

Genetic Variability and Associations of Yield and Yield Related Traits of Lentil (*Lens culinaris* Medik.) Genotypes at Dire Dawa, Ethiopia

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Abstract

Lentil (*Lens culinaris* Medikus) is a self-pollinated diploid ($2n = 14$) annual cool season legume crop that is produced throughout the world and valued as high protein food. Genetic diversity is essential for genetic improvement of crops to make selection and improvement for a given trait. The objective of the study was to study the genetic variation for different agronomic traits of lentil, the phenotypic and genotypic correlation coefficients among these traits and the direct and indirect effects of these traits on seed yield. In the present study, 30 lentil genotypes were used for the study and evaluated for genetic variability and associations of yield and yield related traits at Dire Dawa, Tony farm, from July 6, 2017 to October 10, 2017 in a completely randomized block design (CRBD). The genotypes were obtained from Institute of Biodiversity Conservation (IBC), Addis Ababa, Ethiopia. The collected data were analyzed to determine significant varietal difference by employing analysis of variance for each trait. High significant differences among genotypes for all traits were recorded indicating the presence of genetic variability. The broad sense heritability estimates were high for all traits except for pod length and biological yield which showed moderate heritability and seed yield which showed low heritability, thus, indicating little environmental influence on the traits. Correlation analysis indicated that the values of genotypic correlation coefficients were slightly higher than their corresponding phenotypic correlation coefficients for all except for 100 seed weight, signifying that the association among various traits is of genetic cause rather than environmental effect. The path analysis revealed that days to 95% maturity (1.41633), plant height (1.01723), number of pods per plant (0.98701), number of seeds per pod (0.29773), pod length (0.07098), 100 seed weight (0.29655) and days to emergence (0.11418) contributed positive direct effects on seed yield at genotypic level; so direct selection for these traits may be given more emphasis while selecting high yielding lentil genotypes at the genotypic level whereas at phenotypic level days to 50% flowering (0.17214), plant height (2.4178), number of pods per plant (2.47851), number of seeds per pod (0.09475) and pod length (1.42147) contributed positive direct effect along with their positive significant phenotypic association with seed yield, signifying that direct selection for these traits may be desirable for yield improvement in lentil at the phenotypic level.

Keywords: correlation analysis, heritability, path analysis, seed yield, trait

1. INTRODUCTION

Lentil (*Lens culinaris* Medik) is a self-pollinated diploid ($2n = 14$) annual cool season legume crop that is produced throughout the world and valued as high protein food. Lentil probably originated in the Near East and rapidly spread to Egypt, central and southern Europe, the Mediterranean basin, Ethiopia, Afghanistan, India and Pakistan, China and later to the New World including Latin America (Ladizinsky, 1979). It is probably the oldest of grain legumes to be domesticated. It is now cultivated in most subtropical countries in the Northern hemisphere such as Canada and Pacific North West regions. Globally lentil is an important food legume crop component of farming and food systems of many countries (Sarker *et al.*, 2002). It plays an important role in human, animal and soil health improvement occupying a unique position in cereal-based cropping systems. Its ability in nitrogen fixation and carbon sequestration improves soil nutrient status, which in turn provides sustainability in crop production systems. Lentil can be grown on different soil types and of low fertility and this has assured its important place as a crop of both fertile and marginal lands.

Globally lentil productivity was only 560 kg/ha during the period 1961-1963 and reached 950 kg/ha by 2004-2006 (Erskine, 2009). Despite such productivity increase, the current yield level is still low by comparison with other crops, which might be attributed to the limited yield potential of lentil landraces and vulnerability to an array of stresses. The nutritional value of lentil protein is determined by its amino acids, which are needed by humans to build and/or repair and as structural proteins, enzymes, peptides, antibodies, neurotransmitters and other important components (Reeds and Beckett, 1996). Generally lentil has good amino acid pattern in that it contains all the human essential amino acids sufficient in proportions as recommended by the World Health Organization (Grusak, 2009). The exceptions are the sulfur containing amino acids, methionine and cysteine, which (as with most legume seeds) are the most limited amino acids. On the contrary, lentil has adequate to high levels of lysine. This is why lentil and other legumes are suggested as ideal complementary foods to cereals (rice, wheat, maize), which are low in lysine and generally better sources of the sulfur amino acids (Shewry and

Halford, 2002).

Lentil is an important dietary component in Afghanistan, Bangladesh, India, Nepal, Pakistan, Turkey, Egypt, Iraq and Ethiopia. It makes nutritious soups frequently combined with cereals, since lentils and cereals nutritionally complement each other to form a more complete protein. The crop is used throughout Mediterranean and Middle East, and major food in India, where it is cooked to a purée. Farmers and their families in Ethiopia use it to make *nifro*, *sambusa*, *wot*, and soup, which supplements their diet with lysine where barley and teff are the staple food (Yadav *et al.*, 2009). In Ethiopia, Lentils, currently cover an area of about 105,956.04 hectares with an annual production of 1,237,772 tons; the average national productivity being about 11.68 tons/ha (CSA, 2010). They are mostly cultivated for domestic consumption. However the demand for both grain and split red cotyledon is very high in India, Lebanon and Srilanka. Because of significant economic role and social conditions, lentil production is expanding in Ethiopia in both stressed and non-stressed environments (Asnake and Geletu, 2003). The production and productivity of lentil in Ethiopia is also showing an improving scenario from 2000-2010, whereby the productivity surpassed a tone per hectare. Both biotic (rust, wilt, and root rot) and abiotic (drought, frost, and water logging) stresses are important constraints of lentil production in Ethiopia.

Genotypes with multiple resistance, high adaptability to diverse agro ecological zones, high yields, better grain size and color as desired by producers and consumers are priorities of the national breeding program (Asnake and Geletu, 2003). Improved seeds are among the limiting input factors that contribute to an increase in productivity. The necessity of improved seed is also expanding as more and more peasants aspire to have increased production. In Ethiopia, among pulses the larger area to which improved seeds were applied was under haricot bean (8,482 ha) and lentil (2,908 ha) (CSA, 2009). The total improved seed users in 2015/2016 main cropping season is estimated to be 19,164; 10,871 and 7,608 for haricot bean, chickpea and lentil, respectively (CSA, 2013).

The Ethiopian National Agricultural Research System in collaboration with ICARDA has so far released many lentil varieties since 1980. Among the officially released lentil varieties ‘Alemaya’, ‘Aadaa’ and ‘Teshale’ are the dominant ones. A successful breeding program is likely to generate genetic gain in yield overtimes which is one component of grain yield potential (Heisey *et al.*, 2002). Genetic improvement can be studied either by estimating level of genetic advance from a single or a series of selection cycles made at a time or from a long-term breeding effort made by a breeding program (Waddington *et al.*, 1986). Likewise, estimation of genetic progress from a breeding program and periodic evaluation of advancement in the genetic gain of a crop is required to understand changes produced by breeding activities, to assess the efficiency of past improvement works in genetic yield potential and suggest the future selection direction to facilitate further improvement and fulfill farmers need in seed and grain production. Progress made in genetic yield potential and associated traits produced by different crop improvement programs was evaluated and documented in Ethiopia and concluded that genetic improvement in those crops has produced modern cultivars with improved yield potential (Amsal, 1995a and b; Yifru and Hailu, 2005; Kebere *et al.*, 2006; Tamene, 2008; Wondimu, 2010; Demissew, 2010; Ersullo, 2010; Tafese, 2011; Tibebu, 2011). Therefore, this study was designed to evaluate the heritability, genetic advance and associations among characters of lentil genotypes and to estimate the contribution of each trait to yield improvement in lentil genotypes. Hence, the current study was initiated with the following objectives:

General Objective

- To assess the genetic variability and associations of yield and yield related characters of lentil accessions and their contribution to yield.

Specific Objectives

- To estimate the phenotypic and genotypic coefficients of variation, heritability, and genetic advance of agronomic characters in lentil accessions.
- To assess the extent of association among agronomic characters of lentil accessions.
- To estimate the relative contributions of the different agronomic characters of lentil to the yield of lentil.

2. LITERATURE REVIEW

2.1. Origin, Phylogeny, and Botanical Description of lentil

Lens is a genus in the family Leguminaceae (*Fabaceae*), commonly known as the legume family. The genus *Lens* consists of the species: *Lens culinaris* (Medikus), its progenitor *Lens orientalis* (Boiss.), *Lens nigricans* (M. Bieb.), *Lens ervoides* (Bring.), *Lens odemensis* (Ladiz.), *Lens lamottei* (Czefranova) and *Lens tomentosus* (Ladiz.) Ladizinsky (1979). The three main problems regarding the biological nature of any crop are: (i) where and when the biological species originated; (ii) where and when that species became a crop; and (iii) how it has evolved as a crop (Cubero *et al.*, 2009). For lentil, archaeological data were given by Cubero (1981). The oldest remains were found in Hacilar (Turkey), Ramad (Syria), Jarmo (Iraq), Jericho (Palestine), Beidha (Jordan) and Ali Kosh (Iran) dated around 9000 BC, in ceramic Neolithic layers. Even older remains were found

in Mureybit (Syria), 10,500 BC, but they were wild lentils. The Near East is the obvious candidate for the center of origin of lentil, according to the archaeological data, the distribution of wild species and the existence of the remains of both wild and cultivated lentils in the same region. Lentil was one of the first domesticated plant species, its remains being as old as those of einkorn, emmer, barley and pea (Harlan, 1992). It has been cultivated for 10,000 years in the most difficult agricultural environments, being perhaps second only to barley in this sense. *Lens orientalis* is the wild form out of which the cultigens developed. *Lens culinaris* forms show, in general, greater height, longer rachis and greater number of leaflets per leaf, greater leaflet area, greater number of flowers per peduncle, peduncle shorter or equal to the rachis, higher frequency of white flowers, and also larger pods and seeds. All these characters are related to the increase in yield (Cubero *et al.*, 2009).

According to Balayan and Singh, 1986 the botanical features of *Lens culinaris* can be described as annual bushy herb, slender, almost erect or sub erect, much-branched, with 15-75 cm in height. Ten to sixteen leaflets are subtended on the rachis (40-50 mm); the leaves are alternate, compound, pinnate, usually ending in a tendril or bristly. Seeds are biconvex, rounded, and small, 4-8 mm × 2.2-3 mm, lens-shaped, flowers are small, pale, blue, purple, white or pink. One to four flowers are borne on a single peduncle and a single plant can produce up to 10-150 peduncles each being 2.5-5 cm long. Reproductive nodes of lentil generally bear single flowers, sometimes two or three and, rarely, four flowered racemes on short peduncles. The typical butterfly-like (papilionaceous) flowers are small, from 4 to 8 mm long, and white, pale purple or purple black. Flowering in lentils proceeds acropetally. So lower nodes may bear pods close to maturity while younger nodes continue to initiate flowers (Erskine *et al.*, 1989). Testa colors range from pale tan to brown and black, with purple and black mottles or speckles common to some cultivars (Jain *et al.*, 1995). Germination is hypogeal (cotyledons remain below the ground), which helps prevent environmental damage to seedlings. In the event of shoot damage, new lateral branches can initiate from nodes below ground. The size of lentil seeds increase from the types grown in eastern regions to western types. Two types, namely; macrosperma, found mainly in the Mediterranean region and the New World (seed size ranging from 6 to 9 mm in diameter and yellow cotyledons with little or no pigmentation), and microsperma (2 to 6 mm with red orange or yellow cotyledons) found on the Indian subcontinent, Near East and East Africa, respectively, are known (Singh, 2010).

2.2. Present status of lentil production and consumption in the world.

Lentil is currently an important pulse crop grown widely throughout the Indian Subcontinent, Middle East, Northern Africa and East Africa, Southern Europe, North and South America, Australia and West Asia (Erskine, 1997; Taylor *et al.*, 2003). It is a primary component for farming systems of these areas (Sarker, and Kumar 2011). The major lentil-growing countries of the world are Canada, India, Turkey, Australia, USA, Nepal, China, and Ethiopia. Out of the total global production in recent years, the most is coming mainly from Canada and India (Figure 1).

The total lentil cultivated area in the world is estimated around 4.34 million hectares with annual production and productivity of 4.95 million tons and 1260 Kg ha⁻¹ respectively (FAO, 2014). The production of the crop is increased significantly from year to year through expansion of net cropped area along with its productivity. This increment was stimulated by greater improvement in demand of both domestic and international market of the crop. Even though lentil producing nations are striding in skyrocketing of their production to fill domestic demand and the overwhelming export market, still the supply gap remains wide which is aggravated by rapid population growth, ever changing client demand and limitation in genetic improvement of the crop. Most of the production, around 56% is consumed locally and only 44% of the production is supplied to the global market (Kumar *et al.*, 2013).

Canada is the leading exporting nation, while India is the leading lentil consuming and producing nation (Bedard *et al.*, 2010).

The enrichment of lentil with high protein makes it the preferred pulse crop to rural poor household in the world who cannot afford expensive animal products. Because of this, lentil is called poor man's meat due to its low price compared to meat. It efficiently complements the carbohydrate rich food in making nourishing meal by balancing the amino acid and micronutrient content of the diet. Enhancement of productivity of lentil is very vital as most of the poor people in the world depend on it for protein supply to meet their food, nutritional, and health benefits. Lentil cultivation is expected to increase rapidly in the future due to its demand for consumption and agronomic ability to assimilate atmospheric nitrogen.

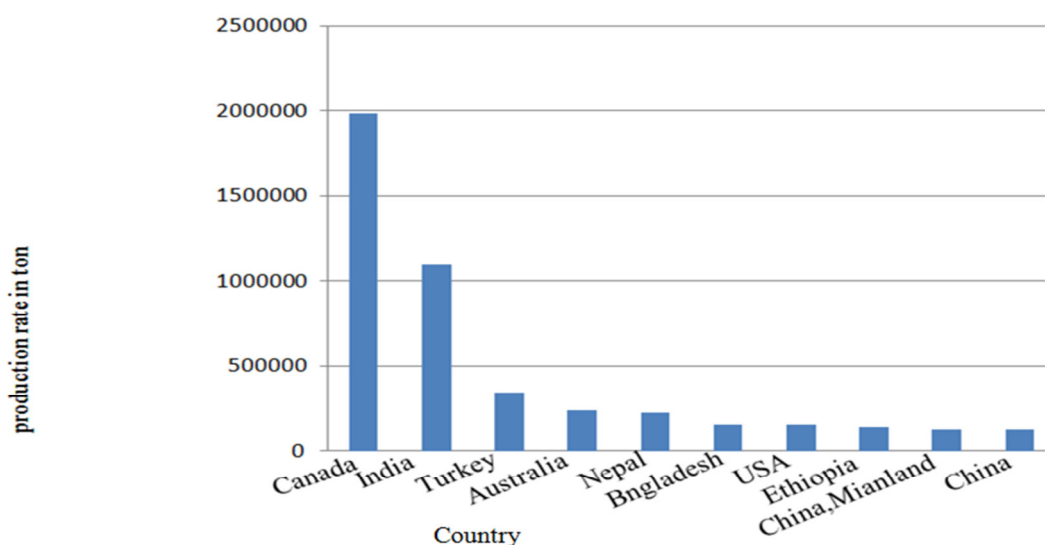


Figure1: Global Major Lentil producing nations (in 1000'tons) in 2014/2015 (FAO, 2014).

2.3. Lentil Breeding and Variety Adoption in Ethiopia

Lentil improvement program was initiated at DebreZeit Agricultural Research Center in the early 1970s, with the focus of increasing yields, development of disease resistance and improvement of management practices (Geletu and Yadeta, 1993). In 1976, the Center took the responsibility of coordinating lentil research at the national level. Since the 1970's the lentil research programme has collaborated with ICARDA's Lentil Improvement Programme. The collaboration has led to the release of one regional 'Assano' and ten nationwide varieties 'R-186', 'Chekol', 'Chalew', 'Gudo', 'Adaa', 'Alemaya', 'Alemtena', 'Teshale', and 'Derso' with their full management packages. EL-142 was released through selection of germplasm from Ethiopian land race collections. Since the late 1990s, the DZARC has started an outreach and on-farm technology popularization programme, involving FRGs (Farmers Research Groups) in several districts. The aim was to increase farmers' awareness and accelerate adoption of the new technologies among farmers who were able to access information about the technology and seed through this programme (Aw-Hassan *et al.*, 2009).

Research on lentil is being undertaken at DebreZeit, Adet, Holetta, Sinana, Debre Birhan and Sirinka Agricultural Research Centers (Senait *et al.*, 2006). Global studies on the impact of lentil research have revealed the advances of lentil improvement research in developing countries (Aw-Hassan *et al.*, 2003). According to Aw-Hassan *et al.* (2009), in Ethiopia, the adoption rate of improved varieties of lentil was 19% in 2004, with higher adoption rates in Ada-Liban (30%) and Gimbichu districts (35%). Moreover, the factors that affect adoption of improved lentil varieties are the gender of the head of the household, access to seeds of improved cultivars, participation in extension activities such as demonstration, verification trials, training and membership of a FRG. In Lume and Gimbichu woredas, out of 140 farmers 71% of the farmers who participated in the demonstration and on-farm experiments adopted an improved variety 'Challew' in 1997/98 crop season whereas only 29% of the non-participated farmers adopted the said variety (Teklu, 1998). Senait *et al.* (2006) reported a rapid increase in area coverage from 156 ha in 2003/2004 to 2460 ha in 2005 under 'Alemaya', particularly in Gimbichu district. In addition, an average yield of 1.6–2.4 ton ha⁻¹ was reported for the variety 'Alemaya' compared to 0.6 ton ha⁻¹ for the local varieties (Legesse and Adam, 2003).

2.4. Lentil Production in Ethiopia

Small scale farmers in Ethiopia grow various crops for own consumption and economic benefits. Pulses are among the crops produced in all the regions of the country following cereals in terms of total production and area coverage CSA (2013). Lentil is one of the major highland pulses of Ethiopia that grows in rotation with teff, wheat and barley particularly on the heavy black soils (Jarso *et al.*, 2009). It is an important part of the farming system and essential to nutrition in the subsistence farming community in Ethiopia Korbu (2009). In such culture, a yield advantage of the succeeding cereal crop is realized as a result of the fixed nitrogen by the predecessor legume and also due to breakage of the life cycle of important diseases and insect pests (Bedard *et al.*, 2010).

Lentil production mainly depends on soil type, altitude and agro-ecologic conditions. In Ethiopia, its production is not mechanized and produced by small holder farmers with fragmented plots of land mainly for household consumption (Jarso *et al.*, 2009). The average annual total harvest of lentil for the last ten years in Ethiopia was about 90,159.63 tons of grains from about 92,998.61 hectares of land CSA (2013). Annual

agricultural sample survey by CSA indicated that the country's pulse production (particularly lentil) shows an increasing pattern since 2003/2004 till now (Figure 2). The total annual area covered by pulses for the last 10 years increased on average by 6% and that of lentil increased by 11.1%. Annual average production growth rate of lentil for the last 10 years was 19.03% (Figure 2). The total lentil production harvested during 2013/2014 growing season was 151,499.93 tones which were out yielded by 18.35% to 128,008.8 tons obtained in 2012/2013 cropping season (figure 2).

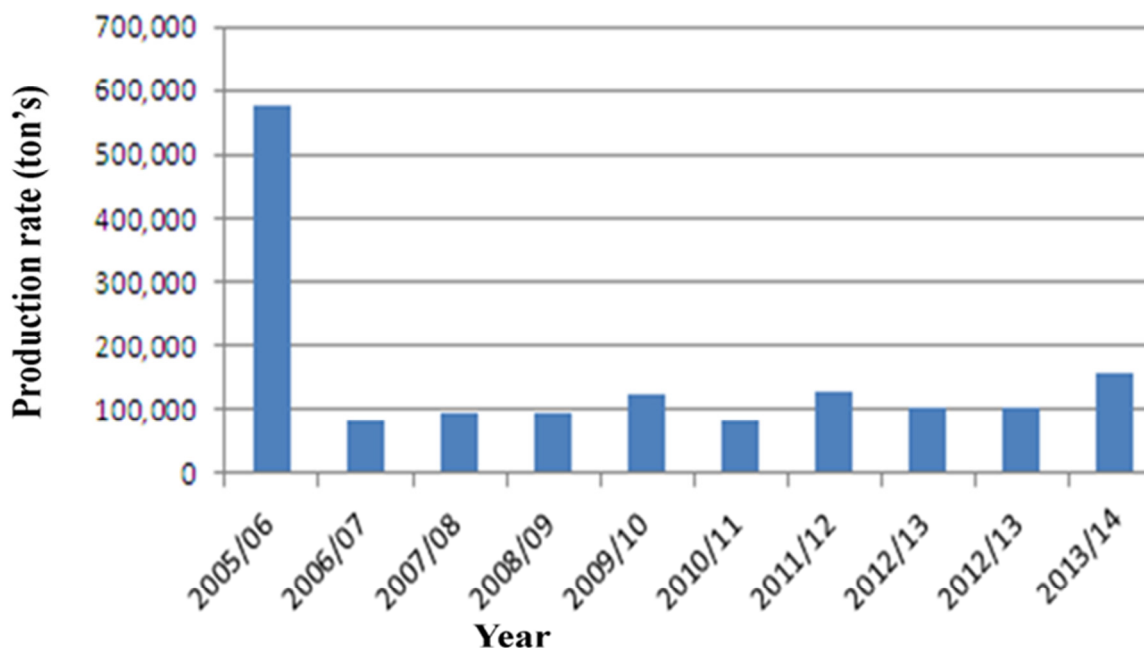


Figure 2: Lentil production in Ethiopia (in 1000'tons) from 2005/06 to 2013/2014 (FAO, 2014).

2.5. Genetic Variability, Heritability and Genetic Advance

Genetic variability is a measure of the tendency of individual accessions in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to environment and genotype. Genetic variability in a population is important for biodiversity, because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction. Variability is an important factor in evolution as it affects an individual's response to environmental stress and thus can lead to differential survival of organisms within a population due to natural selection of the fit variants (Visscher *et al.*, 2008).

Determining the genetic variation within and among breeding population involved in active sharing of germplasm will provide useful information on integrating new germplasm into the programs. Populations from crosses between genetically diverse parents are expected to have greater genetic variation than populations developed from less diverse parents. But, phenotypic assessment of the underlying diversity of parental lines is problematic. At molecular level, molecular markers such as AFLP and RAPD are useful tools to assess the underlying genetic variability not apparent from the phenotype (Engida *et al.*, 2007).

The value observed when a quantitative character is measured on an individual, is the phenotypic value. The phenotypic value is divided into genotypic and environmental components. An important objective is to assess the relative importance of the genotype versus environment. Hence, information about genetic parameters, such as heritability is relevant to decide which, are the most suitable quantitative traits to be used in germplasm evaluation focused on pre-breeding and breeding activities (Ara *et al.*, 2009).

The heritability expresses the proportion of the total variance that is attributable to the average effects of genes, and this is what determines the degree of resemblance between relatives. The heritability has a predictive role expressing the reliability of the phenotypic value as a guide for

breeding value. In the latest part of the 19th century, it was indicated that only a part of continuous variation was due to heredity (Hamdi, 1992).

(Hamdi *et al.*, 2003), the first person to separate genetic variance into sub-components: additive effect of

genes, dominance deviation from the additive scheme and deviation from the additive scheme attributed to inter-allelic interactions. He defined heritability in “Broad sense” as the ratio between the genotypic variance as a whole and that due to phenotype variance. But, broad-sense heritability does not give a clear picture of transmissibility of variation from one generation to the next. Its utility in plant improvement program was limited since the genetic variation included is fixable additive effect and non-fixable dominance and epistatic effect. Thus, heritability in the “Narrow- sense” was defined as the ratio of additive genetic variance to the phenotypic variance (Wortmann *et al.*, 2004).

Selection for traits having high heritability would be very effective as there would be a close correspondence between genotype and phenotype. But heritability estimates along with expected genetic gain are considered to be more useful in predicting the outcome of selecting the best individuals. Improvement in the performance of selected over the original population can be termed as genetic advance. The ultimate goal of the plant breeder is to have higher genetic advance for the material selected, since it is an indicator for the genetic improvement made in a population under selection. The genetic gain that can be expected for a particular character through selection is the product of heritability, phenotypic standard deviation and selection differential (Colasanti *et al.*, 2006).

It is clear that the heritability estimates either “Broad Sense” or “Narrow Sense” is useful only for the population or genotypes under consideration as these estimates vary with the sets of genotypes considered (Faure and Laurie, 2007). Chopra (2000), examined performance, variability, correlation and co-heritability estimates in raj mash. They found significant differences for traits such as plant height, branches per plant, pod length, seeds per pod, yield per plant, 100-seeds weight, and days to 50% flowering. All the traits except branches per plant and pod length exhibited wide range of variability.

The phenotypic and genotypic variances were maximum for yield per plant and minimum for branches per plant. The PCV had higher estimate than the corresponding GCV for all the traits. The small difference between PCV and GCV for days to flowering and pod length indicates that the variability was due to genotypic differences. The heritability estimates were higher for days to flowering, pod length and seeds per pod; and low for plant height, branches per plant, 100-seeds weight and yield per plant. Genetic advance and expected genetic advance (as percent of mean) was maximal for yield per plant (42.2) and seeds per pod (57.5) and minimum for pod length and plant height of lentil.

As Singh (1995) reported, Genetic gain was high for plant height, pods per plant, length of main root and primary branches per plant. However, genetic gain was of low magnitude for days to flowering, days to maturity and harvest index may be expected to be mainly due to non-additive gene action, whereas for those characters having high heritability and high genetic advance, was due to additive gene action.

2.6. Association of Characters

2.6.1. Correlation co-efficient

Correlation coefficient is a linear association between two variables (Gomez and Gomez, 1984). Knowledge of correlations that exist between important characters may facilitate the interpretation of the result obtained and provide the basis for planning more efficient program for the future (Johnson *et al.*, 1955). It is indicated by the correlation coefficient (r) and measures the degree of association, genetic or non-genetic, between two or more traits (Hallauer and Miranda, 2000). It measures the mutual association between two variables but does not indicate the cause and effect relationship of traits contributing directly or indirectly towards economic yield (Shivanna *et al.*, 2007). The value of correlation coefficient, which is a ratio of the covariance between the two variables and the geometric mean of their variances, ranges from -1 to +1, the extreme values indicating perfect negative and positive association, respectively (Gomez and Gomez, 1984).

Sadek *et al.* (2006) pointed out that estimation of simple correlation between various agronomic characters may provide good information necessary for crop breeders, when selection is based on two or more traits simultaneously. Information obtained from correlation coefficients for characters could also be useful as indicators of the more important ones under consideration.

Mevlut *et al.* (2008) stated that correlation analyses are being widely used in many crop species by plant breeders to understand the nature of complex interrelationships among traits and to identify the sources of variation in yield. Yield is a complexly inherited trait as its manifestation is an outcome of intricate interaction of several traits and environment. Therefore, proper understanding of association of different traits provides more reliable criterion for selection to achieve the goal of high yield (Muhammad *et al.*, 2001). Yield components, not only directly affect the yield, but also indirectly by affecting other yield components in negative or positive ways (Roopa and Ravikumar, 2008). High yield through yield attributes, as primary interest in crop improvement, requires understanding the magnitude of correlations among various yield traits (Tadele *et al.*, 2009). Becker (1993) stated that correlation studies are of interest to plant breeders because traits that are correlated with the main breeding objectives may be useful for indirect selection. (Tadele *et al.*, 2009) noted that information on the extent and nature of interrelationships among characters help in formulating efficient scheme of multiple trait

selection. Traits under consideration may have strong correlation or not at all. Grafius (2010) indicated that a positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. On the other hand, a negative correlation between two desirable traits impedes or makes it impossible to achieve a significant improvement in both traits.

Therefore, knowledge of the relationship that exists between yield and other characters and also interrelationships among various characters is necessary to be able to design appropriate selection criteria in lentil breeding program. According to Grafuis (2010), increasing total yield would be made easier by selecting for yield components because the components are more simply inherited than the total yield itself. Thus, studies on correlation enable the breeder to know the mutual relationship between various characters and determine the component characters on which selection can be based for yield environment. Yield is a complex character associated with many interrelated components (Murat and Vahdettin, 2004).

Environment plays an important role in correlation. In some cases, environment affects two traits simultaneously in the same direction or sometimes in different directions. Genetic and environmental causes of correlation combine together and give phenotypic correlation. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation (Usman *et al.*, 2006).

Phenotypic and genotypic correlations have been computed by calculating the appropriate components of variance. Phenotypic correlation (r_p) involves both genetic and environmental effects. It can be directly observed from measurements of the two characters in a number of individuals in a population (Hallauer and Miranda, 2000). Genetic correlation is the association of breeding values (i.e., additive genetic variance) of the two characters (Falconer, 1999). Both measure the extent to which degree the same genes or closely linked genes cause co-variation in two different characters (Hallauer and Miranda, 2000). Correlation coefficient provides a measure of the association between characters (Cerna and Beaver, 1990).

2.6.2. Path co-efficient analysis

Although information about the correlation of agronomic and morphological characters with yields is helpful in the identification of the components of this complex character, yet these do not provide precise information on the relative importance of direct and indirect influences of each of the component characters. With increasing number of variables it becomes necessary to measure the contribution of these variables to the observed correlation and hence partition the correlation coefficient into components of direct and indirect influence (Guler *et al.*, 2001, Onder and Babaoglu, 2001). This, in turn, allows separation of the direct effects of one variable (other variables are kept constant) from indirect effects of other variables, giving a clearer picture of the individual contributions of each variable to yield (Radovan, 2002).

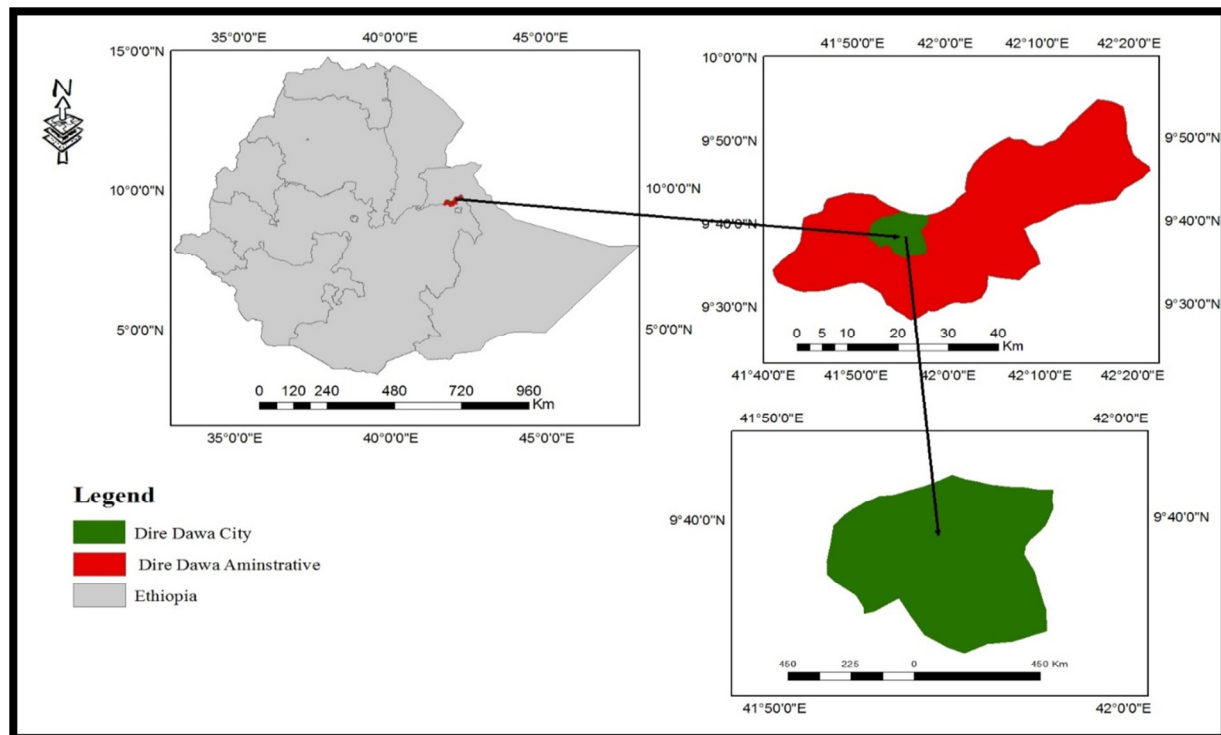
Assuming yield is a contribution of several characters which are correlated among them and to the yield; path co-efficient analysis was developed by (Wright, 1991). According to Dewey and Lu (1957) unlike the correlation coefficient which measures the extent of relationships, path coefficient measures the magnitude of direct and indirect contribution of the component characters to a complex character and it has been defined as a standardized, regression coefficient which splits the correlation coefficient into direct and indirect effects.

Mehmet and Telat (2006) recommended that study of direct and indirect effects of yield components to increase the yield provides the basis for its successful breeding program and hence the problem of yield decrease can be more effectively tackled on the basis of performance of yield components and selection for closely related characters. In order to get a clear picture of the interrelationships between different traits, the direct and indirect effects of different characters worked out using path coefficient analysis in respect of the yield (Singh *et al.*, 2004). Since path analysis permits a critical examination of the specific factor that produces a given correlation, it could be successfully employed in formulating an effective selection strategy (Kumbhar *et al.*, 1980).

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The study was conducted at Tonny farm in Dire-Dawa town. Dire-Dawa town is located in the eastern part of Ethiopia which is located at latitude of 10° 15' 00" N and longitude of 42° 10' 00" E. The town is a commercial and industrial center located on the Addis Ababa-Djibouti railroad. The town lies between 950 and 1250 meters above sea level, and is characterized by warm and dry climate with a relatively low level of precipitation. The mean annual temperature of Dire-Dawa is about 25.4°C (Selamta, 2012). The town has two raining seasons; the small rain season from March to April, and a main rainy season that extends from August to September. The aggregate annual rainfall that the town gets from these two seasons is about 604 mm. On the other hand, the town is believed to have an abundant underground water source (Selamta, 2012). The town has an estimated land area of 29.24 km².



3.2. Experimental Materials

The experiment was conducted using thirty lentil accessions obtained from Institute of Biodiversity Conservation (IBC), Addis Ababa, Ethiopia indicated in Table 1, below

Table 1. Lentil accessions used for the study

Acc No	Region	Zone	Woreda	Locality	Altitude
1. 28747	Oromiya	BALE	Goro	Adale found on the Eastern direction Around 55km away from Goro	1767.00
2. 28748	Oromiya	BALE	Goro	Jebo found on the wester direction around 15 km away	2140.00
3. 28745	Oromiya	BALE	Gadere	Chifaro found on the east direction around 4km awy of Gadaro	2414.00
4. 28744	Oromiya	BALE	Gasara	Bawba Around Found on the North direction Around	2393.00
5. 28743	Oromiya	BALE	Ginir	Found west direction around 2.5 km away from Ginir	1992.00
6. 28742	Oromiya	BALE	Ginir	Found on the west direction 12.5km away from Ginir town	2070.00
7. 28718	Oromiya	BALE	Ginir	Harawa 2 found on the North direction of Ginir town around 23	1934.00
8. 243447	Tigray	MEHAKELEGNAW	DEGUA TEMBEN	4 Km from H/Selam to Melfamaehgeza village	2620.00
9. 243449	Amara	SEMEN GONDAR	DABAT	13.4 Km from Wokini to Deroamay kebele	2605.00
10. 244603	Amara	DEBUB WELLO	WERE ILU	Geteno, 1Km from Kabe to Were Ilu	2846.00
11. 244604	Amara	DEBUB WELLO	WERE ILU	KunoAgere 7 Km from kabe to Were Ilu	2796.00
12. 244605	Amara	DEBUB WELLO	WERE ILU		2743.00
13. 244606	Amara	DEBUB WELLO	WERE ILU	Aba karie, 16 Km from Kabe to Were Ilu	2739.00
14. 244607	Amara	DEBUB WELLO	WERE ILU	Nigasie, 5 Km from Were Ilu to Kabe town	2634.00
15. 244608	Amara	DEBUB WELLO	WERE ILU	Sirgigie/ Bushira Ager, 6 Km from Were Ilu to Kabe town	2640.00
16. 244609	Amara	DEBUB WELLO	WERE ILU	Golelsha	2640.00
17. 244610	Amara	DEBUB WELLO	WERE ILU	Aba Jale, 10 Km from Were Ilu to Kabe	2654.00
18. 244611	Amara	DEBUB WELLO	WERE ILU	Aba Jale	2640.00
19. 241781	Amara	DEBUB GONDAR	TACH GAYINT	2km. West of Arb gebeya town 27km. NE of Nefas mewchia	2615.00
20. 241782	Amara	DEBUB GONDAR	ESTE	63km. East of Nefas mewchia town near Wegeda town	3055.00
21. 241783	Amara	DEBUB GONDAR	LAY GAYINT	31Km.S.East of Nefas mewchia, the Road Wegeda	2890.00
22. 238969	Oromiya	SEMEN SHEWA	YAYA GULELENA D/LIBA	Selie 82km from Adiss Ababa to Fitche	2680.00
23. 238970	Oromiya	SEMENSHEWA	WUCHALENA JIDO	Enwari 90km from on the way to Fitche	2680.00
24. 238971	Oromiya	SEMEN SHEWA	WUCHALENA JIDO	Kasim 95km from Addis Ababa on the way to Fitche	2700.00
25. 238972	Oromiya	SEMEN SHEWA	GERAR JARSO	Abeye104km from Addis Ababa	2620.00
26. 238977	Amara	SEMEN GONDAR	GONDAR	Market	2880.00
27. 238978	Amara	MIRAB GOJAM	BAHIR DAR ZURIA	23 Km. west of Bahirdar	1930.00
28. 238979	Amara	MISRAK GOJAM	DEJEN	Krar 8km Dejen to Addis Ababa	1940.00
29. 237503	Tigray	DEBUBAWI	OFLA	KoremAdiabare, 24km. korem to Sokota	2680.00
30. 237504	Tigray	DEBUBAWI	ALAMATA	Alamata Market	1500.00

3.3. Experimental design and procedure

The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. Each plot was 1.5 m long by 0.8 m width (1.2 m²) and consisting of four rows placed 20cm apart. The distance between plants in a row was 5cm and thus 30 plants per row and 120 plants per plot. There was a distance of 40 cm between the plots and a distance of 1.5m between blocks (Mekonnen *et al.*, 2014). The total plots and blocks used for the study were 90 and 6 respectively. The first weeding was carried out at twenty days after crop emergence and the second weeding was performed as per the emergence of weed. Insecticide was sprayed at the rate of one liter ha⁻¹ in 200 liter of water to control pea aphid. Agronomic characters and yield and yield related traits were determined by taking the two middle rows on plot basis. As to other agronomic practices, irrigation

water was applied to the plants on surface to facilitate plants establishments, and then up to the time of full plant establishments, water was applied using watering can once a day as necessary. Plant protection was part of the field practices where cultural and chemical control measures were taken.

3.4. Data Collection

The following data were collected.

1. **Days to emergence of seedling:** The number of days taken from planting to emergence of the seedlings.
2. **Days to 50 % flowering:** It was recorded as number of days from planting to a stage where 50% of the plants in a plot produce flower.
3. **Days to 95 % physiological maturity:** It was recorded as the number of days from planting to a stage when 95% of the plants in a plot produce mature pods.
4. **Grain filling period:** The period in days from 50 % flowering to 95 % maturity.
5. **Plant height:** The height in centimeters from the ground level to the tip of the plant for 5 randomly selected plants at physiological maturity.
6. **Number of pods per plant:** It is the average number of pods per plant for five randomly selected plants per plot at harvest.
7. **Number of seeds per pod:** The average number of seeds per pod which was recorded from ten randomly taken pods from each plot.
8. **Pod length (cm):** The average length of pod for five randomly taken pods from each plot was measured using ruler.
9. **100 Seed weight (g):** Hundred seed weight was recorded from 100 seeds taken from each plot by counting 100 seeds.
10. **Seed yield (kg/ha):** It was obtained by weighing the seeds from each experimental plot at standard moisture level.
11. **Biomass yield (kg/ha):** It was recorded by weighing the total above ground biomass harvested from each experimental plot at the time of harvest.

3.5. Data Analysis

Data was subjected to analysis of variance using the generalized linear model procedure of SAS software version 9.1. Genotypes were considered as fixed effects whereas replications were taken as random effects in the statistical model. Treatment means that exhibited significant differences were separated using the student-Neuman Keuls test (SNK) at 5% level of significance.

3.5.1. Estimation of Genetic Parameters

The genotypic and phenotypic coefficients of variability were undertaken according to the formulae of Singh and Chaundary (1991).

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\sigma_g}{\bar{x}} \times 100\%$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma_p}{\bar{x}} \times 100\%$$

Where, σ_g and σ_p are genotypic and phenotypic standard deviations, respectively; and \bar{x} is sample mean

3.5.2. Broad-sense Heritability and Genetic Advance

From breeding point of view usefulness of heritability is related to its onward transmission from the parent to the progeny (Raiz and Chowdhury, 2003). Heritability in broad sense (H^2) is expressed as the ratio of the genotypic variance (σ_g^2) to the phenotypic variance (σ_p^2) and was estimated on genotype mean basis as: Heritability in broad sense calculated as:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100\%$$

The genotypic and phenotypic variances were estimated as:

$$\sigma_g^2 = \frac{Ms_g - Mse}{r}$$
$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where, σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance, σ_e^2 = Environmental variance, Ms_g = Mean square due to accessions, Mse = Mean square of error, and r = number of replications. Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the accessions was estimated as:

$$GA = K \sigma_p H^2$$

$$GAM = \frac{GA}{x} \times 100 \%$$

Where, k = the standardized selection differential at 5% selection intensity and ($K = 2.063$), σ_p = phenotypic standard deviation, H^2 = Heritability in broad sense and x = Grand mean

3.5.3. Analysis of Phenotypic and Genotypic Correlation Coefficients

The estimate phenotypic and genotypic correlation coefficients between all pairs of characters were computed by the following formula.

$$\text{Genotypic correlation coefficient, } r_g = \frac{\text{COV}_g(xy)}{\sigma_g(x) * \sigma_g(y)}$$

$$\text{Phenotypic correlation coefficient, } r_{ph} = \frac{\text{COV}_{ph}(xy)}{\text{ph}(x) * \text{ph}(y)}$$

Where, $\text{COV}_g(xy)$ and $\text{COV}_{ph}(xy)$ are the genotypic and phenotypic covariance of two variables (X and Y), respectively. $\sigma_g(x)$ and $\sigma_g(y)$ are the genotypic standard deviations for variables X and Y , respectively. $\sigma_{ph}(x)$ and $\sigma_{ph}(y)$ are the phenotypic standard deviations of variables X and Y , respectively.

The residual effect was obtained by the following relation:

$$P_{ry} = \sqrt{1 - (P_{1y}r_{1y} + P_{2y}r_{2y} + \dots + P_{ky}r_{ky})}$$

Where: P_{ry} = Residual effect.

r_{1y} = the correlation coefficient between i^{th} independent variable X (yield components) and g^{th} dependent variable Y (Seed yield).

P_{iy} = Direct effect of X on Y

3.5.4. Path coefficient analysis

Path coefficient analysis was carried out using the phenotypic correlation coefficients as well as genotypic correlation coefficients to determine the direct and indirect effects of the yield components and other morphological characters on seed yield. Path coefficient analysis was also conducted to determine the direct and indirect effects of various traits on seed yield using the general formula of Dewey and Lu (1957).

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

Where, r_{ij} = mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficients p_{ij} = components of direct effects of the independent character (i) on the dependent variable (j) as measured by the path coefficients and $\sum r_{ik}p_{kj}$ = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k).

4. RESULTS AND DISCUSSION

4.1. Mean, Range and Analysis of Variance

4.1.1. Mean and range

The results of mean, minimum, maximum values and standard error of mean for the 11 quantitative traits of the lentil accessions are summarized in Table 2.

On average all the genotypes emerged five days after planting. Accession numbers “238977”, “238979” and “237503” were late in emergence as compared to the rest accessions. On the other hand, the minimum days to emergence was 4 and the accessions that emerged were “28748”, “28743”, “243447”, “244607”, “244608” and “244609”. The mean and range values for days to emergence were 5.133 days and 3 days respectively (Table 2). The mean value recorded for days to 50% flowering was 38.25 and the range value was 23 days. An accession that flowered early was “244603” among the other accessions. On the other hand “244603” and 28742 were the latest (Table 2). Days to ninety five percent maturity was shortest for accession “244603” and it took 59 days to produce matured pods whereas the longest days to produce matured pods were recorded for accession “244611” which took 80 days to produce matured pods. The mean value for days to ninety five percent maturity and range in the study were 70.1 days and 21 days respectively.

The mean and range values for grain filling period in the study were 31.4 days and 16 days respectively. Accession “244607” took the shortest date with a value of 24 days for grain filling period whereas accession “244611” took the longest day with a value of 40 days for grain filling period. The highest plant height at maturity was recorded from accession “28743” with a score of 52cm whereas the least plant height was recorded from accession “28745” with a score of 21cm. The mean and range value for plant height in the study were

35.6cm and 31cm respectively.

The least number of pods per plant were recorded from accession “28743” with a value of 8 pods per plant whereas the highest number of pods per plant were recorded from accession “28748” with a value of 25 pods per plant. The mean and range value for number of pod per plant were 15.61 and 17 respectively.

The longest pods at maturity were recorded from accession “238971” with a score of 1.8cm whereas the shortest pod length was recorded from accession “243449” with a score of 0.81cm. The mean and range values for pod length were 1.18cm and 0.99cm respectively. The highest score for 100 seed weight was obtained from accession “28748” with a score of 3.59g. On the other hand the least score for 100 seed weight was obtained from accession “243449” with a score of 2.96g. The mean and range values for 100 seed weight were 3.124g and 0.63g respectively.

The highest score for seed yield per plot (kg/ha) was obtained from accession “28748” with a score of 0.654kg/ha. On the other hand the least score was obtained from accession “241782” with a score of 0.512 kg/ha. The mean and range score for seed yield in the study were 0.568kg/ha and 0.142kg/ha respectively. The least score for biological yield per plot (kg/ha) was obtained from accession “238978” with a score of 0.723kg/ha on the other hand the highest score was obtained from accession “243499” with a score of 0.884kg/ha. The mean and range score for biological yield in the study were 0.785kg/ha and 0.161kg/ha respectively.

Table 2. Minimum, maximum, mean values and SE of mean for the 11 quantitative traits of the lentil accessions

Traits	Minimum			Maximum				
	Value	Accessions		Value	Accession	Range	Mean	SE
DE	4	28748,28743,243447,244607,244608,244609		7	238977,238979,237503	3	5.133	0.096
DFF	26	244603		49	244603,28742	23	38.25	4.72
DNPM	59	244603		80	244611	21	70.11	5.161
GFP	24	244607		40	244611	16	31.94	3.529
PH	21	28745		52	28743	31	35.6	6.88
NPPP	8	28743		25	28748	17	15.61	4.162
NSPP	1	243447, 241781, 244605, 238971, 244610		2	All the rest accessions	1	1.6	0.465
PL	0.81	243449		1.8	238971	0.99	1.18	0.223
HSW	2.96	243449		3.59	28748	0.63	3.124	0.309
SY	0.512	241782		0.654	28748	0.142	0.568	0.034
BY	0.723	238978		0.884	243449	0.161	0.785	0.054

Where, DE: Days to emergence seedling, DFF: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biomass yield.

4.1.2. Analysis of variance (ANOVA)

The analysis of variance for the 11 characters studied is given in (Table 3). Highly significant ($p \leq 0.001$) differences were observed for all the traits. The mean sum of squares due to genotypes was significant for all the characters indicating that the variation was genetic (Table 3). Thus, there appears to be a greater scope for bringing about improvement in these traits. There was a highly significant difference ($P \leq 0.001$) among the tested genotypes for days to 50% flowering, days to 95% maturity, plant height, number pods per plant, pod length, hundred seed weight, seed yield and biomass yield which is due to genotype. Significant difference ($P \leq 0.05$) was observed for days to emergence, grain filling period and number of seeds per pod due to genotype. Similar results were reported by Mondal *et al.* (2007). All lentil characters show non-significant difference due to replication i.e. the traits were no longer affected by replication significantly. Similar wide variability for days to fifty percent maturity, days to 95% maturity, plant height, pods per plant, seeds per plant and seed yield per plant has also been reported in lentil by Chakraborty and Haque (2000), Kishore and Gupta (2002), Rathi *et al.* (2002), Bicer and Sakar (2004), Haddad (2004) and Singh *et al.* (2005).

Table 3. ANOVA table showing mean squares for genotypes, error mean square and replication mean squares

Source of variation	DF	DE	DFF	DNPM	GFP	PH	NPPP	NSPP	PL	HSW	SY	BY
Rep	2	4.13 ^{ns}	6.54 ^{ns}	21.67 ^{ns}	8.14 ^{ns}	61.76 ^{ns}	31.67 ^{ns}	0.544 ^{ns}	0.166 ^{ns}	0.062 ^{ns}	0.000097 ^{ns}	0.00009 ^{ns}
Genotype	29	1.5*	47.46**	50.62**	21.51*	128.8**	42.58**	0.366*	0.096**	0.23**	0.0033**	0.0089**
Error	58	0.511	10.14	15.04	8.07	8.05	5.12	0.14	0.027	0.032	0.0001	0.00002
Cv %	-	13.92	8.32	5.53	8.89	7.97	14.49	22.5	13.99	5.76	7.3	1.42

Where, Df= Degrees of freedom, DE: Days to emergence seedling, DFF: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biomass yield, ns=non-significant, * and ** indicate significant and highly significant respectively

4.2. Estimates of Genetic Parameter

4.2.1. Estimates of genotypic and phenotypic coefficient of variation

In the present study, the phenotypic and genotypic variances were maximum for plant height and minimum for seed yield (Table 4). PCV and GCV values were categorized as low, moderate and high values as indicated by Sivasubramaniah and Menon (1973) as follows: Low = 0-9%, Moderate = 10-20%, High > 20 %. In general, phenotypic coefficient of variability was slightly higher than the corresponding genotypic coefficient of variability for all the traits except for seed yield. Thus, traits with high phenotypic coefficient of variation indicating that all the characters studied had interacted with the environment i.e. the apparent variation is not only due to genotypes but also due to the influence of environment. The highest phenotypic coefficient of variability was recorded for biological yield (31.35%), number of pods per plant (22.99%) and number of seeds per pod (20.83%). On the other hand, relatively moderate values were observed for plant height (17.98%), days to emergence (12.66%) and 100 seed weight (10.58%). Low phenotypic coefficient of variation were observed for days to 50% flowering (8.32%), grain filling period (7.56%), days to 95% maturity (4.9%) and seed yield (4.29%).

The estimates of genotypic coefficient of variability were slightly higher than its corresponding phenotypic coefficient of variability for seed yield, this shows small effect of the environment on this trait. The highest estimates of genotypic coefficient of variability were observed for number of pods per plant (22.63%); seed yield (21.48%). On the other hand plant height (17.85%), biological yield (16.73%), number of seeds per pod (16.079%), pod length (12.89%) and days to emergence (11.11%) showed moderate genotypic coefficient of variation. In line with this result, Malik *et al.* (2013) found sufficient genetic variability in lentil genotypes in traits like plant height, number of pods per plant, seed yield and biomass yield. Tigist (2003) had also reported high GCV for plant height and days to emergence. Seifu, (1998) had also reported high GCV for days to 95% maturity and plant height. Low genotypic coefficient of variation was observed for 100 seed weight (8.99%), days to 50% flowering (8.13%), grain filling period (7.36%) and days to 95% maturity (4.8%). These results are not in agreement with the findings of Singh *et al.* (2003) and Abo *et al.* (2012). The difference between PCV and the corresponding GCV values was relatively higher for seed yield and biomass yield indicating the higher influence of the environment on the traits and indicating that environment is important in determining these traits. Whereas pod length, number of seeds per pod, 100 seed weight, days to emergence, number of pods per plant, grain filling period, days to 50% flowering, plant height and days to 95% maturity showed low difference between PCV and GCV indicating that there is a minimal influence of environment on the expression of these traits. In addition, it indicates the presence of sufficient genetic variability for observed traits which may facilitate the selection process (Tadele *et al.*, 2013). Therefore, selection based on phenotypic performance of the traits would be effective to bring considerable improvement in these traits.

4.2.2. Heritability Estimates in Broad Sense

The heritability values for the 11 characters ranged from 24.9% for seed yield to 98.23% for plant height (Table 4). As reported by Wright (1991), genetic advance values are helpful in predicting the expected progress to be achieved through the process of selection. Genetic advance along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. The heritability percentages are categorized as low, moderate and high after Robinson *et al.* (1949), as follows. Low=0-30%, Moderate=31-60%, High >60%. High heritability estimates were obtained for plant height, number of pods per plant, days to 95% maturity, days to 50% flowering, grain filling period, days to emergence, 100 seed weight and number of seeds per pod. Singh and Ceccerelli (1996) stated that if heritability of a character is very high, say 80% or more, selection for such character should be fairly easy. This is because there would be a close correspondence between the genotypes and phenotypes due to the relatively small contribution of the environmental effect on the phenotypes. This finding agreed with the findings of the previous report by Singh (2010), Chakraborty and Haque (2000), Kishore and Gupta (2002), Rathi *et al.* (2002), Bicer and Sakar (2004), Singh *et al.* (2005).

High heritability for different traits indicated that large proportion of the phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression (Maurya *et al.*, 2015). On the other hand, relatively moderate estimates of heritability were found for pod length and biological yield whereas seed yield shows low estimates of heritability. Thus, selection for this trait may be considerably difficult or virtually impractical due to the masking effect of the environment. The results do not agree with Bicer and Sarkar (2004), Yadav *et al.* (2003).

High heritability values were observed for number of pods per plant (96.6%) coupled with high PCV (22.99) and GCV (22.63), also high heritability (98.23%) coupled with high PCV (17.98%) and GCV (17.85%) was observed for plant height indicating that selection for these traits may respond effectively for phenotypic selection of lentil grown in low land area. This result is in agreement with Alemayehu *et al.* (2014). In general, all the traits except pod length, biological yield and seed yield had higher heritable variation.

4.2.3. Genetic advance

The genetic advances as percent of mean (GAM) at 5% selection intensity is presented in Table 4 and the values ranged from 2.206 for seed yield to 45.77 for number of pod per plant. The GA as percent of mean was categorized as low, moderate and high as described by Johnson *et al.* (1955) as follows. Low= 0-10%, Moderate= 11-20% and High>20%. Maximum genetic advance as percent of mean (GAM) at 5% selection intensity was recorded for number of pods per plant (45.77%), plant height (36.37%), number of seeds per pod (26%), biomass yield (22.25%) and days to emergence (20.35). On the other hand moderate genetic advance as percent of mean was observed for pod length (18.33%), days to emergency (16.33%) and 100 seed weight (15.06). Low genetic advance as percent of mean at 5% selection intensity was observed for days to 95% maturity (9.63%) and seed yield (2.206%).

Even if heritability estimates provide basis for selection on the phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously. High heritability is not always associated with high genetic advance as reported by Yadav *et al.* (2003).

In the present study, high GAM for number of pods per plant (45.77%) was coupled with high heritability (96.6%), high GAM for plant height (36.37%) was coupled with high heritability (98.23%) and the high GAM for days to emergence (20.35%) was coupled with high heritability (77.51%) was observed (Table 4). Thus, GAM coupled with high heritability offers opportunities for selection, and indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits which could be improved through either pure line selection or simple mass selection (Janaki *et al.*, 2015). Similar results were also obtained by Gowda *et al.* (1997) who reported high heritability coupled with high genetic advance for most of the quantitative characters in lentil genotypes.

A low GAM coupled with low GCV were observed for characters like days to 95% maturity, 100 seed weight and grain filling period indicating that these characters were under high environmental influence, governed by non-additive genes and that selection based on these characters would be ineffective so for improving this characters heterosis breeding or recurrent selection should be followed. This result also recorded by Alemayehu *et al.* (2014).

Table 4. Estimates of genetic parameters

Traits	(σ^2_p)	(σ^2_g)	PCV%	GCV%	PCV-GCV	H%	GA	GAM%
DE	0.4287	0.3323	12.66	11.11	1.56	77.51	1.03	20.35
DFF	10.25	9.76	8.32	8.13	0.21	95.17	6.27	16.33
DNPM	11.8	11.32	4.90	4.8	0.11	95.4	6.76	9.63
GFP	5.83	5.44	7.56	7.36	0.22	93.2	4.6	14.53
PH	40.97	40.25	17.98	17.85	0.14	98.23	12.95	36.37
NPPP	12.9	12.49	22.99	22.63	0.38	96.6	7.15	45.77
NSPP	0.12	0.089	20.83	16.079	4.76	60.58	0.44	26.003
PL	0.046	0.023	17.79	12.89	4.91	50	0.21	18.33
HSW	0.11	0.076	10.58	8.99	1.6	69.09	0.47	15.06
SY	0.0049	0.0013	4.29	21.48	-17.18	24.9	0.0036	2.206
BY	0.0086	0.003	31.35	16.73	14.63	34.44	0.064	22.25

Where, DE: Days to emergence of seedling, DFF: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biomass yield, ns=non-significant, * and ** indicate significant ($p \leq 0.05$) and highly significant ($p \leq 0.001$) respectively

4.3. Association of Characters

4.3.1. Correlation Analysis

4.3.1.1. Phenotypic correlation

In the present investigation, phenotypic correlation coefficients were computed among 11 lentil characters and are presented in (Table 5). The attributes revealed that seed yield per plot showed highly significant positive association with 100 seed weight and biological yield on the other hand showed significant ($p \leq 0.05$) positive association with number of pods per plant, number of seeds per pod and pod length, but it showed significant and negative association with days to emergence. Thus, these characters emerged as most important associates for seed yield per plant in lentil at the phenotypic level. The available literature has also identified the above characters as important associates of seed yield in lentil (Naresh *et al.*, 2009 and Tyagi and Khan, 2010). Biological yield showed highly significant and positive association with plant height, seed yield per plot, pod length and number of pods per plant. Similar result was also reported by Sirohi *et al.* (2007). In similarly way 100-seed weight and number of seeds per pod shows significant positive association with biological yield while it showed non-significant and negative association with days to emergence and grain filling period.

100 seed weight showed highly significant and positive association with pod length and seed yield in

addition it showed significant positive association with days to 50% flowering and biological yield while it showed significant negative association with grain filling period at the phenotypic level. Similar result was also reported by Barghi *et al.* (2012). Pod length shows highly significant positive associations with number of seeds per pod while it showed non-significant negative association with days to emergence, days to 50% flowering and grain filling period. Plant height shows highly significant negative association with number of pods per plant as well as significant negative association with days to emergence while it showed highly significant positive association with biological yield. Days to 95% maturity showed highly significant positive associations with days to 50% flowering and grain filling period. This finding is in conformity with Hamdi *et al.* (2003). Grain filling period showed significant negative association with days to 50% flowering, 100 seed weight and number of pods per plant. Occurrence of positive significant association of seed yield with most of its yield component revealed less complex inter-relationship between yield and yield components. Such situation is favorable from breeding point of view because phenotypic selection for one trait may bring correlated response for improvement of other traits which are positively associated with it. These findings are broadly in agreement with some of the earlier reports (Karadavut *et al.*, 2009; Tyagi and Khan, 2010).

Table 5. Phenotypic correlation coefficient (r_p) of yield and yield related 11 quantitative traits of lentil.

Variables	DE	DFF	DNPM	GFP	PH	NPPP	NSPP	PL	HSW	SY	BY
DE	1										
DFF	-0.094	1									
DNPM	0.072	0.714**	1								
GFP	0.212*	-0.263*	0.487**	1							
PH	-0.256*	0.028	0.163	0.190	1						
NPPP	-0.068	0.041	-0.128	-0.228*	-0.52**	1					
NSPP	-0.007	0.009	0.031	0.032	-0.184	0.085	1				
PL	-0.148	0.005	-0.036	0.056	-0.145	0.016	0.71**	1			
HSW	-0.193	0.261*	0.053	-0.253*	0.019	0.173	0.214	0.432**	1		
SY	-0.313*	0.115	-0.012	-0.161	0.056	0.267*	0.255*	0.218*	0.53**	1	
BY	-0.207	0.167	0.132	-0.028	0.400**	0.443**	0.265*	0.406**	0.222*	0.510**	1

Where, DE: Days to emergence, DFF: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biological yield, ns=non-significant, * and ** indicates significant and highly significant, respectively.

4.3.1.2. Genotypic correlation

In the present study, the estimates of correlation coefficient between seed yield and yield related traits indicated that genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients except for 100 seed weight, signifying that the association among various characters was of genetic causes rather than environmental effect. Similar results were also obtained by Sharma (2009), Singh *et al.* (2013), Tyagi and Khan (2011).

Biological yield showed highly significant positive association (0.532) with seed yield. Similarly it showed significant positive association with plant height (0.414), number of pods per plant (0.404) and pod length (0.413) (Table 6). Seed yield showed highly significant positive association with biological yield and it showed significant positive association with 100 seed weight. Ayub *et al.* (2001) reported positive and significant correlation between seed yield and biological yield.

Hundred seed weight showed significant and positive association with pod length and seed yield in addition it showed non-significant positive association with days to 50% flowering at genotypic level. Similar result was also reported by Barghi *et al.* (2012).

Pod length showed highly significant positive associations with number of seeds per pod and significant positive association with 100 seed weight. Plant height shows highly significant negative association with number of pods per plant while it showed significant positive association with biological yield. Grain filling period showed significant positive association with days to 95% maturity at genotypic level. Days to 95% maturity showed highly significant positive association with days to 50% flowering and significant association with grain filling period. Days to emergence showed non-significant negative association except with days to 95% maturity, grain filling period and number of pods per plant (Table 6).

Table 6. Genotypic correlation coefficient (rg) of yield and yield related 11 quantitative traits of lentil.

Variables	DE	DFF	DNPM	GFP	PH	NPPP	NSPP	PL	HSW	SY	BY
DE	1										
DFF	-0.135	1									
DNPM	0.059	0.728**	1								
GFP	0.257	-0.264	0.469*	1							
PH	-0.335	0.042	0.226	0.265	1						
NPPP	0.015	0.084	-0.141	-0.307	-0.643**	1					
NSPP	-0.059	0.034	0.053	0.031	-0.161	0.189	1				
PL	-0.232	0.030	-0.091	0.167	-0.057	0.084	0.826**	1			
HSW	-0.271	0.306	0.039	-0.339	0.053	0.185	0.263	0.509*	1		
SY	-0.421*	0.143	-0.013	-0.202	0.089	0.282	0.264	0.227	0.503*	1	
BY	-0.271	0.219	0.176	-0.034	0.414*	0.404*	0.269	0.413*	0.253	0.532**	1

Where, DE: Days to emergence, DFF: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biological yield, ns=non-significant, * and ** indicates significant and highly significant respectively

4.3.2. Path coefficient analysis

4.3.2.1. Phenotypic direct and indirect effect of various characters on seed yield per plot

In the present study, seed yield (SY) was considered as a variable that is dependent on 10 independent variables, which were considered as causes. The independent characters were days to emergence, days to 50% flowering, days to 95% maturity, grain filling period, plant height, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and biological yield.

The path analysis revealed that number of pods per plant followed by plant height, days to 50% flowering, pod length, grain filling period and number of seeds per pod had exerted positive direct effect (Table 7). It means a slight increase in any one of the above traits may directly contribute towards seed yield. Similar results have also been reported by Solanki (2006), Yadav *et al.* (2005) and Joshi *et al.* (2005). Similar results have also been reported for number of pod per plant, plant height, days to 50% flowering and pod length, by Naresh *et al.* (2009) and Sarwar *et al.* (2010).

However, biological yield, days to 95% maturity, 100 seed weight and days to emergence exerted negative direct effect on seed yield. Biological yield had highly significant positive association with seed yield but substantially exerted strong negative (-1.998) direct effect on seed yield. These results agree with Priti *et al.* (2003). The indirect positive effect of biological yield was maximum via number of pods per plant (1.098), plant height (0.871), pod length (0.577), days to 50% maturity (0.363), number of seeds per pod (0.025), and days to emergency (0.012) on seed yield might counter balance the final positive association with seed yield (Table 7). Azizi *et al.* (2009) observed that number of pods per plant, pod length, and days to 50% maturity as important indirect contributors towards expression of seed yield in lentil via biological yield. So this indicating that indirect selection of biological yield through number of pods per plant, plant height, pod length, days to 50% maturity, number of seeds per pod, and days to emergence might be helpful in yield improvement but since the direct effect was negative and strong so direct selection for these traits to improve yield will not be desirable.

Number of pods per plant had significant positive association with seed yield at the phenotypic level as a result it exerted strong positive direct effect (2.47851) on seed yield as well as positive indirect effect via days to 95% maturity, days to 50% flowering, number of seeds per pod, pod length and days to emergence at phenotypic level indicated that this character had maximum contribution in determining yield in this crop. Observation of this investigation also revealed that most of the traits had positive indirect effect on seed yield via number of pods per plant. Thus improving this trait may increase seed yield as well as performance of some traits. It also indicates the true relationship between this trait and seed yield and direct selection through this trait may be effective. Therefore, number of pods per plant may be given more emphasis while selecting high yielding lentil genotypes at the phenotypic level. Similar findings have been reported by Karadavut (2009).

However it applied strong negative indirect effect via plant height. This is due to their highly significant negative phenotypic association with plant height (rp=0.52**). In addition it also showed negative indirect effect via grain filling period, biological yield and 100 seed weight on seed yield at phenotypic level.

Plant height had non-significant positive phenotypic association with seed yield (rp=0.056) yield at the phenotypic level; it exerted strong positive direct effect (2.4178) on seed yield as well as positive indirect effect via days to emergence, days to 50% flowering and grain filling period. Plant height applied negative indirect effect via number of pods per plant, biological yield, days to 95% maturity and pod length on seed yield at the phenotypic level so, direct selection of this trait may improve seed yield but indirect selection is not desirable to improve seed yield because it had exerted maximum negative indirect effect on the essential yield determining characters like number of pods per plant, days to 95% maturity, pod length, number of seeds per pod, 100 seed weight and biological yield.

Days to 50% flowering exerted strong positive direct effect (2.17214) along with its non-significant positive association on seed yield at the phenotypic level similarly it exerted positive indirect effect through number of

Pods per plant and plant height. Days to 50% flowering exerted strong negative indirect effect via days to 95% maturity (-1.4389) but days to 50% flowering had highly significant positive phenotypic association with days to 95% maturity (0.714) so, direct selection of this trait may bring improvement in lentil but due to its negative and negligible positive indirect effect via other traits, indirect selection of this trait is not desirable at the phenotypic level.

In fact, days to 95% maturity had non-significant negative association with seed yield at the phenotypic level; along with its negative association with seed yield it applied strong negative direct effect (-2.0152) on seed yield as well as indirect negative effect via number of pod per plant, biological yield, pod length and 100 seed weight so, direct and indirect selection may not be desirable for these traits to improving seed yield in lentil.

Hundred seed weight applied negative direct effect (-0.1929) on seed yield. It had highly significant positive association with seed yield along with high positive indirect effect via pod length, number of pod per plant, days to 50% flowering and plant height indicating indirect selection of 100 seed weight might be helpful in improvement of these traits but since the direct effect was negative, so direct selection for these traits to improve yield will not be desirable (Table 7).

Number of seeds per pod exerted strong positive direct effect (2.4778) on seed yield at phenotypic level along with its significant positive association with seed yield. It showed positive indirect effect via pod length, number of pods per plant, grain filling period, days to 50% flowering and number of seeds per pod so, direct and indirect selection may be desirable for this trait to improve seed yield in lentil genotypes at the phenotypic level.

In the present study, pod length contributed positive direct effect (1.42147) on seed yield and it applied negative indirect effect on seed yield via biological yield and grain filling period while its indirect effect on seed yield via other traits was negligible. Since, it had positive direct effect on seed yield along with its significant positive phenotypic association with seed yield so direct selection of pod length might be helpful in yield improvement of lentil at the phenotypic level. Whereas, indirect selection of pod length will not be effective due to its negative and negligible indirect effect on seed yield via other traits at the phenotypic level.

Grain filling period contributed positive direct effect (1.47399) on seed yield but it had non-significant negative phenotypic association with seed yield. For this trait negative indirect effect was exerted via days to 50% flowering, days to 95% maturity, number of pods per plant and pod length and positive indirect effect via plant height on seed yield. While, its effect via others trait is negligible. Since, this trait contributed positive direct effect on seed yield but its negative association with negative indirect effect and negligible positive indirect effect via other traits indicating that direct and indirect selection may not be desirable for these traits to improve seed yield in lentil at the phenotypic level. This result agrees with (Karadavut, 2009).

Days to emergence contributed low negative direct effect (-0.0569) on seed yield along with its significant negative association with seed yield at the phenotypic level. This trait exhibited negative indirect effect via days to 50% flowering, plant height, number of pods per plant and pod length while positive indirect effect via days to 95% maturity, grain filling period and biological yield. Since, this trait had negative direct effect along with its significant negative association with seed yield at phenotypic level and negative indirect effect via others traits thus, direct and indirect selection may not be desirable for these traits to improve seed yield in lentil. This result does not agree with Naresh *et al.* (2009). The residual (0.244) indicated that the independent variables included in this study explained (75.6%) of the total variation in the dependent variables that is seed yield per plot at the phenotypic level.

Table 7. Estimates of phenotypic direct effects bold and diagonal and indirect effects off diagonal of traits via other independent traits on seed yield per plot.

Variable	DE	DFF	DNPM	GFP	PH	NPPP	NSPP	PL	HSW	BY	SY(rp)
DE	-0.0569	-0.2042	0.1451	0.31249	-0.6165	-0.1685	-0.0007	-0.2104	0.03724	0.44943	-0.313*
DFF	0.00535	2.17214	-1.4389	-0.3862	0.0677	0.10162	0.00085	0.00711	-0.0504	-0.3643	0.115
DNPM	0.0041	1.55091	-2.0152	0.71783	0.3941	-0.3172	0.00294	-0.0512	-0.0102	-0.288	-0.012
GFP	-0.0121	-0.5691	-0.9814	1.47399	0.45938	-0.5651	0.00303	-0.0796	0.04881	0.06109	-0.161
PH	0.01452	0.06082	-0.3285	0.28006	2.4178	-1.2888	-0.0174	-0.2061	-0.0037	-0.8727	0.056
NPPP	0.00387	0.08906	0.25795	-0.3361	-1.2573	2.47851	0.00805	0.02274	-0.0334	-0.9665	0.267*
NSPP	0.0004	0.01955	-0.0625	0.04717	-0.4449	0.21067	0.09475	1.00924	-0.0413	-0.5781	0.255*
PL	0.00843	0.01086	0.07255	-0.0825	-0.3506	0.03966	0.06727	1.42147	-0.0833	-0.8858	0.218*
HSW	0.01099	0.56693	-0.1068	-0.3729	0.04594	0.42878	0.02028	0.61407	-0.1929	-0.4843	0.53**
BY	-0.07197	0.36275	-0.266	-0.0413	0.86712	1.09798	0.02511	0.57712	-0.0428	-1.998	0.51**

R= 0.244

Where, DE: Days to emergence, DFF: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biological yield.

4.3.2.2. Genotypic direct and indirect effect of various characters on seed yield per plot

The path analysis at the phenotypic level may not provide a true picture of direct and indirect causes (Sood *et al.*, 2009), and it is advisable to understand the contribution of different traits toward the seed yield/plot at the genotypic level. The path analysis revealed that all traits exerted positive direct effect on seed yield except days to 50% flowering (-1.2433), grain filling period (-1.0833), and biological yield (-0.5124) which contributed negative direct effect (Table 8).

In the present study, days to emergence had contributed low positive direct effect (0.1114) along with its significant negative genotypic association with seed yield indicating that this character has minimum contribution in determining yield in this crop at the genotypic level. Observation of the investigation revealed that most of the trait had negative indirect effect on seed yield via days to emergence. Since, it had positive direct effect on seed yield but comparatively low along with its significant negative association with seed yield at genotypic level, indirect effect also low and negative so, direct and indirect selection may not be desirable for these traits to improve seed yield in lentil. The results are not in line with Kar *et al.* (2011) who reported that days to emergence had negative direct effect on seed yield.

Biological yield exerted low negative direct effect (-0.5124) but positive indirect effect via all traits except days to emergence and days to 50% flowering. Since, biological yield had highly significant positive genotypic association on seed yield ($r_g=0.532$) indirect selection of this traits may improve seed yield via days to 95% maturity, grain filling period, plant height, number of pods per plant, number of seeds per pod, pod length, and 100 seed weight. Therefore, biological yield may be given more emphasis while selecting high yielding lentil genotypes. The results were similar to Amarah *et al.* (2005).

Hundred seed weight applied positive direct effect (0.29655) on seed yield along with its significant positive genotypic association with seed yield ($r_g=0.503$) at the genotypic level indicating that this character had maximum contribution in determining yield in this crop. Furthermore, 100 seed weight exerted indirect positive effect on seed yield via days to 95% maturity, grain filling period, plant height, number of pods per plant, number of seeds per pod and pod length so direct selection of this trait will be effective in improvement of seed yield and related traits. This result also recorded by (Tikka *et al.* 2009, Narsinghani *et al.* 2013).

Among the yield attributing traits at the genotypic level, the direct effect of pod length had exerted low positive direct effect (0.07098) on seed yield along with its non-significant positive genotypic association with seed yield (0.227). On the other hand it had applied moderate positive indirect effect on seed yield via grain filling period, number of seeds per pod and 100 seed weight but on the rest traits it had negligible indirect effect at genotypic level. So, direct selection of this trait could relatively improve seed yield and indirectly via grain filling period, number of seeds per pod and 100 seed weight at the genotypic level.

Grain filling period exerted strong negative direct effect (-1.0833) along with its non-significant negative genotypic association (-0.202) with seed yield. In fact, it had positive indirect effect on seed yield via days to 50% flowering, days to 50% flowering and plant height but negligible effect via other traits since the direct effect was negative along with its negative genotypic association with seed yield so direct selection for these traits to improve yield could not be desirable.

Plant height contributed strong positive direct effect (1.01723) along with its non-significant low positive

genotypic association ($rg=0.089$) with seed yield. Plant height contributed positive indirect effect on seed yield via days to 95% maturity and plant height. On the other hand negative effect via grain filling period, number of pods per plant and biological yield while negligible indirect positive effect via days to emergence, days to 50% flowering, number of seeds per pod, pod length and 100 seed weight. Since plant height had positive direct effect along with its positive association with seed yield at genotypic level so direct selection of this trait could improve seed yield in lentil at genotypic level. Similar results have also been reported by Solanki (2007), Yadav *et al.* (2005).

Days to 95% maturity contributed strong positive direct effect (1.41633) on seed yield. It applied strong negative indirect effect via days to 50% flowering (-0.9051) and grain filling period (-0.5081) and moderate negative indirect effect on number of pods per plant and also positive indirect effect on plant height. On the other hand it applied negligible positive indirect effect on seed yield at genotypic level via days to emergence, pod length, 100 seed weight and biological yield. Since, it had positive direct effect on seed yield along with negative association with seed yield, indirect effect also high and negative so, direct and indirect selection may not be desirable for these traits for improving seed yield in lentil. This result do not agree with Joshi *et al.* (2005) who reported that days to maturity applied negative direct effect on seed yield.

Days to 50% flowering contributed strong negative direct effect (-1.2433) on seed yield but applied high positive indirect effect (1.03109) via days to 95% maturity and moderate positive indirect effect via grain filling period. On the other hand it applied negligible indirect effect via other traits on seed yield at genotypic level so indirect selection of this trait should improve seed yield via days to 95% maturity and grain filling period but since the direct effect was negative, so direct selection for these traits to improve yield should not be desirable at genotypic level.

In the present study, number of pods per plant contributed positive direct effect (0.98701) on seed yield at genotypic level but negative indirect effect on seed yield via days to 95% maturity, grain filling period and biological yield while negligible indirect effect via other traits so direct selection of this trait may relatively improve seed yield. Since, it had negative and negligible indirect effect on seed yield along with its non-significant positive genotypic correlation with seed yield indirect selection of this trait may not be desirable for this trait in seed yield improvement in lentil genotypes at the genotypic level. Similar results were recorded by Panse (2012) who reported positive direct effect of pods per plant on seed yield. Similarly number of seed per pod contributed positive direct effect (0.29773) on seed yield but negative indirect effect via days to 50% flowering, grain filling period, plant height and biological yield but positive indirect effect via number of pods per plant. It also showed negligible indirect effect through other traits. Since, it had contributed positive effect on seed yield, direct selection for this trait may improve seed yield at genotypic level but indirect selection may not be desirable because it had negative and negligible indirect effect on seed yield via other traits.

All in all, the path analysis revealed that plant height, number of pods per plant, number of seeds per pod, pod length, and 100 seed weight contributed positive direct effect along with their positive association with seed yield at genotypic level so direct selection for these traits should be given more emphasis while selecting high yielding lentil accessions. The residual (0.195) indicated that the independent variables included in this study explained (80.5%) of the total variation in dependent variables that is seed yield per plot.

Table 8. Estimates of genotypic direct effects bold and diagonal and indirect effects off diagonal of traits via other independent traits on seed yield per plot.

Variable	DE	DFE	DNPM	GFP	PH	NPPP	NSPP	PL	HSW	BY	SY(rg)
DE	0.11418	0.12433	-0.102	-0.2383	-0.3408	-0.0148	-0.0021	-0.0106	-0.059	0.10812	-0.421*
DFE	-0.0114	-1.2433	1.03109	0.286	0.04272	0.04442	0.00327	0.00064	0.07977	-0.0902	0.143
DNPM	-0.0082	-0.9051	1.41633	-0.5081	0.19938	-0.1392	0.0137	-0.0032	0.01157	-0.0902	-0.013
GFP	0.02512	0.32823	0.66426	-0.9887	0.21362	-0.2912	0.00923	-0.0068	-0.0786	0.2737	-0.202
PH	-0.0383	-0.0522	0.2776	-0.2275	1.01723	-0.6346	-0.0479	-0.0089	0.01572	-0.2121	0.089
NPPP	-0.0017	-0.0559	-0.1997	0.31958	-0.6541	0.98701	0.03305	0.00596	0.05486	-0.207	0.282
NSPP	-0.0008	-0.0137	0.06515	-0.0336	-0.1638	0.10956	0.29773	0.05863	0.07799	-0.1332	0.264
PL	-0.0171	-0.0112	-0.0637	0.104	-0.1272	0.08291	0.24592	0.07098	0.15095	-0.2085	0.227
HSW	-0.0227	-0.3344	0.05524	0.28708	0.05391	0.1826	0.0783	0.03613	0.29655	-0.1296	0.503*
BY	-0.0241	-0.2188	0.24927	0.03683	0.42114	0.39875	0.07741	0.02889	0.07503	-0.5124	0.532**

R=0.195

Where, DE: Days to emergence seedling, DFE: Days to fifty percent flowering, DNPM: days to 95% maturity, GFP; grain filling period, PH; plant height, NPPP; number pods per plant, NSPP; number of seeds per pod, PL; pod length, HSW; hundred seed weight, SY; seed yield, BY, biomass yield.

5. SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

5.1. Summary and Conclusion

The present investigation was carried out with 30 genotypes of lentil (*Lens culinaris* Medik) accessions grown in Randomized complete block design with three replications at Tonny Farm, Dire Dawa, Ethiopia; the date of sowing was July 6, 2017.

In the present study, analysis of variance showed that, highly significant differences were observed for all the traits i.e. there is high naturally existing genetic variation among the evaluated genotypes which plays crucial role for selection and adaptation to occur. Thus, there appears to be a greater scope for bringing about improvement in these traits. High coefficient of variation was observed for number of seeds per pod (22.5%) followed by number pods per plant (14.49%) whereas least coefficient of variation belonged to biological yield. Phenotypic coefficient of variability was slightly higher than the corresponding genotypic coefficient of variability for all the traits except for seed yield. Thus, traits with high phenotypic coefficient of variation indicated that all the characters studied had interacted with the environment i.e. the apparent variation is not only due to genotypes but also due to the influence of environment. The difference between PCV and the corresponding GCV values was relatively higher for seed yield and biological yield indicating the influence of the environment on the traits and indicating that environment is important in determining these traits. Pod length, number of seeds per pod, 100 seed weight, days to emergence, number of pods per plant, grain filling period, days to 50% flowering, plant height and days to 95% maturity shows low difference between PCV and GCV indicating that there is a minimal influence of environment on the expression of these traits.

Seed yield showed highly significant ($p \leq 0.001$) positive association with 100 seed weight and biological yield and significant positive association with number of pods per plant, number of seeds per pod and pod length but it showed significant negative association with days to emergence at phenotypic level. Biological yield showed highly significant positive association with plant height, seed yield and number of pods per plant in addition it had significant positive association with 100 seed weight and number of seeds per pod. Plant height showed highly significant negative association with number of pods per plant as well as significant negative association with days to emergence. Days to 95% maturity shows highly significant positive association with days to 50% flowering, 100 seed weight and number of pods per plant at the phenotypic level. On the other hand at the genotypic level biological yield showed highly significant positive association with seed yield and significant positive association with plant height, number of pod per plant and pod length. Seed yield showed highly significant positive association with biological yield and significant association with pod length at the genotypic level.

The path analysis revealed that at phenotypic level days to 50% flowering, grain filling period, plant height, number of pods per plant, number of seeds per pod and pod length contributed positive direct effect on seed yield along with their positive phenotypic association with seed yield except for days to 50% flowering and grain filling period. Thus, direct selection of traits like plant height, number of pods per plant and number of seeds per pod may useful in yield improvement of lentil at the phenotypic level. Whereas, biological yield, 100 seed weight, days to 95% maturity and days to emergence applied negative direct effect on seed yield along with their negative association with seed yield except biological yield and 100 seed weight. So, indirect selection of biological yield and 100 seed weight may be useful in improvement of seed yield because of their positive indirect via other traits. But the direct effect was negative, so direct selection for these traits to improve yield will not be desirable at the phenotypic level. Days to emergence and days to 95% maturity had exerted negative direct effect along with their significant negative association with seed yield at phenotypic level and negative indirect effect via others traits thus, direct and indirect selection may not be desirable for these traits for improving seed yield in lentil at the phenotypic level.

The path analysis at the genotypic level showed that days to 95% maturity, plant height, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and days to emergence contributed positive direct effect on seed yield so direct and indirect selection for this traits may be given more emphasis while selecting high yielding lentil genotypes at the genotypic level.

5.2. Recommendations

Considering the above findings of the present experiment and field observation, the following recommendations and suggestions have been made:

- ❖ From the present study it was noted that number of pods per plant and pod length had high genetic advance along with high heritability PCV and GCV, highly significant association with yield at both the genotypic as well as phenotypic correlations moreover, it had highest positive direct and indirect effect on seed yield. Therefore, emphasis should be laid for this trait while selecting genotypes during yield improvement program.
- ❖ Lentil (*lens culinaris* Medik) is a cool season crop and grows mostly in highland areas but the present study was conducted in low land area characterized by dry and wet environment. So, this

shows lentil is adaptive for such environments as a result this finding should give a clue for other researchers to do further study.

- ❖ This study was carried out with 30 accessions and so more accessions from different area should be included for further study.

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