.50**
Days to maturity	114.21	108.87*	116.50**
Plant height	33.18*	35.72	61.50**
Pod number per plant	14.02*	17.27**	15.50
Pod length	4.56**	4.45	4.00*
Biomass yield	13.42*	14.06	24.00**
Total nodules per plant	15.65	14.68*	29.50**
Effective nodules per plant	8.44	7.24*	11.00**
Root volume	5.00	4.81*	8.50**
Root dry weight	3.42*	3.43	4.50**
Root to biomass ratio	26.14**	25.42	15.71*
Hundred seed weight	12.92*	13.98	19.50**
Harvest index	28.06	36.42**	17.50*

Grain yield	630.78*	1009.67	2130.00**

**= highest value and *= lowest value

4.5.3. Principal component analysis

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre 1998). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998).

The principal component analysis at Jimma revealed that six principal components PC1 to PC6 with Eigen values 4.20, 1.99, 1.91, 1.40, 1.29 and 1.17 respectively, have accounted for 79.90% of the total variation (Table 17).

The PC1 which accounted for 28.00% of the total variation among accessions at Jimma was mainly due to the contrast between days to 50% flowering, days to pod setting, days to maturity, plant height and total nodules per plant. Likewise, 13.27% of the total variation among the tested accessions accounted for the second PC originated from the contrasting effect between biomass yield, root volume, root to biomass ratio and harvest index.

Similarly, the third PC, which explained 12.77% of the total variation was mainly due to the contrast between pod number per plant, effective nodules per plant, harvest index, root dry weight and root to biomass ratio. The PC4 which explained 9.39% of the total variation among the accessions was due to the contrast between root volume, pod number per plant and hundred seed weight. Similarly, PC5, which accounted for 8.64% of the total variation, was mainly due to the average effect of plant height, total nodules per plant, effective nodules per plant and root dry weight. PC6 which explained 7.83% of the total variation among the accessions was due to the contrast between pod length, root dry weight and grain yield.

At Assosa, the principal component analysis in (Table 17) revealed that five principal components PC1 to PC5 with Eigen values 4.27, 2.53, 1.91, 1.28 and 1.08 respectively, have accounted for 73.81% of the total variation.

The PC1 which explained 28.43% of the total variation resulted from the contrast between biomass yield, days to 50% flowering, plant height, total nodules per plant, effective nodules per plant and root to biomass ratio. Correspondingly, the PC2 which accounted for 16.89% of the total variation was attributed to the contrast between days to maturity, pod number per plant, biomass yield, hundred seed weight, harvest index and grain yield.

PC3 which explained 12.71% of the total variability among the tested accessions resulted from the contrast between pod length, root volume, root dry weight, effective nodules per plant and root to biomass ratio. Similarly, the PC4 which accounted for 8.54% of the total variation among the tested genotypes was mainly due to the average effect of days to 50% flowering and days to pod setting. The average effect of total nodules per plant, effective nodules per plant, root dry weight and root to biomass ratio in the fifth PC, accounted for 7.23% of the total variation.

According to Chahal and Gosal (2002), characters with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in the present study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather to the small contribution of each character.

Table 15. Eigenvectors, total variance explained, cumulative and eigen values of the first seven and six principal components (PCs) of soybean genotypes evaluated at Jimma and Assosa respectively.

Eigen vectors											
	Jimma						Assosa				
Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC1	PC2	PC3	PC4	PC5
DF	0.410	-0.166	0.032	0.088	-0.061	-0.085	0.331	-0.035	0.063	0.490	0.128
DPS	0.398	-0.268	-0.022	0.085	0.024	-0.025	0.211	-0.087	0.174	0.649	-0.023
DM	0.367	-0.197	0.045	-0.140	0.209	-0.157	0.255	-0.358	0.007	0.098	-0.297
PH	0.305	-0.034	0.137	-0.296	0.389	0.162	0.344	0.096	0.081	0.152	-0.059
PPP	0.122	0.029	0.451	0.529	-0.135	0.194	-0.250	0.375	-0.060	0.190	-0.001
PL	-0.085	0.254	-0.279	0.001	-0.235	-0.320	-0.107	0.060	-0.465	0.142	0.115
BY	0.254	0.556	0.148	0.022	0.077	0.160	0.329	0.309	0.117	-0.245	-0.088
TNPP	-0.354	0.067	0.108	0.160	0.400	-0.256	0.372	0.055	-0.263	-0.117	0.360
ENPP	-0.242	0.050	0.301	0.159	0.578	-0.128	0.338	0.002	-0.321	-0.139	0.443
RV	0.168	0.314	-0.192	0.479	-0.076	-0.124	0.183	0.137	0.380	-0.240	-0.141
RDW	0.129	0.071	-0.356	0.256	0.319	0.527	0.001	0.215	0.516	-0.017	0.474
RBR	-0.199	-0.449	-0.388	0.141	0.127	0.185	-0.312	-0.165	0.302	0.090	0.471
HSW	-0.029	0.149	0.267	-0.422	-0.097	0.169	0.156	0.390	-0.098	0.021	0.056
HI	-0.134	-0.376	0.433	0.208	-0.273	0.094	-0.266	0.358	-0.192	0.291	0.025
GY	-0.267	0.103	0.004	-0.103	-0.138	0.573	0.048	0.489	0.072	0.073	-0.274
Eigen values	4.20	1.99	1.91	1.40	1.29	1.17	4.27	2.53	1.91	1.28	1.08
Total variance explained	28.00	13.27	12.77	9.39	8.64	7.83	28.43	16.89	12.71	8.54	7.23
Cumulative	28.00	41.28	54.04	63.43	72.07	79.90	28.43	45.32	58.04	66.58	73.81

5. SUMMARY AND CONCLUSION

The progress of crop improvement program depends on the choice of material, the extent of variability present and the knowledge of quantitative characters with grain yield and related traits. The present study comprises 49 soybean genotypes that were evaluated at two locations, namely Jimma and Assosa with the objective of assessing the genetic variability and character associations for 15 characters.

The results of analysis of variance for each location showed the genotypes were significantly different at ($P<0.01$) for all characters except root volume and root dry weight at Jimma. Phenotypic coefficient of variability (PCV) values at Jimma ranged from 5.67% for days to maturity to 49.10% for effective nodules per plant, whereas the genotypic coefficient of variability (GVC) ranged from 5.20% for days to maturity to 48.28% for effective nodules per plant. Phenotypic coefficient of variability values were low for days to pod setting, and days to maturity; medium for pod length and days to 50% flowering and it was high for the rest of the characters. Genotypic coefficient of variability values were low for days to pod setting, days to maturity, and root volume; high for grain yield, biomass yield, number of pods per plant, hundred seed weight, plant height, total nodules per plant, effective nodules per plant, and harvest index. The high GVC values of these characters suggest the possibility of improving these traits through selection.

At Assosa, phenotypic coefficient of variability (PCV) values ranged from 10.50% for days to maturity to 91.14% for effective nodules per plant, whereas the genotypic coefficient of variability (GVC) ranged from 10.47% for days to maturity to 90.00% for effective nodules per plant. The traits such as, grain yield, days to 50% flowering, biomass yield, number of pods per plant, hundred seed weight, plant height, root volume, total nodules per plant, effective nodules per plant, and harvest index had high phenotypic (PCV) and genotypic coefficient of variability (GCV) values.

High heritability coupled with high expected genetic advance (as percent of mean) was observed for effective nodules per plant, total nodules per plant, harvest index, pod number

per plant and grain yield for both locations; biomass yield, plant height and root volume in addition to the fore mentioned traits at Assosa. Thus, these characters can be improved through selection more easily than other characters.

At both locations high phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean was recorded for effective nodules per plant, total nodules per plant, harvest index, pod number per plant, plant height and grain yield.

Correlation analysis at Jimma showed that grain yield had negative and significant association with days to 50% flowering, days to pod setting and days to maturity both at phenotypic and genotypic levels. At Assosa, grain yield showed positive significant association with pod number per plant, hundred seed weight and biomass yield at genotypic and phenotypic level; and with root dry weight at phenotypic level. Grain yield had negative and significant correlation with days to maturity and root to biomass ratio at phenotypic level. Selecting for those traits showing positive and significant correlation coefficient with grain yield supports the possibility to increase grain yield of soybean.

Genotypic correlation coefficients of various characters with seed yield were partitioned into direct and indirect effects. At Jimma, effective nodules per plant exerted the highest positive genotypic direct effect followed by hundred seed weight, root to biomass ratio, pod number per plant, plant height, root dry weight and pod length. The rest of the characters had negative direct effect on grain yield. The highest direct positive effect at Assosa were exerted by pod number per plant followed by hundred seed weight, biomass yield, days to 50% flowering, and plant height. The rest of the characters had negative direct effect on grain yield. Therefore, root to biomass ratio, hundred seed weight and effective nodules per plant; pod number per plant, hundred seed weight and biomass yield at Jimma and Assosa, respectively were the important contributors to seed yield and these traits could be used as an indirect selection criterion.

Based on the relative squared distance values (D^2) between any two genotypes, the 49 soybean genotypes were grouped into five and three distinct clusters at Jimma and Assosa, respectively. This indicates that the soybean genotypes were moderately divergent.

The principal component analysis at Jimma revealed six principal components (PCs) having eigenvalues between 1.17 and 4.20 extracted a cumulative of about 79.90% of the total variation noted among the genotypes. It was also noted that differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the small contribution of each character. The principal component analysis at Assosa indicated five principal components (PCs) having eigenvalues between 1.08 and 4.27 explained a cumulative of 73.81% of the total variation among the genotypes.

The present study generally implied the presence of significant genetic variability among the tested genotypes. Thus, there is an opportunity to bring about improvement through direct selection or hybridization. However, all the above conclusions were derived from results of studies conducted within one season. So, further studies of soybean genotypes with larger sample size in broad environments and seasons should be conducted on soybean variability in order to give confirmative results.

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7. APPENDICES

Appendix Table I. Analysis of variance for mean square of the 15 characters of49 soybean genotypes tested at Jimma (2010/2011)

Mean squares							
Source of variance	Replication	Treatments	Blocks within replications	Error		R^2	Efficiency relative to RCBD
				Intra block	RCBD		
Degrees of freedom	1	48	12	36	48		
DF	13.22	94.83**	6.11	7.26	6.97	94.67	96.06
DPS	13.96	95.56**	5.38	5.66	5.59	95.32	98.77
DM	13.97	93.82**	3.82	8.04	6.99	94.04	97.89
PH	77.23	495.99**	28.75	14.97	18.42	97.18	109.85
PPP	0.82	289.55**	18.11	14.95	15.74	95.67	100.88
PL	0.44	0.52**	0.04	0.05	0.05	92.78	95.16
BY	0.09	136.02**	7.21	11.07	10.11	94.35	91.27
TNPP	58.93	355.25**	3.89	3.42	3.54	99.17	100.39
ENPP	32.00	212.85**	4.07	3.58	3.70	98.59	100.39
RV	11.79	5.59	2.26	4.58	4.00	65.04	87.32
RDW	4.71	0.70	0.43	0.48	0.47	69.58	97.59
RBR	17.67	9.16**	2.89	3.83	3.59	79.13	93.89
HSW	16.32	9.36*	4.08	3.93	3.97	75.65	100.04
HI	223.18	246.96**	36.95	43.31	41.72	88.60	96.32
GY	2140.45	798682.80**	198.26	189.18	191.45	99.98	100.05

*, ** Indicates significance at 0.05 and 0.01 probability levels, respectively.

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod number per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield

Appendix Table II. Analysis of variance for mean square of the 15 characters of49 soybean genotypes tested at Assosa (2010/2011)

Mean squares							
Source of variance	Replication	Treatments	Blocks within replications	Error		R^2	Efficiency relative to RCBD
				Intra block	RCBD		
Degrees of freedom	1	48	12	36	48		
DF	0.04	245.85**	0.87	0.95	0.93	99.70	97.82
DPS	0.01	82.80**	0.01	0.58	0.67	99.36	105.46
DM	0.16	135.60**	0.16	0.76	0.72	99.51	95.18
PH	0.04	198.44**	0.70	1.48	1.29	99.39	86.90
PPP	0.16	35.48**	0.88	0.84	0.85	98.04	100.04
PL	0.04	0.46**	0.05	0.07	0.06	89.23	94.72
BY	0.65	17.40**	2.54	1.82	2.00	92.05	102.59
TNPP	0.04	140.60**	0.52	1.04	0.91	99.43	87.65
ENPP	0.25	49.73**	0.42	1.25	1.04	98.18	83.40
RV	0.16	4.41**	0.30	0.36	0.35	94.44	95.93
RDW	1.02	0.48*	0.29	0.20	0.22	73.76	102.91
RBR	18.87	25.46**	4.63	3.67	3.91	89.13	101.30
HSW	0.09	13.78**	0.77	1.17	1.07	94.08	91.44
HI	1.27	263.42**	1.08	2.08	1.83	99.40	87.95
GY	326.95	153462.34**	823.35	979.09	940.16	99.50	96.02

*, ** Indicates significance at 0.05 and 0.01 probability levels, respectively.

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PlH=Plant height, PPP=Pod number per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield

Appendix Table III. Analysis of variance (ANOVA) for the combined characters of 49 soybean genotypes tested at Jimma and Assosa (2010/2011)

		Mean squares			
Sources of variance	Degrees of freedom	PL	RDW	RBR	HSW
Rep	1	0.377*	0.675	0.010	6.985
Rep x block	12	0.303**	0.806*	11.631*	5.503*
Loc	1	7.602**	18.063**	13455.171**	87.556**
Treatment	48	0.474**	0.396	14.739**	13.528**
Loc x Treatment	48	0.491**	0.732*	21.309**	10.879**
Error	85	0.060	0.390	4.161	2.575
Total	195	0.323	0.593	80.404	7.954
CV		5.69	19.34	11.85	12.33
LSD (5%)		0.070	0.177	0.579	0.455

PL= Pod length, RDW= Root dry weight, RBR= Root to biomass ratio, HSW= Hundred seed weight

Appendix Table IV. Mean values of 15 traits of soybean genotypes grown at Jimma (2010/11)

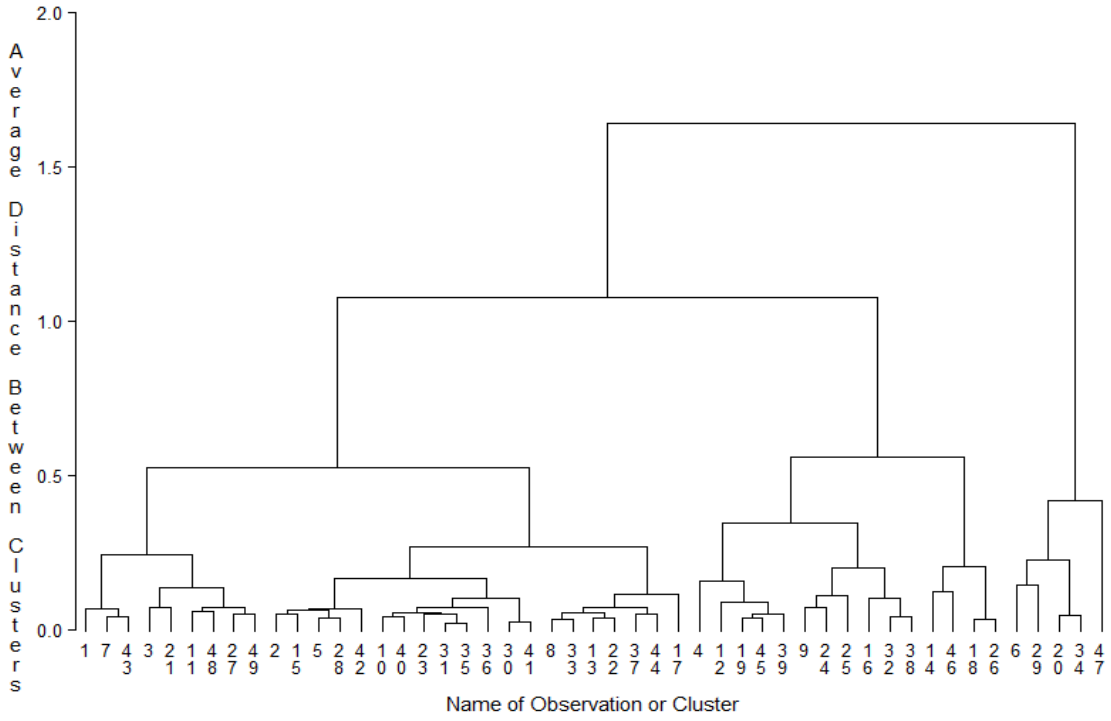
Gen	DF	DPS	DM	PH	PPP	PL	BY	TNPP	ENPP	RDW	RV	RBR	HSW	HI	GY
IAC-6	71.00	76.00	121.40	83.04	52.00	4.00	47.00	16.00	4.00	2.50	8.00	5.27	13.00	32.88	2452.0
SR-4-3	63.00	69.00	133.29	93.07	44.00	4.00	37.00	27.00	25.00	2.50	9.00	6.85	12.00	30.81	2291.0
TGX-1895-33F	63.00	85.00	127.54	93.75	40.00	3.50	36.00	28.00	12.00	2.50	9.00	6.94	12.00	31.25	1680.0
H4	70.00	77.00	124.65	83.83	45.00	4.25	35.00	24.00	8.00	3.50	10.00	10.00	15.00	45.38	2631.0
H1	58.00	64.00	115.25	44.14	37.00	4.75	23.00	48.00	18.00	2.50	9.00	10.98	11.00	41.12	2416.0
TGX-297-6E-1	61.00	76.00	125.00	77.90	36.00	3.70	36.00	22.00	14.00	2.50	5.00	6.91	12.00	28.08	3854.0
AGS-7-1	66.00	74.00	118.12	75.65	28.00	4.75	21.00	44.00	23.00	2.50	6.00	12.05	10.50	31.28	2381.0
Promoveria	68.00	73.00	128.74	82.77	48.00	4.00	21.50	36.00	29.00	2.00	4.00	9.35	12.00	56.78	2188.0
Crowford	64.00	68.00	121.63	84.79	53.00	5.00	43.00	34.00	18.00	2.00	10.00	4.67	12.00	33.17	1515.0
Lotus	63.00	71.00	128.88	94.48	44.00	4.00	48.00	33.00	27.00	3.50	9.00	7.25	11.00	21.12	1861.0
AGS-234	64.00	73.00	126.00	82.56	65.00	4.00	45.00	30.00	21.00	3.50	7.00	7.75	14.00	41.74	2679.0
H14	63.00	72.00	117.60	58.86	39.00	3.75	33.00	20.00	14.00	2.50	9.00	7.50	11.00	28.00	1579.0
HS-82-2136	66.00	74.00	129.35	69.62	47.00	3.75	48.00	16.00	11.00	3.50	13.00	7.26	13.00	24.58	2245.0
Protana	75.00	84.00	144.46	89.38	38.00	3.75	28.00	27.00	14.00	2.50	7.00	8.85	12.00	34.88	1000.0
Essex	70.00	75.00	124.91	85.38	38.00	4.75	37.00	30.00	26.00	2.50	7.00	6.69	10.50	22.59	2442.0
Clark-63k	54.00	71.00	118.58	58.56	32.00	5.00	24.50	40.00	17.00	3.50	9.00	14.25	11.00	29.90	2743.0
PR-41 (339)	73.00	73.00	125.06	70.10	52.00	3.75	38.00	23.00	7.00	2.50	9.00	6.53	11.00	33.54	1863.0
TGX-1895-49-F	64.00	73.00	137.17	99.17	33.00	3.75	30.50	19.00	16.00	2.50	7.50	8.12	11.00	23.43	1285.0
Davis	73.00	81.00	143.77	102.48	27.00	4.00	34.00	13.00	13.00	2.50	8.50	7.29	14.00	22.92	1148.0
H2	60.00	70.00	118.52	59.24	48.00	4.00	38.00	48.00	46.00	2.50	7.00	6.53	14.00	37.22	3233.0
SR-4-1	66.00	73.00	118.63	81.99	55.00	4.00	48.00	23.00	11.00	3.50	6.00	7.25	15.00	34.66	2530.0
IAC-11	71.00	78.00	136.86	80.45	64.00	4.75	37.00	29.00	20.00	2.50	10.00	6.70	12.00	43.52	2058.0
PR-143 (14)	65.00	73.00	126.75	68.47	47.00	4.75	28.50	13.00	2.00	2.50	8.00	8.70	11.00	32.28	2707.0
H18	69.00	77.00	125.00	75.16	60.00	4.25	49.00	30.00	17.00	3.00	12.00	6.13	13.00	35.72	1448.0
PR-160-6	66.00	81.00	129.12	66.73	79.00	4.00	31.00	35.00	24.00	2.50	8.00	8.02	11.00	61.42	1090.0

JSL 1	83.00	97.00	135.71	71.54	48.00	4.00	35.00	22.00	16.00	4.00	9.00	11.67	10.00	28.50	795.00
G9945	67.00	75.00	122.46	66.30	45.00	5.00	21.50	17.00	4.00	2.50	8.00	11.85	11.00	51.27	2619.0
Hardee-1	60.00	70.00	125.58	74.05	38.00	4.00	30.50	28.00	14.00	3.50	8.00	11.42	12.00	32.17	2381.0
G01892	49.00	67.00	114.29	77.87	43.00	4.00	27.00	29.00	13.00	3.00	7.50	10.87	10.00	30.80	3735.0
H3	69.00	76.00	124.68	70.90	46.00	3.75	26.00	18.00	9.00	3.00	7.50	11.53	12.00	38.77	2769.0
IAC-73-5115	64.00	73.00	117.93	41.58	56.00	3.75	25.50	40.00	22.00	2.75	9.50	10.81	9.00	43.09	1610.0
PR-149-81-EP	77.00	87.00	138.05	94.66	43.00	3.75	33.50	28.00	7.00	4.00	10.50	11.96	14.00	38.91	1274.0
AGS 214	63.00	68.00	125.65	56.97	44.00	5.00	36.00	43.00	17.00	2.75	9.00	7.64	16.00	41.72	1961.0
AGS-3-1	65.00	75.00	120.40	66.73	78.00	3.75	32.00	45.50	33.00	2.50	8.00	7.81	13.00	68.19	2982.0
F81-7636-4	64.00	71.00	125.51	53.98	38.00	4.00	20.00	29.00	11.00	2.50	7.00	12.50	14.00	56.90	2658.0
G00391	48.00	59.00	116.97	66.46	29.50	4.00	21.50	94.00	60.00	2.50	6.00	11.69	14.00	41.77	2352.0
G03705	54.00	64.00	111.86	57.49	42.00	4.00	25.50	49.00	20.00	2.50	10.00	9.77	11.00	38.17	1863.0
G01853	76.00	86.00	127.12	118.17	58.00	3.00	31.00	20.50	20.00	2.50	7.00	8.02	9.00	35.63	1327.0
H10	69.00	76.00	125.23	81.25	32.00	5.00	47.00	46.00	23.00	3.00	9.00	6.39	13.00	18.66	2009.0
V1-1	65.00	71.00	124.83	71.56	37.00	4.00	43.00	36.00	15.00	2.25	7.00	5.22	21.00	41.36	2698.0
AGS-299-2	68.00	75.00	122.58	58.82	53.00	4.00	24.00	23.00	12.00	2.00	7.00	8.39	11.00	55.84	2525.0
PR-145-2	59.00	66.00	124.69	89.07	73.00	4.00	46.00	36.00	29.00	3.00	8.00	6.53	11.00	36.31	2202.0
FB1-7636	69.00	77.00	128.86	91.95	38.00	5.00	34.00	25.00	5.00	4.00	7.00	11.93	10.00	21.21	2171.0
F82-7629-2	59.00	71.00	125.75	45.97	36.00	4.00	21.00	53.00	18.00	2.50	8.00	11.82	10.00	36.68	1750.0
G00386	74.00	83.00	135.00	99.66	52.00	3.00	27.00	20.00	9.00	2.50	7.00	9.17	14.00	59.40	1571.0
AGS-3	48.00	65.50	118.12	76.73	31.00	3.75	24.00	32.00	11.00	2.50	4.50	10.31	18.00	47.89	1681.0
G00141	61.00	69.00	125.71	77.04	39.00	4.00	20.50	38.00	35.00	3.00	6.00	14.71	13.00	53.58	3100.0
H5	65.00	72.00	127.46	97.80	63.00	3.00	31.00	38.00	36.00	3.50	8.50	11.25	11.00	46.65	3146.0
Assosa local check-1	70.00	82.00	136.81	94.41	62.00	4.75	37.00	27.00	20.00	2.50	7.00	6.70	14.00	50.84	1348.0
Mean	64.20	75.62	125.74	76.79	46.44	4.10	32.99	31.53	21.18	2.92	8.02	8.93	12.35	38.21	2160.12
CV	3.97	3.16	2.14	5.50	8.62	5.44	9.78	5.96	9.02	22.76	25.07	21.96	16.03	16.70	0.65
LSD (5%)	5.41	4.78	5.70	8.30	7.77	0.46	6.69	3.72	3.80	1.39	4.30	3.93	3.98	13.23	27.65

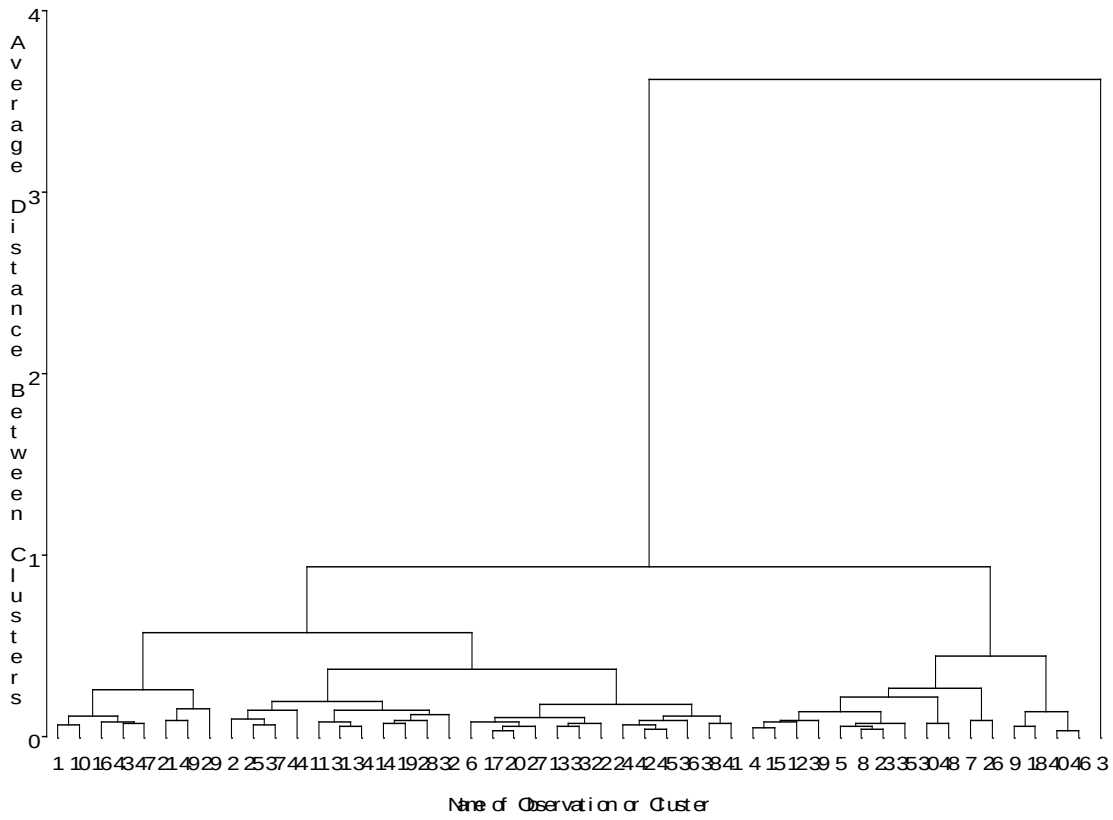
Appendix Table V. Mean values of 15 traits of soybean genotypes grown at Assosa (2010/11)

Name	DF	DPS	DM	PH	PPP	PL	BY	TNPP	ENPP	RV	RDW	RBR	HSW	HI	GY
IAC-6	43.00	71.50	96.00	34.00	21.50	4.75	16.00	4.50	2.50	4.50	4.50	28.04	21.50	57.12	1253
SR-4-3	74.50	94.00	119.50	53.50	12.00	3.75	12.50	15.00	5.50	4.50	3.50	27.92	14.50	27.64	899.55
TGX-1895-33F	65.50	73.50	116.50	61.50	15.50	4.00	24.00	29.50	11.00	8.50	4.50	15.71	19.50	17.5	2130
H4	47.00	69.50	117.00	41.50	12.50	4.00	14.00	8.50	2.50	7.50	3.50	24.87	12.50	24.1	699
H1	42.00	71.00	114.50	21.50	16.50	4.75	13.00	9.00	3.00	4.50	3.50	26.78	11.50	28.5	581
TGX-297-6E-1	44.50	69.50	115.50	34.50	24.00	5.00	12.00	6.00	2.50	4.50	3.00	25.17	14.00	70.54	1002
AGS-7-1	69.50	89.00	115.50	23.50	13.50	5.00	14.50	5.50	2.50	4.50	3.50	24.04	10.50	22.78	964
Promoveria	41.50	72.00	116.50	35.50	18.50	4.00	13.00	4.50	3.50	12.50	4.00	30.95	13.00	37.53	569.5
Crowford	66.50	77.50	116.50	38.50	9.50	5.00	14.00	14.50	5.50	3.50	3.50	24.87	12.00	18.03	519
Lotus	41.50	69.00	98.50	32.00	27.00	4.25	13.00	28.00	11.00	4.50	3.50	26.78	12.50	55.36	1018.5
AGS-234	45.00	70.50	96.00	33.50	24.50	5.00	14.50	10.00	4.50	4.50	3.50	27.61	16.00	59.36	1169.5
H14	42.50	73.50	101.00	25.00	17.50	5.00	13.00	7.00	3.00	5.50	3.50	26.78	12.50	33.61	668.5
HS-82-2136	69.50	72.50	117.00	32.50	19.50	4.00	13.00	12.00	4.50	5.50	3.50	26.78	13.00	42.55	851
Protana	72.50	73.50	112.50	56.50	11.50	4.00	14.50	24.00	14.00	5.00	4.00	27.62	15.50	26.78	875
Essex	49.50	71.50	116.00	31.00	10.00	4.50	13.00	30.00	18.50	5.50	3.50	26.78	18.00	24.32	653
Clark-63k	41.50	69.00	115.50	22.50	12.00	4.00	13.50	7.00	3.50	4.50	3.50	29.66	12.50	21.21	780
PR-41 (339)	68.50	76.00	114.50	34.50	13.50	5.00	13.00	24.00	16.00	4.00	3.50	26.78	12.00	23.57	521
TGX-1895-49-F	66.50	73.50	116.50	52.50	16.50	4.75	14.00	27.50	15.00	4.50	3.50	24.87	14.50	33.23	917.5
Davis	42.50	67.50	95.00	26.50	18.50	3.75	12.00	5.50	2.50	3.50	3.50	29.02	12.50	37.36	945
H2	41.50	68.00	94.50	39.00	19.50	5.00	13.00	6.50	3.50	4.00	3.50	26.78	15.00	43.92	1295.5
SR-4-1	69.50	78.50	115.00	45.50	13.50	3.75	17.50	12.50	4.50	8.50	3.50	22.87	14.50	23.23	855.5
IAC-11	42.50	68.50	115.00	32.50	14.50	4.00	13.00	13.00	6.50	4.00	3.50	26.78	11.50	28.32	533
PR-143 (14)	64.50	71.00	116.00	33.00	20.50	5.00	13.00	25.50	15.00	4.50	3.00	26.78	13.00	45.61	755
H18	46.50	75.50	116.00	41.50	10.00	4.00	15.50	16.50	9.50	6.50	4.50	32.29	12.00	16.19	867.5
PR-160-6	72.50	73.00	115.50	34.00	10.00	5.00	12.00	30.50	17.00	5.50	3.00	25.67	15.50	29.76	684.5
JSL 1	39.50	67.50	98.50	24.00	18.50	4.75	13.00	11.50	4.50	4.50	3.50	27.28	12.00	33.21	871
G9945	42.50	67.50	116.50	32.00	19.00	5.00	14.00	13.50	6.00	4.00	3.50	28.57	15.00	44.85	909.5
Hardee-1	47.50	68.50	95.00	37.00	18.00	4.25	13.00	11.50	4.00	5.50	3.50	26.78	14.50	41.25	1076

G01892	43.00	72.50	117.00	26.00	14.00	4.00	12.00	12.50	5.00	4.00	3.00	26.17	9.50	25	601
H3	44.00	67.00	99.50	23.50	19.50	5.00	13.00	10.50	4.50	4.50	3.50	26.97	11.50	33.14	1284.5
IAC-73-5115	66.00	76.00	116.50	52.00	13.50	4.00	25.50	46.50	24.00	8.00	3.00	11.80	17.00	18.05	938.5
PR-149-81-EP	42.00	69.50	115.50	25.00	12.00	4.00	13.50	17.00	8.50	4.50	3.00	25.83	12.00	22.18	871
AGS 214	46.00	75.00	98.00	26.50	25.50	4.00	14.00	13.50	6.00	5.00	3.50	24.87	11.50	38.17	1155
AGS-3-1	42.50	73.00	98.50	22.00	17.50	4.00	15.50	16.50	8.50	4.00	5.00	32.27	10.50	28.80	718.5
F81-7636-4	37.00	68.00	99.50	29.00	12.50	5.00	14.00	20.50	14.00	4.50	3.50	24.87	16.00	29.15	867
G00391	42.00	69.50	115.00	40.00	12.50	5.00	14.50	10.50	5.50	3.50	3.00	20.71	16.00	28.72	1126.5
G03705	48.50	75.00	116.00	52.00	19.50	5.00	13.00	25.50	12.50	4.00	3.00	22.71	9.50	30.00	929.5
G01853	47.50	72.00	115.50	32.50	12.50	5.00	14.00	21.50	17.50	4.50	3.00	21.54	15.50	30.38	664.5
H10	40.00	68.00	116.00	47.00	11.50	5.00	14.50	7.50	3.50	4.00	3.50	27.62	10.50	17.36	446
V1-1	42.00	67.50	116.00	25.00	15.50	5.00	14.00	11.50	5.00	4.50	3.00	21.55	11.50	27.54	819
AGS-299-2	47.50	69.00	116.00	34.00	22.50	5.00	14.50	12.50	6.00	4.50	3.50	27.62	12.00	37.26	955.5
PR-145-2	46.50	76.50	116.00	31.50	12.50	3.75	12.50	16.50	8.50	5.00	3.00	24.04	14.50	29.00	1026.5
FB1-7636	41.50	65.50	115.50	21.00	16.50	4.00	11.50	6.50	3.50	4.50	3.00	26.13	11.50	37.42	945.5
F82-7629-2	48.50	72.50	115.50	46.00	13.50	4.00	13.00	26.50	13.00	4.00	3.00	23.71	11.00	22.83	740.5
G00386	40.00	68.50	117.00	36.00	12.50	5.00	14.00	11.50	4.50	4.50	3.50	24.87	20.00	37.90	514.5
AGS-3	41.50	69.50	116.50	38.00	15.50	4.00	12.00	6.50	3.50	4.50	3.00	26.17	11.00	28.40	1209
G00141	41.50	72.50	116.50	46.50	14.50	4.50	13.50	16.50	9.50	4.00	3.00	22.25	13.00	28.78	517.5
H5	42.00	66.50	99.00	25.00	15.50	5.00	14.50	14.50	9.00	4.50	3.00	20.71	19.00	49.75	1177
Assosa local check-1	63.50	102.00	117.00	40.50	16.50	4.50	13.50	15.50	8.00	4.00	3.50	22.25	16.50	39.61	1025
Mean	50.06	72.60	111.10	35.27	15.98	4.49	14.02	15.37	7.79	4.96	3.45	25.50	13.68	32.79	888.84
CV	1.90	1.11	0.79	3.36	5.73	5.80	9.48	6.50	13.76	11.86	13.50	7.59	7.69	4.17	3.43
LSD (5%)	1.96	1.62	1.75	2.45	1.84	0.53	2.71	2.05	2.25	1.21	0.91	3.85	2.17	2.90	62.91



Appendix figureIDendrogram of 49 soybean genotypes based on evaluation for 15 characters grown at Jimma (2010/11).



Appendix figure II. Dendrogram of 49 soybean genotypes based on evaluation for 15 characters grown at Assosa (2010/11).