Research
Journal of Botany

OPEN ACCESS

Genetic Variability and Association of Characters in Ethiopian Basil (*Ocimum basilicum* L.) Germplasm

Aynalem Gebre Gossa
Ethiopian Institute of Agricultural Research, Wondo Genet Agricultural Research Center, P.O. Box 198, Shashemene, Ethiopia

ABSTRACT

Background and Objective: Sweet basil (*Ocimum basilicum* L.) is an important herbaceous aromatic and medicinal plant that belongs to the Lamiaceae family. The extent of genetic diversity is not well investigated. Therefore, the objective of this study was to evaluate the genetic variability of sweet basil using quantitative morphological traits. Assessing variability is essential to identify the most important traits in sweet basil accessions which help in crop improvement programs. **Materials and Methods:** An experiment was carried out in a simple lattice design with forty-nine accessions of sweet basil in two replications. After three months, five plants per plot from the central rows were randomly selected and data was collected from a total of 10 plants for each accession from two replications. Estimation of variance components and association of characters analyzed for quantitative traits were performed using the R software. **Results:** High estimates of GCV and PCV were recorded for essential oil yield (58.87%; 78.25%), fresh leaf weight per plant (36.79%; 42.89%), petiole length (27.80%; 30.88%) and leaf length (25.81%; 27.67%). High heritability estimates were observed for leaf length (86%), length of inflorescence (84%), petiole length (81%), fresh leaf weight per plant (72%), plant height (70%) and leaf width (64%). High genetic advance over a mean (GAM%) recorded for essential oil yield (90.03%), fresh leaf weight per plant (65.01%), petiole length (51.57%), leaf length (49.61%), length of inflorescence (29.72%) and leaf width (27.36%). Estimation of genotypic correlation coefficient among traits indicated that there was a positive and highly significant correlation between fresh leaf weight per plant was significantly and positively correlated with leaf width (r = 1), leaf length (r = 0.99) and length of inflorescence (r = 0.77). **Conclusion:** Thus, the result indicated that higher values of heritability showed lesser environmental and greater genetic effects which can be used in future breeding programs.

KEYWORDS

Association of characters, basil, genetic variability, heritability, Lamiaceae, *Ocimum basilicum*

INTRODUCTION

The *Ocimum* genus belongs to the family Lamiaceae. The genus contains over 150 species that are herbaceous and shrubs, which are distributed across tropical regions of Asia, Africa and Central and South America[1]. Since ancient times, *Ocimum* has been the most significant aromatic medicinal plant[2]. As a

ISSN: 2152-0461 (Online)
ISSN: 1816-4919 (Print)
https://doi.org/10.3923/rjb.2024.92.101

Received: 24 Sep. 2024
Accepted: 24 Nov. 2024
Published: 25 Nov. 2024

group of economically useful herbs that have multiple forms, it is a significant source of naturally occurring essential oils and aromatic chemicals. In the Labiatae family, sweet basil (*O. basilicum*, x = n = 12) is a major crop of essential oils that are used in cosmetics, medications and food[3]. Additionally, linalool, eugenol, methyl chavicol, methyl cinnamate, ferulate, methyl eugenol, triterpenoids and steroidal glycosides are present in the essential oil that is extracted from its aerial parts, along with other significant ingredients including eugenol and chavicol and its derivatives[4,5]. Basil has long been used as a medicinal herb to treat a variety of conditions, including headaches, coughs, diarrhoea, constipation, warts, worms and renal malfunctions[6]. It has also been used to treat malarial fever[7], as well as to prevent mosquito vectors and plasmodium parasites from spreading[8].

For thousands of years, Ethiopians have utilized basil as a spice and medicinal herb. The leaves and flowers are dried, ground and added to different kinds of locally prepared food. Sweet basil is cultivated and widely used throughout the country; it is cultivated in every province of Ethiopia. Farmers use this crop for household consumption as well as to supply the local market[9-11]. It has a strong domestic market demand for essential oil in Ethiopia with an estimated value of 5-7 million dollars per year.

Understanding the genetic diversity available in existing crop species for the trait being improved is critical to the success of any plant breeding program. Knowledge of specific genetic factors is required for proper understanding and manipulation in any crop improvement strategy. The observed variability is the result of the interaction of genetic and environmental variables. Only genetic factors were heritable out of the two. As a result, understanding the extent to which genetic factors influence trait performance is critical. When efficient selection is in place, heredity with genetic improvement is more predictive of gain. Thus, it is essential to estimate genetic parameters. Genetic variables that are useful biometrical tools for assessing genetic variability include heritability, genetic advance (GA), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability[12]. By measuring genetic factors such as heritability and genetic progress, the transfer of features from parent plants to offspring can be predicted with substantial accuracy. Additional significant genetic markers that indicate whether a trait is influenced by the environment or not are PCV and GCV. When the PCV and GCV values are well aligned or exhibit minimal variation, it indicates that the genotype's genetic composition is primarily responsible for the phenotype. The more the PCV and GCV values diverge, the more the environment affects how well the genotype functions. Plant breeders can identify the features for which selection will be carried out by considering other crucial selection parameters such as heritability and genetic advancement. Nikam *et al.*[13] found that genetic improvement in aromatic plants for quantitative characters is useful for the determination of yield components to enhance essential oil yield through the selection of genotypes from the population. Yield, however, is the main complex trait that results from the interplay of various plant traits. Selecting solely for a plant's yield without taking into account other desirable features could lead to confusion. Conducting association along with a path coefficient analysis is a more effective way to examine yield and yield contributing traits[14]. An examination of the connections between a dependent variable and two or more independent characteristics or variables is possible through the use of structural techniques like path analysis. But before selection, it's important to understand how genotype and environment affect final yield by taking into account path coefficient analysis and trait correlation[15]. With these considerations in mind, an attempt has been made in the current study to analyze a collection of genotypes of basil with the objective of evaluating the genetic variability, heritability and genetic advancement for morpho-agronomic variables and essential oil yield. Furthermore, the study intended to estimate the association among various traits present in basil accessions.

MATERIALS AND METHODS

Description of the study area: From November, 2019 to March, 2020, the study was conducted in the Wondo Genet Agricultural Research Center's experimental field. Situated in the Sidama Regional State, Wondo Genet is 1780 m above sea level and is roughly 264 km from Addis Ababa. Its geographic coordinates are 7°19'N and 38°38'E. The average annual rainfall at the location is 1120 mm, with mean maximum and lowest temperatures of 26 and 12°C, respectively. In the experimental region, the soil type is nittosols, which have a pH of 6.4 and a sandy clay loam texture[16].

Plant material and experimental design: Forty-nine basil accessions were utilized in the study (Table 1). These comprised twenty-two accessions from the Ethiopian Biodiversity Institute (EBI), two sweet basil varieties released by the Wondo Genet Agricultural Research Center, 23 accessions gathered from various regions of the country (SNNP, Oromia and Harari) and two accessions from overseas (one from Norway and one from Israel).

The experimental fields were organized in a 7×7 simple lattice design with two replications. A spacing of 1.5 m between replications and 1 m between plots was maintained. Each experimental plot measured 2.4×3.6 m, containing six rows with 40 cm intra-row and 60 cm inter-row spacing. Basil seeds were sown in 10 cm polyethylene bags in 2019 at the Wondo Genet Agricultural Research Center greenhouse. Watering was conducted twice a week after seedling emergence. After 5 weeks, the seedlings were moved to a lath house for 1 week of hardening off. The experimental plot was prepared by plowing, hoeing and leveling before transplanting the seedlings to the main field, which took place after 6 weeks. Each experimental plot consisted of 36 plants, with all necessary horticultural practices being carried out.

Data collection: After 3 months, five plants per plot from the central rows were randomly selected and data was collected from a total of 10 plants for each accession from two replications. Data collection was started during the full blooming stage where maximum morphological growth is achieved. Quantitative morphological data such as plant height (cm), number of internodes, length of internode (cm), length of inflorescence, number of inflorescence, inflorescence weight, days to 10% flowering, petiole length (cm), leaf length (cm), leaf width (cm), fresh leaf weight per plant and flowering stem length (cm) were collected.

Data analysis: Estimation of variance component and association of characters analyzed for quantitative traits was performed using the package "MASS" (version 7.3-61) (Venables and Ripley, 2002)[17]. Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane[18]. Categorization of PCV and GCV was based on the ranges of variation as reported by Burton and Devane[18]. Heritability in a broad sense was estimated as per the formulae suggested by Allard[19]. Genetic advance was estimated as per the formula proposed by Robinson *et al.*[20]. The ranges of h 2 b and GAM were categorized as suggested by Johnson *et al.*[21].

Estimation of variance components: Genotypic and phenotypic coefficients of variability were calculated following[18].

Genotypic variance:

$$\sigma^2 g = \frac{MSt - MSe}{r}$$

Where:

MSt = Mean sum of squares for genotypic characteristic
MSe = Mean sum of squares for genotyping error
r = Number of replications

Table 1: Accession code, region and source of sweet basil accessions used for the study

No.	Accession code	Region	Source	Latitude (°)	Longitude (°)	Altitude (m)	Origin
1	OB001	Tigray	EBI	14.092210N	38.633967E	2317	Ethiopia
2	OB002	Tigray	EBI	14.131408N	38.771450E	2017	Ethiopia
3	OB003	Tigray	EBI	14.165868N	38.900548E	2108	Ethiopia
4	OB004	Tigray	EBI	14.282391N	38.075276E	2172	Ethiopia
5	OB005	Tigray	EBI	14.276690N	39.462396E	2170	Ethiopia
6	OB006	Oromia	EBI	7.678924N	36.836128E	2198	Ethiopia
7	OB007	Oromia	EBI	7.673607N	36.831364E	2433	Ethiopia
8	OB008	Oromia	EBI	7.672788N	36.822438E	2336	Ethiopia
9	OB009	Oromia	EBI	7.675862N	36.830592E	1835	Ethiopia
10	OB010	Oromia	EBI	7.679945N	36.834111E	1611	Ethiopia
11	OB011	Oromia	EBI	7.679438N	36.834054E	1719	Ethiopia
12	OB012	Oromia	EBI	7.679751N	36.831301E	2107	Ethiopia
13	OB013	Amhara	EBI	10.684177N	37.345815E	1840	Ethiopia
14	OB014	Amhara	EBI	10.404703N	37.029965E	1840	Ethiopia
15	OB015	Amhara	EBI	10.618046N	37.422726E	1940	Ethiopia
16	OB016	Amhara	EBI	10.642327N	37.392513E	2570	Ethiopia
17	OB017	SWE	EBI	7.579963N	36.028147E	1944	Ethiopia
18	OB018	SWE	EBI	7.305727N	36.120158E	1791	Ethiopia
19	OB019	SWE	EBI	7.301587N	36.070719E	1378	Ethiopia
20	OB020	SWE	EBI	7.318825N	37.836348E	2532	Ethiopia
21	OB021	SWE	EBI	7.335819N	36.158994E	1768	Ethiopia
22	OB022	Sidama	EBI	6.799455N	38.435200E	1789	Ethiopia
23	OB023	Oromia	WGARC	8.982323N	37.867920E	1776	Ethiopia
24	OB024	Oromia	WGARC	8.979610N	37.875645E	1764	Ethiopia
25	OB025	Oromia	WGARC	8.976049N	37.881138E	1789	Ethiopia
26	OB026	Oromia	WGARC	8.705492N	37.888570E	1776	Ethiopia
27	OB027	Oromia	WGARC	8.436618N	37.885823E	1731	Ethiopia
28	OB028	Oromia	WGARC	9.033854N	38.355489E	1722	Ethiopia
29	OB029	Oromia	WGARC	9.066403N	38.580709E	1770	Ethiopia
30	OB030	Oromia	WGARC	8.976887N	37.652364E	2411	Ethiopia
31	OB031	Oromia	WGARC	8.995877N	38.124776E	2354	Ethiopia
32	OB032	SNNPR	WGARC	5.782638N	36.506218E	1733	Ethiopia
33	OB033	SNNPR	WGARC	6.091336N	36.462273E	1745	Ethiopia
34	OB034	SNNPR	WGARC	5.413618N	36.684746E	1432	Ethiopia
35	OB035	SNNPR	WGARC	6.109518N	37.759921E	1453	Ethiopia
36	OB036	SNNPR	WGARC	7.408383N	38.058499E	2132	Ethiopia
37	OB037	SNNPR	WGARC	7.309640N	38.120297E	2250	Ethiopia
38	OB038	SNNPR	WGARC	7.344373N	38.125104E	2050	Ethiopia
39	OB039	SNNPR	WGARC	7.272520N	38.067082E	1912	Ethiopia
40	OB040	SNNPR	WGARC	7.320455N	38.070350E	1961	Ethiopia
41	OB041	Oromia	WGARC	9.066403N	38.566976E	2031	Ethiopia
42	OB042	Harari	WGARC	9.322035N	42.114757E	1875	Ethiopia
43	OB043	SNNPR	WGARC	6.851478N	37.755629E	1785	Ethiopia
44	OB044	SNNPR	WGARC	6.848751N	37.759749E	1793	Ethiopia
45	OB045	Oromia	WGARC	8.971461N	37.542501E	2031	Ethiopia
46	OB046	Harari	WGARC	9.319817N	42.115138E	1965	Ethiopia
47	OB047	Norway	Norway	9.422338N	42.037339E	2034	Norway
48	OB048	Israel	Israel	13.782239N	39.515557E	2054	Israel
49	OB049	Harari	WGARC	13.954230N	39.574608E	2363	Ethiopia

Phenotypic variance:

$$\sigma^2p = \sigma^2g+\sigma^2e$$

Where:

σ^2p = Phenotypic variance for each trait of genotype
σ^2g = Genotypic variance for each trait of genotype
σ^2e = Environmental variance among evaluated genotype traits

Phenotypic and genotypic coefficients of variance: The PCV and GCV expressed as percentages were calculated as suggested by Burton and Devane[18]. Meanwhile, PCV and GCV were divided into three categories: Less than 10% (Low), 10 to 20% (Moderate) and more than 20% (High):

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean}} \times 100$$

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Mean}} \times 100$$

Heritability: Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage[19]:

$$\text{Heritability (broad sense)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

It was categorized according to Robinson *et al.*[20] one to three classes: 0-30% (Low), 31-60% (Medium) and more than 60% (High).

Genetic advance: The extent of genetic advance expected by selecting a certain proportion of the superior accession was calculated by using the following formula[20]:

$$\text{Genetic advance (GA)} = k \times \sigma p \times H^2$$

Where:

k = Selection intensity at 5% ($k = 2.06$)
σp = Phenotypic standard deviation
H^2 = Heritability in a broad sense

Genetic advance expressed as percentage over mean (GAM %):

$$\text{GAM (\%)} = \frac{\text{GA}}{\text{Mean}} \times 100$$

Where:

GAM (%) = Genetic advance over
GA = Genetic advance

Meanwhile, GAM was categorized into three classes: Less than 10% (Low), 10-20% (Moderate) and more than 20% (High)[21].

RESULTS AND DISCUSSION

Phenotypic and genotypic variance: The degree and character of phenotypic and genotypic diversity present in the population's agronomic traits determine the success of selection in any crop. Generally, genetic parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are prerequisites for the genetic improvement of crops. The extent of variability present in the accessions was measured in terms of genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (Table 2). Regarding plant height and essential oil yield per plant, the genotypic coefficients of variation varied from 9.56 to 58.25, respectively. The genotypic coefficients of

Table 2: Estimates of variance components, heritability and genetic advance for 12 agro-morphological traits of basil accessions

Characters	GV	PV	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
Plant height (cm)	16.36	23.26	9.56	11.40	70	6.99	16.52
Number of inter node	0.14	0.44	10.07	17.76	32	0.44	11.75
Length of inter node	0.56	1.14	13.68	19.81	47	1.04	19.46
Length of inflorescence	3.16	3.76	15.73	17.16	84	3.36	29.72
Number of inflorescences	1393.53	3037.00	11.40	16.82	45	52.09	15.90
Petiole length	0.16	0.20	27.80	30.88	81	0.74	51.57
leaf length	0.93	1.07	25.81	27.67	86	1.86	49.61
Leaf width	0.13	0.21	16.53	20.57	64	0.60	27.36
Fresh leaf weight per plant	4957.25	6734.90	36.79	42.89	72	12.43	65.01
Inflorescence weight	256.42	1085.47	12.80	26.16	24	16.25	12.90
Days to 10% flowering	24.61	96.69	16.21	32.12	25	5.15	16.85
Essential oil yield	0.08	0.15	58.25	78.25	55	0.45	90.03

GV: Genotypic ($\sigma^2 g$) components of variance, PV: Phenotypic ($\sigma^2 p$) components of variance, PCV: Phenotypic coefficient of variability, GCV: Genotypic coefficient of variability, H^2 (%): Broad-sense heritability, GA: Expected genetic advance and GAM (%): Genetic advance as percent of the mean

variation for plant height and essential oil output per plant ranged from 9.56 to 58.25, respectively. The GCV and PCV values less than 10% are regarded as low, values between 10 and 20% are regarded as medium and values more than 20% are regarded as high, according to Burton and Devane[18]. As a result, for fresh leaf weight per plant, petiole length, leaf length and essential oil output, high GCV and PCV values were observed. Additionally, leaf width, days to 50% flowering, length of inflorescence, length of internode, number of inflorescences and number of internodes showed moderate GCV and PCV values, with the least GCV and PCV values recorded for plant height.

The highest magnitudes of GCV, coupled with the highest value of PCV, indicated the presence of a wide range of genotypic and phenotypic variability, ensuring ample scope for improvement of these traits through selection. This result aligned with previous findings on *Ocimum* species[2,22-25]. In the present study, the values of PCV were relatively higher than GCV for all the characters studied, indicating the role of environmental variance in the total variance. It is pertinent to mention here that the differences between the values of GCV and PCV were minimal, implying the slightest influence of the environment and indicating that genotypes can be improved and selected for these characters[23].

Estimates of heritability in a broad sense: Although it does not provide the entire range of variation that is heritable or not, the genotypic coefficient of variation shows the contribution of genetic variables to the observed phenotypic variability. Consequently, in order to forecast the predicted gain from the selection process, an estimate of heritability is required. Evidence on heritability in broad sense estimates and genetic advance of yield attributing traits and their association helps plant breeders to identify characters for effective selection[26]. The concept of heritability explains whether differences observed among individuals rose as a result of deference in genetic makeup or due to environmental forces. According to Robinson *et al.*[20], heritability values are categorized as low from 0-30%, moderate from 30-60 and 60% and above are high. Considering this benchmark, the heritability estimate of this study is described as follows. In the present study, heritability in a broad sense estimate ranges from 24% for inflorescence weight to leaf length 86%. High heritability in a broad sense was observed for leaf length (86%) followed by length of inflorescence (84%), petiole length (81%), fresh leaf weight per plant (72%), plant height (70%) and leaf width (64%). Higher heritability values for these variables showed that the large additive gene influence would make selection based on phenotypic performance simple and that the environmental factor contributed relatively little to the phenotype. Additionally, high broad-sense heritability estimates have been found in *Ocimum* Specie[2,21-23,25,27,28].

Genetic advance over mean (GAM %): The utility of the information on heritability estimate would be increased when used in combination with genetic advance expressed on a percentage of the mean[29]. According to Johnson *et al.*[21], the value of genetic advancement as a percent of the mean is categorized as low (<10%), moderate (10-20%) and high (>20%). Based on this category, high genetic advance over mean were observed for the traits essential oil yield (90.03%), fresh leaf weight per plant (65.01%), petiole length (51.57%), leaf length (49.61%), length of inflorescence (29.72%) and leaf width (27. 36%). Other traits like the length of inflorescence (19.46%), days to 10% flowering (16.85%), plant height (16.52%), number of inflorescences (15.90%), inflorescence weight (12.90%) and number of inter-node (11.75%) displayed moderate genetic advance over mean. Understanding the sort of gene activity involved in the development of different polygenic features is made easier with the aid of estimations of genetic advancement. Gene action that is additive is indicated by high genetic advance values, while non-additive gene action is shown by low values. A comparable outcome revealed by Smita and Kishori[23] on basil showed high genetic advance over the mean on inflorescence length (86.43%), fresh herb yield per plant (40.79%) and days to maturity (36.01%).

Less environmental influence and more genetic influence were indicated by higher heritability scores. Higher values of relative genetic progress were linked to a wide range of variability and high heritability, as evidenced by the highest values of genotypic and phenotypic covariance. It would also measure the heritability for significant physical features and use the theory that the additive gene effect was more significant. Thus, genetic progress and heritability are important selection factors. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates[30]. Similar, results were reported in some earlier studies including in different species of *Ocimum*. Smita and Kishori[23] reported that *Ocimum* speices have high genetic advance over mean on essential oil yield per plant (89.89%), inflorescence length (86.43%), fresh herb yield per plant (40.79%) and plant height (26.42%). Likewise, Smita and Kishori[23] reported that the genus *Ocimum* has high genetic advance over mean on inflorescence length (94.87%), days to 50% flowering (72.78%) and plant height (71.08%). A similar result was also reported by Gowda *et al.*[2] on plant spread (68.96%), fresh weight of plant (66.61%) plant height (43.25%) and number of primary branches per plant (26.75%).

Correlation coefficient: Every crop development effort requires a thorough grasp of the relationship between crop yield and its associated attributes[31]. Genotypic correlation coefficients for different pairs of characters and yield are presented in (Table 3). Fresh leaf weight per plant was significantly and positively correlated with leaf width (r = 1), plant height (r = 1), leaf length (r = 0.99) and length of inflorescence (r = 0.77). Essential oil yield correlated positively with length of inflorescence (r = 1), plant height (r = 0.86), number of inter-node (r = 0.62), petiole length (r = 0.62), leaf width (r = 0.56), leaf length (r = 0.40) and length of internode (r = 0.32). Therefore, any change in these traits will have a considerable effect on fresh leaf weight per plant and essential oil yield. Essential oil content can be improved through the selection of these yield components. Inflorescence length showed positive and strongly correlated for all traits, plant height (r =1), number of inter-node (r = 1), length of internode (r =1), length of inflorescence (r =1), number of inter-node (r = 1), fresh leaf weight per plant (r = 1), leaf width (r = 0.88), petiole length (r = 0.68) and leaf length (r = 55). This indicated that this trait is important for the selection of a superior genotype. On the other hand, the length of inter showed a negative correlation with inter-node number (r = -0.65) and plant height (r = -0.32). Similarly, the length of inflorescence showed a negative correlation number of internodes (r = -0.75) and the length of internodes (r = -0.66). Similar association was also reported by Yaldiz and Camlica[15].

Path coefficient analysis: Estimates of correlation coefficients show the interrelationship between different characteristics but do not quantify the direct and indirect influence of each component on yield[32]. Path analysis divided correlation coefficients into direct and indirect effects, offering a clearer understanding of the relationship between yield and other attributes. Categorizing traits into direct and indirect effects enhances comprehension of each trait’s contribution to yield. Path coefficient analysis was

Table 3: Genotypic correlation coefficient between 12 morpho-agronomic quantitative characters in 49 basil accessions

Character	PH	NIN	LIN	LI	NI	PL	LL	LW	FLWPP	IW	ND10	EOC
PH	-	-	-	-	-	-	-	-	-	-	-	-
NIN	0.66**	-	-	-	-	-	-	-	-	-	-	-
LIN	-0.32**	-0.65**	-	-	-	-	-	-	-	-	-	-
LI	0.06^{ns}	-0.75**	-0.66**	-	-	-	-	-	-	-	-	-
NI	0.03^{ns}	0.28*	-0.08^{ns}	-0.69**	-	-	-	-	-	-	-	-
PL	0.47**	0.38**	-0.10^{ns}	0.24^{ns}	-0.65**	-	-	-	-	-	-	-
LL	0.34*	-0.59**	0.28*	0.23^{ns}	0.65**	0.80**	-	-	-	-	-	-
LW	0.39**	0.98**	0.11^{ns}	0.03^{ns}	-0.21**	0.65**	0.65**	-	-	-	-	-
FLWPP	1.00**	0.30*	0.42**	0.77**	-0.06^{ns}	1.00^{ns}	0.99**	1.00**	-	-	-	-
IW	1.00**	1.00**	1.00**	1.00**	1.00**	0.68**	0.55**	0.88**	1.00**	-	-	-
ND10	0.88**	0.49**	0.11^{ns}	0.11^{ns}	0.58**	0.51**	0.51**	0.39**	1.00**	0.88**	-	-
EOY	0.86**	0.08^{ns}	0.32**	1.00**	0.62**	0.62**	0.40**	0.56**	0.09^{ns}	0.13^{ns}	0.33*	-

*Significant ($p<0.05$), **Significant ($p<0.01$) and ***Significant ($p<0.001$), PH: Plant height, NIN: Number of inter-node, LIN: Length of internode, LI: Length of inflorescence, NI: Number of inflorescence, PL: Petiole length, LL: Leaf length, LW: Leaf width, FLWPP: Fresh leaf weight per plant, IW: Inflorescence weight, ND10: Number of days to 10% flowering and EOC: Essential oil content

Table 4: Path coefficient analysis showing direct and indirect effect of yield component on essential oil yield in 49 basil accessions

Character	PH	NIN	LIN	LI	NI	PL	LL	LW	FLWPP	EOC
PH	2.1288	0.6648	-0.2239	-2.3484	0.3898	1.5449	0.1386	1.1998	0.2384	0.86
NIN	0.9781	0.5419	-0.0986	-1.0835	0.174	0.6128	0.0533	0.4846	0.0905	0.08
LIN	1.2471	0.3733	-0.1865	-1.3825	0.2616	0.8655	0.0745	0.7511	0.1271	0.32
LI	1.2473	0.3911	-0.1318	1.7806	0.2194	0.9481	-0.0867	0.6789	0.1462	1.00
NI	1.1608	0.3521	-0.1399	-1.2301	-0.342	0.6652	0.0606	0.6292	0.0932	0.62
PL	0.9113	0.2456	-0.0917	-0.0529	0.1317	1.0314	0.0874	0.639	0.1416	0.62
LL	0.9647	0.2521	-0.0931	-1.1358	0.1415	1.0314	-0.0956	0.6799	0.1447	0.40
LW	1.2404	0.3405	-0.1394	-1.3215	0.2185	1.12	0.101	0.9278	0.1544	0.56
FLWPP	0.6588	0.1701	-0.0631	-0.0865	0.6635	0.0574	0.4125	0.4125	-0.1533	0.09

PH: Plant height, NIN: Number of inter-node, LIN: Length of internode, LI: Length of inflorescence, NI: Number of inflorescence, PL: Petiole length, LL: Leaf length, LW: Leaf width, FLWPP: Fresh leaf weight per plant and EOC: Essential oil yield

conducted to evaluate the contributions of various characters to essential oil yield per plant in terms of cause and effect (Table 3). Among the nine considered causal factors, six characters showed a positive direct influence, while the remaining four had a negative direct impact on essential oil yield per hectare (Table 4).

Plant height exhibited the highest positive direct effect (2.1288) on essential oil yield per plant. It also positively influenced the number of internodes, number of inflorescences, petiole length, leaf length, leaf width and fresh leaf weight indirectly. The high positive direct and indirect effects of plant height counterbalanced any negative effects and led to a significantly positive correlation with essential oil yield per hectare ($rg = 0.86$***). Therefore, plant height emerges as a crucial component and selecting directly for this trait would be the most effective means of getting higher essential oil yield for basil. Inflorescence length demonstrated a considerable positive direct effect (1.7806) on essential oil yield per plant. This trait also exhibited a positive and highly significant phenotypic correlation ($rg = 1$***) with essential oil yield. This also detected that selection for this trait should also be considered for getting a higher essential oil yield of bail. Petiole length, number of internodes, leaf width and fresh leaf weight per plant had positive indirect effects, while leaf length had a negative direct effect. Based on the findings of the present investigation it could be enforced that the most desirable genotype of basil possesses higher plant height, long inflorescence, long petiole, many internodes, wider leaves and higher fresh leaf weight.

CONCLUSION

The study analyzed the genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), broad-sense heritability, genetic advance and genetic advance as a percentage of the mean (GAM) for twelve different characteristics to assess the variability of sweet basil accessions. The study reported high GCV and PCV values for essential oil yield, fresh leaf weight, petiole length and leaf length. Leaf width, days to 10% flowering, inflorescence length, internode length and inflorescence weight all showed moderate GCV and PCV. All evaluated variables had high to moderate heritability and high to moderate genetic advance as a percentage of the mean, indicating the possibility of improvement by selection. Correlation coefficient and path coefficient analysis highlighted plant height, length of inflorescence, petiole length and leaf width as key traits for selecting plants with improved basil essential oil yield.

SIGNIFICANCE STATEMENT

The main objective of assessing the genetic variability of basil germplasm is important for the improvement of the basil through future breeding programs. And also, the understanding of the association between the traits used for crop improvement. The result of this study showed that there is high genetic variability and the traits are highly heritable which can be transferred from generation to generation. Traits with high heritability and genetic advancement over mean can be used for future improvement programs of basil.

REFERENCES

1. Bailey, L.H., 1924. Manual of Cultivated Plants. Macmillan Company, London, United Kingdom, Pages: 851.
2. Gowda, M.P., A.V.D. Dorajeerao, M. Madhavi and D.R.S. Suneetha, 2019. A study on genetic variability for yield and its attributes in sweet basil (*Ocimum basilicum* L.). Int. J. Curr. Microbiol. Appl. Sci., 8: 2995-3003.
3. Carović-Stanko, K., Z. Liber, V. Besendorfer, B. Javornik, B. Bohanec, I. Kolak and Z. Satovic, 2010. Genetic relations among basil taxa (*Ocimum* L.) based on molecular markers, nuclear DNA content, and chromosome number. Plant Syst. Evol., 285: 13-22.
4. Siddiqui, B.S., H. Aslam, S.T. Ali, S. Begum and N. Khatoon, 2007. Two new triterpenoids and a steroidal glycoside from the aerial parts of *Ocimum basilicum*. Chem. Pharm. Bull., 55: 516-519.
5. Siddiqui, B.S., H. Aslam, S. Begum and S.T. Ali, 2007. New cinnamic acid esters from *Ocimum basilicum*. Nat. Prod. Res., 21: 736-741.
6. Simon, J.E., M.R. Morales, W.B. Phippen, R.F. Vieira and Z. Hao, 1999. Basil: A Source of Aroma Compounds and a Popular Culinary and Ornamental Herb. In: Perspectives on New Crops and New Uses, Janick, J. (Ed.), ASHS Press, Alexandria, Virginia, pp: 499-505.
7. Devi, C.U., N. Valecha, P.K. Atul and C.R. Pillai, 2001. Antiplasmodial effect of three medicinal plants: A preliminary study. Curr. Sci., 80: 917-919.
8. Ntonga, P.A., N. Baldovini, E. Mouray, L. Mambu, P. Belong and P. Grellier, 2014. Activity of *Ocimum basilicum*, *Ocimum canum*, and *Cymbopogon citratus* essential oils against *Plasmodium falciparum* and mature-stage larvae of *Anopheles funestus* s.s. Parasite, Vol. 21. 10.1051/parasite/2014033.
9. Egata, D.F., W. Geja and B. Mengesha, 2017. Agronomic and bio-chemical variability of Ethiopian sweet basil (*Ocimum basilicum* L.) accessions. Acad. Res. J. Agric. Sci. Res., 5: 489-508.
10. Abewoy, D., 2021. Review on effects of genotypes and harvesting age on herbage and oil production of sweet basil (*Ocimum basilicum* L.). Int. J. Novel Res. Interdiscip. Stud., 8: 1-6.
11. Tadesse, N., M. Chala and B. Degu, 2019. Intercropping of sweet basil (*Ocimum basilicum* L.) with maize (*Zea mays* L.) as supplementary income generation at Wondo Genet Agricultural Research Center, South Ethiopia. Int. J. Res. Stud. Agric. Sci., 5: 37-43.
12. de Masi, L., P. Siviero, C. Esposito, D. Castaldo, F. Siano and B. Laratta, 2006. Assessment of agronomic, chemical and genetic variability in common basil (*Ocimum basilicum* L.). Eur. Food Res. Technol., 223: 273-281.
13. Nikam, M.S., G.C. Shinde, V.R. Awari, M.S. Shinde and N.S. Kute, 2021. Genetic variability, correlation and path analysis studies in Rabi sorghum (*Sorghum bicolour* (L.) Moench) genotypes. Int. J. Curr. Microbiol. Appl. Sci., 10: 185-192.
14. Kumari, P., N. De, A. Kumar and A. Kumari, 2020. Genetic variability, correlation and path coefficient analysis for yield and quality traits in wheat (*Triticum aestivum* L.). Int. J. Curr. Microbiol. Appl. Sci., 9: 826-832.

15. Yaldiz, G. and M. Camlica, 2021. Agro-morphological and phenotypic variability of sweet basil genotypes for breeding purposes. Crop Sci., 61: 621-642.
16. Kassahun, B.M., D.F. Egata, T. Lulseged, W.B. Yosef and S. Tadesse, 2014. Variability in agronomic and chemical characteristics of spearmint (*Mentha spicata* L.) genotypes in Ethiopia. Int. J. Adv. Biol. Biomed. Res., 2: 2704-2711.
17. Venables, W.N. and B.D. Ripley, 2002. Modern Applied Statistics with S. 4th Edn., Springer, New York, ISBN: 978-1-4419-3008-8, Pages: 498.
18. Burton, G.W. and E.H. Devane, 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J., 45: 478-481.
19. Allard, R.W., 1960. Principles of Plant Breeding. Wiley, Hoboken, New Jersey, ISBN: 9780471023159, Pages: 485.
20. Robinson, H.F., R.E. Comstock and P.H. Harvey, 1949. Estimates of heritability and the degree of dominance in corn. Agron. J., 41: 353-359.
21. Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.
22. Marwat, S.K., Fazal-Ur-Rehman, M.S. Khan, S. Ghulam, N. Anwar, G. Mustafa and K. Usman, 2011. Phytochemical constituents and pharmacological activities of sweet basil-*Ocimum basilicum* L. (Lamiaceae). Asian J. Chem., 23: 3773-3782.
23. Smita, S. and R.L. Kishori, 2017. Estimation of genetic variability, heritability and genetic advance for essential oil yield and related traits in genus *Ocimum*. Adv. Crop Sci. Technol., Vol. 6. 10.4172/2329-8863.1000350.
24. Zaki, H.E.M. and K.S.A. Radwan, 2022. Response of potato (*Solanum tuberosum* L.) cultivars to drought stress under *in vitro* and field conditions. Chem. Biol. Technol. Agric., Vol. 9. 10.1186/s40538-021-00266-z.
25. Jambhale, V., V. Awari, A. Aher and A. Patil, 2023. Genetic variability studies in jute (*Corchorus olitorius* L.). Pharma Innovation J., 12: 720-724.
26. Magar, B.T., S. Acharya, B. Gyawali, K. Timilsena, J. Upadhayaya and J. Shrestha, 2021. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon, Vol. 7. 10.1016/j.heliyon.2021.e07939.
27. Singh, S., R.K. Lal, R. Maurya and C.S. Chanotiya, 2018. Genetic diversity and chemotype selection in genus *Ocimum*. J. Appl. Res. Med. Aromat. Plants, 9: 19-25.
28. Regmi, S., B. Poudel, B.R. Ojha, R. Kharel, P. Joshi, S. Khanal and B.P. Kandel, 2021. Estimation of genetic parameters of different wheat genotype traits in Chitwan, Nepal. Int. J. Agron., Vol. 2021. 10.1155/2021/6651325.
29. Deepthi, B., P.S.S. Reddy, A.S. Kumar and A.R. Reddy, 2016. Studies on PCV, GCV, heritability and genetic advance in bottle gourd genotypes for yield and yield components. Plant Arch., 16: 597-601.
30. Shanko, D., M. Andargie and H. Zeleke, 2014. Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp). Res. Plant Biol., 4: 21-26.
31. Aparna and I. Deo, 2021. Correlation and path coefficient analysis for yield and its related traits in rice (*Oryza sativa* L.). Int. J. Chem. Stud., 9: 1757-1760.
32. Hiywotu, A.M., A. Abate and F. Worede, 2023. Correlation and path coefficient analysis of yield and yield components of some Ethiopian faba bean (*Vicia faba* L.) accessions. Acta Agric. Slov., Vol. 119. 10.14720/aas.2023.119.1.2911.