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RESEARCH

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Genetic variability and characters association for yield, yield attributing traits and protein content of lentil (*Lens Culinaris* Medikus) genotype in Ethiopia

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Abstract

Background: Lentil is a multipurpose annual legume crop grown in many environments of Ethiopia and recognized as the second center of diversity in the country. However, there is limited information on genetic variation, association of yield, yield-attributing traits, and protein content of lentil in the country. Therefore, this study was conducted to assess the genetic variability, traits association, direct and indirect effects of yield-related traits and protein content on seed yield of lentil genotypes.

Methods: A total of 64 lentil genotypes were evaluated for morpho-agronomic traits and protein content in an 8 × 8 simple lattice design at Debre Berhan Agricultural Research Center in 2018.

Results: The analysis of variance displayed significant differences among the genotypes for all traits indicating the existence of variability and potential for selection of the genotypes for desirable traits. High heritability and high genetic advance were observed for seed yield (96.57%, 81.32%), above-ground biomass (79.03%, 57.99%), days to 50% flowering (70.97%, 23.17%), and the number of seeds per pod (69.41%, 38.23%), respectively. High heritability and moderate genetic advance were detected in plant height (62.63%, 19.77%) and protein content (73.2%, 17.13%), respectively. A positive and significant correlations was observed in phenotypic and genotypic levels of seed yield and above-ground biomass (r = 0.90, 0.93), number of seed per pods (r = 0.79, 0.85), number of pods per plant (r = 0.52, 0.64), plant height (r = 0.49, 0.55), harvest index (r = 0.38, 0.45), secondary branches (r = 0.48, 0.56) and protein content (r = 0.24, 0.26), respectively. Above-ground biomass, harvest index, secondary branches, plant height, number of pods per plant, and protein content were exerted positive and direct effect on yield at phenotypic and genotypic level. This suggested that seed yield, above-ground biomass, harvest index, number of pods per plant, number of seed per pod, plant height, secondary branches, and protein content are the most important traits in selection of lentil improvement.

Conclusion: The study results showed that the presence of wide range of genetic variations among lentil genotypes with desirable traits in above-ground biomass, harvest index, number of pods per plant, number of seeds per pod, plant height, seed yield, and protein content. This variation among traits could be used to develop varieties through selection and hybridization for lentil seed improvement.

Keywords: Correlation, Genotype, Heritability, Lentil, Nutritional quality, Variability

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Introduction

Lentil (*Lens culinaris* Medik) is described as an edible self-pollinated and diploid (2n = 2x = 14) annual legume crop with a genome size of about 4Gbpsp (Arumuganathan and Earle 1991). It is an ancient pulse crop grown for more than eight thousand years. Lentil was originated in the fertile crescent area of Near East and further distributed in the other areas of Europe, the middle east, and Africa (Zohary 1972; Cokkizgin and Munqez 2013). Globally, it is the second pulse crop among the legumes (Shahvar et al. 2017). Nepal, India, Turkey, Australia, the United States, Iran, Syria, Ethiopia, Canada, China, are the uppermost lentil-producing county in the world (FAOSTAT 2019).

Ethiopia ranks tenth in the world and first in Africa in terms of lentil production (FAOSTAT 2019). Global and Africa productivity of lentils covers an area of about 87,443.29 hectares with an annual production of 1193, 28.893 t and the average estimation of national productivity is being about 1.365t/ha (CSA 2019/2020). Ethiopia is one of the centers of diversity for lentils until much of the acreage allocated to the crop is covered by landrace cultivars that are *microsperma* types generally early maturing. The other distinct morphological characters of lentils are also large-seeded (*macrosperma*) types which are native to West Asia and North Africa and Southern Europe (Dugassa et al. 2014).

Lentil is rich in protein, micronutrients, minerals, vitamins, soluble and insoluble dietary fibers. It has also a minimum level of nutrition-hindering factors (Karakoy et al. 2012). Due to this reason, it is more preferred grain legumes crop in human nutrition for preventing and tackling malnutrition (Shrestha et al. 2018). It is attributable to important dietary sources and effective complementary foods with cereals like wheat maize and rice making a nourishing meal by balancing most essential amino acids (Mekonnen et al. 2014).

The crop is commonly cultivated as a rotation with cereals to break the different cereal disease cycles by suppressing pests, avoiding pathogen infection, and fixing atmospheric nitrogen. Because of having better carbon sequestration, lentil is very important for improving soil health (Kumar et al. 2013). It is also used for foods in the form of soup, loaf, salad, stew, *nifro (Ethiopian traditional food)*, and *asambusa (Ethiopian traditional food)* which prepared as a snack and baking flour included in many healthy recipes of the country. It is also an important cash crop fetching a lot of money for the domestic and international markets compared to other legume crops in the county. Lentil straw is also a valued animal feed and the vegetative part that can be used as green manure.

In Ethiopia, poor cultivation practice is the cause of low productivity of lentil. The most essential lion share reason for this bottleneck is biotic stress, abiotic stress, and narrow genetic base of local landrace. The use of diverse germplasm in breeding of lentil cultivars is still inadequate as only a few lines have frequently been used in hybridization causing in narrowing of the genetic base. To increase the genetic resource and productivity as well as to solve such types of problems, widening the genetic base and avoiding vulnerability of resources for the crop is an important issue. An approach that can be used to increase yield and nutritional quality traits in lentils is identifying natural variants that have promising traits and using these variants to develop the best new cultivars (Bailey et al. 2015).

To get crucial information about the availability of such variation, producing differences in the genetic background of lentil is needed. To exploit the available gene pool, unraveling the information on the degree and nature of genetic variability of the population and the interrelationships among traits that would assistance to formulate an efficient scheme of selection based on multiples of traits is vital. The exploitation of crop genetic resources is the most effective ways to increase seed yield and nutritional quality in lentil. Identifying genotypes that produce high mineral concentrations and hopeful plant traits and using these genetic resources in breeding programs are the keys to fruitful crop improvement (Roy et al. 2013).

Yield is one of the major complex traits that are an outcome of the interaction of plant traits. It is highly influenced by environmental fluctuation (Tadesse et al. 2014). The direct selection based on the seed yield of plants without considering others traits of interest may be ambiguous. In the examination of yield and yield contributing traits, conducting association together with a path coefficient analysis is a more effective method (Mahajan et al. 2011). Path analysis is a structural technique to assess the relationships between a dependent variable and two or more independent traits or variables. Though, correlation of traits and path coefficient analysis must be considered to understand the impact of genotype and environment towards the final yield before selection (Kumar et al. 2013; Dugassa et al. 2014; Hussan et al. 2018). Therefore, considering the importance of generating information on genetic variability, heritability, genetic

advance, and association of traits that could be made in introduced lentil genotypes as pre-requisite for improving the crop, and the importance of information on the association of protein content and agro-morphological traits in lentil breeding programs.

Several scholars in Ethiopia explained the genetic variability of lentil germplasm, especially for local genotypes for yield and yield-related traits (Edossa et al. 2010; Tadesse et al. 2014; Dugassa et al. 2014). Understanding the genetic relationships and diversity of lentil germplasm from other countries is important to widen the genetic base of germplasm. However, information is not exhaustive for different population structures of exotic genotypes on the genetic variability for important traits, and nutritional quality traits. Hence, the objectives of this study were to assess the genetic variability, heritability, and genetic advance in lentil genotypes for morpho-agronomic traits and protein content. Furthermore, the study intended to estimate the association of traits and determine the direct and indirect effect on seed yield, yield component traits, and protein content of lentil genotypes.

Materials and methods

Description of study site

The experiment was conducted in the 2018 main cropping season at the research site of Debre Berhan Agricultural Center, Enewari which is located at 9° 52′ 10.7″ North and 39°10 ′46.5″ East at an altitude of 2665 m.a.s.l. Enewari is far from Addis Ababa (the capital city of Ethiopia) around 195 km to the North (Adamu 2018). The area is characterized by highland agroecology which received a mean monthly rainfall of 121.3 mm with average maximum and minimum temperatures of 18.9 and 9.3 °C, respectively. The most common type of soil in the experimental site is vertisol which is known for its high waterlogging and drainage problems with a PH value of 5.9. As different research findings show, even if it has such problems through appropriate management, it is well-known and very appropriate for Lentil growth (Daniel et al. 2010).

Experimental materials

The genotypes used in this study were obtained from Debre Berhan and Debre Zeit Agricultural Research Center's high land pulse and oil crops improvement program. This study includes 64 genotypes in total. Of these, five of them are commercially released varieties from national and regional research centers (Alemaya-98, Chekol, Teshale, Alem Tena, and Jiru) which were used as a standard check. From these genotypes, about 70% of the accessions were from International Center for Agricultural Research in Dry Areas (ICARDA) based on their superiority for agronomic traits and phonologically adapted exotic lines introduced from other countries. The detailed description and list of experimental materials used in this study are explained in Table 1.

Experimental design and procedures

This study was conducted in 8×8 simple lattice designs with two replications. The plot sizes of the experimental field were 3 m × 0.8 m (2.4 m^2) with a row to row spacing of 20 cm, 40 cm between plots, and 150 cm between blocks. To drain excess water, planting was carried out on first August with a broad bed furrow (BBF). Throughout the experimental period, plots were made free of weeds using hand weeding. Insecticide (Dimethoate) was sprayed at the rate of 1.8-L ha^{-1} in 200 L of water to control pea aphid. The collection and calculation of seed protein content was performed at the proper and pertinent time. When the pod turned yellowish, harvesting of the crop was done.

Data collection

Data were recorded on morpho-agronomic traits and yield for days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, number of secondary branches, grain filling period, number of seeds per pod, number of pods per plant, harvest index, biomass yield, 1000 seed weight (g), seed yield (kg ha^{-1}), and protein content. The data were also recorded on plant and plot bases. Plot base records were from the central two rows as well as plant base records were ten randomly selected plants used to represent the genotypes in each replication. Protein analysis was performed with the Kjeldahl method using KjelTech nutrient analyzer as per the Association of Official Analytical Chemists. Protein content was estimated by multiplying total nitrogen content with a factor of 6.25 Altschul (1958). The analysis of protein was performed by the ground seeds using the formula to calculate crude protein by;

$$\mathrm{CP}\ (\%) = (\mathrm{T} - \mathrm{B}) \times \mathrm{N} \times 14 \times 100 \times 6.25\mathrm{Ws} \times 1000$$

where, CP = Crude protein = Titration reading = Blank titration reading = HCl normality.

Ws = Sample weight, 1000 = to convert in to mg.

Data analysis

The statistical analysis of variance was done in statistical procedure for simple lattice design using SAS software version 9.0 (SAS Institute 2004) following the Gomez and Gomez (1984). Duncan's multiple range test (DMRT) at 5% probability levels was used to compare the difference between treatment means.

Table 1 Description of plant material used in the experiment

Source of origin	Number of genotypes	Name of genotypes	Pedigree
ICARDA	45	FLIP-2011-33L, FLIP-2010-21L,FLIP-2011 22L, FLIP-2010-26L, FLIP-2011 30L, FLIP-2010- 22L,FLIP-2010- 23L, FLIP-2010-20L FLIP-2011-20L, FLIP-2010-31L,FLIP-2010 19L, FLIP, 2011-25L, FLIP-2011-37L, FLIP-2011-23L,FLIP-2011 21L, FLIP-2010-21L FLIP-2010-24L, FLIP-2011-29L,FLIP-2011-27L, FLIP-2010- 30L,FLIP-2010-28L, FLIP-2011-36L, FLIP-2007-1L, 97011L, FLIP-2011-24L, FLIP 2011-25L,PRECOZ, FLIP-2011-62L, FLIP-2011-42L, FLIP-2011 82L,FLIP-2011 41L, FLIP-2010-74L, 09S 82,109–04, 010S 96,134–3, ILL-1323, ILL 2261, 2009S 9657 s-L, 2009s -9651 s-L, 010S 96,122–3, 2009S-96101-209S 83,227–04, ILL 2303, 010S-96143–4, 010S 96,105–1, FLIP-2010-29L	ILL7949XILL7686,ILL702XILL2125,ILL8116XILL5562,ILL8116024XIL,L0098,ILL8116XILL5562,LL7012XILL2125,ILL712XILL2125,ILL0590XILL5769,ILL0590XILL5562, ILL8090XILL7686,ILL7949XILL7686,ILL8090XILL5769,ILL8090XILL7685,ILL7683XILL5562,ILL8116XILL5562,ILL6467XILL8009,ILL8116XILL5562,ILL8116XILL5562,ILL2126XILL6199,ILL8090XILL7685,ILL8090XILL673,ILL7683XILL5562,ILL7620XILL7686,ILL10933,ILL8116XILL5562,LL8116XILL5562,ILL4353XILL4400,ILL7537XILL590,ILL818XILL5883,ILL7620ILL8113,ILL6467XILL8009,WA8649090XILL7559,ILL1005XILL5883,ILL4400XILL7947,NEL1323,IG2261,ILL4400XILL7949,LL4400XILL7956,ILL1005XILL5883,ILL323XILL4605,ILL1005XILL5883,IG2303,ILL323XILL9977,ILL8072XILL7162,ILL8090XILL6783
DZARC& DBARC	5	Alemya98, Alem Tena, Checol, Teshale and Jiru	Released (1997, 2004, 1994, 2004 and 2015) respectively
AUS	8	94-028L, 95-005L, 96-034L, 97039LX99R064,97039LX99R120,97011L,193S-180L,97-039LX99RO60	ILL10933, ILL10932, ILL10930, ILL10925ILL10924, ILL10924, ILL10935, ILL7683X-ILL5562
JORDAN	3	8IS-15, UIJ-29L,1b1a-1	UJL197XILL4400, ILL5244, Ibla-1
ARGENTINA	1	2009S 96,575-L	ILL6434XILL7938
USA	1	LC-8603–59-L	ILL10923
TURKEY	1	78S-26052	ILLU2SELECTION

Estimation of variance components

The estimation of phenotypic and genotypic coefficients of variation was applied according to the method suggested by Burton and de Vane (1953) indicated below:

$$\text{Genotypicvariance} = \sigma^2 g = [Msg - Mse],$$

$$\text{Phenotypicvariance}\left(\sigma^2 \text{p}\right) = \sigma^2 \text{g} + \sigma^2{}_\text{e}$$

Genotypic and phenotypic coefficient of variation.

$$(\text{GCV}) = \frac{\sigma \text{g}}{\text{x}} \times 100 (\text{PCV}) = \frac{\sigma \text{p}}{\text{X}} \times 100,$$

Estimation of heritability in broad sense

Heritability (h^2) in a broad sense for all traits was computed using the formula adopted by Allard (1960).

$$h^2 = [\sigma_g^2/\sigma_p^2] \times 100.$$

Estimation of genetic advance

Genetic advance in the absolute unit (GA) and presence of the mean (GAM), selection of superior 5% of the genotypes were assessed by the approaches elucidated by Johnson et al. (1955) as GA = K σp H and GA (as 5% of the mean)

$$\text{GAM} = \frac{\text{GA}}{\overline{\text{x}}} \text{x} 100$$

where, K = the standardized selection differential at 5% selection intensity (k = 2.063), σp = phenotypic standard deviation on the mean basis, H = heritability in a broad sense.

Estimation of correlation coefficients

Phenotypic and genotypic correlations between yield and yield-related protein content were assessed using the typical method described by (Miller et al. 1958). Phenotypic and genotypic correlation coefficient (rp_{xy}) between trait x and y, was estimated using the following formula.

$$rpxy = \frac{\sigma pxy}{\sqrt{\sigma^2 p \times \sigma^2 px}} rgxy = \frac{\sigma gxy}{\sqrt{\sigma^{2gx \times \sigma^2 gy}}}$$

Phenotypic correlation coefficients were tested for their significance using the formula suggested by Sharma (1998). $t = \frac{r}{\sqrt{\frac{1-r^2}{n-2}}}$, where, r = replication and n = number of tested genotypes.

Genotypic correlation coefficients were tested for their significance using the formula suggested by Robertson (1959).

$$t = \frac{\mathbf{rg_{xy}}}{\mathbf{SErg_{xy}}} \quad \text{where} \quad SErg_{xy=}\sqrt{\frac{(1 - \boldsymbol{r^2 g_{xy}})2}{2\boldsymbol{h^2 x} \times \boldsymbol{h^2 y}}}$$

SErgxy = Standard error of genotypic correlation coefficient between trait X and Y.

h^2x = heritability for character x, h^2y = heritability for trait y.

The calculated absolute t value was tested against the tabulated t- value at g-2 degree of freedom for both phenotypic and genotypic correlations.

Path coefficient analysis

Path coefficient analysis (direct and indirect relation) was done according to the method advised by Dewey and Lu (1959) considering seed yield per hectare as a dependent variable and other traits used as an independent variable.

$$rij = pij + \sum rik + Pkj$$

$r_{ij} = P_{ij+} \Sigma r_{ik} p_{kj}$ Where, r_{ij} = mutual association between the independent traits (i) and dependent trait (j) as measured by the correlation coefficient. P_{ij} = the element of direct effects of the independent trait (i) and dependent trait (j) as measured by the path coefficient and $\sum r_{ik-}$ p_{kj} = summation of constituents of an indirect effect of a certain independent traits (i) on the given independent traits (j) via all other independent traits (k). The contribution of the remaining unknown factor was measured as the residual factor (PR) which is calculated as.

$PR = \sqrt{(1 - \sum r_{ij} p_{ij})}$. PR specifies how best the causal factors explain the variability of the dependent factor (seed yield) (Singh and Chaudhary 1999). That is, the small PR value (for instance, nearly zero), the dependent trait considered fully described by the variability in the independent traits, while PR value is higher shows that some other factors which have not been considered, need to be incorporated in the analysis to complete the variation in the dependent trait (seed yield).

Results and discussion

Analysis of variance

In the present study, analysis of variance showed that highly significant genotypic ($P \leq 0.01$) difference for days to 90% maturity, days to 50% flowering, number of primary branches per plant, number of secondary branches, plant height, grain filing period, number of seeds per pod, above-ground biomass, seed yield, harvest index, thousand seed weight, and protein content. Two traits

Table 2 Mean squares for the different sources of variations for 13 quantitative traits and protein content of lentil genotypes evaluate at Debre Berhan, in 2018

Trait	Rep (df = 1)	Blocks/ reps(adj.) (df = 14)	TreatmentsUnadj (df = 63)	Intrablock Error (df = 49)	RCBD error (df = 63)	Total (df = 127)	RE of SL over RCBD	CV (%)
DF	4.130	27.357	118.62**	19.092	20.929	69.322	102.720	6.0
DM	11.883	25.106	89.33**	26.737	26.375	57.490	106.230	3.7
PB	2.494	25.106	20.28**	0.144	0.140	0.228	97.512	14.6
SB	0.007	0.192	1.19**	0.442	0.386	0.784	98.140	14.3
PH	5.755	5.111	19.56**	3.784	4.079	11.771	101.910	6.6
GFP	0.281	24.755	36.86*	21.411	22.154	29.275	100.450	7.6
NPPP	1.872	13.543	30.12*	14.890	14.561	22.181	100.870	12
NSPP	0.174	0.211	0.565**	0.079	0.108	0.335	120.460	10.4
TSW	0.151	6.123	61.28**	7.178	6.943	33.844	96.735	6.9
BM	417,666	1,410,772	1,519,748**	118,891	154,914	779,968	115.49	11.5
SY	49,743	8455.7	302,336**	4427.73	5322.83	153,010	108.71	5.3
HI	2.79	15.0	42.49**	13.88	14.09	28.31	108.08	9.7
PC	0.4016	1.232	5.472**	0.715	0.832	3.1311	106.05	4.2

** and * = Significant at 1% and 5% probability level respectively, ns = none significant, Rep = replication, df = degree of freedom, RCBD = Randomized complete block design; RE of SL = relative efficiency of simple lattice, CV = Coefficient of variance, DF = Days to 50% flowering, DM = Days to 90% maturity, BP = Number of primary branches per plant, SB = Number of secondary branches,PH = Plant height (cm),GFP = grain filing period and NSPP = Number of Seed per pod, BY = above ground biomass kgha^{-1}, SY = Seed yield kgha^{-1}, HI = Harvesting index, TSW = Thousand seed weight(g)and PC = protein content

(number of pods per plant and grain filling period) were displayed significant differences at ($P \leq 0.05$) probability level (Table 2). This designated that the manifestation of a sufficient degree of variability in the tested genotypes will improve the possibility of getting better lentil genotypes through selection. Various scholars formerly explained that high significant morpho-agronomic trait differences among lentil genotypes (Crippa et al. 2009; Edossa et al. 2010; Pandey et al. 2015; Hussan et al. 2018; Sakthivel et al. 2019).

Mean performance and range of genotypes

Estimates of mean separation for the 13 traits have been depicted below along with traits and genotype-wise mean value (Additional file 1: Table S1). Analysis of variance showed that the presence of ample variation for phenology, growth parameters, yield, yield-related traits, and protein contents were varied for accessions from their corresponding traits Additional file 1: Table S1.

Phenology traits

Flowering time is very important for crop adaptation and seed yield. Earliness is a desirable trait that ensures the maturity of crops in a relatively short period thereby avoiding losses due to high temperature during the grain filling and maturity period. The estimated range and mean for all studied traits also indicated wide ranges of variation which revealed a possible amount of variability among the genotypes in Table 3. The variation of days to 50% flowering ranges from 58.5 to 86 days with a mean of 71 days and coefficient variation of 6%. Genotypes Jiru, Alem Tena, LC-8603-59L, ILL2303, 010S96105-1, FLIP-2011-82L, PRECOZ, Chekol, FLIP-2011-62L, 2009S 96,575–1, and FLIP-2011-62L were early flowering genotypes when compared to others. Genotypes FLIP-2010-19L and FLIP-2010-28L were recorded late flowering when compared to other genotypes. Days to maturity varied from 115.5 to 143 and 3.7% coefficient of variation with an average value of 132. FLIP-2011-62L and FLIP-2011-82L were earlier maturing than nationally released variety Chekol and Alem tena by 5 days and more than one week (8 days). 193S-180L and FLIP-2010-28L were late matured from other genotypes which took 141 and 143 days, respectively. Among 64 tested genotypes, 37.5% had a mean maturity period below the overall mean of the genotypes (Additional file 1: Table S1). Grain filling period ranges from 54 to 69.5 recorded for 193S-180L and 09S 82,109–04 genotypes, respectively with a mean of 61.03 and coefficient of variation 6.66. Similar findings were found in the previous studies. Alemayehu et al. (2014) reported that ample variation in lentil genotypes for grain filling period. Pandey et al. (2015) asserted that a wide range of days to 50% flowering and days to maturity in lentil genotypes.

Growth traits

Regarding the growth of traits, the number of primary branches ranges from 2.05 to 3.6 with a mean of 2.56, number of secondary branches ranges from 3.25 to 6.2 with a mean of 4.46. Plant height ranges from 23.5 to 38.4 with mean values of 31.62 and coefficient of variation 14.6, 14.3 and 6.6, respectively. The highest values were recorded for primary branches in genotype Alemaya 98, secondary branches in genotype 2009S 9657s-1, and

Table 3 Estimates of range mean and genetic variability components of lentil genotypes evaluated at Debre Berhan in 2018

Trait	Range	Mean	$\sigma^2 g$	$\sigma^2 p$	GCV (%)	PCV (%)	H^2 (%)	GA	GA (%)
DF	58.5–86	71.03	89.66	126.32	13.33	15.82	70.97	16.46	23.17
DM	115.5–143	132.12	48.2	97.21	5.26	7.46	49.59	10.09	7.63
PB	2.05–3.6	2.53	0.12	0.39	13.65	24.77	30.37	0.39	15.52
SB	3.25–6.2	4.46	0.76	1.57	19.58	28.11	48.52	1.25	28.14
PH	23.5–38.4	31.62	14.66	23.41	12.11	15.3	62.63	6.25	19.77
GFP	54–69.5	61.03	15.04	58.23	6.35	12.5	25.83	4.07	6.66
NPPP	21.6–42.0	32.17	14.21	43.99	11.72	20.62	32.31	4.42	13.74
NSPP	2.15–3.95	2.84	0.4	0.57	22.25	26.7	69.41	1.08	38.23
TSW	26.1–54.0	37.95	48.22	61.9	18.3	20.73	77.91	12.65	33.32
BM	2019.9–5539.2	3274.1	1,071,727	1,356,026.4	31.62	35.57	79.03	1898.67	57.99
SY	869.4–2401.5	1269.6	259,295	268,497.77	40.11	40.82	96.57	1032.34	81.32
HI	31.4–55.7	38.9	25.65	53.95	13.08	18.86	47.47	7.2	18.47
PC	17.5–26.2	21.68	4.43	6.05	9.71	11.34	73.2	3.71	17.13

DF = Days to 50% flowering, DM = Days to 90% maturity, BP = number of primary branches per plant, SB = secondary branches per plant, PH = Plant height(cm), GFP = grain filing period and NSPP = Number of Seed per pod, BY = Above ground biomass kg/ ha, SY = Seed yield kg/ha, HI = Harvesting index, TSW = Thousand seed weight (g) genotypic ($\sigma^2 g$) and phenotypic ($\sigma^2 p$) components of variance, phenotypic (PCV) and genotypic (GCV) coefficient of variability, H^2 (%) = broad-sense heritability, expected genetic advance (GA) and genetic advance as percent of the mean (GA%)

plant height in genotype PRECOZ. The lowest value of primary branches was recorded in genotype LC860359L, for secondary branches in genotype FLIP-2010-21L, for plant height in genotype 010S 96,134–3, and for number of pods per plant in genotype FLIP-2010-19L. In line with this result, highly significant genetic variability for plant height was recorded by Sarker et al. (2017) and (Ghimire and Mandal, 2019). Hussan et al. (2018) also reported significant differences for primary branches and secondary branches.

Yield and yield components

In this study, seed yield ranges from 869.4 kg ha^{-1} to 2401.5 kg ha^{-1} with a mean value of 1269.56 kg ha^{-1} and a coefficient of variation of 5.3% (Table 3). Genotype 96-034L possessed high seed yield followed by Jiru, ILL 2303, and PRECOZ which make them differed significantly from all the other genotypes. On the other hand, genotype 97-039LX-99R120 had the lowest yield compared with the other tested genotypes. Depending on the mean performances, 34.37% of the genotypes had high mean value than the overall tested genotypes. Among the tested genotypes, 8.33% of genotypes had mean performances higher than the nationally released variety (Chekol). These high-yielding genotypes could be utilized in further breeding programs. Wide ranges were recorded for above-ground biomass kg ha^{-1} from 2019.9 to 5539 with a mean of 3274.1 and a coefficient of variation of 11.5%. Genotypes Alemaya 98, Jiru, ILL 2303, 96-034L, and PRECOZ had high above-ground biomass compared to other tested genotypes. While the minimum above-ground biomass was obtained in genotype FLIP-2010-21L (Additional file 1: Table S1).

Harvest index exhibited significant differences among the tested genotypes which ranges from 31.4 to 55.7 with a mean value of 38.9 and coefficient of variation of 9.7%. Genotype FLIP-2010-20L followed by FLIP-2011-82L and 95-005L had a high harvest index, but genotype 09S 82,109–04 had the lowest harvest index compared to other tested genotypes.

The values for thousand seed weight ranges from 26.1 to 54.0 with a mean value of 37.9 g and coefficient of variation 6.9%. Accordingly, genotypes FLIP-2010-26L and FLIP-2010-20L exhibited high thousand seed weight, while genotype 97-011L had a minimum thousand seed weight from others. The number of pods per plant was ranged from 23.3 to 40.9 with a mean value of 32.17 and coefficient of variation 12%. The highest and lowest number of pods per plant were recorded from genotypes Jiru and FLIP 2010-19L, respectively. The number of seeds per pod ranges from 3.95 to 2.15 and the coefficient of variation 10%. Higher numbers of seeds per pod were recorded in genotypes FLIP-2011-62L, whereas lower values were recorded from genotype 97-039LX-99R120 among other tested genotypes. This high variation in the number of seeds per pod was reported by Yadav et al. (2016) and Darai et al. (2017). Sharma et al. (2014) and Hussan et al. (2018) reported high significant variation in lentil genotypes for above-ground biomass and seed yield. Variations on thousand-seed weight due to genotypes were also reported by Yadav et al. (2016). Lego et al. (2016) report that the harvest index of lentil genotypes ranges from 5.92 to 54.22 with a mean value of 28.9.

Nutritional quality traits

Protein contents were ranges from 17.5 to 26.2 and coefficient of variation 4.2 with a mean value of 21.6. Genotypes 2009S 9657 s^{-1} and PRECOZ had high protein content compared to other genotypes. Whereas, the minimum protein content was recorded for genotype ILL-1323 97-011L. This result was consistent with the study conducted by Hussan et al. (2018).

Estimation of variance component

Phenotypic and genotypic coefficient of variation

The amount of genotypic and phenotypic variability exists in a species is essential and a pre-request in developing better varieties and initiating a breeding program. The estimation of variance components, genotypic and phenotypic coefficient variation are explained in Table 3. Genotypic and phenotypic coefficient of variation were categorized as high > 20%, medium 10%—20%, and low < 10% according to Deshmukh et al. (1986). Based on this explanation, high phenotypic coefficient of variation (PCV) estimates were observed for seed yield (40.82%), above-ground biomass (35.57%), secondary branches (28.11%), number of seeds per pod (26.70%), 1000 seed weight (20.73%), and number of pods per plant (20.62%). This result is similar with Sarwar et al. (2013), Al-aysh (2014) and Pandey et al. (2015) who reported a high magnitude of PCV for 1000 seed weight, number of pods per plant, above-ground biomass, secondary branches, number of seeds per pod, and seed yield. Medium PCV was observed for harvest index (18.86%), days to flowering (15.82%), plant height (15.30%), grain filling period (12.50%), and protein content (11.3%). Low PCV was found in days to maturity. This result is in line with Paliya et al. (2015) who explained harvest index, days to 50%, and plant height had medium PCV.

Genotypic coefficient of variation (GCV) ranges from 5.26% to 44.3%. The high magnitude of GCV value estimates were recorded for seed yield (40.11%), above-ground biomass (31.62%), harvest index (32.39%), and number of seeds per pod (22.25). These high GCV values in the studied genotypes suggested that the possibility of improving traits through selection. This result is similar

with Hussan et al. (2018) and Sakthivel et al. (2019) who noticed high GCV for the number of seeds per pod, and seed yield. Medium GCV was observed for primary branches (13.65%), secondary branch (19.58%), days to flowering (13.33%), 1000 seed weight (18.3%), number of pods per plant (11.27%), and plant height (12.11%). The present finding was similar to Pandey et al. (2015) and Chowdhury et al. (2019) who observed medium GCV for plant height, number of pods per plant, number of seeds per pod, and 1000 seed weight. On the other hand, the low GCV was exhibited for days to maturity (5.26%), grain filling period (6.35%), and protein content (9.7%). This finding is in line with Dugassa et al. (2014) who reported low GCV for the grain-filling period.

The differences between PCV and GCV were recorded for days to 50% flowering, days to maturity, plant height, seed yield, harvest index, and 1000 seed weight which were relatively less than the other considered traits. This minimum difference between PCV and GCV expressed that more of the phenotypic expression came from genotypic influences and as well as it indicated that the environmental influence was less. Similar results were observed by Lego and Nath (2016) and Gautam et al. (2014).

Broad-sense heritability and genetic advance

Estimates of heritability in a broad sense ranges from 25.83% for the grain filling period to 96.57% for seed yield (Table 3). Robinson et al. (1949) categorized heritability value as high (> 60%), moderate (40–60%), and low (< 40). Considering this benchmark, the heritability estimation value was high for seed yield (96.57%), above-ground biomass (79.03%), days to 50% flowering (70.97%), number of seeds per pod (69.41%), plant height (62.63%), 1000 seed weight (77.91%), and protein content (77.3%). This high value indicated that these traits were less influenced by environmental conditions. It reflected that the phenotypes were the true descriptive of their genotypes and mass selection based on phenotypic performance would be reliable for lentil improvement by increasing the frequency of favorable alleles through hybridization. Heritability was moderate for days to maturity (49.58%), secondary branches (48.52%), and harvest index (47.47%). It was low for primary branches (30.31%), number of pods per plant (32.31%), and grain filling period (25.83%). This low heritability of traits indicated that the environmental effect was high.

This result is in line with previous reports by Hussan et al. (2018) who found high heritability for protein content, seed yield, 1000 seeds weight, and number of seeds per pod and moderate heritability in days to maturity. Umakant et al. (2017) explained that protein content and seed yield had high heritability. Lego and Nath (2016) reported that days to 50% flowering and plant height had high heritability. Ali et al. (2011) revealed that above-ground biomass and seed yield had high heritability. Al-Aysh (2014) reported that high heritability for above-ground biomass, seed yield, and number of seeds per pod. Dugassa et al. (2014) reported that several primary branches and grain filling periods had low heritability and harvest index had moderate heritability.

Genetic advance as percent of mean is categorized as low, moderate, and high which ranges from < 10%), 10–20%, > 20%, respectively (Johson et al. 1955). Accordingly, seed yield (81.32%), above-ground biomass (57.99%), number of seeds per pod (33.32%), secondary branches (28.14%), and days to 50% flowering (23.17%) showed high genetic advance. Primary branches (15.52%), plant height (19.77%), harvest index (18.47%), protein content (17.13%), and the number of pods per plant (13.74%) had moderate genetic advance. It was low for day to maturity (7.63%) and grain filling period (6.6%). High heritability together with high expected genetic advance as percent of mean was recorded from seed yield, above-ground biomass, days to 50% flowering, and the number of seeds per pod. This occurrence is because of additive gene effect through selection. Depending on this impression, this trait is highly desirable. On the other hand, plant height, harvest index, protein content, and the number of pods per plant had high heritability and moderate genetic advance. This indicates that equal influence of additive and non-additive gene action in their manifestation. This result was consistent with Pandey et al. (2015) who reported days to 50% flowering and number of seeds per pod had high heritability with high genetic advance. Raturi et al. (2015) for seed yield and number of seeds per pod and Dugassa et al. (2014) for above-ground biomass were reported considerably high heritability with high genetic advance. Chowdhury et al. (2019) explained that plant height and number of pods per plant had high heritable with moderate genetic advance. Hussan et al. (2018) for protein and Tyagi and Khan (2010) for harvest index were reported high heritability and moderate genetic advance.

The results in Table 3 showed that highly heritable traits with high genetic advance and better GCV were observed for seed yield and above-ground biomass. These were providing a reliable indication and estimate of the expected amount of improvement through selection for these traits of interest. High heritability might not necessarily lead to increased genetic gain (Sardana et al. 2007). In this study, plant height, harvest index, and the number

of pods per plant possess high estimates of heritability, but they fail to show a high estimate of genetic advance as a percentage of the mean. This is indicative of non-additive gene actions predominance which could be exploited over heterosis breeding.

Association among traits

Seed yield is the outcome of many mutually dependent traits. Some of these traits are vastly related among themselves and with seed yield. The analysis of the relationship among these traits and their association with seed yield is important to launch selection criteria (Singh and Ceccerelli 1996). In this investigation, GCV was higher in magnitude than that of phenotypic correlation coefficients in almost all the traits which indicated that the presence of inherent association among various traits. The current investigation revealed that each studied trait was associated negatively and positively representing the traits under this study were influenced and supported by one another.

Phenotypic association of seed yield with yield-related traits

The estimates of phenotypic and genotypic correlation coefficients between each pair of traits were presented in Table 4. Seed yield ha^{-1} showed positive and significant phenotypic correlation at ($P \leq 0.01$) with above-ground biomass (0.90) followed by number of seeds per pod (0.79), number of pods per plant (0.52), plant height (0.49), harvest index (0.45), secondary branch (0.48), l000 seed weight(g) (0.30), harvest index (0.38), and protein content (0.24). The existence of a strong positive correlation between seed yields with yield-related traits helps to identify traits that could be used for indirect selection for the improvement of seed yield in the tested genotypes. This observation is similar with Hamdi et al. 2012 who showed a high positive correlation for plant height, number of pods per plant, number of seeds per pod, and seed yield. Sarwar et al. 2013 and Dugassa et al. 2014 were also observed a positive and significant correlation of plant height, above-ground biomass, and harvest index at the phenotypic level. Nath et al. (2015) and Ghimire and Mandal (2019) were reported a positive and highly significant association of 1000 seeds weight, plant height, number of pods per plant, and number of seeds per pod. Paliya et al. (2015) and Kumar et al. (2017) were indicated seed yield had a positive significant phenotypic correlation with the number of pods per plant, 1000 seeds weight, number of secondary branches per plant, above-ground biomass, and harvest index. Sharma et al. (2014) reported that above-ground biomass yield, number of pods per plant, number of seeds per pod, and harvest index had a positive and highly significant association for seed yield. A positive correlation between two desirable traits is important for plant breeders easy for improving both traits simultaneously (Bhima et al. 2016).

Based on the present finding, it is important to give more attention to those traits having the greatest positive influence on seed yield for lentil improvement in a breeding program. Days to 50% flowering ($r_p = -0.51$) and days to maturity ($r_p = -0.57$) exhibited a negative and significant correlation with seed yield. These genotypes that exhibit longer flowering period results

Table 4 Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient of quantitative and nutritional traits for 64 lentil genotypes

Trait	DF	DM	PB	SB	PH	GFP	NPPP	NSPP	TSW	BM	SY	HI	PC
DF	1	0.812**	−0.096	−0.31*	−0.19	−0.48**	−0.38**	−0.47*	−0.24	−0.53**	−0.55**	−0.19	−0.29*
DM	0.76**	1	−0.265*	−0.27*	−0.15	0.11	−0.37**	−0.61**	−0.22	−0.57**	−0.65**	−0.36**	−0.29*
PB	−0.07	−0.23*	1	0.03	−0.11	−0.23	0.07	0.36**	−0.09	0.09	0.17	0.28	0.25*
SB	−0.22*	−0.16	−0.02	1	0.50**	0.08	0.59**	0.43**	0.36	0.56**	0.56**	0.16	0.28*
PH	−0.16	−0.12	−0.12	0.38**	1	0.08	0.58**	0.45**	0.01	0.58**	0.55**	0.05	0.08
GFP	−0.43**	0.23**	−0.20*	0.07	0.06	1	0.10	−0.13	0.08	0.05	−0.04	−0.21	0.06
NPPP	−0.30**	−0.29**	0.00	0.49**	0.50**	0.06	1	0.48**	0.24	0.67**	0.64**	0.11	0.29*
NSPP	−0.42**	−0.51**	0.32**	0.32**	0.38**	−0.09	0.34**	1	0.14	0.79**	0.85**	0.38**	0.23
TSW	−0.22*	−0.19*	−0.13	0.31**	0.02	0.06	0.19	0.13	1	0.23	0.30*	0.29*	0.07
BM	−0.48**	−0.48**	0.09	0.49**	0.49**	0.05	0.54**	0.75**	0.24**	1	0.93**	0.09	0.26*
SY	−0.51**	−0.57**	0.14	0.48**	0.49**	−0.04	0.52**	0.79**	0.30**	0.90**	1	0.45**	0.26*
HI	−0.14	−0.27**	0.17	0.06	0.05	−0.16	0.04	0.24**	0.21*	−0.06	0.38**	1	0.05
PC	−0.24**	−0.21*	0.18*	0.22*	0.08	0.05	0.22*	0.20*	0.07	0.20*	0.24**	0.10	1

*Significant at 5 percent level; **Significant at 1 percent, *DF* Days to 50% flowering, *DM* Days to 90% maturity, *BP* number of primary branches per plant, *SB* Number of secondary branches, *PH* Plant height (cm), *GFP* grain filing period, *NSPP* Number of Seed per pod, *BY* Above ground biomass kg/ ha, *SY* Seed yield kg/ha, *HI* Harvesting index, *TSW* Thousand seed weight (g)

wastage of critical pod setting periods and exposing for stress conditions in terminal moisture stress environment. The negative association of these traits with seed yield indicates simultaneous selection of such traits is difficult though independent selection has to be used for the improving these genotypes. This result was in line with the study done by Mekonnen et al. (2014).

Genotypic association of seed yield with yield-related traits

Seed yield ha^{-1} showed positive and significant correlation at ($P \leq 0.01$) probability level with above-ground biomass ha^{-1} (0.93), number of seeds per pod (0.85), number of pods per plant (0.64), secondary branches (0.56), plant height (0.55), and harvest index (0.45), while significant associations at ($P \leq 0.05$) probability level with 1000 seeds weight (0.30) and protein content (0.26) (Table 4). These results showed that the greater the number of branches per plant, number of pods per plant and other eventually contributing positively towards yield. However, seed yield ha^{-1} showed a highly significant negative correlation with days to 50% flowering (−0.55) and days to maturity (**−**0.65). This indicated that a longer day to 50% flowering and maturity delivered a low seed yield. The result is in line with Pandey et al. (2017). Mekonnen et al. (2014) was observed a positive genotypic association of seed yield with above-ground biomass, plant height, number of pods per plant, number of seeds per pod, and 1000 seeds weight. Kumar et al. (2017) was also reported a highly significant and positive genotypic association of seed yield per plant with harvest index, above-ground biomass, number of secondary branches, number of pods per plant, 1000 seeds weight, and number of seeds per pod. Ali et al. (2011) revealed a positive and significant correlation between the number of pods per plant and protein content.

Path coefficient analysis

Path coefficient analysis provides the real indication of the direct and indirect influence of each trait associated with the other traits. Genotypic and phenotypic correlations were classified into direct and indirect effects to identify the importance of different traits for seed yield under this investigation. In most cases, the magnitudes of the phenotypic direct and indirect effects were somewhat greater than the genotypic effects. Path analysis was carried out both at the genotypic and phenotypic levels by using seed yield as a dependent variable to see the causal factors and to identify the common components responsible for producing better seed yield.

Phenotypic path analysis of seed yield with other characters

The phenotypic direct and indirect effect of different traits on seed yield ha^{-1} was presented in Table 5. In the present investigation, above-ground biomass ha^{-1} ($r_p = 0.905$) followed by harvest index ($r_p = 0.426$) exerted high positive direct effects on seed yield ha^{-1}, and had a highly significant positive phenotypic correlation for seed yield ha^{-1} (Table 5). This finding was detected that selection for this trait would be the most effective means of getting higher seed yield for lentils. Secondary branches, number of pods per plant, plant height, and days to 50% flowering had positive direct effects, but weak (negligible) influences on seed yield ha^{-1}. These traits also exhibited a positive and highly significant phenotypic correlation with seed yield ha^{-1}. This result is in agreement with the finding of Latif et al. (2010) who reported plant height and number of pods per plant had positive phenotypic direct effects in determining the seed yield of lentils. Fikru et al. (2014) observed that the number of pods per plant, plant height, and above-ground biomass had a positive direct effect on seed yield. Nath et al.

Table 5 Estimates of direct (bold diagonal) and indirect effects (off-diagonal) at a phenotypic level for different traits on seed yield and protein content in lentil genotype

Trait	DF	DM	SB	PH	NPPP	NSPP	TSW	BM	HI	PC	r_p
DF	**0.0112**	−0.0277	−0.0014	−0.0035	−0.0006	0.0070	0.0022	−0.4339	−0.0600	−0.0037	−0.510**
DM	0.0085	**−0.0363**	−0.0010	−0.0027	−0.0006	0.0085	0.0019	−0.4307	−0.1156	−0.0033	−0.571**
SB	−0.0024	0.0057	**0.0064**	0.0084	0.0010	−0.0053	−0.0031	0.4415	0.0241	0.0034	0.480**
PH	−0.0018	0.0044	0.0024	**0.0223**	0.0010	−0.0063	−0.0002	0.4468	0.0224	0.0013	0.492**
NPPP	−0.0034	0.0104	0.0031	0.0111	**0.0020**	−0.0057	−0.0019	0.4864	0.0182	0.0033	0.524**
NSPP	−0.0047	0.0184	0.0020	0.0085	0.0007	**−0.0167**	−0.0013	0.6749	0.1026	0.0030	0.787**
TSW	−0.0025	0.0071	0.0020	0.0004	0.0004	−0.0022	**−0.0100**	0.2201	0.0886	0.0010	0.305**
BM	−0.0054	0.0173	0.0031	0.0110	0.0011	−0.0124	−0.0024	**0.9050**	−0.0245	0.0030	0.896**
HI	−0.0016	0.0098	0.0004	0.0012	0.0001	−0.0040	−0.0021	−0.0520	**0.4267**	0.0015	0.380**
PC	−0.0027	0.0078	0.0014	0.0018	0.0004	−0.0033	−0.0007	0.1768	0.0406	**0.0154**	0.238*

**,* Significant level at 0.01 and 0.05 probability level, Residual for phenotypic 0.089, *DF* Days to 50% flowering, *DM* Days to maturity, *SB* secondary branches, *PH* Plant height (cm), *NSPP* Number Seeds per pod, *NPPP* number of pods per plant, *BY* above ground biomass kg ha^{-1}, *HI* Harvesting index, *TSW* Thousand seed weight (g), *PC* protein content, r_g *and* r_p genotypic and phenotypic correlation coefficient

(2015) reported that above-ground biomass ha^{-1}, harvest index, number of pods per plant, plant height, and secondary branches had the positive phenotypic direct effect on seed yield. Sakthivel et al. (2019) reported that above-ground biomass ha^{-1} and harvest index had a positive direct effect on the seed yield of lentils.

However, a hundred seed weight ($r_p = -0.0167$) and the number of seeds per pod (−0.01) had a negligible negative direct effect on seed yield ha^{-1}, but it exerted a significant positive correlation. This might be related to the counterbalancing of the positive indirect effect of other parameters. Days to maturity had a negative direct effect on seed and a highly significant negative correlation on seed yield of lentil genotype. This result was in line with Dalbeer et al. (2013) who reported days to maturity had a negative direct effect on seed yield.

The path analysis revealed that a high positive indirect effect at the phenotypic level on seed yield ha^{-1} was exerted by number of seeds per pod ($r_p = 0.6749$) followed by the number of pods per plant ($r_p = 0.4864$), plant height ($r_p = 0.4468$), secondary branches ($r_p = 0.4415$), and 1000 seed weight ($r_p = 0.2201$) all via above-ground biomass ha^{-1}. In addition, these traits had a positive and highly significant phenotypic correlation with seed yield ha^{-1} (Table 6). The results indicated that above-ground biomass is the most noticeable trait contributing directly to seed yield and most other traits were correlated to seed yield indirectly through above-ground biomass. Number of seeds per pod ($r_p = 0.103$) via harvest index indirectly showed a positive contribution to seed yield. While days to maturity showed a negative indirect effect on seed yield via harvest index ($r_p = -0.115$). In general, except for traits like above-ground biomass and harvest index, the indirect effect of seed yield via other traits was small and negligible.

The residual effect determines the unaccounted variability of the dependent factor (seed yield ha^{-1}). Its magnitude (0.089) indicated that the traits included in the path analysis explained 91.1% of the variation in seed yield ha^{-1} of tested lentil genotypes. Favorable direct effects of those traits on seed yield indicated that with other variables kept constant, improvement of these traits will increase seed yield. In other words, the independent variables included in the study had sufficiently captured the variation in seed yield of lentil genotypes. In the present study, traits that showed considerable positive indirect effects via other traits should be considered simultaneously as indirect selection criteria for seed yield improvement.

Genotypic path analysis of seed yield with other characters

The maximum positive genotypic direct effect on seed yield was exerted by above-ground biomass ha^{-1} (rg = 0.874) and harvest index (rg = 0.365) in Table 6. Both traits had highly significant positive genotypic correlations with seed yield ha^{-1}. Hence, it should be considered in further selection procedures for higher seed yield in the tested lentil genotypes. Days to 50% flowering, plant height, and number of pods per plant also had positive direct effects on seed yield ha^{-1}. Correspondingly, all these traits had a positive association with seed yield ha^{-1} which showed the importance of the traits to be used as direct selection criteria to improve seed yield though direct selection of this trait may ultimately lead to the development of high-yielding lentil genotypes. This result was similar to Tyagi and Khan (2010) who revealed harvest index and above-ground biomass showed the highest positive direct effect towards seed yield. Latif et al. (2010) observed a high positive direct effect of number of pods per plant and plant height on seed yield. Tadesse et al.

Table 6 Estimates of direct (bold diagonal) and indirect effects (off-diagonal) at a genotypic level for different traits on seed yield and protein content in lentil genotype

Trait	DF	DM	SB	PH	NPPP	NSPP	TSW	BM	HI	PC	rg
DF	**0.0193**	−0.034	0.0001	−0.005	−0.0006	0.0067	0.0010	−0.468	−0.0705	−0.0028	−0.552**
DM	0.0157	**−0.042**	0.0001	−0.004	−0.0006	0.0086	0.0009	−0.495	−0.1308	−0.0027	−0.650**
SB	−0.0059	0.0114	**−0.0003**	0.0117	0.0010	−0.0060	−0.0015	0.4918	0.0578	0.0026	0.563**
PH	−0.0036	0.0064	−0.0001	**0.0237**	0.0009	−0.0063	0.0000	0.5089	0.0199	0.0008	0.551**
NPPP	−0.0074	0.0152	−0.0002	0.0137	**0.0016**	−0.0067	−0.0009	0.5815	0.0389	0.0028	0.639**
NSPP	−0.0092	0.0254	−0.0001	0.0106	0.0008	**−0.0140**	−0.0006	0.6902	0.1403	0.0022	0.846**
TSW	−0.0046	0.0091	−0.0001	0.0002	0.0004	−0.0020	**−0.0040**	0.1999	0.1048	0.0007	0.304**
BM	−0.0103	0.0236	−0.0002	0.0138	0.0011	−0.0111	−0.0009	**0.8741**	0.0335	0.0025	0.926**
HI	−0.0037	0.0149	0.0000	0.0013	0.0002	−0.0054	−0.0011	0.0800	**0.3656**	0.0005	0.452**
PC	−0.0057	0.0121	−0.0001	0.0020	0.0005	−0.0033	−0.0003	0.2274	0.0192	**0.0095**	0.261*

**,*Significant level at 0.01 and 0.05 probability level, Residual for genotypic 0.076, *DF* Days to 50% flowering, *DM* Days to maturity, *SB* secondary branches, *PH* Plant height (cm), *NSPP* Number Seeds per pod, *NPPP* number of pods per plant, *BY* above ground biomass kg ha^{-1}, *HI* Harvesting index, *TSW* Thousand seed weight (g), *PC* protein content, r_g *and* r_p genotypic and phenotypic correlation coefficient

(2014) also revealed that the number of pods per plant and the number of seeds per pod had a positive direct effect on seed yield. Lego *et al.* (2016) explained that harvest index, plant height, and number of pods per plant had a direct effect on seed yield ha^{-1}.

Days to maturity and days to flowering had negative direct effects followed by weak influence for number of seeds per pod, secondary branches, and 1000 seed weight on seed yield ha^{-1}. Except days to maturity and days to flowering, these traits had a highly significant and positive correlation with seed yield ha^{-1}. This result was in line with Tadesse et al. (2014) and Akter et al. (2020). Latif et al. (2010) and Chowdhury et al. (2019) observed that days to 50% flowering had negative direct effect on the number of seeds per pod and days to maturity for 1000 seed weight.

Above-ground biomass contributed to seed yield ha^{-1} mainly via its positive indirect effects with secondary branches, plant height, number of pods per plant, and number of seeds per pod. Similarly, high positive direct effect for harvest index on seed yield was increased by its positive indirect effects via the number of seeds per pod and 1000 seed weight. Hence, except for the two traits above-ground biomass and harvest index, the indirect effect of seed yield via other traits was negligible.

The residual (0.076) indicated that the traits included in the genotypic path analysis explained 92.4% of the total variation in seed yield ha^{-1}. These low residual effects of a genotypic path (0.076) and phenotypic path (0.089) for seed yield indicated that there may not be any important characters that were not utilized in the present study. It is worthy to mention that almost all the traits had a considerable positive indirect effect via above-ground biomass ha^{-1}. As a result of this study, traits that exerted positive direct effect, positive and significant correlation with seed yield need much attention in the selection program. Hence, traits that showed considerable positive indirect effects via other traits should be considered simultaneously as indirect selection criteria for seed yield improvement.

Conclusion

The analysis of variance revealed that the presence of highly significant differences among the tested genotypes for all traits considered. This indicates the existence of variability among the tested genotypes. Genotypes PRECOZ FLIP-2010-20L, Alemaya 98, Jiru, ILL 2303, FLIP-2011-82L, and 96-034L FLIP-2010-26L were the best with seed yield, protein content, and other important traits compared to other tested genotypes in the study area. Seed yield was positively and significantly correlated with yield attributing traits in this finding. Maximum phenotypic coefficient of variation (PCV) was noted for seed yield and the lowest PCV was detected for days of maturity.

Generally, the magnitudes of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for secondary branches, number of seeds per pod, above-ground biomass thousand seed weight, and seed yield. High heritability and genetic advance as percent of mean simultaneously were observed for days to 50% flowering, thousand seed weight, number of seeds per pod, above-ground biomass, and seed yield indicating presence of additive gene effect for these traits. Direct selection may improve seed yield on these important traits. Plant height and protein content had high heritability with moderate genetic advances. This shows that additive and non-additive gene action has an equal influence on the expression. On the other hand, the date of maturity and grain filling period had low genetic advances.

Correlation analysis displayed that seed yield had positive and significant correlations with above-ground biomass, number of seeds per pod, number of pods per plant, plant height, harvest index, protein content, and secondary branches at both phenotypic and genotypic levels. These traits paid positive correlation towards yield. Thus, attention should be given to those traits when selecting the best seed yield genotypes. The path analysis indicated that above-ground biomass, harvest index, secondary branches per plant, number of pods per plant, plant height, and protein content exerted positive direct effects on seed yield at phenotypic and genotypic levels.

Meanwhile, this study was conducted for one location in one season and was not deal with the determination of the genetic diversity using molecular markers. Therefore, replicated evaluation of genotypes over varied locations is recommended to assess the genetic diversity of genotypes based on molecular markers.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s43170-022-00079-6.

Additional file 1. Mean values of 13 quantitative traits of 64 lentil genotypes grown at Debre Berhan 2018.

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Authors' contributions
ET: Participated in conception, design, analysis and writing of the manuscript and serve as the lead author of the paper. FM and FM are participated in designing, revising and writing the manuscript. All authors read and approved the final manuscript.

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Availability of data and materials
Data will be made available up on reasonable request.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no conflict of interest.

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