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Family *Neuradaceae* J. G. Agardh in Saudi Arabia

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Morphological characters, seed coat sculpturing (SEM) of seed, leaf, pollen grains and also a key aspects were revisited to revise relationships between dissimilar taxa of the genus *Neurada* in Saudi Arabia. The present revision shows the occurrence of three distinctive varieties (var. *procumbens*, var. *al-eisawii* and var. *stellate*); the last two varieties considered a new registration in Flora of Saudi Arabia.

Key words: Morphological characters, *Neuradaceae*, Saudi Arabia.

INTRODUCTION

Neurada L. is a desert monotypic plant labeled from Aegypto-Arabia. It has a very wide circulation from North Africa, East Mediterranean region, Sahara, Sudan to Indian desert. *Neurada* L. among subfamily *Neuradaceae* of the family *Rosaceae* (Thorne, 1983). Later, Takhtajan (1980), Cronquist (1981) and Dahlgren (1983) divided *Neurada* into two genera (*Neuradopsis* and *Grielum*) which comprised subfamily *Neuradaceae*.

According to Zohary (1966) two varieties *Neurada procumbens* L. var. *procumbens* and var. *stellate* were recognized. *Neurada al-eisawii* was described by Barsotti et al. (2000) as a new species from the Southern desert of Jordan. He described the new species by some morphological characters in the fruit in insertion to the plant habit.

In Egypt *Neuradaceae* is recognized as a monotypic

family (Tackholm, 1956, 1974; Boulos, 1995, 1999; El Hadidi and Fayed, 1994-1995). According to a study carried out by Turki (2007), three distinctive varieties were found from Egyptian *Neuradaceae*.

In Saudi Arabia, *N. procumbens* is comprised in the family *Neuradaceae* as a monotypic genus (Migahed, 1974; Mandaville, 1990; Chaudhary, 1999).

Family *Neuradaceae*

Family *Neuradaceae* is a densely pubescent, prostrate and annual herb. Leaves alternate stipulate, sinuate to pinnately lobed. Flowers are usually solitary, bisexual, 5-merous, perigynous to epigynous, the receptacle discoid and woody in fruit. Sepals are valvate and petals free,

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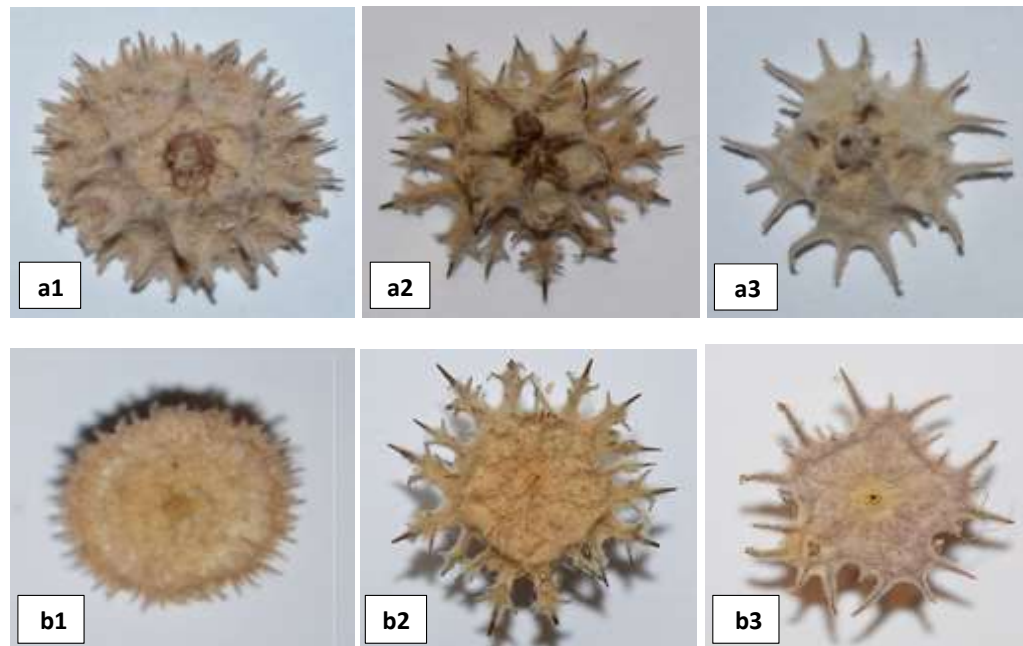


Figure 1. Photographs of fruits of the deliberate taxa (a: abaxial surface, b: adaxial surface): 1) *Neurada procumbens* var. *al-eisawii*; 2) *N. procumbens* var. *procumbens*; 3) *N. procumbens* var. *stellata*. Key: 1. Fruit circular in adaxial surface; var. *procumbens*; 1. Fruit pentagonal in adaxial surface; 2, Fruit having branched spine; var *al-eisawii*; 2, Fruit having unbranched spine; var. *stellata*.

and pentamerous. It has ten free stamens, and gynaecium of 3-10 carpels immersed in the receptacle. Fruits are discoid, woody, spiny with winged bound formed from the enlargement of sepals in fruit, the seeds develop inside the stiff discoid pericarp, the radicles and the plumules perforate the pericarp and grow down and up correspondingly and the old spiny hypanthium often continue as a collar curved the base of the new plants. Furthermore, *Neurada* seeds are likely heteromorphic, with both spinose and spineless sides, which involve the vertical scattering of seeds and diaspores, and the exact site in which they lie in the soil (Hegazy et al., 2014).

This family is symbolized by its connate carpels inside the calyx tube.

Neurada are wide-ranging in distribution in Saudi Arabia, it is found in all sandy soil of the Kingdom.

For all the field excursions during the spring of consecutive years 2014 -2015, *Neurada* samples were found which clearly differ from *N. procumbens* in pattern and structures of fruit (Figure 1).

MATERIALS AND METHODS

This work was done on fresh plant material collected from the natural habitations in Saudi Arabia (Al-Oassim, Al Kharj, (NJw); Nafud, (NF) and Nuairiya, Dammam and Dahran (E), and kept in

College of Science of Herbarium, Imam Abdulrahman Bin Faisal University.

Morphologically, fruits and leaf characters were examined on fresh material. Photographs was taken for SEM on leaf, and seed and pollens grains were examined from fresh resources by escalating them on stubs and covered with a tinny coating of gold using Fei, Inspect S50, Czech Republic SEM at the electron microscopic unit, Institute For Research And Medical Consultation (IRMC). Terms of pollen conferring to El-Ghazaly (1991).

RESULTS

N. procumbens L. var. *procumbens*

Annual herb 15-40 cm, densely grey-tomentose; stem prostrate; leaves 0.5-3.1 x 0.3-1.5 cm, oblong-ovate, sinuate-pinnatifid; sepals 2-2.5 x 1-1.5 mm, ovate-triangular, acute; petals 1 x 1 mm, white, cream or pinkish; fruit 1-2.3 mm diam. With 2-8 mm spines. Figure 1. (1 a, b).

N. procumbens var. *al-eisawii* (Barsotti, Borzatti & Garbari) Turki, comb. nova

Syn.: *Neurada al-eisawii* Barsotti, Borzatti & Garbari,

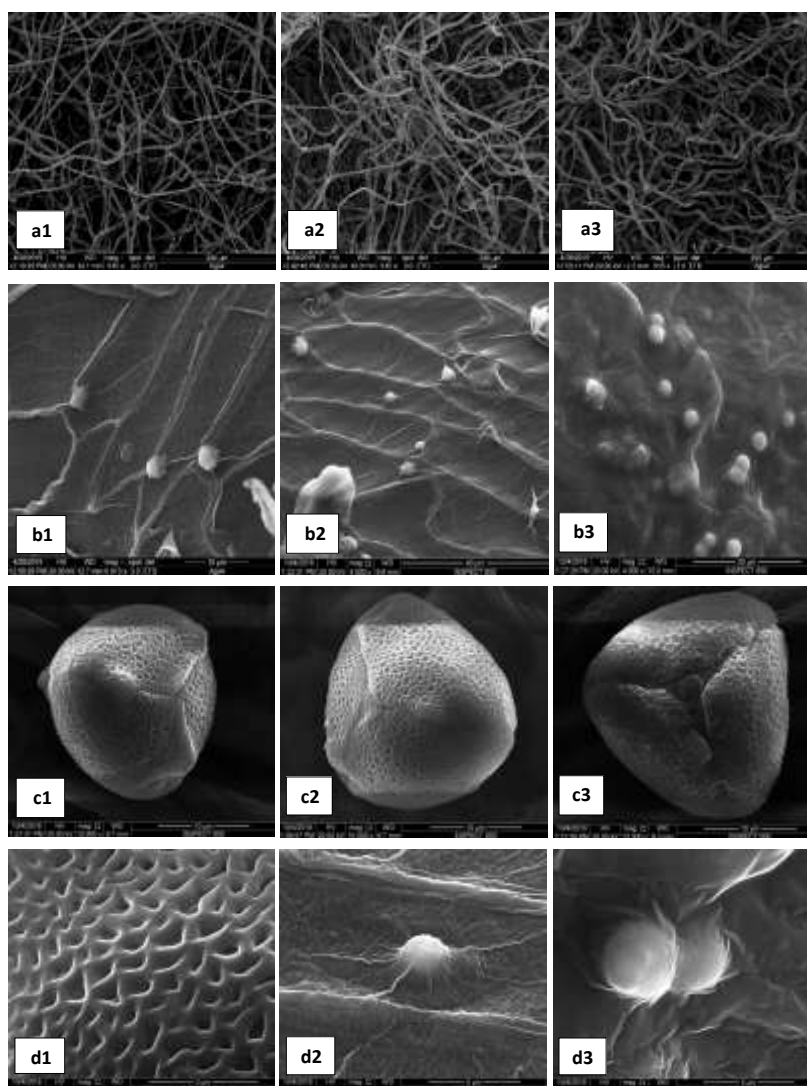


Figure 2. SEM micrographs of leaf hair (a), sculpture of seed (b), pollen grains (c) and type of granules (d) of the studied taxa (1, *Neurada procumbens* var. *procumbens*; 2: *N. procumbens* var. *al-eisawii*; 3: *N. procumbens* var. *stellata*).

Bot. Chron. 13: 113 (2000) Holotypus: Giabal El Guzman, Barsotti 368.4.98.1 (PI).

Leaves: greenish white; 1.7-2.2 cm long; 1.0-1.9 cm wide; petiole 0.9-1.2 cm; flowers with white petals; fruit with external obvious branched spines (Figure 1, 2a, b).

***N. procumbens* var. *stellata* M. & D. Zohary in Zohary & Angelis, de, Palest. J. Bot. Jerusalem, ser. 5,: 249 (1952)**

Leaves: greenish white; 1.9-2.4 cm long, 1.0-1.3 cm wide; petiole 1.0 -1.4 cm; flowers with white petals; fruit boundaries intensely 5- lobed; each lobe with 3 spines, (unbranched spine) (Figure 1, a3, b3).

Morphological feature

The following key is suggested for delimiting the taxa studied on the basis of morphological characters of fruits.

Leaf hair: leaf of all studied taxa was covered with densely unicellular branched hair (Figure 2a1, a2 and a3).

Seed coat sculpturing

The seed coat sculpturing (SEM) of the studied taxa was investigated. The spermoderm patterns were reticulate with granules (Figure 2b1, b2, b3, d2 and d3).

Pollen grains

In polar view, the pollen grain of the revised taxa are tricolpate, triangular, isopolar, exine microreticulate, with asymmetrical carinate profile; lumina subcircular polygonal and Homobrochate (Figure 2 (c1, c2, c3 and d1)).

DISCUSSION

The morphological features of the taxa *N. procumbens* indicate diversity. In the field, they can be differentiated by stem pattern, plant stature, extent of leaves and fruit type. Borzatti De Loewenstern and Garbari (2002) stated no noteworthy changes in the karyotype morphology of *N. procumbens* var. *stellata* and *N. al-eisawii*. Turki (2007) revealed the presence of three distinct varieties on Egyptian specimens depending on fruit characters and stated that anatomical and pollen types seem to be irrelevant. The specimens collected from Saudi Arabia almost close by in the dimensions of the leaves and pedicels extent from that designated by Turki from Egypt. Seed cote of *N. procumbens* var. *procumbens* and var. *al-eisawii* have the same sculpture and also the same kind and density of granules (solitary granules) while var. *stellata* carries out a densely two types of granules, (single and double granules). Pollen types appear to be irrelevant in typifying the deliberate taxa.

Consequently, fitting to identify *Neurada al-eisawii* as a variety under *N. procumbens* instead of a distinct species is suggested. Therefore, the three deliberate Saudi Arabian taxa may be deliberated as three dissimilar varieties of *N. procumbens*.

This result agrees with the investigation by Turki (2007) and contradicts that by Barsotti et al. (2000) of *Neurada al-eisawii* as a new species.

N. procumbens var. *al-eisawii* and var. *stellata* are considered new registration in Flora of Saudi Arabia.

ACKNOWLEDGMENTS

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CONFLICT OF INTERESTS

The author has not declared any conflict of interests.

REFERENCES

- Barsotti G, Borzatti de Loewenstern A, Garbari F (2000). *Neurada al-eisawii* (Neuradaceae), a new species from the southern desert of Jordan. *Botanika Chronika* 13:111-115.
- Borzatti de Loewenstern A, Garbari F (2002). Karyological aspects of the genus *Neurada* (Neuradaceae J. G. Agardh). – *Caryologia* 55(4):361-365.
- Boulos L (1995). *Flora of Egypt Checklist*. Al Hadara Publishing, Cairo; First edition.
- Boulos L (1999). *Flora of Egypt, Vol 1. (Azollaceae-Oxalidaceae)*. – Cairo. Available at: <https://doi.org/10.1111/j.1756-1051.1999.tb01119.x>
- Cronquist A (1981). *An Evolution and classification of flowering plants*. Second edition. The New York Botanical garden, New York, USA. Available at: http://www.nybgpress.org/Content/Site185/FilesSamples/180865GeneralBo_00000103182.pdf
- Chaudhary SA (1999). *Flora of the Kingdom of Saudi Arabia*. (vol. 1) Ministry of Agriculture and Water. National Agriculture and Water Research Center Kingdom of Saudi Arabia, Riyadh.
- Dahlgren RM (1983). General aspects of angiosperm evolution and macrosystematics. *Nordic Journal of Botany* 3:119-149.
- El-Ghazaly GA (1991). *Pollen flora of Qatar*. Scientific and applied research center, Doha: Qatar University.
- El Hadidi MN, Fayed AA (1994-95). *Materials for Excursion Flora of Egypt*. *Taekholmia* 15:57.
- Hegazy AK, Alatar AA, Khan MA, Lovett-Doust J (2014). Interaction Between “Safe Sites” and “Safe Sides” for Germination of *Neurada procumbens* (Neuradaceae) in the Middle East. *Folia Geobotanica*. 49. 10.1007/s12224-013-9187-8.
- Mandaville JP (1990). *Flora of eastern Saudi Arabia*. London: Kegan Paul International jointly with the National Commission for Wildlife Conservation and Development, Riyadh. 130-155.
- Tackholm V (1956). *Students, Flora of Egypt*. Cairo University. p. 649.
- Tackholm V (1974). *Students, Flora of Egypt, ed. 2*. Cairo University, p. 888.
- Takhtajan AL (1980). Outline of the classification of flowering plants (*Magnoliophyta*). *Botanical Review* 46(3):225-359.
- Thorne RF (1983). Proposed new realignments in the angiosperms. *Nordic Journal of Botany* 3:85-117.
- Turki ZA (2007). *Neuradaceae* J.G. Agardh in Egypt. *Flora Mediterranea* 17:137-142.
- Zohary M (1966). *Flora of Palestine*. Israel Academy of Sciences and Humanities, Jerusalem 346 p.

Full Length Research Paper

Genetic variability studies of some quantitative traits in cowpea (*Vigna unguiculata* L. [Walp]) under water stress

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This research was conducted to study genetic variability of some quantitative traits in varieties of cowpea (*Vigna unguiculata* L. [Walp.]) under water stressed in Zaria Sudan Savannah, Nigeria. Seven varieties of cowpea (Sampea 1, Sampea 2, IAR1074, Sampea 7, Sampea 8, Sampea 10 and Sampea 12) collected from Institute for Agricultural Research, Samaru, Zaria, were screened for tolerance to water stress. The seeds were sown in poly bags containing sandy-loam arranged in Completely Randomized Design with three replications for quantitative traits evaluation. The result obtained revealed highly significant difference ($P \leq 0.01$) in the effects of water stress on the number of wilted and dead plants at 40 days after sowing. However, variety sampea-10 has the highest mean performance in terms of number of wilted plants at 34, while sampea 2 and IAR 1074 have the lowest mean performance. However, sampea 7 was found to have the highest mean performance for the number of wilted plants at 40 days and sampea 2 is the lowest. The result for quantitative traits study indicated highly significant difference ($P \leq 0.01$) in the plant height, number of days to 50% flowering, number of days to maturity, number of pods per plant, pod length, number of seeds per plant and 100 seed weight, and significant ($P \leq 0.05$) at seedling height and number of branches per plant. Similarly, IAR1074 was found to have high performance in terms of most of the quantitative traits under study. However, sampea 8 has the highest mean performance at nutritional level. It was therefore concluded that, all the seven cowpea genotypes were water stress tolerant and produced considerable yield that contained significant nutrients. It was recommended that IAR1074 should be grown for yield, while sampea 8 should be grown for protein supplements.

Key words: Quantitative traits, water stress, genetic variability, carbohydrate, protein, cowpea.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp) belongs to the Leguminosea family. It is widely grown and distributed in many tropical regions of the world. Cowpea cultivation in West Africa is the most common in the dried part of the

sub-region. Nigeria is one of the leading cowpea producers in the sub-region. It provides most of the needed source of protein for people. It also accounts for about 60% of the daily dietary poultry intake of most

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Nigerians. In addition, the cowpea plant enriches the soil through nitrogen fixation process (the major food legume cultivated in Nigeria is Cowpea (*V. unguiculata* L. Walp) (Nielson et al., 1997).

One of the major challenges facing the world is food security as well as how to address the phenomenon of malnutrition among the teeming and ever rising population of poor rural dwellers of the third world countries. In the wake of climate changes, fluctuating global economy and intensification of low-input agricultural production has led to a rapid increase in soil degradation and nutrient depletion in many parts of sub-Saharan Africa. This has constituted serious threats to food production and food security, there is need to promote crops that could fix into global nutrient requirements and one of such crop is cowpea.

Production of cowpea has been found with a number of problems or constraints, which includes the biotic and abiotic constraints that resulted into low grain and fodder yield. In most West African countries, development and release of improved varieties that adapts well and yield better have been slow in getting to the farmers (FAO, 2000). Development of cultivars with early maturity, acceptable grain quality, resistance to diseases and pests is necessary to overcome the ever-growing food shortage (Ehlers and Hall, 1997). Hence, there is need to generate more information on variability among the existing germplasm and cultivars and also broadening the gene pool of the crop for selection and development of more improved varieties not just in yield but with better nutritional values.

As a legume grain, cowpea is an important source of human dietary protein and calories. The grains contain about 25% proteins and 64% carbohydrate, while young leaves, pods and peas contain vitamins and minerals (Nielson et al., 1997). Its high protein and lysine content makes it natural supplement for high carbohydrates tubers and cereals, which are common staple foods among the sub-Saharan people. Malnutrition among the children in developing countries is mainly due to the consumption of cereal-based meal, which is bulky, high energy and anti-nutrients. Therefore, cowpea provides protein constituent of the daily diet of the economically depressed rural class, due to its potential to reduce malnutrition; it is sometimes being referred to as "poor man's meat" (Geissler et al., 1998). Its utilization is majorly as grain crop, vegetables and fodder for livestock (Hall et al., 2003).

The study of variability and diversity in accessions of cultivated crops could provide vital information for the establishment of breeding programme, especially when intraspecific hybridization is necessary for the incorporation of new features or for mapping purposes. Assessment of genetic diversity and variability in cowpea would enhance development of cultivars for adaptation to specific production constrain. Therefore, sufficient information is necessary on genetic variability among the

available germplasm to formulate and accelerate breeding programme. Previous workers have reported on genetic variability among different varieties of cowpea (Omoigui et al., 2006; Nwosu et al., 2013) and crop nutritional value (Henshaw, 2008; Mamiro et al., 2011; Odedeji and Oyeleke, 2011). However, only few of these reports compared nutrient composition of different varieties and in particular the early maturing varieties.

In order to achieve a successful breeding programme to improve the yield potentials of the crop, the quality of the grains in term of its nutritional values should also be a pivot concern. This enables the breeder to operate selection efficiently and subsequently developed appropriate breeding strategies to solve the problems of poor yield as well as improve the nutritive quality of the crop. Effort was made to examine the genetic differences among the studied cultivars to group them into relatively homogenous groups of baseline parents for breeding purposes.

Despite the increasing importance of cowpea in the diet of many Nigerians, yield per hectare remains low. Although yields of 2500 kg/ha are achievable, several constraints have kept farmers' yields constantly low at levels between 350 and 700 kg/ha. To overcome the yield barrier, a new strategy to improve the genetic potential of cowpea plants by introducing new genes is required. For this to be achievable, genotypes with a potential for better quality traits are needed as parent stocks to develop improved varieties (Adeigbe et al., 2011). The aim of the research is to assess the genetic variability among screened water stressed tolerant varieties of cowpea for improved quantitative traits in northern Guinea savannah zone of Nigeria.

MATERIALS AND METHODS

Study area

The experiment was conducted under screen house in the Department of Biological Sciences, Ahmadu Bello University, Zaria (lat: 11°, 21¹N and long: 7°, 37¹ E, Alt: 550 to 700 m above sea level).

Sources of materials

The experimental seeds were obtained from the cowpea unit of Institute of Agricultural Research (IAR), Samaru, Ahmadu Bello University, Zaria.

Screening for water stress

The screening for water stress was conducted using box screening method in a completely randomized design (CRD) with three replications in a screen house. The box was half-filled with a soil in a ratio of 1:1 of top soil and humus; it was watered to sufficiently moist it for planting and two seeds were sown per hole. The watering continued regularly up to three weeks after sowing where a complete withdrawal of the water was applied. The data collected at 28 days after sowing, 34 days after sowing and 40 days after

Table 1. Mean square for water stress tolerance screening of seven different cowpea genotype.

Sources of variation	Df	Number of wilted plants	Number of dead plants	Number of wilted	Number of dead plants	Number of wilted plants	Number of dead plants	Number of healthy plants
Variety	6	0.00 ^{ns}	0.00 ^{ns}	0.21 ^{ns}	0.02 ^{ns}	1.22*	0.21 ^{ns}	1.52 ^{ns}
Water level	1	0.00 ^{ns}	0.00 ^{ns}	6.72*	0.00 ^{ns}	10.89**	6.72**	72.00**
Variety and water level	2	0.00 ^{ns}	0.00 ^{ns}	0.06 ^{ns}	0.00 ^{ns}	0.06 ^{ns}	0.06 ^{ns}	0.17 ^{ns}
Error	32	0.00	0.00	0.92	0.03	1.09	0.92	7.34

ns= No significant difference; *Significantly different (P=0.05), **Highly significant difference (P=0.01).

sowing were for the number of wilted plants, number of dead plants and the number of healthy plants, respectively.

Pot experiment for growth and yield

Polythene bags were used in place of pot and were filled with soil in a ratio of 1:1 humus and top soil. They were watered sufficiently to moist it for planting, and were arranged in completely randomized design with three replications. Four seeds were planted in each polythene pot and watered regularly until harvest. The data collected include germination percent, seedling height (cm), plant height at maturity (cm), number of branches per plant, number of leaves per plant, leaf area, number of days to fifty percent flowering, number of days to maturity, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, and dry weight of the plant.

Proximate analysis

Proximate analysis was performed to determine the relationship between Protein, Arsh, Crude Fibre, Fat and Moisture contents by extraction and using standard method by AOAC (2000). Carbohydrate content was determined using the formula:

$$\% \text{ Carbohydrate} = 100 - (\% \text{ Moisture} + \% \text{ Ash} + \% \text{ Crude protein} + \% \text{ Crude fat} + \% \text{ Crude fibre})$$

Data analysis

All the data collected were subjected to analysis of variance (ANOVA) with Duncan's Multiple Range Test (DMRT) used to separate the means. All tests of relationships were done using Pearson's Product Moment Correlation Co-efficient.

RESULTS

The result for the ANOVA obtained due to the exposure of seven different cowpea varieties to water stress is shown in Table 1. The result indicated a highly significant difference ($P \leq 0.01$) in the effects of water stress on the number of wilted and dead plants at 40 days after sowing (DAS). Similar result was obtained in the number of healthy plants. However, a significant difference ($P \leq 0.05$) was found in the number of wilted plants at 34 DAS. While no significant difference was found in the effects of

water stress from 28 DAS to 34 DAS in the remaining parameters. Furthermore, no significant difference was found in the interaction of the varieties to water level.

However, Table 2 shows the results of the mean performance of the seven cowpea varieties to water stress. The result shows that sampea 10 has the highest mean performance in terms of number of wilted plants at 34 DAS, while sampea 2 and IAR 1074 have the lowest mean performance. However, sampea 7 was found to have the highest mean performance for the number of wilted plants at 40 DAS and sampea 2 is lowest. Meanwhile the number of dead plants at 40 DAS, sampea 7 and sampea 10 have the highest mean performance, while the lowest was found in sampea 2, 12 and IAR1074. Nevertheless, in the number of healthy plants sampea 1 shows high mean performance, while sampea 7 has the lowest mean performance. At 34 DAS, sampea 12 was found to be the highest.

The combine ANOVA of the mean performance for seven cowpea genotypes to water stress is shown in Table 3. High mean performance was found in the water stressed plants for the number of wilted plants at 40 DAS, while the lowest mean performance was found in the number of wilted plants at 34 DAS. A high mean performance was found for the number of dead plants at 40 DAS. However, in the unstressed plants, the high mean performance was found in the number of wilted plants at 40 DAS and the lowest was obtained in the number of dead plants at 34 DAS. Similarly, a high mean performance was found in the water stressed healthy plants, while the lowest was found in the unstressed healthy plants.

Table 4 shows the results for the relationships between the seven cowpea varieties to water stress, which indicated that positive relationship ($P \leq 0.05$) exists between the number of wilted plants at 40 DAS and number of wilted plants at 34 DAS. Also, positive relationships exist between the number of dead plants at 40 DAS and the number of wilted plants at 40 DAS. Nevertheless, negative relationship was found in the number of healthy plants and number of wilted plants at 34 DAS; also, between number of wilted plants at 40 DAS and number of dead plants at 40 DAS. However, no significant difference was found in the others.

Table 2. Mean performance of seven cowpea varieties under water stress.

Variety	No. of wilted plants (28DAS)	No. of dead plants (28 DAS)	No. of Wilted plants (34 DAS)	No. of dead plants (34 DAS)	No. of wilted plants (40 DAS)	No. of dead plants (40 DAS)	No. of healthy plants
Sampea1	0.00 ^a	0.00 ^a	0.50 ^b	0.00 ^a	0.83 ^d	0.50 ^d	10.17 ^a
Sampea2	0.00 ^a	0.00 ^a	0.67 ^c	0.00 ^a	0.67	0.67 ^c	10.00 ^a
IAR1074	0.00 ^a	0.00 ^a	0.67 ^c	0.00 ^a	0.83 ^d	0.67 ^c	9.83 ^b
Sampea7	0.00 ^a	0.00 ^a	1.00 ^a	0.00 ^a	1.67 ^a	1.00 ^a	8.83 ^d
Sampea8	0.00 ^a	0.00 ^a	0.83 ^b	0.00 ^a	1.00 ^b	0.83 ^b	9.33 ^c
Sampea10	0.00 ^a	0.00 ^a	1.00 ^a	0.00 ^a	1.00 ^b	1.00 ^a	9.00 ^c
Sampea12	0.00 ^a	0.00 ^a	0.67 ^c	0.17 ^a	1.00 ^b	0.67 ^c	9.50 ^b
Means	0.00	0.00	0.76	0.02	0.93	0.76	9.52
SE(+)	0.00	0.00	0.36	0.06	0.39	0.36	1.02

a=Higher mean; b, c, d=lowest mean.

Table 3. Mean performance (Combine ANOVA) of the seven cowpea genotype.

Water level	NWP 28 DAS	NDP28 DAS	NWP 34 DAS	NDP34 DAS	NWP 40 DAS	NDP 40 DAS	NHP
Water stressed	0.00 ^a	0.00 ^a	1.22 ^a	0.03 ^a	1.56 ^a	1.22 ^a	9.94 ^a
Control	0.00 ^a	0.00 ^a	0.64 ^a	0.00 ^a	0.76 ^b	0.64 ^b	8.00 ^b
Means	0.00	0.00	0.93	0.02	1.94	0.93	8.97
S E (+)	0.00	0.00	0.89	0.00	0.41	0.71	0.89

a= Highest mean; b= lowest mean.

Table 4. Relationships among the wilted and dead plants at different time of water stress of the seven cowpea.

Genotype	No. of wilted plants (28DAS)	No. of dead plants (28 DAS)	No. of Wilted plants (34 DAS)	No. of dead plants (34 DAS)	No. of wilted plants (40 DAS)	No. of dead plants (40 DAS)	No. of healthy plants
NWP 28	1.00						
NDP 28	0.00	1.00					
NWP 34	0.00	0.00	1.00				
NDP 34	0.00	0.00	0.20 ^{ns}	1.00			
NWP 40	0.00	0.00	0.65 [*]	0.31 ^{ns}	1.00		
NDP 40	0.00	0.00	1.00 ^{ns}	0.20 ^{ns}	0.65 [*]	1.00	
NHP	0.00	0.00	-0.95 [*]	-0.31 ^{ns}	-0.85 [*]	-0.95 [*]	1.00

ns= No significant difference; *Significantly different ($P \leq 0.05$), **Highly significant difference ($P \leq 0.01$).

Table 5 shows the results of ANOVA for genetic variability for growth and yield of seven cowpea varieties. The result shows that a highly significant difference ($P \leq 0.01$) was found in the plant height, number of days to 50% flowering, number of days to maturity, number of pods per plant, pod length, number of seeds per plant and 100 seed weight, while significant difference ($P \leq 0.05$) was found in seedling height and number of branches per plant. No significant difference was found

on the other growth and yield parameters.

The mean performance of seven cowpea varieties is shown in Table 6, which shows that IAR1074 and sampea 2 has the highest mean performance in terms of germination percentage and the lowest mean performance was found in sampea 8. Similarly, IAR1074 was found to have the highest mean performance in the seedling height and least was found in sampea 10. However, sampea 1 has the higher mean performance in

Table 5. Mean square for the genetic variability studies among seven cowpea variety.

Source of variation	Df	G7	SH (cm)	PH (cm)	B/p	L/p	LA	D 50% F	DM	P/ p	PI (cm)	S/p	SW	DW (g)
Variety	6	1.49 ^{ns}	13.43*	749.34**	2.74*	27.11 ^{ns}	154.59 ^{ns}	3679.56**	6727.89**	15.75**	82.15**	47.60**	144.96**	52.44**
Error	14	2.00	-	-	0.95	14.57	89.38	3.09	2.24	1.95	1.63	0.95	0.19	1.24

ns= No significant difference; *Significantly different ($P \leq 0.05$), **Highly significant difference ($P \leq 0.01$).

Table 6. Mean performance of the seven cowpea genotypes for growth and yield.

Variety	G %	SH (cm)	PH (cm)	B/P	L/P	LA	D50% F	DM	P/P	P L	S/p	100 SW	DW
Sampea1	11.33 ^a	32.40 ^{bc}	91.00 ^a	6.00 ^{bc}	19.33 ^a	34.47 ^b	0.00 ^d	0.00 ^e	0.00 ^c	0.00 ^d	0.00 ^e	0.00 ^f	16.90 ^a
Sampea2	11.00 ^a	36.23 ^{ba}	67.33 ^b	5.33 ^{bc}	12.33 ^{ba}	44.50 ^{ba}	94.33 ^a	125.67 ^b	5.00 ^{ba}	12.83 ^{ba}	10.00 ^{bc}	15.23 ^e	10.33 ^b
IAR1074	11.67 ^a	36.63 ^a	71.67 ^b	5.67 ^{bc}	16.67 ^{ba}	47.63 ^{ba}	96.67 ^a	132.00 ^a	5.67 ^{ba}	14.00 ^{ba}	9.33 ^{bcd}	19.30 ^b	14.87 ^a
Sampea7	11.33 ^a	36.17 ^{ba}	70.67 ^b	4.67 ^c	11.33 ^b	54.00 ^a	96.33 ^a	128.33 ^b	7.33 ^a	13.67 ^{ba}	10.67 ^{ba}	16.23 ^d	10.73 ^b
Sampea8	09.67 ^a	32.30 ^{bc}	49.00 ^{cd}	7.00 ^{ba}	17.00 ^{ba}	39.57 ^{ba}	91.00 ^b	126.33 ^b	5.67 ^{ba}	12.33 ^b	8.67 ^{cd}	16.93 ^{dc}	15.83 ^a
Sampea10	10.67 ^a	31.73 ^c	43.67 ^d	7.33 ^a	12.33 ^{ba}	39.57 ^{ba}	86.67 ^b	121.67 ^c	4.33 ^b	15.17 ^a	12.33 ^a	17.10 ^c	6.57 ^c
Sampea12	11.67 ^a	34.43 ^{bc}	59.50 ^{bc}	5.33 ^{bc}	13.67 ^{ba}	52.23 ^{ba}	73.33 ^c	105.67 ^d	5.33 ^{ba}	8.83 ^c	7.67 ^d	21.07 ^a	7.17 ^c
Mean	11.05	34.27	64.69	5.90	14.67	44.57	77.33	105.67	4.76	10.98	8.38	15.12	11.76
S E (+)	0.51	1.03	6.28	0.46	1.62	3.94	12.55	1.69	0.93	1.92	1.46	2.49	1.54

a = High mean; b a, b, b c, c, b c d, c d, and d = lowest mean.

terms of plant height and sampea 10 is having the lowest mean performance. Meanwhile the highest mean performance for the number of branches per plant was obtained in sampea 10, while the least was found in sampea 7. In terms of the number of leaves per plant, the highest mean was found in sampea 1, while sampea 7 has the lowest. The highest mean performance in the leaf area was found in the sampea 7 while sampea1 has the lowest mean performance. However, IAR1074 has the highest mean in the number of days to 50% flowering and the number of days to maturity, while sampea 7 has the higher mean performance in terms of number of pod per plant and in the pod length, the high mean was found in sampea 10 similarly in the number of seeds per plants. However, sampea 12 was found to have

the highest mean performance in 100 seed weight and sampea 1 is found to be the lowest in all yield parameters. Meanwhile, sampea 1 was found to be the highest interms of dry weight and sampea 10 was having the lowest mean performance.

On the other hand, Table 7 shows the relationships between different parameters of the seven cowpea varieties. The result indicated a positive relationship between the number of days to 50% flowering and the number of days to maturity. Similar relationship exists between the number of days to maturity and number of pod per plant; between the number of days to 50% flowering and number of pod per plant; pod length and number of days to 50% flowering; seed per pod and number of days to 50% flowering; seed per pod and number of days to maturity; pod per

plant and pod length. Similarly, the result indicated that positive relationship exists between 100 seed weight and number of days to flowering, days to maturity, pod per plant, pod length and seed per pod. A positive relationship was also found between leaf area and seedling height, pod per plant and 100 seed weight. While no relationship was found on germination percentage and other parameters. Similarly, no relationship was found between leaf area and days to 50% flowering days to maturity. However, negative relationship was found between plant and other parameters; while no relationship was in the remaining parameters.

Result for the ANOVA of proximate analysis for seven cowpea genotypes is shown in Table 8. The result indicated a highly significant difference

Table 7. Relationship between the growth and yield parameters of the seven cowpea genotypes under study.

Correlation	Germ%	SDH	PLH	BRP	LVP	LFA	DFL	DMT	PPP	SPP	PL	SW	DW
Germ%	1.00												
SDH	0.18	1.00											
PLH	0.26	0.15	1.00										
BRPP	-0.42	-0.16	-0.51*	1.00									
LVPP	-0.27	-0.16	-0.45*	0.21	1.00								
LFA	0.21	0.53*	-0.13	-0.32	-0.44	1.00							
DFL	-0.09	0.31	-0.55*	-0.06	-0.45*	0.37	1.00						
DMT	-0.09	0.31	-0.61**	-0.03	-0.44	0.37	0.99**	1.00					
PPP	-0.18	0.40	-0.35	-0.24	-0.35	0.51*	0.88**	0.81**	1.00				
PL	-0.16	0.23	-0.60**	0.05	-0.40	0.21	0.95**	0.94**	0.69**	1.00			
SPP	-0.15	0.17	-0.66**	0.08	-0.51*	0.32	0.92**	0.92**	0.70**	0.94**	1.00		
100SW	0.01	0.27	-0.63**	-0.06	-0.39	0.44	0.89**	0.91**	0.76**	0.80**	0.81**	1.00	
DW	-0.14	-0.13	0.48*	-0.05	0.51*	-0.27	-0.41	-0.42	-0.33	-0.43	-0.58**	-0.54*	1.00

ns=No relationship; *=Relationship; **= strong relationship.

Table 8. Result for the mean squares of the seven cowpea genotypes.

Sources of variation	Df	Moisture	Ash	Fibre	Fat/oil	Protein	Carbohydrate
Variety	5	2.22 ^{ns}	1.54**	2.10*	0.21 ^{ns}	12.69**	21.70 ^{ns}
Error	12	2.43	0.11	0.83	0.43	3.76	16.94

ns= No significant difference; * =Significant difference ($P \leq 0.05$); **= Highly Significant difference ($P \leq 0.01$).

Table 9. Mean performance of the proximate analysis for the six cowpea genotypes under study.

Variety	Moisture	Ash	Fibre	Fat/oil	Protein	Carbohydrate
Sampea 2	6.67 ^a	2.17 ^b	3.00 ^{ab}	3.33 ^a	23.79 ^{ab}	62.29 ^a
IAR 1074	5.00 ^a	2.35 ^b	2.33 ^b	3.33 ^a	21.05 ^b	65.94 ^a
Sampea 7	6.67 ^a	3.97 ^a	4.00 ^{ab}	3.75 ^a	20.99 ^b	59.38 ^a
Sampea 8	5.83 ^a	2.22 ^a	4.33 ^a	3.32 ^a	26.40 ^a	58.72 ^a
Sampea 10	6.67 ^a	2.20 ^b	3.00 ^{ab}	3.33 ^a	24.10 ^{ab}	59.73 ^a
Sampea 12	7.50 ^a	2.16 ^b	2.33 ^b	2.92 ^a	22.70 ^{ab}	62.25 ^a
Mean	6.39	2.51	3.17	3.33	23.17	61.39
S E (+)	0.63	0.30	0.45	0.25	1.03	1.75

a = Higher mean; ab, b = lowest mean.

($P \leq 0.01$) in the ash and protein content, while a significant difference ($P \leq 0.05$) was observed in the fiber content; whereas no significant difference was found in the remaining parameters. Table 9 shows the result of mean performance for the proximate analysis of seven different cowpea varieties that indicated that sampea 12 has the highest moisture content, while IAR1074 has the lowest. The highest ash content was found in sampea 7 and the lowest was found in sampea 12. In terms of amount of fibre, the highest mean performance was found in sampea 8 while IAR 1074 and sampea 12 has

the least mean performance. However, for fat content, the highest mean was found in sampea 7 and the lowest was found in sampea12. Sampea 8 shows a high mean performance in terms of protein content while sampea 7 has the lowest. However, the carbohydrate content of cowpea varieties was found to have the highest mean performance in IAR1074 and the lowest was sampea 8.

The relationship among the seven cowpea varieties for the proximate analysis is shown in Table 10 which indicated that there is a negative relationship ($P \leq 0.01$) between moisture content and carbohydrate, fibre and

Table 10. Relationship among the nutritional content of cowpea.

Correlation	Moisture	Ash	Fibre	Fat/oil	Protein	Carbohydrate
Moisture	1.00					
Ash	0.09 ^{ns}	1.00				
Fibre	0.20 ^{ns}	0.28 ^{ns}	1.00			
Fat/oil	0.06 ^{ns}	0.39 ^{ns}	0.21 ^{ns}	1.00		
Protein	0.08 ^{ns}	-0.38 ^{ns}	0.24 ^{ns}	-0.11 ^{ns}	1.00	
Carbohydrate	-0.63 ^{**}	-0.24 ^{ns}	-0.58 ^{ns}	-0.21 ^{ns}	-0.58 [*]	1.00

ns = No relationship; * = relationship; ** =strong relationship.

Table 11. Some of the qualitative traits found in the seven cowpea varieties under study.

Variety	Growth habit	Flower color	Seed coat color	Seed shape	Seed texture	Eye color
Sampea1	Spreading	-	-	-	-	-
Sampea2	Spreading	White	Brown	Kidney	Smooth	Brown
IAR1074	Spreading	White	Brown	Kidney	Smooth	Brown
Sampea7	Erect	White	Brown	Rhomboid	Smooth	Brown
Sampea8	Erect	White/Violet	White	Rhomboid	Rough	Black
Sampea10	Erect	White	White	Rhomboid	Rough	Black
Sampea12	Spreading	White	Brown	Kidney	Smooth	Brown

carbohydrate and also between protein and carbohydrate, while there are no relationships among other.

Also from Table 11 it shows some important qualitative traits found in the seven cowpea varieties that include Growth habit, Flower Color, Seed Coat Color, Seed Shape, Seed texture and Eye Color.

DISCUSSION

The screening for water stress tolerance in cowpea is a vital phenomenon that increases the potential of cowpea production in Nigeria especially in areas where drought is rampant. The significant difference and highly significant differences exhibited for number of wilted plants at 34 and 40 days. The number of dead plants at 40 days as well as number of healthy stands would be as an evidence that values of all the growth parameters decreased with the period of growth as the water stress increased. This is in conformity with the findings of Okon (2013). The different (highest and lowest) mean performances obtained in the different varieties under water stress based on the number of wilted, dead and healthy plants at different days interval could be as a result of variation that exist in the rate of decrease of growth parameters among the different varieties (in different fortnight) with respect to corresponding variation in water stresses. It was observed that, under intense water stress conditions, there was a sharp changes in the values obtained. Similar result was reported by Ba et al. (2004) in soya bean seedlings.

High differences in the mean performance were observed in the different cowpea varieties to water stress at different days based on the wilted, dead and healthy plants, with the highest mean performance (8.97) obtained in the number of healthy plants and lowest (0.02) obtained in the number of dead plants at 34 days. This indicates the existence of a high degree of genetic variability in the different cowpea varieties. However, certain factors such as height of the culms, size of the leaves, the distance between the veins and the stomata openings are all affected when the varieties are developing under water stress. This is in line with findings of Zia-ul-haq et al. (2010) who reported that water stress causes changes (significant difference) in the different varieties.

The positive relationships that exist between number of wilted plants at 40 days also between number of dead and wilted plants at 40 days showed that traits might not be independent in their action and are interlinked likely to bring simultaneous change for other characters. They can be effectively used as selection criteria for cowpea yields (varieties) under water stress conditions.

The negative relationships that exist between number of healthy plants and number of wilted plants at 34 days, number of wilted plants conditions can influence genetic interactions among the traits as well as genetic variance in the traits themselves. This is in line with the findings of Coulibaly et al. (2002) who suggested exposure to water stress conditions may induce positive relationships for among the traits and expression of new gene will break

negative correlations. The highly significant difference ($P \leq 0.01$) and significant difference ($P \leq 0.05$) exhibited the characters (parameters) studied indicated the existence of sufficient genetic variability among the selected traits for improve yield in cowpea. While the non-significant difference ($P \leq 0.05$) exhibited for some few characters (parameters) is line with the report of Manggoel et al. (2012) who suggested that traits with such significant difference might be under genetic control rather than environmental influence.

The differences (highest and lowest) in mean performance of different cowpea varieties studies based on their different traits measured could be as a result of durations of the experiment which affects the differential changes that might occur in the morphological features of the varieties of the plants at a given time. The growth habits of different varieties studied also varied which result to differences in the mean performance, with highest mean performance in a particular trait such as maturity and lowest in another trait in a given variety. This observation is in line with the findings of Ekpo et al. (2012) who observed that there is variability in the growth habit of cowpea in different species.

The results from this research are similar to those found by Lobato and Costa (2011) where reduction in leaf relative to water content was reported. The study also recorded reduced vegetative growth due to water stress. This finding agrees with that of Nwofia et al (2012). Nwofia et al. (2012) reported similar results on decrease in growth and yield which can be attributed to the effects water has on the physiology of cowpea. The finding also agrees with that of Samson and Helmut (2007) on cowpea that reduction in leaf area in cowpea varieties (with sampea 1 had the lowest 34.47 cm^2) is a mechanism adapted to avoid higher rate of transpiration and reduced surfaces for radiation due to water deficit. The reduction in number of pods result of increase in with the lowest found in sampea 10, which is (4.33), could be because of increase in reduction of soil moisture, thereby reducing the number of seeds that may contribute to low yield in water, stressed cowpea. This is in line with the findings of who reported reduction in number of pods in different cowpea varieties Abayomi and Abidoye (2009).

The positive relationships that exist between yield traits or parameters could be as a result of the fact that cowpea varieties height studied contributed to yield as it leads to resulting increase in the number of days to maturity, days to flowering, number of pods and other yield traits. The result obtained is in line with the findings of Cursky et.al (2002) who reported that plant height contribute positively to different yield parameters or traits. In addition, yield improvement would be possibly achieved by selecting for the number of pods per plant, since the study revealed that, number of pods per plants increased significantly.

Correlations has used in indirect selection for breeding characters (Diouf, 2011). The highly significant difference ($P \leq 0.01$) and significant difference ($P \leq 0.05$) obtained in the ash, protein content and fibre contents showed that

the range of values were within the recommended values, this range of values fall within the values reported for cowpea Longe (1980). In this study, the ash have 2 to 3%; protein, 20 to 27%; and fiber, 2 to 4%.

The best mean performance of the proximate analysis was found in carbohydrate in all the cowpea varieties (58.72-65.94%), while the least mean performances in all the varieties were found in Ash content (2-4%). The high and low mean performance of the studied varieties may not depend on genetic factor alone, but also on environmental influences. The result obtained is in line with the findings of Nwosu et al. (2013) who worked on the different cowpea varieties and discovered high and low in the mean performance of the proximate analysis contents. However, from the result obtained, high variability was found in the mean performances of the different varieties in terms of their yield traits (ash content, protein, moisture, fibre, fat and carbohydrates). The observed variability was in agreement with the work of Nwosu et al. (2013) and could serve as an important purpose in improving the crop as selected would be effective for population with broad genetic variability as opened by previous workers (Omoigai et al., 2006; Animasaun et al., 2015). The negative relationship that exist shows that moisture content had the highest relationship (0.63) and the least values or relationships were found in fibre and protein (0.58). The significance of the result would be better interpreted to mean that the cowpea varieties cultivated under wide cultural conditions such as soil compositions climate and agronomic practices vary widely in moisture and carbohydrate, contents, followed by the fibre and protein. These components are important in determining nutritive quality and processing quality of cowpea seeds. The content of fat was the least with no relationship. The non-relationship that exists between fat content and carbohydrate is an advantage during processing to flour; unlike other legumes such as soya bean, there is no need for a defatting stage in flour production. Similar finding was obtained by Henshaw (2008) who studied varietal differences in physical characteristics and proximate composition of cowpea (*V. unguiculata*).

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

- Abayomi YA, Abidoye TO (2009). Evaluation of cowpea genotypes for soil moisture stress tolerance under screen house conditions. African Journal of Plant Science 3(10):229-237.
- Adeigbe OO, Adewale BD, Fawole IO (2011). Genetic variability, stability and relationship among some Cowpea, *Vigna unguiculata* (L.) Walp breeding lines. Journal of Plant Breeding and Crop Science 3(9):203-208.
- Animasaun DA, Oyedeji S, Mustapha OT, Azeez MA (2015). Genetic variability study among ten cultivars of cowpea (*Vigna unguiculata* L.

- Walp) using morpho-agronomic traits and nutritional composition. *Journal of Agricultural Sciences* 10(2).
- Ba FS, Pasquet RE, Gepts P (2004). Genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp.] as revealed by RAPD markers. *Genetic Resources and Crop Evolution* 51:539-550.
- Coulibaly S, Pasquet RS, Papa R, Gepts P (2002). AFLP analysis of the phenetic organization and genetic diversity of cowpea [*Vigna unguiculata* (L.) Walp.] reveals extensive gene flow between wild and domesticated types. *Theoretical and Applied Genetics* 104:258-266.
- Cursky RJ, Vanlauwe B, Lyasse O (2002) Cowpea rotation as a resource management technology for cereal-based systems in the savannas of West Africa. In: Fatokun CA, Tarawali SA, Singh BB, Kormawa PM, Tamo M (eds) *Challenges and Opportunities for Enhancing Sustainable Cowpea Production*. International Institute of Tropical Agriculture, Ibadan, Nigeria pp. 252-266.
- da Costa RC, Iobato AK, da Silveira JA, Laughing house IV HD (2011). ABA-mediated proline synthesis in cowpea leaves exposed to water deficiency and rehydration. *Turkish Journal of Agriculture and Forestry* 35(3):309-317.
- Diouf D (2011). Recent advances in cowpea (*Vigna unguiculata* (L.) Walp). *Omics Research for Genetic Improvement*. *African Journal of Biotechnology* 10:2803-2810.
- Ehlers JD, Hall AE (1997). Cowpea (*Vigna unguiculata* L. Walp). *Field Crops Research* 53:18-204.
- Ekpo IA, Agbor RB, Osuagwu AN, Okpako EC, Ekanem BE (2012). Evaluation of eight cowpea (*Vigna unguiculata* L. Walp) species for yield and associated traits. *International Journal of Pure and Applied Sciences and Technology* 12(2):1-7.
- Food and Agriculture Organization (FAO) (2000). The state of food insecurity in the world (SOFI) Rome. Italy: FAO-UN. Available at: www.fao.org/FOCUS/E/SOFI00/sofi001-e.html.
- Geissler PW, Mwaniki DL, Thiong'o F, Michaelsen KF, Friis H (1998). Geophagy, iron status and anemia among primary school children in Western Kenya. *Tropical Medicine and International Health* 3(7):529-534.
- Hall AE, Cisse N, Thiaw S, Elawad HOA, Ehlers JD (2003). Development of cowpea cultivars and germplasm by Bean/Cowpea CRSP. *Field Crop Research* 82:103-134.
- Henshaw FO (2008). Varietal differences in physical characteristics and proximate composition of cowpea (*Vigna unguiculata*), *World Journal of Agricultural Sciences* 4(3):302-306.
- Longe OG (1980). Carbohydrate composition of different varieties of cowpea (*Vigna unguiculata*). *Food Chemistry* 6(2):153-161.
- Mamiro PS, Mbwaga AM, Mamiro DP, Nmanri AW, Kinabo JL (2011). Nutritional quality and utilization of local and improved cowpea varieties in some regions in Tanzania. *African Journal of Food, Agriculture, Nutrition and Development* 11(1):4490-4506.
- Manggoel W, Uguru MI, Ndam ON, Dasbak MA (2012). Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions. *Journal of Plant Breeding and Crop Science* 4(5):80-86.
- Nielson S, Ohler T, Mitchell C (1997). Cowpea leaves for human consumption: production, utilization and nutrient composition. In: Singh SR, Rachie KO (eds.). *Cowpea researches, production and utilization*. Wiley, New York pp. 145-162.
- Nwofia GE, Nwanebu M, Agbo CU (2012). Variability and inter-relationship between yield and associated traits in cowpea (*Vigna unguiculata* L. Walp) as influenced by plant population, *World Journal of Agricultural Sciences* 8(4):396-402.
- Nwosu DJ, Olatunbosun BD, Adetiloye IS (2013). Genetic variability, heritability and genetic advance in cowpea genotypes in two agro-ecological environments, *Greener Journal of Biological Science* 3(5):202-207.
- Odedeji JO, Oyeleke WA (2011). Proximate, physiochemical and organoleptic properties of whole and dehulled cowpea seed flour (*Vigna unguiculata*), *Pakistan Journal of Nutrition* 10(12):1175-1178.
- Okon JE (2013). Effect of water stress on some growth aspects of two varieties of cowpea, *Vigna unguiculata* (L.) Walp Fabaceae. *Bulletin of Environment, Pharmacology and Life Sciences* 2(5):69-74.
- Omoigui LO, Ishiyaku MF, Kamara AY, Alabi SO, Mohammed SG (2006). Genetic variability and heritability studies of some reproductive traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *African Journal of Biotechnology* 5(13):1191-1195.
- Samson H, Helmut H (2007). Drought effect on yield, leaf parameters and evapotranspiration efficiency of cowpea. In *Conference of International Agricultural Research for Development*, University of Kassel-Witzenhause and University of Gottingen.
- Zia-Ul-Haq M, Ahmad S, Chiavaro E, Ahmed S (2010). Studies of oil from cowpea (*Vigna unguiculata* (L.) Walp.) cultivars commonly grown in Pakistan. *Pakistan Journal of Botany* 42(2):1333.

Full Length Research Paper

Correlations and path Analysis of some quantitative characters in barley (*Hordeum vulgareum* L.) landraces in western Oromia, Ethiopia

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Barley is recognized as one of the oldest cereal crop in Ethiopia grown for various uses. The knowledge of the association between various yield components and yield is paramount important for effective selection in crop improvement. The present study was to determine the interrelationship and direct and indirect effects of yield component traits on grain yield of Ethiopian landraces barley for further breeding activities of yield improvement. One hundred barley landraces were laid out in 10 x 10 simple lattice design with two replications in 2017 main cropping season at Mata sub site of Haro-Sabu Agricultural Research Center (HSARC). The analysis of variance revealed highly significant ($p \leq 0.01$) to low significant ($p \leq 0.05$) difference for all the characters. Sixteen parameters were evaluated to assess the inter relationship among yield and yield-related agronomic characters and their effect on grain yield. Grain yield showed positive and significant genotypic correlations with grain weight per spike ($r_g = 0.36$), spike weight per plant ($r_g = 0.38$), 1000-seed weight ($r_g = 0.66$), biological yield ($r_g = 0.83$), awn length ($r_g = 0.34$) and plant height ($r_g = 0.23$). The result revealed that biological yield, 1000-seed weight, productive tillers per plant and grain weight per spike were the most important yield components as they exerted positive direct effect on grain yield as well as positive genetic association with each other explaining the existence of significant correlation. This suggests that simultaneous improvement in these characters might be possible.

Keywords: Barley, phenotypic association, genotypic association, direct and indirect effects.

INTRODUCTION

Barley has a long history as a domesticated crop, as one of the first to be adopted for cultivation. In Ethiopia, barley is 5th major crop after maize, tef, sorghum and wheat in production (CSA, 2016/2017). It has been cultivated in

different regions of Ethiopia and produced twice annually, during the main season (Meher) and during the short rainy season (Belg). Moreover, Oromia, Amara, South Nation and Nationality of People (SNNP) and Tigray are

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the major barley growing regions which account more than 85% of the total production (Chilot et al., 2008). It is used for human consumption, food and feed (Harlan, 2008). It is prepared in different forms of indigenous food and homemade beverages (Fekadu et al., 2005). Additionally, barley has health benefits, such as barley β -glucans used to reduce blood cholesterol, glucose and weight loss by increased satiety, controls heart disease and type-2 diabetes (Behall et al., 2004; Ripple et al., 2009).

Selection of desired genotypes increased diversity and is used for modern plant breeding (Von Bothmer et al., 2003). In Ethiopia, barley landraces show high diversity mainly due to cultivation under variable climatic, farming systems, ecological and human management. Ethiopian barley landraces are important source of genes for several traits like barley yellow dwarf virus resistance, powdery mildew, high lysine content, good vegetative vigor, drought resistance and resistance to several barley diseases (Qualset, 1975; IBC, 2008). Furthermore, Ethiopian barley landraces have useful characteristics such as high tillering capacity; tolerance to marginal soil conditions, barley shoot fly, aphids and frost resistance; vigorous seedling establishment; and quick grain filling period (Birhanu et al., 2005).

Yield is a complex quantitative trait controlled by a large number of genes with small cumulative effect which, is highly influenced by environment (Dyulgerova, 2012). Hence, selection of barley lines based on direct selection for yield would not be effective. For better and successful yield improvement, selection has to be made for the component traits of yield. This requires understanding of interrelationship between component characters that help in determining which character to select when improvement of the related complex character is desired. Correlation between different traits is generally due to the presence of linkage disequilibrium, pleiotropic gene actions and epistatic effect of different genes (Falconer, 1985). A knowledge of correlations that exists between desirable characters can facilitate the interpretation of results obtained and provide the basis for planning more efficient program for the future (Martintell et al., 2005).

Genotypic correlation coefficient offers a measure of the genetic association between characteristics and may provide an important criterion of the selection procedures (Can and Yoshida, 1999). Although correlation coefficient is very important to determine traits that directly affect grain yield, it is insufficient to determine indirect effect of these traits on grain yields. Thus, path-coefficient analysis is one of the reliable statistical techniques which, allow quantifying the interrelations of different components and their direct and indirect effects on grain yield through correlation estimates (Dyulgerova, 2012). Path coefficient analysis is simply a standardized partial regression coefficient that, measures the direct and indirect effects for one variable upon another. And also permits the

separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959). Using path coefficient analysis, it is easy to determine which yield component/s is/are influencing the yield substantially and so that selection can then be based on that criterion thus making possible great progress through selection (Garcia et al., 2003; Kashif, et al., 2004).

The magnitude of association between yield and its component as well as their utilization in the selection has been reported in barley by many researchers (Dyulgerova, 2012; Tofiq et al., 2015; Hailu et al., 2016; Amardeep et al., 2017). Breeding for grain yield improvement is dependent on the presence of genetic diversity which is an important factor in any successful hybridization program. Quantitative characters like as grain yield is a complex character influenced directly or indirectly by several genes present in the plant (Bhutta et al., 2005) that making difficult for direct selection. In most breeding programs, the strategy is based on simultaneous selection for several traits and therefore the knowledge on the genetic association between traits is very useful for the establishment of selection criteria.

Therefore, the main objective of the study was to examine the prevailing genetic variability, the effects and the association among agronomic characters in Ethiopia landraces barley for further breeding activities of yield improvement. The specific objectives were to assess the variability and associations among yield and yield-related agro-morphological characters of barley landraces and to assess the direct and indirect effects of yield components on yield of barley landraces.

MATERIALS AND METHODS

Study area

The experiment was conducted during the main cropping season in 2017 at HSARC, Mata research sub-site, Western Oromia, Ethiopia. The area is located at 8°53'33"N latitude and 34°80'11"E longitude at the Mata research sub-site found with an elevation of 1900 m.a.s.l. Soil types is classified as about 90% loam, 6% sand and 4% clay soil. The nine years (2009- 2017) mean annual rainfall of the area was 1219.15 mm. The relative humidity was 67.5%. The nine years (2009- 2017) mean minimum and maximum annual temperatures were 16.21 and 27.77°C, respectively (Appendix 1 and 2) (Sayo Agriculture and Natural Resource office, Dembi Dollo, Unpublished).

Breeding materials and experimental design

A total of 100 food barley, of which 97 were landraces and two released varieties as standard checks (HB 1307 and Abdane) and one local check were evaluated (Table 1). Materials were sown in the second week of August 2017 in Mata sub site in 10 x 10 simple lattice design with two replications. Seed was drilled on 20 cm row spacing, 1.65 m row length and 1 m spacing between each block. Seed rate of 85 kg ha⁻¹ and recommended dose of fertilizer (41:57:00, NPK kg per ha) were applied (50 kg/ha Urea and 100 kg/ha DAP). Other crop management practices were undertaken as

Table 1. Passport description of the test barley landraces.

Entry code	Acc. No	Genus name	species name	Region	Zone	Woreda	Latitude	Longitude	Altitude (m.a.s.l)
1	64197	<i>Hordeum</i>	<i>Sp.</i>	Amara	MirabGojam	Merawi	12-24-00-N	37-05-00-E	2090
2	3239	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Dembia	12-23-00-N	37-17-00-E	1830
3	3240	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Dembia	12-18-00-N	37-10-00-E	1830
4	4560	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabWellega	Gimbi	09-10-00-N	35-42-00-E	1900
5	3465	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabShewa	Ambo	08-57-00-N	37-46-00-E	1800
6	3583	<i>Hordeum</i>	<i>vulgare</i>	SNNP	Semen Omo	Damot Gale	07-00-00-N	37-53-00-E	2140
7	3612	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Jimma	TiroAfeta	07-14-00-N	36-55-00-E	1810
8	3617	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Jimma	Sokoru	07-55-00-N	37-24-00-E	1890
9	3632	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabWellega	Jarso	09-32-00-N	35-28-00-E	1800
10	3638	<i>Hordeum</i>	<i>vulgare</i>	Amara	Debub Gondar	Fogera	11-49-00-N	37-37-00-E	1780
11	3763	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gonder	Chilga	12-31-00-N	37-10-00-E	1870
12	3940	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Chiro	08-54-00-N	40-46-00-E	1830
13	3941	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Habro	08-54-00-N	40-46-00-E	1890
14	3943	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Habro	09-05-00-N	40-50-00-E	1870
15	235286	<i>Hordeum</i>	<i>vulgare</i>	Tigray	Debubawi	Enderta	13-38-00-N	39-17-00-E	1780
16	4193	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Chiro	09-02-00-N	40-44-00-E	1870
17	4194	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Chiro	09-03-00-N	40-44-00-E	1840
18	4195	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Doba	09-26-00-N	41-02-00-E	1800
19	202561	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Bale	Gololcha	07-32-00-N	40-42-00-E	2090
20	239513	<i>Hordeum</i>	<i>Sp.</i>	Oromiya	Bale	Ginir	07-04-77-N	40-31-71-E	2050
21	64022	<i>Hordeum</i>	<i>sp.</i>	SNNP	Semen Omo	Damot Gale	06-53-00-N	37-48-00-E	2140
22	64053	<i>Hordeum</i>	<i>sp.</i>	SNNP	Semen Omo	Chencha	06-12-00-N	37-35-00-E	2150
23	64248	<i>Hordeum</i>	<i>sp.</i>	SNNP	Semen Omo	SodoZuria	07-02-00-N	37-54-00-E	1900
24	64260	<i>Hordeum</i>	<i>sp.</i>	Oromiya	Arssi	Digelunatuo	07-29-00-N	39-15-00-E	1910
25	237021	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Shewa	Shenkora	08-50-00-N	39-20-00-E	1750
26	64344	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Jimma	LimuSeka	07-33-00-N	36-36-00-E	1880
27	64345	<i>Hordeum</i>	<i>vulgare</i>	SNNP	KefichoShekicho	Decha	07-10-00-N	36-21-00-E	2140
28	202536	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Wegera	12-47-00-N	37-40-00-E	1750
29	202537	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Wegera	12-47-00-N	37-40-00-E	1750
30	202538	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Wegera	12-47-00-N	37-40-00-E	1750
31	202539	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Dabat	13-03-00-N	37-47-00-E	1810
32	202540	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Dabat	13-03-00-N	37-47-00-E	1810
33	202541	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Dembia	12-23-00-N	37-17-00-E	1830
34	202542	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Gondar	Dembia	12-18-00-N	37-10-00-E	1830
35	202660	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Jimma	TiroAfeta	07-41-00-N	36-58-00-E	1810
36	202661	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Jimma	TiroAfeta	07-41-00-N	36-58-00-E	1810

Table 1. Contd.

37	202670	<i>Hordeum vulgare</i>	Oromiya	Jimma	Sokoru	07-55-00-N	37-24-00-E	1890
38	202676	<i>Hordeum vulgare</i>	Amara	Debub Gondar	Fogera	11-49-00-N	37-37-00-E	1780
39	202820	<i>Hordeum vulgare</i>	Oromiya	MirabHarerge	Tulo	09-09-00-N	41-07-00-E	1910
40	202536	<i>Hordeum vulgare</i>	Amara	Semen Gonder	Wegera	12-47-00-N	37-40-00-E	1750
41	12970	<i>Hordeum sp.</i>	SNNP	Semen Omo	Chencha	37-36-00-N	06-09-00-E	2150
42	212972	<i>Hordeum sp.</i>	Oromiya	Borena	Yabelo	37-44-00-N	05-01-00-E	1850
43	217010	<i>Hordeum vulgare</i>	Amara	Semen Gonder	Chilga	12-38-00-N	37-06-00-E	2090
44	217173	<i>Hordeum vulgare</i>	Oromiya	Jimma	LimuSeka	07-33-00-N	36-36-00-E	1880
45	217175	<i>Hordeum vulgare</i>	Oromiya	Jimma	LimuSeka	07-33-00-N	36-36-00-E	1880
46	217176	<i>Hordeum vulgare</i>	SNNP	KefichoShekicho	Decha	07-10-00-N	36-21-00-E	2140
47	219151	<i>Hordeum vulgare</i>	Oromiya	MirabHarerge	Doba	09-19-00-N	41-03-00-E	2020
48	219152	<i>Hordeum vulgare</i>	Oromiya	MirabHarerge	Doba	09-11-00-N	41-03-00-E	2100
49	219148	<i>Hordeum vulgare</i>	Oromiya	MirabHarerge	Habro	08-49-00-N	40-28-00-E	1800
50	219307	<i>Hordeum vulgare</i>	Oromiya	Borena	Hagermariam	05-39-00-N	38-13-00-E	1880
51	219311	<i>Hordeum vulgare</i>	Oromiya	Borena	Yabelo	04-52-00-N	38-05-00-E	1870
52	219316	<i>Hordeum vulgare</i>	Oromiya	Borena	AdolanaWadera	05-53-00-N	39-11-00-E	1820
53	219317	<i>Hordeum vulgare</i>	Oromiya	Borena	AdolanaWadera	05-44-00-N	39-20-00-E	1800
54	220677	<i>Hordeum sp.</i>	Amara	Semen Shewa	Shenkora	08-48-00-N	39-21-00-E	2000
55	221312	<i>Hordeum sp.</i>	SNNP	Hadiya	Soro	07-13-00-N	37-46-00-E	2130
56	221313	<i>Hordeum sp.</i>	SNNP	Hadiya	Soro	07-13-00-N	37-46-00-E	2130
57	221324	<i>Hordeum sp.</i>	SNNP	Semen Omo	Chencha	06-09-00-N	37-36-00-E	2150
58	223192	<i>Hordeum sp.</i>	Tigray	Misrakawi	Wukro	13-43-00-N	39-28-00-E	1930
59	223194	<i>Hordeum sp.</i>	Tigray	Misrakawi	Wukro	12-42-00-N	39-31-00-E	1940
60	225179	<i>Hordeum vulgare</i>	SNNP	Semen Omo	Damot Gale	06-57-00-N	37-51-00-E	2100
61	225992	<i>Hordeum vulgare</i>	Amara	Semen Gondar	Dembia	12-22-00-N	37-17-00-E	1830
62	229997	<i>Hordeum sp.</i>	Oromiya	Bale	Nensebo	06-64-00-N	39-01-00-E	1940
63	230614	<i>Hordeum vulgare</i>	Oromiya	Bale	Goro	07-01-00-N	40-29-00-E	1870
64	230620	<i>Hordeum vulgare</i>	Oromiya	Bale	Ginir	07-05-00-N	40-36-00-E	1800
65	219307	<i>Hordeum vulgare</i>	Oromiya	Borana	Hagermariam	05-39-00-N	38-13-00-E	1880
66	230622	<i>Hordeum vulgare</i>	Oromiya	Bale	Ginir	07-05-00-N	40-36-00-E	1820
67	225176	<i>Hordeum vulgare</i>	SNNP	Semen Omo	Damot Gale	06-57-00-N	37-51-00-E	2100
68	230624	<i>Hordeum vulgare</i>	Oromiya	Bale	Ginir	07-08-00-N	40-42-00-E	1800
69	230628	<i>Hordeum vulgare</i>	Oromiya	Bale	Ginir	07-11-00-N	40-44-00-E	1790
70	232372	<i>Hordeum vulgare</i>	Oromiya	MisrakHarerge	Meta	09-22-00-N	41-47-00-E	2020
71	231223	<i>Hordeum vulgare</i>	Oromiya	Arssi	Merti	08-35-00-N	39-53-00-E	1780
72	232373	<i>Hordeum vulgare</i>	Oromiya	MisrakHarerge	Meta	09-22-00-N	41-47-00-E	2020
73	233028	<i>Hordeum vulgare</i>	SNNP	Semen Omo	Bonke	05-55-00-N	37-20-00-E	2050

Table 1. Contd.

74	234337	<i>Hordeum</i>	<i>vulgare</i>	Tigray	Mehakelegnaw	Adwa	14-05-00-N	38-57-00-E	1810
75	235264	<i>Hordeum</i>	<i>sp.</i>	Tigray	Debubawi	HintaloWajirat	12-58-00-N	39-34-00-E	1850
76	235274	<i>Hordeum</i>	<i>sp.</i>	Tigray	Mehakelegnaw	Abergele	13-31-00-N	39-07-00-E	1620
77	235283	<i>Hordeum</i>	<i>vulgare</i>	Tigray	Debubawi	Enderta	13-38-00-N	39-15-00-E	1900
78	235284	<i>Hordeum</i>	<i>vulgare</i>	Tigray	Debubawi	Enderta	13-40-00-N	39-15-00-E	1840
79	233030	<i>Hordeum</i>	<i>vulgare</i>	SNNP	Semen Omo	Bonke	05-58-00-N	37-17-00-E	2030
80	235299	<i>Hordeum</i>	<i>vulgare</i>	Tigray	Debubawi	Samre	13-23-00-N	39-21-00-E	1860
81	235635	<i>Hordeum</i>	<i>sp.</i>	SNNP	Bench Maji	Dirashe Special	05-17-00-N	37-39-00-E	2150
82	235636	<i>Hordeum</i>	<i>sp.</i>	SNNP	Bench Maji	Dirashe Special	05-17-00-N	37-39-00-E	2150
83	235637	<i>Hordeum</i>	<i>sp.</i>	SNNP	Bench Maji	Dirashe Special	05-17-00-N	37-39-00-E	2150
84	235651	<i>Hordeum</i>	<i>sp.</i>	Oromiya	Borena	Yabelo	04-56-00-N	38-11-00-E	1780
85	235652	<i>Hordeum</i>	<i>sp.</i>	Oromiya	Borena	Yabelo	04-56-00-N	38-11-00-E	1780
86	235654	<i>Hordeum</i>	<i>sp.</i>	Oromiya	Borena	Hagermariam	05-28-00-N	38-15-00-E	1880
87	235746	<i>Hordeum</i>	<i>sp.</i>	Amara	Semen Gonder	Chilga	12-24-00-N	37-07-00-E	1920
88	237021	<i>Hordeum</i>	<i>vulgare</i>	Amara	Semen Shewa	MinjarnaShenkora	08-50-00-N	39-20-00-E	1750
89	237022	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MisrakShewa	Ada'aChukala	08-50-00-N	39-00-00-E	1800
90	239514	<i>Hordeum</i>	<i>sp.</i>	Oromiya	Bale	Ginir	07-09-00-N	40-40-88-E	2050
91	241675	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	MirabHarerge	Mieso	07-17-36-N	38-22-98-E	1720
92	242098	<i>Hordeum</i>	<i>vulgare</i>	Amara	DebubWello	Kalu	11-06-00-N	39-47-00-E	1760
93	242574	<i>Hordeum</i>	<i>vulgare</i>	Tigray	Debubawi	HintaloWajirat	13-52-10-N	39-35-24-E	1820
94	242581	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Bale	Goro	07-00-00-N	40-27-40-E	1828
95	243182	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Bale	Goro	07-00-00-N	40-27-40-E	1828
96	243184	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	Bale	Goro	06-59-44-N	40-28-04-E	1830
97	243614	<i>Hordeum</i>	<i>vulgare</i>	Amara	Agewawi	Guangua	10-39-00-N	36-38-00-E	1815
98	HB1307	<i>Hordeum</i>	<i>vulgare</i>	Oromiya					
99	Abdane	<i>Hordeum</i>	<i>vulgare</i>	Oromiya					
100	Local	<i>Hordeum</i>	<i>vulgare</i>	Oromiya	K.Wollega	Sayo (Mata)	08-53-33-N	34-80-11-E	1700

per the recommendation.

Method of data collection

Ten plants were selected randomly before heading from each row and tagged with thread and all the necessary

plant based data were collected from these sampled plants.

Plant-based

These were peduncle length (cm), grain weight per spike (gm), plant height (cm), spike length (cm), spike weight per

plant (g), number of spikelets per spike, productive and total tillers per plant, flag leaf length (cm) and awn length (cm).

Plot based

These were days to heading (days), days to physiological

maturity(days), thousand seed weight(g), grain yield (g), biological yield(g) and harvest index (%).

Statistical analysis

ANOVA of the tested genotypes was conducted both for the simple lattice and randomized complete block design (RCBD) for the quantitative data. Associations between all possible pairs of quantitative traits were evaluated for their significance using SAS software version 9.2 (SAS, 2008). Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by Miller et al. (1958) and Kashiani and Saleh (2010) from the corresponding variance and covariance components as follows:

Phenotypic correlation coefficient:

$$r_{pxy} = \frac{pcov\ x.\ y}{\sqrt{\delta^2_{px} * \delta^2_{py}}}$$

Genotypic correlation coefficient:

$$r_{gxy} = \frac{gcvov\ x.\ y}{\sqrt{\delta^2_{gx} * \delta^2_{gy}}}$$

Where, r_{pxy} = Phenotypic correlation coefficient between characters X and Y, r_{gxy} = genotypic correlation coefficients between characters X and Y, $pcovx.y$ and $gcvov.x.y$ are phenotypic and genotypic covariance between variables x and y, respectively, σ^2_p =Phenotypic Variance between characters X and Y, σ^2_g =Genotypic Variance between characters X and Y.

The calculated phenotypic correlation value was tested for its significance using t-test according to Sharma (1998):

$$t = \frac{r_p}{SE(r_p)}$$

Where, r_p = Phenotypic correlation; $SE(r_p)$ = Standard error of phenotypic correlation obtained using in the following procedure (Sharma, 1998).

$$SE(r_p) = \sqrt{\frac{(1 - r_p^2)}{(n - 2)}}$$

Where, n is the number of genotypes tested, and r_p is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were tested for their significance using the formula described by Robertson (1959) as indicated below:

$$t = \frac{r_{gxy}}{SEr_{gxy}}$$

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% and 1% level of significance.

Where, n = number of genotypes:

$$SEr_{gxy} = \sqrt{\frac{1 - r_{gxy}^2}{2H_x.H_y}}$$

Where, H_x^2 = Heritability of trait x and H_y^2 = Heritability of trait y.

Path coefficient analysis

Path coefficient analysis was computed by Dewey and Lu (1959) using the phenotypic and genotypic correlation coefficients as: $r_{ij} = P_{ij} + \sum r_{ik} * P_{kj}$

Where, r_{ij} = mutual association between the independent character i (yield-related trait) and dependent character, j (grain yield) as measured by the genotypic correlation coefficients; P_{ij} = components of direct effects of the independent character (i) on the dependent character (j) as measured by the path coefficients; and $\sum r_{ik}p_{kj}$ = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The residual factor (P_R), was calculated as:

$$P_R = \sqrt{(1 - \sum p_{ij}r_{ij})}$$

Where, i=any trait in the model, j=dependent variable (grain yield) and r=correlation coefficient between any trait i and the dependent variable j. Residual (R) is the square root of non-determination; the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999).

RESULTS AND DISCUSSION

Analysis of variance

The result of relative efficiency of the design showed that, for most characters' (more than 68%), simple lattice design was more efficient than randomized complete block design (RCBD) (Table 2). However, for traits like YLD, GWS, SWPP, BYLD and HI, the error variance of the blocks within replications were smaller than or equal to the intra-block error (Table 2), which, was decided to partition various source of variation by RCBD analysis of variance (Appendix 3). Analysis of variance (ANOVA) exhibited that significant ($P < 0.05$ and $P < 0.01$) differences were obtained for all traits evaluated (Table 2). Significant differences were recorded for parameters like days to heading, days to maturity, plant height, peduncle length, spike length, awn length, flag leaf length, productive tillers per plant, grain yield, grain weight per spike, spike weight per plant, number of spikeletes per spike, 1000-seed weight and biological yield at ($P \leq 0.01$) probability level. Whereas, total tillers per plant and harvest index were recorded at $P \leq 0.05$. The significant differences of the parameters indicated that, there is considerable amount of genetic variation among the studied landraces (Table 2). This variation would offer scope of selection for development of desirable genotypes which, could also be attributed to the diverse composition of the populations

Table 2. Mean squares, degrees of freedom and some of statistical parameters of all studied traits of barley landraces evaluated in 2017 season using simple lattice design.

Traits	Source of variation				R ² (%)	CV%	Mean	SE(±)	LSD (5%)	Efficiency Relative to RCBD (%)
	Replication	Blocks within Replications	Genotypes	Error						
	DF=1	DF=18	DF=99	DF=81						
DH	33.62*	11.04 ^{ns}	50.62**	7.83	89.79	4.63	60.36	0.52	5.75	102.07
DM	206.04**	13.15**	50.15**	8.21	90.04	3.12	91.8	0.53	5.99	103.85
PH	2288.26**	37.37**	134.18**	35.83	86.02	7.17	83.54	0.87	11.92	100.03
PDL	34.53*	6.03**	27.98**	5.77	87.2	16.92	14.19	0.39	4.78	103.04
SL	19.16**	1.19*	1.51**	0.64	80.6	9.52	8.43	0.09	1.71	106.56
AL	4.65*	1.3 ^{ns}	7.02**	1.21	88.54	8.81	12.46	0.19	2.19	100.1
FLL	62.16**	7.38*	7.69**	3.73	76.86	12.99	14.87	0.2	4.16	108.07
PTPP	27.16**	1.01*	1.29**	0.58	79.77	16.88	4.51	0.08	1.61	105.33
TTPP	27.23**	1.05 ^{ns}	1.09*	0.68	74.81	16.45	5.02	0.08	1.72	103.23
YLD	16.3**	0.36 ^{ns}	1.25**	0.5	78.17	19.67	3.58	0.08	1.37	94.63
GWPS	0.37**	0.03 ^{ns}	0.07**	0.03	77.74	16.73	1.06	0.02	0.35	99.11
SWPP	1.48**	0.04 ^{ns}	0.13**	0.04	82.37	14.82	1.39	0.03	0.41	99.41
NSTPS	54.71*	10.82 ^{ns}	72.90**	7.34	93.34	15.26	17.76	0.64	5.6	102.62
TSW	2751.34**	57.4 ^{ns}	110.10**	54.24	76.9	23.8	30.94	0.74	14.69	100.06
BYLD	60.72**	1.4 ^{ns}	8.37**	1.86	87.03	15.27	8.93	0.22	2.64	95.48
HI	10.95*	42.02*	58.47.*	45.81	60.82	18.61	41.21	0.58	14.82	94.81

^{ns} *, ** non-significant, significant at 0.05 and 0.01 probability levels, respectively. DF= degree of freedom R²= R- square; CV= Coefficient of variation; SE= standard error; LSD=least significant difference; DH = days to heading; DM= days to maturity; PH=plant height; PDL= peduncle length; SL= spike length; AL =awn length; FLL =flag leaf length; PTPP =productive tillers per plant; TTPP=total tillers per plant; YLD = grain yield; GWPS =grain weight spike⁻¹; SWPP =spike weight plant⁻¹; NSTPS = number of spikelets spike⁻¹; TSW =thousand seed weight; BYLD=biomass yield; HI=harvest index; RCBD = random complete block design.

evolved through time. Similarly, Assefa (2003) reported that, barley landraces showed significant variations for many traits like 1000 seed weight, spike length, heads per square meter, grain yield per spike, days to heading, days to maturity and plant height in Ethiopian barley landraces. Study by Oettler et al. (2009) showed significant differences among nine barley genotypes for grain yield, spikes/m², 1000 seed weight, dry matter, days to anthesis and plant height.

Genotypic and phenotypic correlation of grain yield with other traits

In the present study, the estimated values of phenotypic and genotypic correlation coefficients between all pairs of characters are presented in Table 3. The analyses revealed, genotypic correlation coefficient values were greater for most of the characters than their corresponding phenotypic correlation coefficient values, indicating inherent association of the characters so, that selection for the correlated characters could give a better yield.

Phenotypic correlations

Grain yield per plant showed positive and high significant

($p < 0.01$) correlation with spike length ($r_p = 0.25$), awn length ($r_p = 0.25$), plant height ($r_p = 0.32$), thousand seed weight ($r_p = 0.54$), biological yield ($r_p = 0.76$), harvest index ($r_p = 0.30$) and grain weight per spike ($r_p = 0.32$) (Table 3). It appears that phenotypic selection of phenotypically high values of these characters' result in increasing yield potential. Similarly, positive and highly significant phenotypic correlation of grain yield with 1000-kernel weight and biological yield in all environments was reported by Azeb et al. (2016). This finding is also in agreement with those of Acevedo et al. (1991) and Alam et al. (2007) who reported the association of grain yield with plant height in barley. At phenotypic level, grain yield per plant was positively and significantly associated with biological yield and harvest index (Amardeep et al., 2017). Moreover, grain yield showed negative and significant phenotypic correlation with days to heading ($r_p = -0.36$) and days to maturity ($r_p = -0.38$) (Table 3) which is in agreement with the finding of Bhutta et al. (2005) and Blanco et al. (2010) on barley.

Genotypic correlations

Grain yield showed positive and significant correlation with grain weight per spike ($r_g = 0.36$), spike weight per plant ($r_g = 0.38$), 1000-seed weight ($r_g = 0.66$), biological

Table 3. Phenotypic (r_p) and genotypic (r_g) correlation coefficients of studied traits of barley landraces evaluated in 2017 season.

Traits		DH	DM	PH	PDL	SL	AL	FLL	PTPP	TTPP	YLD	GWPS	SWPP	NSTPS	TSW	BYLD	HI
DH	rp	1	0.74**	0.03	-0.19*	-0.05	-0.16*	0.23**	-0.33**	-0.15*	-0.36**	-0.01	-0.16*	-0.24**	-0.32**	-0.14	-0.36**
	rg		0.81**	0.1	-0.22*	0	-0.16	0.38**	-0.42**	-0.19	-0.43**	-0.02	-0.16	-0.27**	-0.40**	-0.17	-0.43**
DM	rp		1	-0.01	-0.23**	0.02	-0.05	0.28**	-0.32**	-0.15*	-0.38**	-0.02	-0.18*	-0.15*	-0.35**	-0.18*	-0.30**
	rg			0.09	-0.25*	0.1	-0.08	0.47**	-0.38**	-0.17	-0.42**	0.02	-0.15	-0.16	-0.37**	-0.18	-0.42**
PH	rp			1	0.60**	0.41**	0.21**	0.32**	0.23**	0.22**	0.32**	0.32**	0.36**	0.02	0.27**	0.41**	-0.15*
	rg				0.60**	0.27**	0.32**	0.23*	0.1	0.07	0.23*	0.39**	0.37**	-0.02	0.18	0.36**	-0.26**
PDL	rp				1	0.21**	0.16**	0.15*	0.16*	0.13	0.31**	0.09	0.09	0.13	0.31**	0.30**	0.03
	rg					0.17	0.19	0.1	0.20*	0.17	0.35**	0.11	0.11	0.14	0.36**	0.30**	0.05
SL	rp					1	0.17*	0.37**	0.38**	0.40**	0.25**	0.11	0.12	0.32**	0.30**	0.27**	-0.06
	rg						0.23*	0.20*	0.28**	0.30**	0.18	0.08	0.01	0.37**	0.21*	0.23*	-0.12
AL	rp						1	0.11	0.13	0.09	0.25**	0.30**	0.32**	0.01	0.19**	0.22**	0.04
	rg							0.07	0.2	0.15	0.34**	0.39**	0.41**	0.02	0.27**	0.27**	0.05
FLL	rp							1	0.07	0.16*	0.13	0.20**	0.21**	-0.07	0.14	0.17*	-0.11
	rg								-0.12	-0.02	0.01	0.22*	0.17	-0.11	-0.02	0.16	-0.30**
PTPP	rp								1	0.94**	0.39**	0.11	0.14*	0.31**	0.39**	0.32**	0.11
	rg									0.93**	0.37**	0.03	0.02	0.35**	0.34**	0.26**	0.20*
TTPP	rp									1	0.31**	0.06	0.08	0.26**	0.33**	0.27**	0.06
	rg										0.25*	-0.05	-0.09	0.28**	0.27**	0.20*	0.1
YLD	rp										1	0.32**	0.36**	0.23**	0.54**	0.76**	0.30**
	rg											0.36**	0.38**	0.24*	0.66**	0.83**	0.15
GWPS	rp											1	0.82**	-0.09	0.32**	0.34**	-0.03
	rg												0.88**	-0.2	0.23*	0.40**	0.88**
SWPP	rp												1	-0.16*	0.33**	0.38**	-0.05
	rg													-0.28**	0.20*	0.41**	-0.11
NSTPS	rp													1	0.22**	0.15*	0.13
	rg														0.27**	0.15	0.15
TSW	rp														1	0.51**	0.01
	rg															0.55**	11
BYLD	rp															1	-0.37**
	rg																-0.41**
HI																	1

DH = days to heading; DM= days to maturity; PH=plant height; PDL= peduncle length; SL=spike length; AL =awn length; FLL=flag leaf length; PTPP =productive tillers per plant; TTPP=total tillers per plant; YLD= grain yield; GWPS =grain weight per spike; SWPP =spike weight per plant; NSTPS=number of spikelets per spike; TSW =thousand seed weight; BYLD = biological yield and HI =harvest index; rp = phenotypic correlation coefficients; rg = genotypic correlation coefficients.

yield ($r_g = 0.83$), awn length ($r_g = 0.34$) and plant height ($r_g = 0.23$). Similarly, grain yield had positive and highly significant genotypic correlation with 1000-kernel weight and biological yield in all environments (Azeb et al., 2016) and with biological yield and plant height at the genotypic level (Amardeep et al., 2017). However, days to heading ($r_g = -0.43$) and days to maturity ($r_g = -0.42$) had negatively significant correlation with grain yield (Table 3) which was also similarly reported by Bhutta et al. (2005). Azeb et al. (2016) also reported negative and highly significant genotypic correlation of grain yield with days to heading and days to maturity at Ofla site. This might be due to the presence of common genetic elements that controlled the characters in the same and/or in different direction. The observed significant positive correlation could be either due to the strong coupling linkage between the genes or was the result of pleiotropic genes that controlled these characters in the same direction (Kearsey and Pooni, 1996). Thus, the negative correlations of grain yield with days to heading and maturity indicates that, late varieties would produce low grain yield. Normally, inverse relationship between earliness characters and grain yield is necessary especially if stresses such as terminal heat and drought are expected. That means even if long duration of the growing period would mean that there would be more accumulation of dry matter over the extended growing period; and there should be certain compromise between earliness as a stress escape mechanism and the possible yield reduction in moisture stress areas. Previous studies have confirmed this result (Gebeyehou et al., 1982; Amin et al., 1992; Van Oosteron and Acevedo, 1992; Gashaw, 2007), which means that early heading genotypes with adequate grain filling period escape terminal moisture stress and, thus give better grain yield. The yield components exhibited varying trends of association among themselves.

Furthermore, plant height had positive significant association with peduncle length, spike length, awn length, grain weight per spike, spike weight per plant, and biological yield. Peduncle length had positive and significant correlation with productive tillers per plant, 1000-seed weight and biological yield. Spike length had positive and significant correlation with awn length, productive and total tillers per plant, number of spikelets per spike, 1000-seed weight and biological yield. The correlation of awn length with grain weight per spike, spike weight per plant, 1000-seed weight and biological yield was positive and significant. Productive tillers per plant had positive and significant correlation with total tillers per plant, number of spikelets per spike, 1000-seed weight, biological yield and harvest index (Table 3). The positive significant associations between grain yield and plant height because of these tall genotypes generally excelled in their capacity to support kernel growth by stem reserve mobilization (Blum et al., 1989). Therefore, selection for tall plants tends to increase grain yield per plant.

Path coefficient analysis

Path coefficient analysis provides more effective means of separating direct and indirect factors, permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. Genotypic and phenotypic correlations were partitioned into direct and indirect effects using grain yield as a dependent variable. In this study, grain yield was the result of days to heading, days to maturity, plant height, peduncle length, awn length, total tillers per plant, productive tillers per plant, grain weight per spike, spike weight per plant, number of spikelets per spike, 1000-seed weight, biological yield, harvest index and residual factor that included other factors affecting grain yield (Tables 4 and 5).

Genotypic path coefficient

Biological yield had positive and significant correlation coefficient and it showed the highest positive direct effect (0.68) on grain yield. Biological yield has also exerted large indirect effects thousand seed weight, total tillers per plant, grain weight per spike than other characters included in the analysis showing its high contribution for a better partitioning of the photosynthetic products into the grain. The direct effect of 1000-seed weight followed by productive tillers per plant, awn length, grain weight per spike, peduncle length, and number of spikelets per spike on grain yield was positive with significant correlation and so exerted positive direct effect (Table 4). Biological yield, thousand kernel weight, productive tillers per plant and grain weight per spike revealed positive direct effect and had positive genetic correlation explaining the existence of real relation between the characters and yield indicating that, indirect selection of yield via this characteristic is effective. Similarly, Getachew et al. (2007) reported positive direct effect of the number of productive tillers per plant on grain yield in Ethiopian barley landraces. Azeb et al. (2016) indicated that biological yield exerted maximum positive direct effect on grain yield across locations. In another study the highest positive direct effect on seed yield per plant was exerted by biological yield, number of productive tillers per plant, plant height, length of spike, days to maturity, harvest index (Amardeep et al., 2017). Mogghadam et al. (2009) and Blanco et al. (2010) reported positive direct effect of 1000-seed weight on grain yield. Bhutta et al. (2005) reported positive maximum association between peduncle length and number of spikelets with grain yield in six rowed barleys.

Plant height exerted higher negative direct effects on grain yield but positive and highly significant association at genotypic levels. The indirect effects of plant height on grain yield via biological yield was however positive and

Table 4. Estimates of direct (bold diagonal) and indirect (off diagonal) effect of traits on grain yield on the basis of genotypic correlation.

Traits	DH	DM	PH	PDL	AL	PTPP	TTPP	GWPS	SWPP	NSTPS	TSW	BYLD	rg
DH	-0.07	-0.06	-0.01	-0.02	-0.01	-0.05	0.02	-0.00	0.00	-0.01	-0.05	-0.11	-0.43**
DM	-0.05	-0.07	-0.01	-0.02	-0.01	-0.05	0.02	0.00	0.00	-0.01	-0.05	-0.12	-0.42**
PH	-0.01	-0.01	-0.13	0.04	0.03	0.01	-0.01	0.03	-0.00	-0.00	0.02	0.25	0.23**
PDL	0.01	0.02	-0.08	0.07	0.02	0.03	-0.02	0.01	-0.00	0.01	0.05	0.21	0.35**
AL	0.01	0.01	-0.04	0.01	0.09	0.03	-0.02	0.03	-0.01	0.00	0.04	0.19	0.34**
PTPP	0.03	0.03	-0.01	0.02	0.02	0.13	-0.09	0.00	0.00	0.02	0.05	0.18	0.37**
TTPP	0.01	0.01	-0.01	0.01	0.01	0.12	-0.10	-0.00	0.00	0.01	0.04	0.14	0.25*
GWPS	0.00	-0.00	-0.05	0.01	0.03	0.00	0.01	0.09	-0.01	-0.01	0.03	0.27	0.36**
SWPP	0.01	0.01	-0.05	0.01	0.04	0.00	0.01	0.08	-0.01	-0.01	0.03	0.28	0.38**
NSTPS	0.02	0.01	0.00	0.01	0.00	0.04	-0.03	-0.02	0.00	0.05	0.04	0.10	0.24**
TSW	0.03	0.03	-0.02	0.03	0.02	0.04	-0.03	0.02	-0.00	0.01	0.13	0.38	0.66**
BYLD	0.01	0.01	-0.05	0.02	0.02	0.03	-0.02	0.04	-0.01	0.01	0.07	0.68	0.83**

DH = days to heading; DM= days to maturity; PH=plant height; PDL= peduncle length; AL =awn length; PTPP =productive tillers per plant; TTPP=total tillers per plant; GWPS =grain weight per spike; SWPP; =spike weight per plant; NSTPS=number of spikelets per spike; TSW =thousand seed weight; BYLD=biological yield; rg =genotypic correlation.

Table 5. Estimates of direct (bold diagonal) and indirect (off diagonal) effect of traits on grain yield on the basis of phenotypic correlation.

Traits	DH	DM	PH	PDL	SL	AL	PTPP	TTPP	GWPS	SWPP	NSTPS	TSW	BYLD	HI	r_p
DH	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	-0.14	-0.24	-0.36**
DM	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	-0.18	-0.20	-0.38**
PH	0.00	0.00	0.01	-0.01	0.01	0.00	0.00	-0.01	-0.01	0.01	0.00	0.00	0.41	-0.10	0.32**
PDL	0.00	0.00	0.00	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.29	0.02	0.31**
SL	0.00	0.00	0.00	0.00	0.01	0.00	0.00	-0.01	0.00	0.00	0.00	0.01	0.27	-0.04	0.25**
AL	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	-0.01	0.01	0.00	0.00	0.23	0.03	0.25**
PTPP	-0.01	0.00	0.00	0.00	0.01	0.00	0.01	-0.03	0.00	0.00	0.00	0.01	0.32	0.07	0.39**
TTPP	0.00	0.00	0.00	0.00	0.01	0.00	0.01	-0.03	0.00	0.00	0.00	0.01	0.27	0.04	0.31**
GWPS	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	-0.03	0.01	0.00	0.01	0.34	-0.02	0.32**
SWPP	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	-0.03	0.02	0.00	0.00	0.38	-0.03	0.36**
NSTPS	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	0.00	0.00	0.00	0.00	0.15	0.09	0.23**
TSW	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	-0.01	0.01	0.00	0.02	0.51	0.01	0.54**
BYLD	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	-0.01	0.01	0.00	0.01	0.99	-0.25	0.76**
HI	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.37	0.67	0.30**

Residual effect = value (0.1731) is unexplained; 82.7% is explained; DH = days to heading; DM= days to maturity; PH=plant height; PDL= peduncle length; SL=spike length; AL =awn length; PTPP =productive tillers per plant; TTPP=total tillers per plant; GWPS =grain weight per spike; SWPP =spike weight per plant; NSTPS=number of spikelets per spike; TSW =thousand seed weight; BYLD=biomass yield; HI=harvest index; r_p =phenotypic correlation.

high. Smaller negative direct effects were also exerted by days to heading, days to maturity, total tillers per plant and spike weight per plant. However negative genotypic correlation was obtained only for days to heading and days to maturity. Days to heading, days to maturity and plant height had negative direct effect. The indirect effects of days to heading, days to maturity and plant height with other characters were mostly negatives and negligible. The total negative correlation coefficient of days to heading and maturity with grain yield were due to mainly direct effect while the positive correlation for plant height with grain yield was due to large indirect effect of biological yield (Table 4). The present study is in agreement with those of Pathak (2008) and Azeb et al. (2016) reporting negative direct effect of plant height on grain yield. The negative direct effect of days to heading, days to maturity and plant height on grain yield suggests the possibility that grain yield could be improved by focusing on early maturing genotypes with shorter or medium plant height. Shorter plant height is also responsive to high input resulting higher yield. Singh and Chaundhary (1985) suggested an indirect effect seemed to be the cause of correlation and hence, these indirect causal factors (traits) should be considered simultaneously for selection. Besides to significant, awn length, grain weight per spike, productive tillers per plant and thousand seed weight exhibited positive direct effects on grain yield indicating that, increasing in those traits could possibly to increase grain yield. The genotypic residual value (0.4326) showed that, the characters under study accounted for 56.74% of the variability with grain yield components (Table 4).

Phenotypic path coefficient analysis

Biological yield and harvest index showed positive and significant correlation ($r = 0.76$) and ($r = 0.30$) with grain yield and they had the highest direct effect (0.99) and (0.67) on grain yield respectively. The existence of negligible and positive indirect effect of biological yield and harvest index with most of the other characters determines that, the correlation of these traits with grain yield were found to be due to the direct effect (Table 5). Days to maturity has negligible positive direct effect on grain yield. The correlation of days to maturity with grain yield was because of indirect effect. Plant height, spike length, awn length, productive tillers per plant and 1000-seed weight have positive and negligible direct effect on grain yield and the phenotypic correlation they had with grain yield were positive. The indirect effect of biological yield through days to heading, total tillers per plant, grain weight per spike and harvest index counter balanced the direct effect of biological yield on grain yield. The indirect effect of harvest index through biological yield (-0.37) counter balanced the direct effect of harvest index on grain yield (0.67). The residual value (0.1731) showed the characters under the study accounted 82.7% of the

variability in grain yield (Table 5).

Conclusion

Characters that showed positive direct effect as well as positive and significant correlation coefficient with grain yield were known to affect grain yield to the favorable direction. The present study revealed that, biological yield, thousand kernel weight, productive tillers per plant and grain weight per spike were the most important yield components as they exerted positive direct effect on grain yield as well as positive genetic association with each other explaining the existence of real correlation. This suggests that, simultaneous improvement in these characters might be possible. Generally, significant differences of the characters showed that, there is substantial amount of genetic variation among the studied materials and is a strong correlation between most of the studied desirable characters that can afford basic information for further breeding activities for crop improvement.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

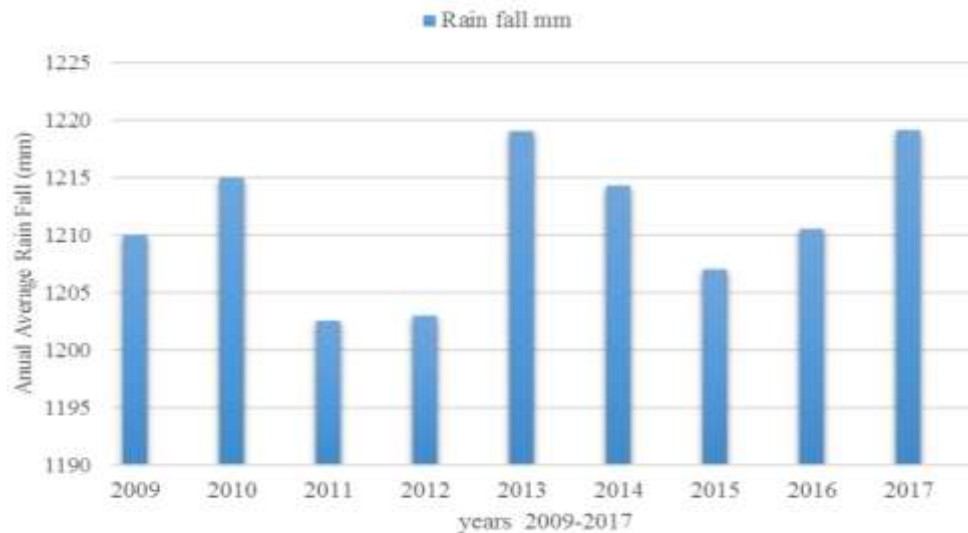
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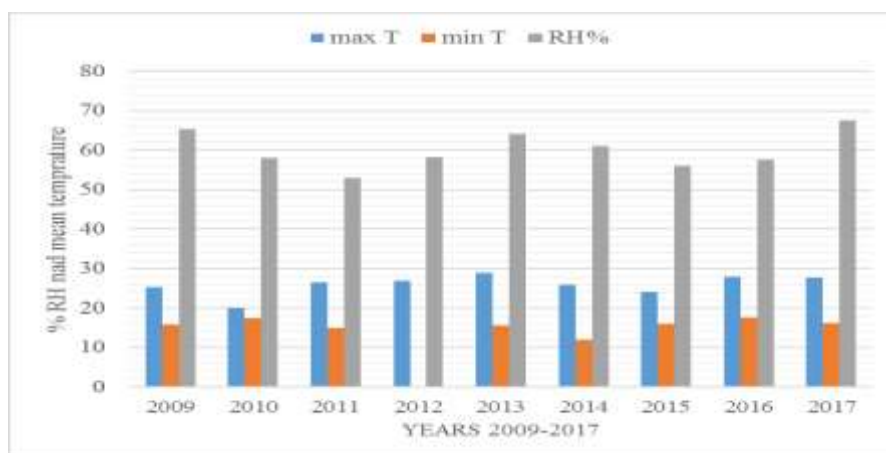
REFERENCES

- Acevedo E, Craufurd PQ, Austin RB, Perez-Marco P (1991). Traits associated with high yield in barley in low-rainfall environments. *The Journal of Agricultural Science* 116(1):23-36.
- Alam MZ, Haider SA, Pau NK (2007). Yield and Yield Components of Barley (*Hordeum vulgare* L.) cultivars in Relation to Nitrogen Fertilizer. *Journal of Applied Sciences Research* 3(10):1022-1026.
- Amardeep L, Singh V, Piyushmalik (2017). Studies on correlation and path coefficients analysis in barley (*Hordeum vulgare* L.). *Bulletin of Environment, Pharmacology and Life Sciences* 6(12):75-80.
- Assefa A (2003). "Genetic variability and Breeding Potential of Barley (*Hordeum vulgare* L.) Landraces from North Shewa in Ethiopia," PhD Thesis, Faculty of natural and agricultural sciences university of Free State, Bloemfontein, South Africa.
- Azeb H, Sentayehu A, Mandefro N, Ermias A (2016). Correlation and Path Coefficient Analysis of Yield and Yield Associated Traits in Barley (*Hordeum vulgare* L.) Germplasm. *Advances in Crop Science and Technology* 4:2.
- Behall KM, Scholfield DJ, Hallfrisch J (2004). Diets containing barley significantly reduce lipids in mildly hypercholesterolemic men and women. *The American Journal of Clinical Nutrition* 80(5):1185-1193.

- Bhutta WM, Tahira B, Ibrahim M (2005). Path-coefficient analysis of some quantitative characters in husked barley. *Caderno de PesquisaSØr. Universidade de Santa Cruz do Sul* 17(1):65-70.
- Birhanu B, Fekadu A, Berhane L (2005). Food barley in Ethiopia. In: Grando S, Macpherson HG (eds.), *Food Barley: Importance, Uses and Local Knowledge*, Proceedings of the International Workshop on Food Barley Improvement, 14-17 January 2002, Hammamet, Tunisia. ICARDA, Aleppo, Syria pp. 53-82.
- Blanco A, Rajaram S, Kronstad WE (2010). Agronomic potential of some barley genotypes. *Crop Science* 41:670-676.
- Blum A, Golan G, Mayer J, Sinmena B, Shpiller L, Burra J (1989). The drought response of landraces of wheat from the northern negev desert in Israel. *Euphytica* 4:87-96.
- Can ND, Yoshida T (1999). Genotypic and phenotypic variances and covariance's in early maturing grain sorghum in a double cropping. *Plant Production Science* 2(1):67-70.
- Chilot Y, Fekadu A, Woldeyesus S (2008). Barley Livestock Production System in Ethiopia: An overview. In: Chilot Y, Fekadu A, Woldeyesus S (ed.) *Barley-based Farming System in the highlands of Ethiopia*. Ethiopian Agriculture Research Organization, Addis Ababa, Ethiopia.
- Central Statistical Agency (CSA) (2017). The Federal Democratic Republic of Ethiopia Agricultural Sample Survey 2016/2017: Area and production of major crops, (private peasant holdings, Meher season). Addis Ababa, Ethiopia.
- Dewey DR, Lu K (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy Journal* 51(9):515-518.
- Dyulgerova B (2012). Correlations between grain yield and yield related traits in barley mutant lines. *Journal of Agriculture, Science and Technology* 4(3):208-210.
- Falconer DS (1985). *Introductions to Quantitative Genetics*. Longman, London.
- Fekadu F, Lakew B, Hailu G (2005). Barley production and breeding in Ethiopia. Breeding for disease resistance with emphasis on durability Proceedings of the Regional Workshop for Eastern, Central, and Southern Africa, Njoro, Kenya, Oct. 2-6, 1994.
- Garcia LF, del M, Rharrabti Y, Villagas D, Royo C (2003). Evaluation of grain yield and its components in durum wheat under Mediterranean conditions. Anontogenic approach. *Agronomy Journal* 95(3):266-274.
- Gebeyehou G, Knott DR, Baker RJ (1982). Rate and duration of grain filling in durum wheat cultivars. *Crop Science* 22:337-340.
- Getachew B, Tesemma T, Becker HC, Merker A (2007). Variation and interrelationships of agronomic traits in Ethiopian Barley landraces *Euphytica* 71(3):181-188.
- Hailu A, Alamerew S, Nigussie M, Assefa E (2016). Correlation and Path Coefficient Analysis of Yield and Yield Associated Traits in Barley (*Hordeum vulgare* L.) Germplasm. *Advances in Crop Science and Technology* 4:216.
- Harlan JR (2008). *Evolution of Crop Plants*. New York, Simmonds NW (eds.), University of Illinois Urbana Iii USA, Longman.
- Institute of Biodiversity Conservation (IBC) (2008). Ethiopia: Second Country Report on the State of PGRFA to FAO, January, 2008. Addis Ababa P 45.
- Kashiani P, Saleh G (2010). Estimation of genetic correlations on sweet corn inbred lines using SAS mixed model. *American Journal of Agricultural and Biological Sciences* 5(3):309-314.
- Kashif M, Khaliq IH (2004). Heritability, correlation and path coefficient analysis for some metric traits in wheat. *International Journal of Agriculture and Biology* 6(1):138-142.
- Kearsey MJ, Pooni HS (1996). *The Genetic Analysis of Quantitative Traits*. Chapman and Hall, London, Weinhein, New York.
- Martintell P, Delocu G, Boggini G, Odoardi M, Stanca AM (2005). Breeding progress in grain yield and selected agronomic characters of winter barley (*Hordeum vulgare* L.) over the last quarter of a century. *Plant Breeding* 99:289-294.
- Miller PA, Williams JC, Robinson HF, Comstock RE (1958). Estimates of Genotypic and Environmental Variances and Covariance in Upland Cotton and Their Implications in Selection 1. *Agronomy Journal* 50(3):126-131.
- Mogghhadam M, Ehdai B, Waines JG (2009). Genetic variation and interrelationships of agronomic characters in landraces of spring barley from south eastern Iran. *Euphytica* 95(5):361-369.
- Oettler GS, Wietholter S, Horst WJ (2009). Genetic variation for yield and other agronomic traits of barley grown on an acid, aluminum-toxic soil in Southern Brazil pp. 267-272.
- Pathak NN (2008). Correlation and path analysis in barley under high temperature and moisture stress conditions. *Agronomy Journal* 50(3):126-131.
- Qualset CO (1975). Sampling germplasm in a center of diversity: an example of disease resistance in Ethiopian barley. Frankel OH, Hawkes JG (eds), *Crop Genetic Resources for Today and Tomorrow*, Cambridge University Press, Cambridge pp. 81-96.
- Ripple T, William L, Mary SPC, Michael W, Craig IC (2009). The effects of barely-derived soluble fiber on serum lipids. *Annals of Family Medicine* 7(2):157-163.
- Robertson A (1959). The sampling variance of the genetic correlation coefficient. *Biometrics* 15(3):469-485.
- SAS Institute Inc (2008). *Statistical analysis Software version 9.2*, Cary, NC: SAS Institute.
- Sharma JR (1998). *Statistical and biometrical techniques in plant breeding*. New Delhi, New Age International (P) limited, publishers.
- Singh RK, Chaundhary BD (1985). *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi, Kalyani Publishers.
- Singh RK, Chaudhary BD (1999). *Biometrical methods in quantitative genetics analysis*. New Delhi, Kalyani Publishers.
- Tofiq SE, Hama TN, Amin SM, Sheikh A, Abdulkhaleq DA (2015). Correlation and path coefficient analysis of grain yield and yield components in some barley genotypes created by full diallel analysis in sulaimani region for F2 generation. *International Journal of Plant, Animal and Environmental Sciences* 5(4):76-79.
- Von Bothmer R, Kazuhiro S, Helmut K, Theo van Hintum (2003). Barley diversity- an introduction. In: *Diversity in Barley (Hordeum Vulgare)*. Elsevier Science P 280.



Appendix 1. Annual average rainfall (2009-2017).
Source: (Sayo Agriculture and Natural Resource office, Demba Dollo)



Appendix 2. Mean min and max temperature (°C) and relative humidity (%) (2009-2017).
Source: (Sayo Agriculture and Natural Resource office, Demba Dollo).

Appendix 3. Mean squares, degrees of freedom and some of statistical parameters of five studied traits of barley landraces evaluated in 2017 season using RCBD.

Source of Variation	Rep	Genotypes	R ² (%)	CV(%)	Mean ±SE	LSD(5%)
	DF=1	DF= 99				
YLD	16.30**	1.25**	75	19.13	3.61±0.07	1.37
GWPS	0.37**	0.08**	73	16.66	1.06±0.02	0.35
SWPP	1.48**	0.14**	79	14.78	1.39±0.02	0.41
BYLD	60.72**	9.34**	85	14.92	8.93±0.17	2.64
HI	10.95 ^{ns}	66.94 ^{ns}	55	18.12	41.21±0.55	14.82

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