Morphological Characterization, Variability, and Diversity among Amaranth Genotypes from Ethiopia

Mekonnen Degefu Yeshitila (mekonnenyeshitila19@gmail.com)
Hawassa University College of Agriculture
Andargachew Gedebo
Hawassa University College of Agriculture
Temsgen Magule Olango
Hawassa University College of Agriculture
Bizuayehu Tesfaye
Hawassa University College of Agriculture

Research Article

Keywords: genetic diversity, genotype performance, heritability, variability, genetic gain

Posted Date: February 21st, 2023

DOI: https://doi.org/10.21203/rs.3.rs-2554556/v1

Abstract

Amaranths are dicotyledonous plants with high yield potential, a high mineral uptake rate, short days, and high adaptability. It has been extensively investigated as a model C4 plant. The objectives of the current study were to estimate genetic diversity, heritability, and genetic advance for yield and yield-contributing traits of amaranth genotypes based on agro-morphological traits. The study was done on one hundred twenty amaranth genotypes planted over two growing seasons using an alpha lattice design with two replications. The analysis of variance showed the presence of significant variation ($P \leq 0.001$) between genotypes, years, and their interactions for most of the studied traits. Among the genotypes, based on their performance, promising genotypes KAZ-059, 225713, KAZ-058 and KEN-019, 242530, and 212890 exhibited higher leaf area, branch number, and plant height at maturity, and plant height at flowering. Selection based on these traits could be effective for amaranth leaf yield improvement. On the other hand, KEN-016, KEN-020, KAZ-060, KEN-010, KEN-018, and 22571 produced high grain yield along with better leaf area, axillary inflorescence length, terminal inflorescence lateral length, terminal inflorescence stalk length, grain sink filling rate, and thousand seed weight, indicating phenotypic-based selection on these traits might be reliable for grain yield improvement in amaranth genotypes. These genotypes were chosen as a result due to their high yield potential and good yield-related traits. Future selection efforts for amaranth should therefore continue to evaluate the genotypes under various environmental conditions. These genotypes were selected as a result because they had a high potential for yield and desirable traits that might boost yield.

Introduction

The genus Amaranthus (L.) belongs to the order Caryophyllales, which includes quinoa, spinach, and beetroot. Amaranthus is a dicotyledonous mesophyte that uses a special C4 carbon-fixation pathway (Morrison, 1985; Wang *et al*., 1999). Amaranth is a herbaceous plant or shrub that is found all over the world and is either annual or perennial (Stevens, 2012). The Amaranthus genus has 50–70 species and belongs to the Amaranthaceae family (Costea & DeMason, 2001). It is now referred to be a third-millennium crop plant (Rastogi & Shukla, 2013). The genus encompasses both cultivated and wild species, according to historical records. The Mayan civilization of South and Central America was the first to domesticate and cultivate amaranths some 8000 years ago (Rastogi & Shukla, 2013). They are one of the few non-kinds of grass that produce considerable amounts of small-seeded grain (Santra & Schoenlechner, 2017).

Amaranth has long been a component of traditional African agriculture and is semi-domesticated, mostly as a vegetable, in Ethiopia and other East African countries (Alemayehu *et al*., 2015). Amaranth is now grown as a grain crop in far-flung areas such as Ethiopia's mountains, South India's hills, Nepal's Himalayas, and Mongolia's plains, with exceptional seed quality and the highest potential for use as a food ingredient (Brink *et al*., 2006; Sokolova *et al*., 2021). The widespread usage of local names and the large genetic variation present in Ethiopia have also been suggested as a hub of amaranth diversity. In the Flora region of Ethiopia and Eritrea, eleven species have been identified (Demissew, 2010). Ethiopia is endowed with a wide range of food crops, the majority of which have received little to no attention in terms of research and the creation of regulatory frameworks that can encourage efficient commercial and industrial exploitation. One such underappreciated and neglected but double-duty species is amaranth. Amaranths are gluten-free (Rastogi & Shukla, 2013).

The morphological diversity of *Amaranthus species* is remarkable, as is their adaptation to a wide range of eco-geographical conditions (Lee *et al*., 2008). Despite the enormous morphological variability between and within *Amaranthus species*, there are only a few taxonomic traits that are unique to the genus (Sammour *et al*., 1993; Juan *et al*., 2007). Amaranths have a considerable genetic variation, which indicates that they have a lot of room for improvement. The determination of genetic diversity relies heavily on agro morphological genotype characterization. As a result, it is required for the successful conservation of amaranth biodiversity and crop enhancement programs (Shah *et al*., 2018).

Amaranth is not a true grain or cereal because the plant is not a member of the Poaceae family of grasses, but it is referred to as a "pseudo-cereal" since the species exhibits traits of grain in terms of flavor, appearance, and cooking (Alvarez-Jubete *et al*., 2010). Amaranth is an annual herbaceous or transient perennial, a stunning plant with vividly colored flowers, stems, and leaves. Amaranth is a crop that mostly self-pollinates and outcrosses to various degrees (Hauptli & Jain, 1985; Petruzzello, 2016). Being C_4 plants, they use an extremely effective type of photosynthesis to transform the raw materials of soil, co_2, sunshine, and water into tissue.

Amaranth is a high-yielding, climate-smart, nutrient-rich plant that is essential for meeting rising world demand while also reducing dependency on a few cereal crops. The potential of both native and exotic species for food or industrial must be harnessed, or new types must be created (Janovská *et al*., 2012). Therefore, amaranth has become more important in recent years as a substitute crop for other major cereals. The amaranth plant not only thrives in a variety of climates (Lakshmi & Vimala, 2000), but it is also one of the few exceptionally nutritionally multi-purpose crops. It is used as a vegetable, cereal, medicinal plant, dye plant, forage plant, ornamental plant, as well as a fuel source (Mlakar *et al*., 2009; Sheikh & Singh, 2013). Historically an important component of African agriculture, amaranth is currently farmed in Ethiopia and other East African nations, mostly as a vegetable (Emire & Arega, 2012; Corke *et al*., 2016). Due to the great nutritional value of both its leaves and seeds, amaranth is a superior food source value (Barba de la Rosa *et al*., 1992; Fasuyi *et al*., 2007). The protein, calcium, dietary fiber, and gluten-free starch content of the seeds is a higher and better balance of essential amino acids than that of grains and legumes (Singhal & Kulkarni, 1988; Barba de la Rosa *et al*., 1992; Venskutonis & Kraujalis, 2013; Schnetzler, 2018). Due to its high amounts of lysine and methionine and negligible prolamin content, which are the seed storage proteins that cause the symptoms of celiac disease and cerebropathy, amaranth has become a popular alternative crop (Angel Huerta-Ocampo & Paulina Barba de la Rosa, 2011). Despite these advantages, Ethiopia has yet to fully utilize amaranth as a crop, partly because there aren't many improved varieties from which farmers may choose.

Yield and its component is a multi-genic trait, impacted by the contribution of many loci across the genome for various physiological, abiotic, and biotic stress tolerance factors that all interact overtime during the growing season to determine final yield (Das, 2016). Direct selection of yield-related traits, which are easier to precisely quantify than the yield itself, has also been an effective yield improvement technique (Samonte *et al*., 1998; Kumar *et al*., 2014). Thus, selection based on yield coupled with yield components can be efficient since yield-contributing traits are less complex in heredity and less impacted by the environment (Samonte *et al*., 1998; Gatti *et al*., 2005; Kumar *et al*., 2014).

The introduction of genetic variability, selection, and usage of variance found in selected genotypes are all components of the contemporary breeding program used to produce new breeding materials. Heritability and variance components are important parameters of interest to disclose the genetic expression controlling the target trait. A genetic advance is also a potent instrument for looking for the first advance predicted by selection. To take advantage of the existing variations in amaranth genotypes, determining the extent of genetic diversity using markers of agro-morphological traits is crucial. Historic and less expensive morphological markers, which are the most straightforward measures of phenotypes, are frequently used to evaluate the extent of genetic diversity in populations (Samarina *et al*., 2022). Therefore, this study attempted to specify promising genotypes for selection and future amaranth breeding programs and to quantify the extent of genetic variability, heritability, and expected genetic gain in amaranth genotypes using markers of agro-morphological traits.

Materials And Methods

Experimental site

In the years 2020 and 2021, the experiment was carried out at Hawassa University, which is located at the agricultural experimental site. Geographically, the location is in Ethiopia's Sidama region, around 275 kilometers from the capital, Addis Ababa. The experimental area is located at latitude 7°2' 54.7503"N and longitude 38°30' 17.1608" E, at an elevation of 1709 meters above sea level. The soil texture class in the experimental area was clay loam, and the pH ranged from 6–to 6.5. The district's mean monthly minimum and maximum temperatures are 14.1.0 0C and 27.9 0C, respectively. For two growing seasons, the experimental farm received an average of 1379.16mm of rain throughout the growing seasons.

Plant materials

A total of 120 amaranth genotypes were used in this study (Table **S1**), 34 from the Ethiopian Biodiversity Institute (EBI), 2 from the Melkasa research center, 15 from the Werere research center (Afar region), and 8 from Sidama. The remaining 61 genotypes were collected in the SNNP, Amhara, Benishangul & Gumuz, Oromia, and Tigray regions of Ethiopia in 2019 and characterized for various agro-morphological traits. One hundred and eighteen members have passport information, while the other two do not and are considered released varieties. A two-season experiment was conducted at Hawassa University in Ethiopia to achieve the aforementioned objective.

Experimental Layout And Crop Management

The experimental field was cleared, properly plowed, and harrowed by a tractor, with ridge preparation done by hand hoe. The experimental design was alpha lattice. A layout with 2 replications, 16 blocks, and 15 plots per block for amaranths was conducted. Each unit plot was separated by a 0.60-meter way between plots, a one-meter between blocks, and a three-meter between replications, with a plot size of 1.80 m in length and 1.50 m width of 2.7 m^2 area. Each season required a total space of 1,345.2sq.m (38 m × 35.4 m). On April 15th, 2020, and 2021, the seed was sown at one location in each season, which is under ideal growing circumstances and during the agricultural season. One growing season on the experimental site in one year is considered the environment. Seeds of various genotypes were consistently sowed in two rows with a gap of 0.75 m between them. Seeds are quite tiny, and they were sowed in seedbeds and covered with finely powdered farmyard manure after being combined with sand in a 1:4 ratio. At 14 and 22 days after sowing (DAS), thinning was done twice at a distance of 75 cm between rows and 30 cm between plants. According to Grubben and Van Sloten (1981a) and Sudhir Shukla *et al.* (2006), the experiment followed standard cultural practices. Hand-hoeing was used to control weeds at 2-week intervals following germination and whenever necessary. A total of 12 plants were maintained in each plot. During the first season of the trial cutworms, were identified as important amaranth pests. Diseases such as root rot, stem rot, and white rot were also observed on some plants. But no pests were identified in the second season. Five percent karate was sprayed twice a day for 5 days at a rate of 25 ml per 15 liters of water to control cutworm and leaf folder. 250 EC (0.05 percent) was sprayed around the collar region to reduce root rot, and Redomil Gold (0.2 percent) was sprayed twice to control white rust.

Data Collection And Measurements

To characterize the material under study, observations were made on various morphological traits at distinct phenological stages (Table **S2**). In each plot, the phenotypic characteristics of 10 randomly tagged plants were assessed. Plants were grown to maturity and defined using amaranth descriptors, as recommended by the International Board for Plant Genetic Resources based on taxonomic keys (Grubben & Van Sloten, 1981b). Characters not on the list that were considered necessary for the characterization were included. In this investigation, a total of 24 quantitative characters were recorded. In each season, data was collected from the field at four phases of growth: germination, vegetative stage, 50% of the plants' developing inflorescences, and plant maturity shortly before and after harvesting. Plant height at flowering and maturity(cm), petiole length (cm), leaf width (cm), leaf thickness (mm), terminal inflorescence stalk length (cm), inflorescence lateral length(cm), number of branches per plant (number), number of leaves (number), number of nodes, stem diameter (mm), number of days to emergence, number of days to flowering, number of days to maturity, leaf area (cm^2), and 1000-seed weight (g), leaf yield tone ha^{-1}, grain yield tone ha^{-1}, grain filling period days), grain filling rate(kg $ha^{-1}day^{-1}$) are among them. As a result, agro-morphological characteristics were evaluated four times per plot for each replication, for a total of forty observations per plot. Seedling data, vegetative data, inflorescence data, and seed data were among the 24 characteristics evaluated. Except for days to emergence, days to flowering, and days to maturity, which were recorded at the plot level, all ten planted genotypes for each population (two replications) were used to collect quantitative trait data. For the traits, the mean value of 10 plants per plot was measured and recorded. Three different leaf lengths, leaf thickness, leaf width, petiole length, and leaf area (small, medium, and large) were randomly picked per plant for measurement. Leaf length, breadth, thickness, petiole length, and area were computed using the averages of 30 measurements (10 plants per plot for each of the 3 different leaf and petiole sizes). The harvest was done manually, panicles were carefully removed to minimize grain spilling, then the panicles were threshed by a mechanical thresher, seeds were cleaned, and the seeds were held in an electric oven at 100 ^oC for 48 hours to regulate the moisture content to 12 percent, as advised by (Biru, 1978; de Jesus Souza *et al.*, 2016). A digital caliper was used to measure the diameter of the stem and the thickness of the leaves (Digimatic Solar DC-S15 m, Mitutoyo, Japan). The LI-3100 AREA METER, an electronic leaf area meter, was used to measure the leaf area (LI, Cor, Inc, Lincoln, Nebraska, USA).

Statistical analysis

Analysis of variance

The SAS computer program first confirmed Bartlett's test for homogeneity of variance before executing ANOVA for each year's analysis ((Table **S3**). The F-max technique of Hartley (1950), which is based on the ratio of the larger mean square error (MSE) from the separate analysis of variance to the smaller MSE, was also used to test the homogeneity of error variance for the combined ANOVA (Table **S3**). The error variance is considered homogenous if the bigger MSE is not three times greater than the smaller MSE

(Gomez & Gomez, 1984). After determining that the error variance was homogeneous, the combined ANOVA was carried out using the SAS PROC GLM procedure. The genotype and year effects were both accounted for using a linear random model. The denominator degree of freedom was calculated using Satterthwaite's approximation approach, and the mean square of the random effect was compared to the sum of replication and interaction mean squares minus residual mean squares. The interaction effect, however, was assessed against the residual mean square whereas the genotype random effect was tested against the interaction (genotype by year) mean square. So, using the SAS statistical tool, analysis of variance (ANOVA) was performed on the pooled data from a two-year alpha lattice design. The quantitative data was evaluated using a two-way analysis of variance (ANOVA) in SAS 9.4 (Lehman *et al*., 2013), taking into account all sources of variation as random effect blocks, replications, genotypes, and year of planting as variables. All sources of variation were considered random effects, and the interactions between genotypes and years were evaluated. Following Gomez and Gomez (1984), a mean comparison between years was performed using Duncan's Multiple Range Test (DMRT) at a 5% probability level. The numerator degree of freedom for the year F-test was Y-1 while the denominator (combined mean squares) degree of freedom was estimated using Satterthwaite's (Satterthwaite, 1946) formula as indicated below.

$$\mathrm{F1} = \frac{MSy}{(MS_r + MS_{gy-MSe})}$$

1

$$\mathrm{DFcms} = \frac{(MS_r + MS_{gy-MSe})^2}{\frac{(MS_r)^2}{(r-1)} + \frac{(MS_{gr})^2}{(g-1)(y-1)} + \frac{(\mathrm{MSe})^2}{y(g-1)(r-1)}}$$

2

Where Fl is F-test for the year; MSy is the mean square of the year; MSr is the mean square of replication; MSgy is the mean square of genotype by year interaction; MSe is the mean square of error; DFcms is the degrees of freedom for combined mean square; r is replication; y is the year, and g is genotype.

The statistical models for each year and combined across the two years are presented below. The statistical model of the alpha lattice design for individual years is given by:

$$\mathrm{Yijkl} = \mu + \mathrm{Yi} + \mathrm{Rj}\,(\mathrm{i}) + \mathrm{Bk}\,(\mathrm{ij}) + \mathrm{Gl} + (\mathrm{GY})\,\mathrm{il} + \epsilon\mathrm{ijk}\,(3)$$

The statistical model of the alpha lattice design across years is given by:

$$\mathrm{Yijkl} = \mu + \mathrm{Yi} + \mathrm{Rj}\,(\mathrm{i}) + \mathrm{Bk}\,(\mathrm{ij}) + \mathrm{Gl} + (\mathrm{GY})\,\mathrm{il} + \epsilon\mathrm{ijkl}$$

4

where yijk is the measured response of genotypes i at year j and block k; μ is the overall mean; G (k) is the k-th genotype random effect; Y (i) is the i-th year random effect; GY (ki) is the genotype k by year i interaction is random effect; Bj is the j th block random effect, and ε (ijkl) is the random error.

Table 8
Combined analysis of variance (ANOVA) and expected mean square for the random model of alpha lattice design

Sources of variation	Degree of freedom (Df)	Mean square (MS)	Expected means square (EMS)	F- test
Year (y)	y-1	M1	$\delta^2 e+r\delta^2_{gy}+g\delta^2 r'(y)$	M1/M2 + M5-M3
Rep(year)	y(r-1)	M2	$\delta^2 e+g\delta^2 b(ry)$	M2/M3
Block(rep*year)	yr(b-1)	M3	$\delta^2 e+\delta^2 g/r(ry)$	M3/M6
Genotypes (g)	g-1	M4	$\delta^2 e+r'\ \delta^2 gy+r'y\ \delta^2 g$	M4/M5
Genotypes*year	(g-1)(y-1)	M5	$\delta^2 e+r'\ r'\delta^2 gy$	M5/M6
Error	[y(r-1)(g-1)]-[yr(b-1)	M6	$\delta^2 e+g/b\delta^2 b(ry)+g\ \delta^2 r'(y)$	-

Comparison Of Selected Genotypes With The Original Population

To compare with the original population, the means of the top 5% genotypes for each trait were independently computed. The student t-test table was used to determine the significance of the difference between the sample mean and population parameter. When the calculated t-value is higher than the tabulated t-value, the difference is deemed significant (Singh *et al.*, 2001). To compare the performance of the 5% best-selected genotypes with the size of a population, the absolute t-value was obtained using the student's t-test formula as follows:

$$T = (\bar{X} - \mu)/(S/\sqrt{n}) \quad (5)$$

Where n is the number of genotypes selected from the size of a population for better performance, $\bar{x}$ is the mean of the genotypes that were selected, S is the sample standard deviation, andμ is the mean of the size of the population.

Estimates of variance components:
The mean, phenotypic, genotypic, and coefficient of variation were all measured to evaluate the population's level of diversity. According to the approach recommended by Johnson *et al.* (1955), the combined over-year mean squares computed using SAS statistical techniques and the causes of variations in alpha lattice design were utilized to estimate variance components as follows:

$$\sigma^2 y = \frac{(MSy + MSe) - (MSr + MSgy)}{gr'}$$

6

$$\sigma^2 r = \frac{[(MSr) - (MSe)]}{g}$$

7

$$\sigma^2 g = \frac{[(MSg) - (MSgy)]}{r'y}$$

8

$$\sigma^2 gy = \frac{[(MSgy) - (MSe)]}{r'}$$

9

$$\sigma^2 e = MSeand$$

10

$$\sigma^2 p = \sigma^2 g + \frac{\sigma^2 gy}{y} + \frac{\sigma^2 e}{r\prime y}$$

11

where δ^2y is the variation over the year; The term "MSy" refers to the mean square of a year. g represents the number of genotypes, r represents the number of replications, δ^2r represents the replication variance, MSr represents the mean square of replication, δ^2b represents the block variance, MSe represents the mean square of error, and δ^2g represents the genotypic variance. MSgy stands for the mean square of genotype by year interaction. "y" specifies the number of years, while MSg refers to the genotypes' mean square. The phenotypic variance is represented by δ^2p, the environmental variance by δ^2e, and the genotype by year interaction variance is represented by δ^2gy. On the other hand, the technique suggested by Singh and Chaudhary (1977) was also applied to estimate the genotypic (GCV), phenotypic (PCV), and environmental coefficients of variation (ECV).

These estimates of variance were categorized as low when values were less than 10%, medium when values were between 10% and 20%, and high when values were over 20% (Johnson *et al.*, 1955; Sivasubramanian & Menon, 1973; Deshmukh *et al.*, 1986).

$$GCV = \frac{\sqrt{\delta^2 \mathrm{g}}}{\mu} * 100$$

12

$PCV = \frac{\sqrt{\delta^2 \mathrm{P}}}{\mu}$ *100 (13)

$$ECV = \frac{\sqrt{\delta^2 \mathrm{e}}}{\mu} * 100$$

14

Where GCV denotes the genotypic coefficient of variation, PCV denotes the phenotypic coefficient of variation, and ECV denotes the environmental coefficient of variation. Whereas the genotypic variation is represented by δ^2g, the phenotypic variation is represented by δ^2p, the environmental variation by δ^2e, and the genotype by year interaction variation is represented by δ^2gy.

Estimation of heritability

Heritability was defined by **(**Allard (1960); Falconer, 1989**),** as a proportion of the (δ^2g) the genotypic variance, and phenotypic variance (δ^2p). Singh *et al.* (2001) and Pandey and Singh (2011) determined that the heritability estimates were classed as low when they were less than 40%, medium when they were between 40 and 59%, fairly high when they were between 60 and 79, and very high when they were higher than 80% estimated these values as follows:

$$h^2{}_{bs=} = \frac{\frac{[(MSg)-(MSgy)]}{ry}}{\sigma^2 g + \frac{\sigma^2 gy}{y} + \frac{\sigma^2 e}{ry}} * 100$$

15

Whereas δ^2g stands for genotypic variance, δ^2p for phenotypic variance

and h^2 stands for heritability.

4.5.5. Estimation of genetic advance

Using the approach described by **Allard** (Allard, 1960), expected genetic advancement as a component of the mean (GA) for each characteristic at 5% selection intensity (k = 2.06) was calculated. Additionally, using the Comstock and Robinson (Comstock &

Robinson, 1952) method, the expected genetic advance as a percentage of the mean (GAM) was calculated to examine the magnitude of the predicted advance of various characteristics under selection. Johnson (Johnson *et al*., 1955) defined the estimated GAM values as low when values were less than 10%, medium when values were between 10% and 20%, and high when values were greater than 20%.

$GA = K^* \sqrt{\delta^2 p} * h^2$ (16)

$GAM = GA/ \bar{x} * 100$ (17)

Results

Analysis of Variance (ANOVA)

Table 1 illustrates the variance results from a pooled analysis of all traits for 120 genotypes. For all characteristics other than leaf thickness (mm), petiole length (cm), leaf yield (t/ha), top lateral branch length (cm), and thousand seed weight (g), the mean squares resulting from genotypes differed significantly among genotypes ($P \leq 0.001$). The majority of the replicates showed no discernible differences. The effect of cropping season was significant for all traits, including plant height at flowering (days), leaf area (cm^2), leaf yield (t/ha), branch number (number), top lateral branch length (cm), auxiliary inflorescence length (cm), terminal inflorescence stalk length (cm), grain filling periods (days), and thousand seed weight (g). Similarly, genotype by cropping season's interaction effects was significant for all morphological and agronomic traits, except leaf yield (t/ha), and thousand seed weight (gm.) (Table 1). Significant genotype by cropping season's interaction effects was mostly a 'cross-over' type; i.e., interactions were associated with rank order changes among the genotypes (Fig. 1).

Table 1
Combined analysis of variance (over the year) for 24 traits of 120 amaranth genotypes grown at Hawassa University's agricultural research site in the 2020 and 2021 cropping seasons.

Traits	Rep(Year) DF = 2	Block(Rep*year) (DF = 28)	Year (DF = 1)	Genotype (DF = 119)	G*Y (DF = 119)	MSE (DF = 210)	CV (%)
Days to emergence (days) **[DE]**	0.42^{ns}	0.319^{ns}	156.41**	2.475***	1.328***	0.334	8.67
Days to flowering(days) **[DF]**	58.16^{ns}	24.35^{ns}	1836.92**	295.27***	73.17***	22.27	8.92
Plant height at flowering(days) **[PHF]**	348.176^{ns}	235.763^{ns}	439.01^{ns}	1318.99***	468.187***	179.59	18.48
Leaf number (number) **[LN]**	475.967***	18.491***	41458***	70.193***	37.976***	9.982	10.75
Leaf area(cm^2) **[LA]**	33869***	1079.06***	6537.352^{ns}	1986.13***	423.752^{ns}	395.42	30.01
Leaf length(cm) **[LL]**	15.236***	1.607^{ns}	1122.87**	24.03***	5.45***	1.810	9.30
Leaf width(cm) **[LW]**	3.633***	0.481^{ns}	298.67**	5.911***	1.159***	0.446	9.28
Leaf thickness(mm) **[LT]**	0.046***	0.0028^{ns}	3.015**	0.0025^{ns}	0.003***	0.0014	10.09
Petiole length(cm) **[PL]**	4.079**	0.642^{ns}	289.99**	2.86^{ns}	2.580***	0.57	12.06
Leaf yield(t/ha) **[LY]**	369.875***	25.526**	403.59^{ns}	22.57^{ns}	18.722^{ns}	15.567	39.41
Branch number(number) **[BN]**	75.015**	21.589^{ns}	73.907^{ns}	203.614***	32.486***	16.583	14.30
Basal lateral branch length (cm) **[BLBL]**	2797.86***	191.421^{ns}	39905.05^{ns}	5318.31***	1671.72***	315.72	33.84
Top lateral branch length(cm) **[TLBL]**	88.290**	42.599**	290.75^{ns}	165.63^{ns}	173.70***	25.044	24.28
Node number (number) **[NN]**	245.54***	11.53^{ns}	65114**	41.13^{ns}	31.89***	8.175	10.84
Days to maturity(days) **[DM]**	22.10^{ns}	67.56**	682.59**	616.34***	133.81***	43.77	6.56
Plant height at maturity(days) **[PHM]**	59.25^{ns}	370.89^{ns}	377692***	8801.80***	1557.40***	333.12	8.69
Stem diameter (cm) **[SD]**	85.37**	10.82^{ns}	9515.79**	113.29***	20.29***	12.29	12.45
Auxiliary inflorescence length (cm) **[AIL]**	91.50***	11.66^{ns}	70.58^{ns}	112.32***	31.13***	9.52	25.73
Terminal lateral inflorescence length (cm) **[TILL]**	30.57**	6.02^{ns}	23433**	50.37**	33.65***	4.52	11.95
Terminal inflorescence stalk length (cm) **[TISL]**	175.38**	29.89^{ns}	3.06^{ns}	210.34**	121.56***	25.51	17.30
Grain filling periods(days) **[GFP]**	31.95^{ns}	79.26^{ns}	279.99^{ns}	406.91***	149.37***	58.51	15.40
Grain sink filling rate (kg ha^{-1}day $^{-1}$) **[GSFR]**	170.23^{ns}	516.81**	8900.84**	765.95**	551.09***	313.00	59.26
Thousand seed weight(g) **[TSW]**	0.0019^{ns}	0.160^{ns}	0.26^{ns}	0.27^{ns}	0.22**	0.13	41.90
Grain yield (t ha-1) **[GY]**	0.91ns	0.89**	17.05**	1.28**	0.92***	0.57	54.00

DF = Degree of freedom; CV = Coefficient of variation; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively; Rep (L) = Replication nested under location

Effect of test cropping seasons

Table 2 indicates how experimental cropping seasons impacted the mean performance of agro-morphological characters in amaranth genotypes. Several agro-morphological parameters of the amaranth genotypes were significantly different between the two cropping seasons. Days to emergence (days), days to flowering (days), leaf length (cm), leaf width (cm), leaf thickness (mm), petiole length (cm), node number (number), days to maturity (days), plant height at maturity (cm), stem diameter (cm), terminal lateral inflorescence length (cm), grain sink filling rate (kg $ha^{-1}day^{-1}$), thousand seed weight and grain yield (t ha^{-1}) were all significantly higher in 2020 than in 2021. Whereas, plant height at flowering (cm), leaf area (cm^2), leaf yield (t/ha), branch number (number), top lateral branch length (cm), auxiliary inflorescence length (cm), terminal inflorescence stalk length (cm), and grain filling periods (days) did not differ significantly between cropping seasons. The mean performance of all traits was greater in the cropping seasons in 2020 than in 2021 (Table 2).

Table 2
Mean performance for 24 agro- morphological traits of 120 amaranth genotypes grown at Hawassa University's agricultural research site in the 2020 and 2021 cropping seasons.

Traits	Cropping seasons (Years)		R^2	P - Value
	2020	2021		
Days to emergence (days)	7.20[a]	6.10[b]	0.90	0.003
Days to flowering(days)	48.2[a]	44.3[b]	0.91	0.030
Plant height at flowering (cm)	74.70	72.70	0.85	0.378
Leaf number (number)	39.00[a]	20.40[b]	0.96	0.011
Leaf area (cm^2)	73.60	66.20	0.81	0.703
Leaf length(cm)	15.90[a]	12.90[b]	0.92	0.013
Leaf width (cm)	7.90[a]	6.30[b]	0.93	0.011
Leaf thickness (mm)	0.50[a]	0.30[b]	0.92	0.015
Petiole length (cm)	7.00[a]	5.50[b]	0.89	0.01
Leaf yield (t/ha)	11.20	9.40	0.65	0.406
Branch number (number)	29.40	28.60	0.89	0.426
Basal lateral branch length (cm)	61.10[a]	42.80[b]	0.93	0.063
Top lateral branch length (cm)	21.80	20.30	0.88	0.211
Node number (number)	38.20[a]	14.90[b]	0.98	0.005
Days to maturity (days)	97.39[a]	95.00[b]	0.91	0.0205
Plant height at maturity (cm)	237.30[a]	181.02[b]	0.96	0.0002
Stem diameter (cm)	32.80[a]	23.90[b]	0.91	0.008
Auxiliary inflorescence length (cm)	12.40	11.70	0.90	0.472
Terminal lateral inflorescence length (cm)	24.90[a]	10.90[b]	0.97	0.001
Terminal inflorescence stalk length (cm)	29.00	28.90	0.89	0.907
Grain sink filling rate (kg $ha^{-1}day^{-1}$)	34.40[a]	25.80[b]	0.85	0.026
Grain filling periods (days)	50.70	49.20	0.71	0.100
Thousand seed weight (g)	0.88	0.83	0.69	0.007
Grain yield (t ha^{-1})	1.60[a]	1.20[b]	0.70	0.023

Mean Performance Of Genotypes

Over several traits, genotype differences were substantial (Fig. 2). It was clear that most genotypes of amaranth outperformed or had superior agro-morphological performances when compared to the overall mean of the population and newly released variety(AC-NL and Madiira II), including the thousand seed weight (g), leaf number (number), leaf area (cm^2), leaf length (cm), leaf width (cm), leaf thickness (mm), days to emergence (days), petiole length (cm), and node number (number), top lateral branch length (cm), and days to maturity (days) (Fig. 2A). In contrast, several newly introduced varieties outperformed the population mean when evaluated across all agro-morphological parameters, particularly grain and leaf yield traits. So, comparisons at both levels (with population and average

performances of released varieties) showed that there were genotypes comparable to the released genotypes for all 24 traits (Fig. 2B). The differences between the numbers of superior and inferior genotypes for most studied traits were higher when the tested genotypes were compared with the mean of released varieties than the mean of the population.

As shown in Table 3, the performance of the top 5% of leaf yielder amaranth genotypes in comparison with the bottom 5% of leaf yielder genotypes, the population means, and the mean of two released varieties. The findings showed that in the majority of evaluated phenotypic traits, the top leaf yielder genotypes were superior to the least leaf yielder genotypes, the population means, and the mean of released varieties. The top leaf yielder genotypes, however, were inferior to the least leaf yielder genotypes, the population means, and released variety mean in terms of days to emergence (days), basal lateral branch length (cm), top lateral branch length (cm), auxiliary inflorescence length (cm), terminal inflorescence lateral length (cm), terminal inflorescence stalk length (cm), grain filling periods (days), and thousand seed weight. Comparably, Table 3 compares the performance of the top 5% grain yielder amaranth genotypes with the lowest 5% grain yielder genotypes, the population means, and the mean of two released varieties. The most grain genotypes outperformed the least grain-yielding genotypes in terms of leaf area (cm^2), leaf length (cm), leaf width (cm), leaf yield (t/ha), top lateral branch length (cm), auxiliary inflorescence length (cm), terminal inflorescence lateral length (cm), terminal inflorescence stalk length (cm), grain sink filling rate (kg $ha^{-1}day^{-1}$), thousand seed weight (g). On the other hand, the top grain yielder genotypes were inferior to the least grain yielder genotypes in terms of the number of leaf days to emergence (days), days to flowering (days), plant height at flowering cm), leaf number (number), branch number (number), basal lateral branch length (cm), days to maturity (days), plant height at maturity (cm), and grain filling periods (days).

Table 3

Compares the mean of 5% high and low leaf and grain yielder amaranth genotypes to the mean of the population and released varieties for 24 amaranth traits grown at Hawassa University's agricultural research site in the 2020 and 2021 cropping seasons.

Tr Tait	High/low Leaf yielder genotypes							High/low grain yielder genotypes						
	Top	Bottom	MP	MRV	Differences			Top	Bottom	MP	MRV	Differences		
	(A)	(B)	(C)	(D)	A-B	A-C	A-D	(A)	(B)	(C)	(D)	(A-B)	(A-C)	(A-D)
DE	6.50	7.1	6.7	6.1	-0.7	-0.2	0.3	6.6	7.3	6.7	6.1	-0.6	0.0	0.5
DF	49.3	34.7	46.3	53.5	14.7	3.1	-4.2	37.4	47.2	46.3	53.5	-10.4	-8.9	-16.1
PHF	84.3	49.2	73.7	76.0	35.1	10.6	8.3	60.5	72.8	73.7	76.0	-12.3	-13.2	-15.5
LN	29.0	22.9	29.7	27.6	6.2	-0.7	1.5	23.8	29.8	29.7	27.6	-6.0	-5.9	-3.8
LA	83.6	39.5	69.9	72.6	44.1	13.7	11.1	14.3	12.9	69.9	72.6	1.4	-55.7	-58.3
LL	15.9	10.2	14.4	14.6	5.7	1.5	1.3	14.3	12.9	14.4	14.6	1.4	-0.1	-0.4
LW	7.3	5.2	7.1	6.5	2.1	0.2	0.8	7.2	6.1	7.1	6.5	1.1	0.1	0.7
LT	0.4	0.4	0.4	0.4	0.0	0.0	0.0	0.4	0.4	0.4	0.4	0.0	0.0	0.0
PL	6.2	5.2	6.3	5.8	1.0	0.0	0.4	5.7	6.0	6.3	5.8	-0.3	-0.6	-0.2
LY	16.2	6.3	10.3	10.7	9.9	5.8	5.4	9.0	8.5	10.3	10.7	0.5	-1.3	-1.7
BN	28.9	22.3	29.0	26.1	6.7	0.0	2.8	22.2	27.6	29.0	26.1	-5.3	-6.7	-3.9
BLBL	37.8	77.7	51.9	62.6	-39.9	-14.1	-24.8	44.7	59.9	51.9	62.6	-15.2	-7.2	-17.9
TLBL	17.7	28.8	21.1	15.1	-11.1	-3.4	2.6	28.2	20.2	21.1	15.1	8.0	7.2	13.1
NN	27.4	22.2	26.5	25.4	5.2	0.9	2.0	22.1	26.8	26.5	25.4	-4.7	-4.4	-3.3
DM	99.2	90.0	96.2	94.5	9.2	3.0	4.7	87.0	110.6	96.2	94.5	-24.3	43.6	-7.1
PHM	209.	151.0	209.	196.4	58.2	-0.1	12.8	183	191.2	209	196.4	-8.2	-26.2	-13.3
SD	29.7	20.3	28.3	28.0	9.4	1.4	1.7	25.3	26.5	28.3	28.0	-1.2	-3.0	-2.7
AIL	12.8	15.1	12.0	9.6	-2.4	0.7	3.2	18.9	10.0	12.0	9.6	8.9	6.9	9.3
TILL	17.0	18.6	17.9	17.5	-1.7	-1.0	-0.6	24.4	15.9	17.9	17.5	8.5	6.5	6.9
TISL	30.3	32.0	29.0	29.5	-1.8	1.3	0.8	37.6	23.7	29.0	29.5	13.9	8.7	8.1
GFP	49.9	55.3	49.9	47.1	-5.4	-0.1	2.8	49.5	63.5	49.9	47.1	-13.9	-0.4	2.4
GSFR	29.7	25.3	30.1	34.0	4.4	-0.4	-4.3	64.4	7.7	30.1	34.0	56.7	34.3	30.4
TSW	0.8	1.0	0.9	0.9	-0.2	0.0	-0.1	0.9	0.7	0.9	0.9	0.2	0.1	0.0
GY	1.4	1.3	1.4	1.5	0.1	-0.1	-0.2	3.0	0.4	1.4	1.5	2.6	1.6	1.4

Table 4 indicates the results of the top 5% of grain yielder genotypes for the assessed phenotypic variables. The top 5% of grain yielder genotypes were KEN-016, KEN-020, KAZ-060, KEN-010, KEN-018, and 225715. The first top grain yielder genotype (KEN-016) had a higher top lateral branch length (cm), terminal lateral inflorescence length (cm), and grain filling rate (kg $ha^{-1}day^{-1}$). The second top seed yielder genotype (KEN-020) gave a higher basal lateral branch length (cm) and grain filling rate (kg $ha^{-1}day^{-1}$). The traits of the third-best grain yielder genotype were longer terminal inflorescence stalk length (cm) and auxiliary inflorescence length (KAZ-060). Higher top lateral branch length (cm), auxiliary inflorescence length (cm), and terminal inflorescence stalk length (cm) were obtained by the fourth-best grain-yielding genotype (KEN-010). The fifth-best grain-yielding genotype, KEN 018, exhibited the most days to emergence (days), days to flowering (days), plant height at flowering (cm), leaf number (number), leaf area (cm^2), leaf length (cm), and leaf breadth (cm). The top 5% leaf yielder genotypes were KAZ-059, 225713, KAZ-058, KEN-019, 242530, and 212890. Higher days to flowering (days), leaf area (cm^2), leaf thickness (mm), and petiole length (cm) were found in the first top leaf yielder

genotype (KAZ-059). The genotype with the second-highest leaf yield (225713) had higher plant height at blooming (cm), leaf length (cm), branch number (number), basal lateral branch length (cm), days to maturity (days), plant height at maturity (cm), stem diameter (cm), and grain filling durations (days). The third top grain yielder genotype (KAZ-058).has larger leaves (cm) and longer terminal inflorescence stalks (cm). The fourth-best leaf-yielding genotype (KEN-019) developed more leaves and nodes (number).

Table 4
Mean traits performance of top 5% leaf and grain yielder genotypes for 24 traits of amaranth grown at Hawassa University's agricultural research site in the 2020/2021 cropping season.

	Leaf yield-producing genotypes						Grain yield-producing genotypes					
Traits	**1st**	**2nd**	**3rd**	**4th**	**5th**	**6th**	**1st**	**2nd**	**3rd**	**4th**	**5th**	**6th**
Days to emergence (days)	5.8	6.8	5.5	6.8	6.5	7.5	7.0	6.5	6.5	6.5	7.3	6.0
Days to flowering (days)	48.3	59.8	44.5	44.8	46.3	52.5	34.3	43.3	32.3	31.5	50.8	32.5
Plant height at flowering (cm)	71.9	144.9	57.6	62.6	76.1	92.6	44.5	47.4	47.7	52.8	93.0	77.8
Leaf number (number)	28.4	27.8	31.6	34.2	25.8	26.5	15.1	31.3	19.9	17.2	35.3	24.2
Leaf area (cm^2)	92.3	80.7	87.0	62.1	81.0	98.8	63.6	46.0	49.0	49.2	77.7	75.8
Leaf length (cm)	15.6	17.2	14.4	15.6	16.0	16.8	12.5	14.6	12.5	12.6	17.5	16.0
Leaf width (cm)	7.5	6.6	7.9	6.8	7.1	7.8	6.7	6.4	6.4	6.6	10.0	7.0
Leaf thickness (mm)	0.4	0.4	0.4	0.4	0.4	0.5	0.4	0.4	0.4	0.4	0.4	0.5
Petiole length (cm)	7.1	6.1	6.3	5.2	5.9	6.8	4.5	4.6	5.0	4.8	7.5	7.6
Leaf yield (t/ha)	21.7	15.6	15.3	14.9	14.8	14.8	9.3	7.8	8.4	6.8	12.8	8.9
Branch number (number)	25.6	39.9	22.3	25.6	23.9	36.4	18.2	22.8	17.7	17.0	39.2	18.5
Basal lateral branch length (cm)	21.0	71.5	17.9	30.0	58.0	28.4	31.7	57.4	39.7	43.9	48.0	47.7
Top lateral branch length (cm)	15.7	13.2	16.2	17.8	23.2	20.0	38.4	12.3	32.2	34.3	23.9	28.1
Node number (number)	27.2	25.3	27.4	32.3	24.3	27.8	16.6	29.4	19.0	17.9	27.8	22.0
Days to maturity(days)	82.8	128.0	85.5	98.3	93.5	107.3	82.5	80.5	82.5	82.5	106.3	87.5
Plant height at maturity (cm)	181.4	236.3	156.9	190.9	230.0	259.4	153.2	157.7	148.8	137.3	232.5	268.8
Stem diameter (cm)	28.1	36.1	24.9	28.5	32.7	27.8	24.1	29.9	22.0	18.9	34.0	22.9
Auxiliary inflorescence length (cm)	9.0	6.8	16.5	13.1	14.0	17.2	19.7	9.2	23.2	22.4	17.6	21.3
Terminal lateral inflorescence length (cm)	16.6	14.0	19.9	19.4	17.3	14.6	26.8	17.9	28.8	25.6	23.3	24.0
Terminal inflorescence stalk length (cm)	24.7	24.6	32.8	33.4	33.8	32.6	38.2	24.8	42.6	41.8	39.3	39.2
Grain-filling periods (days)	34.5	68.3	41.0	53.5	47.3	54.8	48.3	37.3	50.3	51.0	55.5	55.0
Grain sink filling rate ($kg\ ha^{-1} day^{-1}$)	41.1	19.3	32.8	13.1	43.5	28.3	71.6	94.0	64.5	60.0	50.3	46.1
Thousand seed weight (g)	1.1	0.5	1.1	0.6	0.7	0.9	0.7	1.0	0.8	1.2	0.9	0.9

	Leaf yield-producing genotypes						Grain yield-producing genotypes					
Traits	**1st**	**2nd**	**3rd**	**4th**	**5th**	**6th**	**1st**	**2nd**	**3rd**	**4th**	**5th**	**6th**
Grain yield (t ha^{-1})	1.3	1.3	1.3	0.7	2.0	1.5	3.3	3.2	3.1	2.9	2.9	2.4

Top 5% high leaf yielder amaranth genotypes (1st = KAZ-059; 2nd = 225713; 3rd = KAZ-058; 4th = KEN-019; 5th = 242530; 6th = 212890); Top 5% high grain yielder amaranth genotypes (1st = KEN-016; 2nd = KEN-020; 3rd = KAZ-060; 4th = KEN-010; 5th = KEN-018; and 6th = 225715).

Using certain agro-morphological parameters, the performance of the top 5% of genotypes is compared with the population means and the mean of the released variety (Table 5). When compared to the released varieties, no single genotype consistently outperformed the top 5% of best performers for various parameters such as grain yield, grain sink filling rate (kg $ha^{-1}day^{-1}$), days to maturity (days), and grain filling time (days). Many other superior genotypes for multiple traits of agronomic significance, including grain yield, were also identified. The best genotypes for grain yield (t ha^{-1}) were found to be superior by 71.22–138.85% to the population mean and 53.55–114.9% to the mean of grain yield performance of the released varieties; leaf yield (t/ha) 43.06–110.38% to the population mean and 37.59–102.33% to the mean leaf yield performance of the released varieties; plant height at maturity (cm) 36.86–64.09% to the population mean and 45.85–74.86% to the mean plant height at maturity performance of the released varieties; and grain sink filling rate (kg $ha^{-1}day^{-1}$) 67.92% – 212.19% to the population mean and 15.42% – 28.97% to the released varieties' mean grain sink filling rate performance; grain filling periods (days) 38.67%-100.74% to the population mean and 46.93%-112.71% to the released varieties' mean grain filling periods performance; thousand seed weight (g) 53.49%-68.60% to the population mean and 40.43%-54.26% to the released varieties' mean thousand seed weight performance; days to 50% flowering (days) 33.46%-49.12% to population mean and 15.42%-28.97% days to flowering performance of released varieties; days to maturity (days) 30.98%-61.112% to population mean and 33.33%-64.02% days to maturity performance of released varieties; terminal inflorescence stalk length (cm) 46.75%-65.68% to population mean and 43.97%-62.53% terminal inflorescence stalk length performance of released varieties; and leaf area (cm^2) 44.31%-71.86% to population mean, and 39.01%-65.4% leaf area performance of released varieties (Table 5).

Table 5

Mean performance comparison of top 5% genotypes with mean of the population and released varieties for 10 traits of amaranth grown at Hawassa University's agricultural research site in 2020 and 2021 cropping season.

Genotypes	Mean	Relative advantage (%) over		Genotypes	Mean	Relative advantage (%) over	
		MP	MRV			MP	MRV
1. 1. Plant height at maturity (cm)				**2. 2. Leaf yield (t/ha)**			
215567	343.36	64.09%	74.86%	KAZ-059	21.69	110.38%	102.33%
MEK-084	292.97	40.01%	49.20%	225713	15.56	50.92%	45.15%
KEN-017	292.68	39.87%	49.05%	KAZ-058	15.26	48.01%	42.35%
MEK-083	289.42	38.31%	47.39%	KEN-019	14.88	44.33%	38.81%
BKD-031	287.24	37.27%	46.28%	242530	14.77	43.26%	37.78%
HAL-039	286.39	36.86%	45.85%	212890	14.75	43.06%	37.59%
MP	**209.25**	**———**	**6.56**	**MP**	**10.31**	**——**	**-3.64**
MRV	**196.36**	**-6.16**	**—**	**MRV**	**10.72**	**3.98**	**—**
3. **Grain yield (t ha^{-1})**				4. **Thousand seed weight (g)**			
KEN-016	3.32	138.85%	114.19%	SAA-004	1.45	68.60%	54.26%
KEN-020	3.23	132.37%	108.39%	ALE-074	1.43	66.28%	52.13%
KAZ-060	3.12	124.46%	101.29%	MEK-081	1.38	60.47%	46.81%
KEN-010	2.93	110.79%	89.03%	212890	1.34	55.81%	42.55%
KEN-018	2.87	106.47%	85.16%	BKD-031	1.32	53.49%	40.43%
225715	2.38	71.22%	53.55%	KAZ-078	1.32	53.49%	40.43%
MP	**1.39**	**—**	**-10.32**	**MP**	**0.86**	**–**	**-8.51**
MRV	**1.55**	**11.51**	**–**	**MRV**	**0.94**	**9.30**	**–**
5. **5. Days to 50% flowering(days)**				6. **6. Grain filling period (days)**			
240815	69.00	49.12%	28.97%	212582	100.25	100.74%	112.71%
211456	63.25	36.70%	18.22%	HA-003	79.50	59.19%	68.68%
242531	62.50	35.08%	16.82%	212583	78.75	57.69%	67.09%
CHU-045	62.25	34.54%	16.36%	242534	73.50	47.18%	55.95%
241764	62.00	34.00%	15.89%	WA-001	70.00	40.17%	48.53%
242534	61.75	33.46%	15.42%	SHIA-007	69.25	38.67%	46.93%
MP	**46.27**	**–**	**-13.51**	**MP**	**49.94**	**–**	**5.96**
MRV	**53.50**	**15.63**	**–**	**MRV**	**47.13**	**-5.63**	**–**
7. **7. Grain sink filling rate (kg ha^{-1}day $^{-1}$)**				8. **8. Days to maturity (days)**			
KEN-020	94.00	212.19%	176.88%	212582	155.00	61.12%	64.02%
KEN-016	71.57	137.70%	110.81%	242534	135.25	40.59%	43.12%
KAZ-060	64.49	114.18%	89.96%	242531	130.50	35.65%	38.10%
KEN-010	59.99	99.24%	76.70%	212583	130.50	35.65%	38.10%
242533	55.13	83.10%	62.39%	225713	128.00	33.06%	35.45%

Genotypes	Mean	Relative advantage (%) over		Genotypes	Mean	Relative advantage (%) over	
		MP	MRV			MP	MRV
1. 1. Plant height at maturity (cm)				**2. 2. Leaf yield (t/ha)**			
KEN-014	50.56	67.92%	48.92%	241764	126.00	30.98%	33.33%
MP	**30.11**	**–**	**-11.31**	**MP**	**96.20**	**–**	**1.80**
MRV	**33.95**	**12.75**	**–**	**MRV**	**94.5**	**-1.77**	**–**
9. **9. Leaf area (cm^2)**				10. **Terminal Inflorescence Stalk Length(cm)**			
ALE-023	120.15	71.86%	65.54%	215567	47.98	65.68%	62.53%
KAZ-055	119.90	71.51%	65.20%	CHU-045	46.53	60.67%	57.62%
ALE-034	119.66	71.16%	64.87%	240814	45.11	55.77%	52.81%
DRA-053	109.28	56.32%	50.56%	212892	43.83	51.35%	48.48%
ALE-068	108.67	55.44%	49.72%	KAZ-060	42.57	47.00%	44.21%
KAZ-057	100.89	44.31%	39.01%	219284	42.50	46.75%	43.97%
MP	**69.91**	**–**	**-3.68**	**MP**	**28.96**	**–**	**-1.90**
MRV	**72.58**	**3.82**	**–**	**MRV**	**29.52**	**1.93**	**–**

MP = Mean of the population; MRV = Mean of released varieties

A student t-test was used to compare the mean of the top 5% genotypes to the mean of the population was varied ($P \leq 0.0001$) for all measured phenotypic traits (Table 6). The t -test showed highly significant differences between means of the selected subsets of the top 5% best genotypes ($\bar{x}$) and the population parameters (μ) for days to emergence (days), days to flowering (days), plant height at flowering (cm), leaf area (cm^2), leaf length (cm), leaf yield (t/ha), leaf width (cm), petiole length (cm), leaf thickness (mm), top lateral branch length (cm), node number (number), days to maturity (days), plant height at maturity (cm), leaf number (number), stem diameter (cm), auxiliary inflorescence length (cm), terminal lateral inflorescence length (cm), branch number (number), basal lateral branch length (cm), terminal inflorescence stalk length (cm), grain filling periods (days), grain sink filling rate ($kg\ ha^{-1} day^{-1}$), grain yield ($t\ ha^{-1}$), and thousand seed weight (g) (Table 6). The findings showed that the top 5% of genotypes had greater relative advantages in all agro-morphological variables, with differences between them and the population means performances ranging from 15.90% for leaf thickness to 184.11% for basal lateral branch length. Each day, the top 5% of genotypes produced 119.05% greater grain, per hectare than the population as a whole. Additionally, the top 5% of genotypes exhibited advantages in leaf area(cm^2), leaf yield (t/ha), terminal inflorescence stalk length (cm), thousand seed weight (g), and grain yield ($t\ ha^{-1}$) of 61.77, 56.66, 54.53, and 114.03% above the mean performances of the population, respectively, showing the occurrence of various degrees of amaranths enhancements through selection.

Table 6
Comparison of mean performances of selected top 5% genotypes with the population mean performances for 24 traits of amaranth grown at Hawassa University's agricultural research site in the 2020 and 2021 cropping seasons.

Traits	Mean of selected genotypes ($\bar{X}$)	Population parameter (μ)	Change through selection ($\bar{X}$-μ)	Change as % of a population parameter (μ)	t-test
Days to emergence (days)	8.88	6.65	2.23	33.46	14.37***
Days to flowering (days)	63.46	46.27	17.19	37.15	15.24***
Plant height at flowering (cm)	115.02	73.7	41.32	56.07	6.75***
Leaf number (number)	36.96	29.69	7.27	24.48	25.18***
Leaf area (cm^2)	113.09	69.91	43.18	61.77	13.17***
Leaf length (cm)	17.54	14.39	3.15	21.88	58.16***
Leaf width (cm)	9.06	7.09	1.97	27.79	10.14***
Leaf thickness (mm)	0.44	0.38	0.06	15.90	7.68***
Petiole length (cm)	7.77	6.26	1.51	24.05	11.74***
Leaf yield (t/ha)	16.15	10.31	5.84	56.66	5.24***
Branch number (number)	41.34	28.96	12.38	42.76	19.73***
Basal lateral branch length (cm)	147.54	51.93	95.61	184.11	35.57***
Top lateral branch length (cm)	38.98	21.05	17.93	85.16	11.69***
Node number (number)	32.58	26.51	6.07	22.91	19.04***
Days to maturity (days)	134.21	96.20	38.01	39.51	8.74***
Plant height at maturity (cm)	298.68	209.25	89.43	42.74	9.93***
Stem diameter (cm)	39.07	28.33	10.74	37.92	10.28**
Auxiliary inflorescence length (cm)	23.76	12.04	11.72	97.36	33.19***
Terminal lateral inflorescence length (cm)	27.17	17.91	9.26	51.70	17.13***
Terminal inflorescence stalk length (cm)	44.75	28.96	15.79	54.53	17.51***
Grain-filling periods (days)	105.32	49.94	55.38	110.89	6.11***
Grain sink filling rate (kg $ha^{-1}day^{-1}$)	65.96	30.11	35.85	119.05	5.64***
Thousand seed weight (g)	1.37	0.86	0.51	59.69	22.27***
Grain yield (t ha^{-1})	2.98	1.39	1.59	114.03	11.48***

The tabulated t-value for 5 degrees of freedom is 6.869 for two-tailed tests and 5.894 for one-tailed tests at 0.1% probability. T = Student t-test; *** = significantly different at 0.1% probability level.

Variance Component And Coefficient Of Variation

Genetic parameters such as genotypic variance ($\delta^2 g$), phenotypic variance ($\delta^2 p$), environmental variances ($\delta^2 e$), genotypic variance with year interactions ($\delta^2 gy$), genotypic co-efficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental co-efficient of variation (ECV) were calculated for each of the evaluated quantitative traits indicated in the (Table 7). For all of the traits, the assessment of the variance's components revealed a wide range of variation and substantial disparities. The result reveals that for all examined variables, the phenotypic variance was greater than the comparable genotypic variance. Concerning all examined phenotypic variables; the phenotypic variance was likewise greater than the corresponding genotype-by-year interaction variance and environmental variance. The genotypic variance overshadowed genotype-by-year interactions, except for days to emergence, leaf thickness, petiole length, leaf yield, top lateral branch length, node number, terminal lateral inflorescence length, and terminal inflorescence stalk length, grain sink filling rate, thousand seed weight, and grain yield. Similarly, the genotypic variance was higher than the corresponding environmental variance in the days to flowering, plant height at flowering, leaf area, leaf length, leaf width, branch number, basal lateral branch length, days to maturity, plant height at maturity, stem diameter, auxiliary inflorescence length, and grain filling periods.

More than 33.33 percent of the quantitative variables exhibited high phenotypic and genotypic coefficients of variation (PCV and GCV, respectively). Plant height at flowering, leaf area, branch number, auxiliary inflorescence length, basal lateral branch length, plant height at maturity, grain sink filling rate, and grain yield all had high genotypic and phenotypic coefficients of variation. The traits with medium GCV and PCV comprised days to flowering, leaf length, leaf width, days to maturity, terminal lateral inflorescence length, stem diameter, days to grain filling periods, and thousand seed weight. Leaf yield and top lateral branch length showed high PCV and low GCV values, but days to emergence, the number of leaves, petiole length, and the number of nodes showed medium PCV and low GCV values. Leaf thickness is revealed by low PCV and GCV. Likewise, estimates of the environmental coefficient of variation (ECV) ranged from 6.88 (for days to maturity) to 58.76 for grain sink filling rate. For each trait, the estimates of the genotypic coefficient (GCV) were lower than the corresponding phenotypic coefficient of variation (PCV). The petiole length, leaf yield, basal lateral branch length, node number, top lateral branch length, terminal lateral inflorescence length, grain sink filling rate, thousand seed weight, and grain yield showed a wide difference between the phenotypic and genotypic coefficient of variations, while the remaining traits all exhibited a slight difference (Table 7).

Table 7
Components of variance and coefficient of variation for 24 traits of amaranth grown at Hawassa University's agricultural research site in the 2020 and 2021 cropping seasons.

Trait	Variance component							Coefficient of variation		
	δ^2r	δ^2b	δ^2y	δ^2g	δ^2gy	δ^2e	δ^2p	PCV	GCV	ECV
Days to emergence (days)	0.001	0.000	0.081	0.306	0.529	0.334	0.660	12.210	8.320	8.690
Days to flowering(days)	0.299	0.009	0.442	62.694	27.075	22.270	82.150	19.590	17.110	10.200
Plant height at flowering(cm)	1.405	0.234	-0.015	226.277	153.505	179.598	350.800	25.410	20.410	18.180
Leaf number (number)	3.883	0.036	21.573	8.568	14.890	9.982	18.670	14.550	9.860	10.640
Leaf area(cm^2)	278.946	2.849	3.184	415.526	15.071	395.419	528.230	32.880	29.160	28.440
Leaf length(cm)	0.112	-0.001	0.582	4.942	1.936	1.810	6.390	17.570	15.450	9.350
Leaf width(cm)	0.027	0.000	0.155	1.264	0.379	0.446	1.570	17.680	15.850	9.420
Leaf thickness(mm)	0.000	0.000	0.002	0.000	0.001	0.001	0.001	6.070	0.000	9.850
Petiole length(cm)	0.029	0.000	0.150	0.075	1.069	0.570	0.760	13.930	4.360	12.060
Leaf yield(t/ha)	2.953	0.042	0.201	1.023	1.678	15.567	6.000	23.760	9.810	38.270
Branch number(number)	0.487	0.021	0.022	45.512	8.459	16.583	54.150	25.410	23.300	14.060
Basal lateral branch length(cm)	20.685	-0.518	19.913	969.837	721.280	315.718	1414.440	72.420	59.970	34.220
Top lateral branch length(cm)	0.527	0.073	0.061	-2.146	79.072	25.044	44.050	31.530	0.000	23.770
Node number (number)	1.978	0.000	33.897	2.457	12.614	8.175	10.940	12.480	5.910	10.790
Days to maturity(days)	-0.181	0.099	0.027	136.495	47.894	43.770	172.080	13.640	12.140	6.880
Plant height at maturity(cm)	-2.282	0.157	195.903	1926.699	651.213	333.120	2340.900	23.120	20.980	8.720
Stem diameter (cm)	0.609	-0.006	4.946	24.734	4.255	12.290	30.130	19.380	17.560	12.370
Auxiliary inflorescence length(cm)	0.683	0.009	0.021	21.593	11.495	9.520	29.870	45.400	38.590	25.630
Terminal lateral inflorescence length(cm)	0.217	0.006	12.187	4.447	15.495	4.520	13.400	20.440	11.770	11.870
Terminal inflorescence stalk length(cm)	1.249	0.018	-0.062	23.612	51.090	25.510	55.940	25.830	16.780	17.440
Grain-filling periods(days)	-0.221	0.087	0.068	68.495	48.330	58.510	108.220	20.830	16.570	15.320

Trait	Variance component							Coefficient of variation		
	δ^2r	δ^2b	δ^2y	δ^2g	δ^2gy	δ^2e	δ^2p	PCV	GCV	ECV
Grain sink filling rate (kg $ha^{-1}day^{1}$)	-1.190	0.849	4.349	57.144	126.644	313.000	203.710	47.400	25.110	58.760
Thousand seed weight(g)	-0.001	0.000	0.000	0.013	0.048	0.130	0.070	31.160	13.410	41.930
Grain yield (t ha^{-1})	0.003	0.001	0.008	0.096	0.186	0.570	0.340	41.980	22.260	54.320

σ^2y =year variance; σ^2r = Replication variance; σ^2b = block variance; σ^2g = Genotypic variance; σ^2gy = Genotypic by year interaction variance; σ^2e = Error variance; σ^2p = Phenotypic variance; PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; ECV = Environmental coefficient of variation.

Heritability And Genetic Advance

Estimates of heritability in a broad sense (H^2bs) for 24 quantitative traits of amaranth genotypes are presented in (Fig. 3). The heritability estimates in a broad sense (H^2bs %) in the traits examined revealed large variances, ranging from 4.9% for top lateral branch length to 84.0% for the number of branches. Several branches (84.0%), plant height at maturity (82.3%), stem diameter (82.1%), and leaf width (80.4%) all showed heritability in a broad sense of greater than 80%, revealing very high heritability. Days to maturity (79%), leaf area (78.7%), leaf length (77.3%), days to flowering (76.3%), auxiliary inflorescence length (72.3%), basal lateral branch length (68.6%), plant height at flowering (64.5%), grain filling periods (63.3%), showed moderately high heritability. The estimate of heritability of leaf thickness (50.0%), days to emergence (46.5%), leaf number (45.9%), and terminal inflorescence stalk length (42.2%) was in the medium category, and other traits were low.

As depicted in Fig. 3, the estimates of genetic advance (GA) for evaluated phenotypic variables in amaranth genotypes vary greatly. The values of GA for the phenotypic traits that were examined ranged from 0.0 to 63.0%. Plant height at maturity (63.0%), followed by basal lateral branch length (44.7%), leaf area (29.26%), plant height at flowering (21.59%), days to maturity (16.8%), grain filling periods (11.88%), days to flowering (11.36%), and grain sink filling rate (10.85%) were all observed relatively as having the highest GA values. The GA (10) values for the remaining sixteen phenotypic variables varied from 0.0% for top lateral branch length and leaf thickness to 9.68% for branch number.

The genetic advance as a percent of means (GAM) for measured phenotypic traits in amaranths' genotypes is also presented in Fig. 3. The values of high GAM (> 20%) were recorded for basal lateral branch length (86.1%), auxiliary inflorescence length (55.4%), leaf area (41.8%), grain sink filling rate (36%), grain yield (32%), plant height at maturity (30.1%), plant height at flowering (29.3%), stem diameter (25.2%), days to flowering (24.6%), terminal inflorescence stalk length (24.1%), grain filling periods (23.8%), leaf width (22.8%), and leaf length (22.2%). Thousand seed weight (19.2%), days to maturity (17.4%), terminal inflorescence lateral length (16.9%), leaf yield (14.1%), and days to emergence (11.9%) all had medium GAM (10–20%) values. Node number (8.5%), petiole length (6.3%), leaf thickness, and top lateral branch length both had (0.00%) were the variables with the lowest GAM value.

Discussion

Superior genotypes must be investigated utilizing several traits and multi-environment experiments to make sure that the chosen genotypes perform well in a variety of environments within the targeted area. Due to the extremely significant changes between the seasons and interactions between genotypes and seasons, the best genotypes for specific traits during the planting season were not always the best genotypes for the subsequent planting season. For the majority of the studied variables, the extent of significant differences was seen among years, genotypes, and the genotype-by-year interaction. In most of the studied traits in amaranth genotypes, the test year had a significant impact. Because weather and farming practices, such as soil characteristics, field management, or weather, affect how genes are expressed, this may help to explain the scenario **(Yao**et al., **2008; Persaud**et al., **2022). Debelo**et al.**(2001)**, and **Mbwambo**et al.**(2013)** also observed comparable findings the irregular variations in rainfall from year to year

due to the genotypic difference often have an impact on Ethiopia's agriculture and could influence most of the plant variables in a complex way resulting in their plastic responses.

The mean squares of genotypes from the analysis of variance demonstrated that there was significant variation among the genotypes for the studied variables, except for the leaf thickness, node number, petiole length, leaf yield, and top lateral branch length. The considerable observed variances among the genotypes under study suggest that there was a substantial amount of inherent variability among amaranth genotypes for the variables under analysis. Various researchers have also reported that amaranth genotypes exhibit significant variability (**Andini**et al., **2013**; **Thapa & Blair, 2018**; **Trivedi**et al., **2022**). The evaluation of both genetic and environmental factors may be made more precisely and efficiently by studying the interaction between genotype and environment. For agricultural production to be secure and sustainable, stable genotypes are necessary (**Brammer, 1971**). In the current studies, the genotypes by year interactions were found significant for DE, DF, LN, LL, LW, DM, PHM, SD, TILL, GSFR, and GY. This is due to both the discrepancy response of genotypes to the test year and the influence of the test year on the genotypes differently. Additionally, the inconsistent performance of the genotypes across years suggested the potential for exploring and cultivating superior genotypes in a variety of environmental conditions (**Olaniyi, 2007**) and attributed genotype x year to variations in ecological distribution and genetic variations among the genotypes. Contrarily, the observed significant interactions for the PHF, BN, BLBL, AIL, TISL, and GFP traits were only due to the differential response of genotypes to the test years. However, the observed significant interactions for the remaining three (about 12.5%) traits were only due to differential responses of years to the test genotypes. Because growing conditions can vary, it is typical to expect that a genotype's performance will fluctuate in a variety of environments (**Keneni, 2012**; **Mohammadi, 2017**; **Fekadu**et al., **2022**).

The observed crossover interactions in GY were a result of genotypic performance changes brought on by variable environments, which made it more difficult to create genotypes with stable performance. Significant genotype by environment interaction effects was mostly of the ‘cross-over’ type; i.e., interactions were associated with rank order changes among the genotypes. This indicated that the two environments were distinctly different for some of the characters and that better genotypes in one environment may not be better performers in another (**Temesgen**et al., **2015**; **Sossou**et al., **2021**). Moreover, the significant presence of extensive crossover GY interactions in the two cropping seasons suggests that a systematic effort is needed to screen different genotypes across various environments to identify those that perform well there or within a particular target region of environments (environment trials). The inconsistent genotype rankings for the investigated traits would make it difficult to generate genotypes with stability for these traits (**Moghaddam & Pourdad, 2009**). The results, however, point to significant variations in genotype ranks between the environments; therefore, effort must be used while breeding these characteristics, particularly for grain production.

Plant height, days to flowering, leaf number, leaf area, leaf length, and individual leaf width are all key contributors to amaranth's leaf yield, as are a variety of other yield elements. **Das (2016)**, supported similar findings. The observed high plant height in the top 5% leaf yielder genotypes might be due to the inherent genetic variation, strong light competition, and partition of more assimilates for stem elongation. Similar findings were observed by **Yarnia**et al.**(2010)** in amaranths and taller plants outcompete weeds more successfully than shorter ones (**Fageria**et al., **2004**). Similarly, the leaf area is crucial in determining the yield (**Sarker & Oba, 2021**). The top 5% of leaf yielder genotypes exhibited the biggest leaf area. This is because each leaf's area is estimated as the sum of its leaf length and leaf width, and when water availability grew, plants were able to photosynthesize more effectively (**Shongwe**et al., **2010**). The leaf area intercepts sunlight, take up CO_2 and inorganic nitrogen, and perform photosynthesis and biomass accumulation, among other factors, determining the yield reported for sunflower in several studies (**Hall**et al., **1985**; **Gimenez & Fereres, 1986**). Moreover, photosynthesis has been the precondition for a successful breeding program to increase photo-assimilate production in high-yielding genotypes (**Haritha**et al., **2017**). Although, light absorption and the rate of dry matter production increase as leaf number and size increase during crop growth (**Remison & Akinleye, 1979**). Besides intercepting most of the solar radiation falling on the crop canopy, high leaf area indices ensure the optimum use of other available environmental factors like moisture, carbon dioxide, and nutrients, to achieve high productivity. Overall, our findings indicate that the genotypes that can be selected to increase biomass have superior photosynthetic efficiency (**Vikram**et al., **2016**). Therefore, a successful yield improvement strategy has been the direct selection of yield-related traits, which are simpler to quantify precisely than the yield itself (**Samonte**et al., **1998**; **Kumar**et al., **2014**). The genotypes of amaranth examined for potential grain and leaf yields generally showed genotypic heterogeneity. These variations in agro-morphological trait performance indicate the amaranth's potential for success in future development efforts for various uses.

Grain yield is a tremendously complex feature that cannot determine itself, according to **Grafius (1978)**. It is a resultant effect of actions and interactions of its component traits. Therefore, the identification of plant traits that contribute to high grain yield is

essential for breeding efforts. The observed grain yield was markedly higher in the top 5% of grain yielder genotypes, which may be explained by a stronger relationship between GY and GY-related traits LN, LA, LL, LW, LY, BN, AIL, TILL, TISL, GSFR, and TSW. The relative effect of PHM and DM, however, was less significant for grain yield performance in the top 5% of yielder genotypes. This may be tied to the top grain genotypes' considerably shorter plant heights and earlier maturation. Modern high-yielding genotypes have improved grain production mostly through the reduction of plant height, which boosts the harvest index due to lower yields of straw and increased lodging resistance. The photosynthesis and respiration of the shorter plants are better balanced, and thus require less maintenance respiration (**Peng**et al., **1994**). The study's findings also revealed that genotypes with high grain production typically had shorter plant heights (**Knott & Gebeyehou, 1987**; **Shah**et al., **2018**). According to **Sogbohossou and Achigan-Dako (2014)**, **Brenner**et al. **(2000)**, and **Joshi (1991)**, grain amaranths were chosen for reduced plant heights. Higher photosynthetic efficiency, lower respiration, and increased grain carbohydrate storage are significant physiological processes that can be used to increase yield potential (**Sharma-Natu & Ghildiyal, 2005**). Additionally, similar to the photosynthetic rate, leaf area greatly increase grain output (**Ishii**et al., **1977**). On the other hand, it seems reasonable that any component that influences a plant's ability to fix carbon and/or transfer available or stored assimilates to the grain will likely also affect physiological maturity. For instance, terminal drought or nitrogen stress, which is known to accelerate leaf senescence, could shorten the filling period and advance physiological maturity (**Smith & Hamel, 2012**). The top 5% of genotypes for grain-yielding plants began to bloom earlier but took longer for GFP, which resulted in higher GY due to better use of growth resources. The length of the vegetative growth stage may also have an impact on grain yield (**Bingham, 1969**). A shorter vegetative growth period makes it possible to reserve more growth resources for the reproductive phase, which raises GY due to the effective use of growth resources for yield production (**Feng**et al., **2021**). The final yield is greatly influenced by the grain filling rate (GFR) and is a positive impact on the final grain weight (**Khan**et al., **2014**). High temperature also increases the rate of grain filling to compensate for the shortened grain growth period. Selecting genotypes with high GFR is therefore probably a wise way to proceed for enhancing grain yield under stress.

Any breeding material must have a high level of genetic diversity since it not only serves as a foundation for selection but also offers important insights into the choice of varied parents for use in hybridization programs (**Singh**et al., **2016**; **Upadhyay**et al., **2019**). To determine the additive or heritable portion of variability, agronomic traits must be divided into genotypic, phenotypic, and environmental influences because they are quantitative and interact with the environment being studied. The extent of phenotypic variances was comparatively higher for all agro-morphological traits in amaranth genotypes in the current study compared to the corresponding genotypic and the interaction of genotypic by year variances, indicating a relatively high level of environmental influence on the expression of these traits. For 50% of the examined variables, the magnitude of genotypic (heritable) variance was higher than the corresponding environmental (non-heritable) variances. This suggests that the examined traits were mostly influenced by the genotypic component of variance.

In the current study's variability analysis, all of the characteristics exhibited greater phenotypic than genotypic coefficients of variation, which is generally consistent with the findings of (**Sharma**et al., **1997**; **Varalakshmi, 2004**; **Sravanthi**et al., **2012**; **Parveen**et al., **2013**; **Yadav**et al., **2014**; **Malaghan**et al., **2018**; **Showemimo**et al., **2021**). They consequently suggested that the environment had an impact on how they expressed themselves. High genotypic and phenotypic coefficients of variation were revealed in the plant height at flowering, leaf area, branch number, auxiliary inflorescence length, basal lateral branch length, plant height at maturity, grain sink filling rate, and grain yield. Higher PCV values and correspondingly higher GCV values for these traits suggest that they are of economic importance and are under the control of genetics. As a result, these traits can be relied upon, and simple selection can be used to enhance these traits. Results of a comparable ilk have been reported by **Malaghan**et al.**(2018)** for a number of a branch, and plant height at flowering. A significant difference between PCV and GCV estimates for the traits viz., petiole length, leaf yield, leaf thickness, node number, top lateral branch length, terminal lateral inflorescence length, and thousand seed weight points to a higher level of environmental control or the contribution of non-additive gene effects. The same findings were reported by (**Rana**et al., **2005**; **Showemimo**et al., **2021**). But it was found that the differences between PCV and GCV were comparatively very small for the traits of days to flowering, leaf length, leaf width, days to maturity, and stem diameter. This suggests that these traits had a lot of genetic diversity that could be exploited and it is revealed that this estimated phenotypic variability is a reasonable signal of genotypic variability. As a result, environmental influences had a smaller impact on phenotypic performance (**Sawadogo**et al., **2014**). Six of the examined traits had low ECV estimates (about 25%), suggesting that these traits are less responsive to environmental variables. For the traits of leaf length, leaf breadth, days to maturity, and plant height at maturity, the observed moderate-to-high PCV and moderate GCV along with the accompanying low ECV estimations revealed that improvement in those traits would be possible by direct selection.

The value of selection for a specific characteristic depends mainly on its heritability since selection operates on genetic differences (**Allard, 1960**). Heritability, a degree of the genetic link between parent and offspring, has been frequently used to determine how much a character may be passed down from one generation to the next. Estimates of heritability reveal the degree to which a trait is under genetic control, as well as the accuracy of phenotypic prediction of its breeding value (**Ndukauba**et al., **2015**). Understanding heritability is crucial because it aids breeders in determining how much improvement is feasible through selection (**Robinson**et al., **1949**; **Ene**et al., **2016**). The current research revealed that, for assessed phenotypic traits, the estimated heritability generally showed significant variability. This great genetic improvement potential of the traits under study was suggested by the vast range of variability in the studied traits since the degree of wide variability essentially provides better scope for selection.

The number of branches, plant height at maturity, stem diameter, and leaf width, plant height at flowering, grain filling periods, basal lateral branch length, days to maturity, auxiliary inflorescence length, leaf area, days to flowering, and leaf length all demonstrated substantial heritability in the current investigations. According to **Manal (2009)** and **Yanti (2016)**, high heritability signifies that environmental influences on the expression of these traits were relatively low and that the dominant genetic influence, due to the presence of high additive gene action on the expression of these traits, was largely responsible for the manifested phenotypic performance. For this reason, special consideration should be given to these particular traits that are passable and may be regulated by additive gene action. Therefore, to make selection effective for improving amaranth, these traits can be enhanced using mass selection or the pedigree technique. Similarly, **Showemimo**et al.**(2021)** also obtained high heritability estimates for, the number of branches, and leaf width. Similar findings in amaranth for traits including plant height, stem diameter, and the number of branches were made by **Sravanthi**et al.**(2012)**, **Yadav**et al.**(2014)**, **Mobina and Jagatpati (2015)**, and **Selvan**et al.**(2013)**. Similar results have also been reported by **Trivedi**et al.**(2022)** for the traits of days to flowering, plant height, and stem diameter. The estimations of heritability, however, were moderate for the length of the terminal inflorescence stalk, the number of leaves, and the number of days to emergence. Selection based on the phenotypic performance of these traits may not be beneficial for improvement due to the medium heritability of these traits, which suggested that the environmental effect was relatively strong on the expression of these traits. Moreover, moderate heritability, indicating a weak correlation of phenotype with genotypic value and reflecting the high influence of season by genotypes interaction effects. According to **Singh**et al.**(1993)**, the selection is made significantly more challenging by the medium to low heritability estimates since the environment has a considerable obscuring impact on the genotypic effects. The existence of considerable genotype by environment interactions in 22 (or almost 92%) of the examined traits may be the key cause of the low heritability estimates that were observed in the current study.

There is a sign of genetic variation in the genotypes of amaranth that can be selected, according to the estimates of GA and GAM in the present study, which varied significantly across the observed traits. Whenever we select the top 5% of high-yielding genotypes as parents, the mean performance of the offspring is anticipated to improve based on the assessment of genetic gain in the current study. In light of this, it is expected that the genotypic performance of the new population (progeny) will increase, from 1.39 to 1.83 t/ha for grain yield to 10.31 to 11.76 t/ha for leaf yield. Similarly, leaf area (69.91 to 99.17cm2), leaf length (14.39 to 17.58cm), leaf width (7.09 to 8.70 cm), grain sink filling rate (30.11 to 40.96 kg ha-1day-1), plant height at maturity (209.25 to 272.25cm), plant height at flowering (73.7 to 95.29cm), thousand seed weight (0.86 to 1.03 g), auxiliary inflorescence length (12.04 to 18.71cm), terminal lateral inflorescence length (17.91 to 20.94cm), and terminal inflorescence stalk length (28.96 to 35.93 cm) are expected to be improved. The genetic gain (GAM) that could be estimated from selecting the top 5% of the genotypes as a percent of the mean ranged from 0.0% for leaf thickness to 86.1% for basal lateral branch length.

Only heritability-based trait selection, however, may occasionally be successful since the broad definition of heredity takes into account total genetic variance, which includes additive, dominant, and epistatic variances (i.e. interaction between variations that is not additive). Measuring the heritability of a group of genotypes in conjunction with rapid genetic advance is, therefore, more precise and efficient for the selection of desirable traits for a subset of the population (**Ali**et al., **2002**; **Bhargava**et al., **2004**). High heritability combined with high genetic advance as a percentage of the mean was a more valuable and powerful tool for predicting the effect of selection and producing the resultant effect for selecting the best individuals (**Panse & Sukhatme, 1954**; **Jonhson**et al., **1955**; **S Shukla**et al., **2006**; **Kuralarasan**et al., **2018**; **Chauhan & Singh, 2019**) because heritability is a separate numerical expression of the ratio of the two variances, which may not result in success if the selection is based on heritability estimates alone. High heritability and GA for a particular characteristic show that it is controlled by additive gene action, which makes it the best candidate for selection (**Mohsin**et al., **2009**). High heritability traits, therefore, may not always result in high genetic gain (**Johnson**et al., **1955**). Estimates of very high to moderately high heritability accompanied with high GAM were identified for basal lateral branch length, auxiliary inflorescence length, leaf area, branch number, plant height at maturity, plant height at flowering, stem diameter, days to flowering,

grain filling periods, leaf width, and leaf length. Similar results were recorded by **Popa**et al.**(2010)**; **Venkatesh**et al.**(2014)**, and **Mobina and Jagatpati (2015)**. This implies that additive genetic variables had a significant impact on the development of these traits. The above suggests the existence of gene effects that are additive and, as a result, a significant genetic gain under phenotypic selection. The remaining traits' moderate to low heritability estimates and moderate to low genetic advance as a percentage mean suggested that non-additive genetic variance played a role in how they manifested themselves. The traits for petiole length, top lateral branch length, and nod number showed low heritability and genetic gain. Through hybridization, these traits with low genetic advance and heritability can be improved (**Liang & Walter, 1968**). The superior genotypes of the segregating population obtained from repeated crosses can be accumulated in the lines, whilst the traits that exhibit high heritability with moderate or poor genetic advance can be improved via inter-mating.

Conclusions

The findings of this study suggest that there is substantial genetic variation for grain and leaf yield, as well as related traits, among the 120 genotypes of amaranth. Therefore, special emphasis should be given to these traits while making decisions that aim to improve amaranth. Most of the traits were significantly affected by the test year, suggesting that the test year affects the traits differently. Additionally, the genotype-by-year interaction revealed significant variance in the majority of the evaluated traits. Different traits had varying estimations of their heritability, variability, and genetic advance; selection based on high GCV, PCV, heritability, and GAM, which suggested that these characters can be recognized as favorable features and as an indication of additive gene action features should be prioritized during selection, would be helpful for the improvement of amaranth yield. To improve these traits, phenotypic-based genetic selection on these traits may be reliable. These traits include BLBL, AIL, LA, BN, PHM, PHF, SD, DF, GFP, LW, and LL. It may be possible to increase leaf yield in amaranth genotypes by selecting genotypes with high leaf yield along with traits like higher LA, BN, PHM, and PHF. Conversely, when the selection was done with high GY combined with higher LA, AIL, TILL, and TISL, grain yield improvement in amaranth genotypes might be successful. Accordingly, the selected amaranth genotypes namely KAZ-059, 225713, KAZ-058, KEN-019; 242530, and 212890 had high leaf yield along with better LA, LW, LL, LN, and PH. On the other hand, genotypes KEN-016; KEN-020; KAZ-060; KEN-010; KEN-018; and 225715 produced high GY along with better LN, LA, AIL, TILL, TISL, GSFR, and TSW. Therefore, these genotypes were selected to enhance the current leaf, and grain yield productivity of amaranth genotypes that will be used as parents for improving genetic gain in the amaranth breeding program in the future. Moreover, evaluating the genotypes under diverse environmental conditions will be also very important to release the desirable genotypes to the farming community.

Declarations

Funding: The Norwegian Embassy in Addis Abeba funded this field study through the Institutional Collaboration Program between the Norwegian University of Life Sciences, Mekele, and Hawassa Universities (Ethiopia), until the project was phased out and a training grant was awarded to the Dilla College of Education, Ethiopia

Acknowledgments: I am deeply grateful and indebted to my friend Gezahagn Kebede from the Holetta Agricultural Research Center, Ethiopia, for his unlimited help, kindness, and patience in guiding me during my study. We gratefully acknowledge the financial support of the: Norwegian Embassy in Addis Abeba, and Dilla College of Education, Dilla, Ethiopia.

Compliance with ethical standards

Conflict of Interest: The authors declare that they have no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

References

1. Alemayehu, F. R., Bendevis, M., & Jacobsen, S. E. (2015). The potential for utilizing the seed crop amaranth (Amaranthus spp.) in East Africa as an alternative crop to support food security and climate change mitigation. *Journal of Agronomy and Crop Science, 201*(5), 321-329

2. Ali, Z., Khan, A. S., & Asad, M. A. (2002). Salt Tolerance in Bread Wheat: Genetic Variation and Heritability. *Asian Journal of Plant Sciences, 1*(4), 420-422
3. Allard, R. (1960). Principle of Plant Breeding. New York. London, Jhon Wiley and Sons: Inc.
4. Alvarez-Jubete, L., Arendt, E. K., & Gallagher, E. (2010). Nutritive value of pseudocereals and their increasing use as functional gluten-free ingredients. *Trends in Food Science & Technology, 21*(2), 106-113
5. Andini, R., Yoshida, S., Yoshida, Y., & Ohsawa, R. (2013). Amaranthus genetic resources in Indonesia: morphological and protein content assessment in comparison with worldwide amaranths. *Genetic Resources and Crop Evolution, 60*(7), 2115-2128
6. Angel Huerta-Ocampo, J., & Paulina Barba de la Rosa, A. (2011). Amaranth: a pseudo-cereal with nutraceutical properties. *Current Nutrition & Food Science, 7*(1), 1-9
7. Barba de la Rosa, A. P., Gueguen, J., Paredes-Lopez, O., & Viroben, G. (1992). Fractionation procedures, electrophoretic characterization, and amino acid composition of amaranth seed proteins. *Journal of Agricultural and Food Chemistry, 40*(6), 931-936
8. Bhargava, A., Shukla, S., Chatterjee, A., & Singh, S. (2004). Selection response in vegetable amaranth (A. tricolor) for different foliage cuttings. *J Appl Hortic, 6*, 43-44
9. Bingham, J. (1969). Physiological determinants of grain yield in cereals. *Agr Progr*
10. Biru, A. (1978). Agronomy research manual.
11. Brammer, H. (1971). Soil survey project, Bangladesh. Soil resources.
12. Brenner, D., Baltensperger, D., Kulakow, P., Lehmann, J. W., Myers, R., Slabbert, M., & Sleugh, B. (2000). Genetic Resources and Breeding of Amaranthus (Vol. 19, pp. 227-285).
13. Brink, M., Belay, G., & De Wet, J. (2006). *Plant resources of tropical Africa 1: Cereals and pulses*: PROTA Foundation Wageningen, The Netherlands.
14. Chauhan, C., & Singh, S. (2019). Genetic variability, heritability and genetic advance studies in oat (Avena sativa L.). *IJCS, 7*(1), 992-994
15. Comstock, R., & Robinson, H. (1952). Estimation of average dominance of genes. *Heterosis, 2*, 494-516
16. Corke, H., Cai, Y., & Wu, H. (2016). Amaranth: overview.
17. Costea, M., & DeMason, D. A. (2001). Stem morphology and anatomy in Amaranthus L.(Amaranthaceae), taxonomic significance. *Journal of the Torrey Botanical Society*, 254-281
18. Das, S. (2016). *Amaranthus: A promising crop of future*: Springer.
19. de Jesus Souza, F. F., Devilla, I. A., GuimarÃ, R. T., Teixeira, I. R., & Spehar, C. R. (2016). Physiological quality of quinoa seeds submitted to different storage conditions. *African Journal of Agricultural Research, 11*(15), 1299-1308
20. Debelo, D., Girma, B., Alemayehu, Z., & Gelalcha, S. (2001). Drought tolerance of some bread wheat genotypes in Ethiopia. *African Crop Sci. J, 9*(2), 385-392
21. Demissew, S. (2010). *The Ethiopian Flora Project: Lessons learnt.* Paper presented at the Proceedings of the Fourth Global Botanic Gardens Congress, Dublin
22. Deshmukh, S., Basu, M., & Reddy, P. (1986). Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. *Indian Journal of Agricultural Sciences*
23. Emire, S. A., & Arega, M. (2012). Value added product development and quality characterization of amaranth (Amaranthus caudatus L.) grown in East Africa. *African Journal of Food Science and Technology, 3*(6), 129-141
24. Ene, C. O., Ogbonna, P. E., Agbo, C. U., & Chukwudi, U. P. (2016). Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean journal of agricultural research, 76*(3), 307-313
25. Fageria, N., Castro, E., & Baligar, V. (2004). Response of upland rice genotypes to soil acidity *The Red Soils of China* (pp. 219-237): Springer.
26. Falconer, D. (1989). Introduction to Quantitative Genetics Wiley. *New York*
27. Fasuyi, A., Dairo, F., & Olujimi, O. (2007). Protein supplementary quality of vegetable leaf meal (Amaranthus cruentus) in the diets of laying hens: Egg laying performance, egg quality and heamatological implications.

28. Fekadu, W., Mekbib, F., Lakew, B., & Haussmann, B. I. (2022). Genotype× environment interaction and yield stability in barley (Hordeum vulgare L.) genotypes in the central highland of Ethiopia. *Journal of Crop Science and Biotechnology*, 1-15
29. Feng, T., Xi, Y., Zhu, Y.-H., Chai, N., Zhang, X.-T., Jin, Y., . . . Li, F.-M. (2021). Reduced Vegetative Growth Increases Grain Yield in Spring Wheat Genotypes in the Dryland Farming Region of North-West China. *Agronomy, 11*(4), 663
30. Gatti, I., Anido, F. L., Vanina, C., Asprelli, P., & Country, E. (2005). Heritability and expected selection response for yield traits in blanched asparagus. *Genetics and Molecular Research, 4*(1), 67-73
31. Gimenez, C., & Fereres, E. (1986). Genetic variability in sunflower cultivars under drought. II. Growth and water relations. *Australian journal of agricultural research, 37*(6), 583-597
32. Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research*: John wiley & sons.
33. Grafius, J. E. (1978). Multiple Characters and Correlated Response 1. *Crop science, 18*(6), 931-934
34. Grubben, G., & Van Sloten, D. (1981a). Genetic resources of amaranth-a global plan of action: IBPGR.
35. Grubben, G., & Van Sloten, D. (1981b). Genetic Resources of Amaranths, International Board for Plant Genetic Resources. *Food and Agriculture Organisation, Rome*
36. Hall, A., Chimenti, C., Vilella, F., & Freier, G. (1985). *Timing of water stress effects on yield components in sunflower.* Paper presented at the Proceedings of the 11th International Sunflower Conference
37. Haritha, G., Vishnukiran, T., Yugandhar, P., Sarla, N., & Subrahmanyam, D. (2017). Introgressions from Oryza rufipogon increase photosynthetic efficiency of KMR3 rice lines. *Rice Science, 24*(2), 85-96
38. Hartley, H. O. (1950). The maximum F-ratio as a short-cut test for heterogeneity of variance. *Biometrika, 37*(3/4), 308-312
39. Hauptli, H., & Jain, S. (1985). Genetic variation in outcrossing rate and correlated floral traits in a population of grain amaranth (Amaranthus cruentus L.). *Genetica, 66*(1), 21-27
40. Ishii, R., Samejima, M., & Murata, Y. (1977). Photosynthetic 14CO2 fixation in the leaves of rice and some other species. *Japanese Journal of Crop Science, 46*(1), 97-102
41. Janovská, D., Cepkova, P., & Dzunkova, M. (2012). Characterisation of the amaranth genetic resources in the Czech Gene Bank. *Genetic diversity in plants. Online: InTech*, 457-478
42. Johnson, H. W., Robinson, H., & Comstock, R. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal, 47*(7), 314-318
43. Jonhson, H., Robinson, H., & Comstock, R. (1955). Genotypic and phenotypic correlations in soyabean and their implication. *J Agron47*, 477-483
44. Joshi, B. (1991). Grain Amaranths in the Himalayas. *Indian Journal of Plant Genetic Resources, 4*(1), 45-54
45. Juan, R., Pastor, J., Alaiz, M., & Vioque, J. (2007). Electrophoretic characterization of Amaranthus L. seed proteins and its systematic implications. *Botanical Journal of the Linnean society, 155*(1), 57-63
46. Keneni, G. (2012). *Genetic potential and limitations of Ethiopian chickpea (Cicer arietinum l.) germplasm for improving attributes of symbiotic nitrogen fixation, phosphorus upatke and use efficiency, and adzuki bean beetle (Callosobruchus chinensis l.) resistance*. Adiss Ababa University.
47. Khan, M., Khan, A., Khattak, G., & Subhan, F. (2014). Genetic effects in controlling grain filling duration in wheat crosses. *JAPS: Journal of Animal & Plant Sciences, 24*(3)
48. Knott, D., & Gebeyehou, G. (1987). Relationships between the lengths of the vegetative and grain filling periods and agronomic characters in three durum wheat crosses 1. *Crop science, 27*(5), 857-860
49. Kumar, Dixit, S., Ram, T., Yadaw, R., Mishra, K., & Mandal, N. (2014). Breeding high-yielding drought-tolerant rice: genetic variations and conventional and molecular approaches. *Journal of experimental botany, 65*(21), 6265-6278
50. Kuralarasan, V., Vanniarajan, C., Kanchana, S., Veni, K., & Lavanya, S. A. (2018). Genetic divergence, heritability and genetic advance in mutant lines of urdbean [Vigna mungo (L.) Hepper]. *Legume Research, 41*(6), 833-836
51. Lakshmi, B., & Vimala, V. (2000). Nutritive value of dehydrated green leafy vegetable powders. *Journal of food science and technology, 37*(5), 465-471
52. Lee, J.-R., Hong, G.-Y., Dixit, A., Chung, J.-W., Ma, K.-H., Lee, J.-H., . . . Park, Y.-J. (2008). Characterization of microsatellite loci developed for Amaranthus hypochondriacus and their cross-amplifications in wild species. *Conservation genetics, 9*(1), 243-246

53. Lehman, A., O'Rourke, N., Hatcher, L., & Stepanski, E. (2013). *JMP for basic univariate and multivariate statistics: methods for researchers and social scientists*: Sas Institute.
54. Liang, G. H., & Walter, T. (1968). Heritability estimates and gene effects for agronomic traits in grain sorghum, sorghum vulgate pers. 1. *Crop science, 8*(1), 77-81
55. Malaghan, S. N., Revanappa, S., Ajjappalavar, P., Nagaraja, M., & Raghavendra, S. (2018). Genetic Variability, Heritability and Genetic Advance in Grain Amaranth (Amaranthus spp.). *Int. J. Curr. Microbiol. App. Sci, 7*(7), 1485-1494
56. Manal, H. E. (2009). Estimation of heritability and genetic advance of yield traits in wheat (Triticum aestivum L.) under drought condition. *International Journal of Genetics and Molecular Biology, 1*(7), 115-120
57. Mbwambo, Bwogi, G. V., Ekhuya, N. A., Epel, A. R., & Saidi, M. (2013). *Morphological characteristics, growth and yield of elite grain and leaf amaranth in Northern Tanzania.* Dissertation, Jomo Kenyatta University of Agriculture and Technology.
58. Mlakar, S. G., Turinek, M., Jakop, M., Bavec, M., & Bavec, F. (2009). Nutrition value and use of grain amaranth: potential future application in bread making. *Agricultura, 6*(4), 43-53
59. Mobina, P., & Jagatpati, T. (2015). Genetic variability of Amaranthus hybridus in tropical plains of west Bengal. *Int. J. Pure App. Biosci, 3*(2), 389-395
60. Moghaddam, M., & Pourdad, S. (2009). Comparison of parametric and non-parametric methods for analysing genotype× environment interactions in safflower (Carthamus tinctorius L.). *The Journal of Agricultural Science, 147*(5), 601-612
61. Mohammadi, R. (2017). Interpretation of genotype× year interaction in rainfed durum wheat under moderate cold conditions of Iran. *New Zealand Journal of Crop and Horticultural Science, 45*(1), 55-74
62. Mohsin, T., Khan, N., & Naqvi, F. N. (2009). Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food Agric. Environ, 7*(3-4), 278-282
63. Morrison, P. (1985). Amaranth: Modern Prospects for an Ancient Crop: JSTOR.
64. Ndukauba, J., Nwofia, G., Okocha, P., & Ene-Obong, E. (2015). Variability in egusi-melon genotypes (Citrullus lanatus [Thumb] Matsum and Nakai) in derived savannah environment in South-Eastern Nigeria. *International Journal of Plant Research, 5*(1), 19-26
65. Olaniyi, J. (2007). Evaluation of yield and quality performance of grain amaranth varieties in the Southwestern Nigeria. *Research Journal of Agronomy, 1*(2), 42-45
66. Pandey, R., & Singh, R. (2011). Genetic divergence in grain amaranth (Amaranthus hypochondriacus L.). *Genetika, 43*(1), 41-49
67. Panse, V. G., & Sukhatme, P. V. (1954). Statistical methods for agricultural workers. *Statistical methods for agricultural workers.*
68. Parveen, M., Chattopadhyay, N., & Tah, J. (2013). Biometric evaluation of genotypic variability and genetic advance in amaranth cultivars. *SciTech Journal of Science and Technology, 2*, 26-30
69. Peng, S., Khush, G., & Cassman, K. (1994). *Evolution of the new plant ideotype for increased yield potential.* Paper presented at the Breaking the Yield Barrier: Proceedings of a Workshop on Rice Yield Potential in Favorable Environments. International Rice Research Institute, Los Banos, Philippines
70. Persaud, M., Persaud, R., Gobind, N., Khan, A., & Corredor, E. (2022). Genotype by environment interactions of grain yield performance and lodging incidence in advance breeding lines of rice across environments in Guyana.
71. Petruzzello, M. (2016). Amaranthaceae plant family.
72. Popa, G., Cornea, C. P., Ciuca, M., Babeanu, N., Popa, O., & Marin, D. (2010). Studies on genetic diversity in Amaranthus species using the RAPD markers. *Analele Universităţii din Oradea-Fascicula Biologie, 2*, 280-285
73. Rana, J., Yadav, S., Mandal, S., & Yadav, S. (2005). Genetic divergence and interrelationship analysis in grain amaranth (Amaranthus hypochondriacus) germplasm. *Indian Journal of Genetics and Plant Breeding, 65*(02), 99-102
74. Rastogi, A., & Shukla, S. (2013). Amaranth: a new millennium crop of nutraceutical values. *Critical reviews in food science and nutrition, 53*(2), 109-125
75. Remison, S., & Akinleye, D. (1979). A Note on the Relationship Between Leaf Area and Yield of Maize Varieties. *East African Agricultural and Forestry Journal, 45*(2), 124-129
76. Robinson, H., Comstock, R. E., & Harvey, P. (1949). Estimates of heritability and the degree of dominance in corn.
77. Samarina, L. S., Malyarovskaya, V. I., Rakhmangulov, R. S., Koninskaya, N. G., Matskiv, A. O., Shkhalakhova, R. M., . . . Gvasaliya, M. V. (2022). Population analysis of Diospyros lotus in the Northwestern Caucasus based on leaf morphology and multilocus

DNA markers. *International journal of molecular sciences, 23*(4), 2192

78. Sammour, R. H., Hammoud, M., & Abd Alla, S. (1993). Electrophoretic variations in Amaranthus. *Bot. Bull. Acad. Sin, 34*, 37-42
79. Samonte, Wilson, L., & McClung, A. (1998). Path analyses of yield and yield-related traits of fifteen diverse rice genotypes. *Crop science, 38*(5), 1130-1136
80. Santra, D., & Schoenlechner, R. (2017). Amaranth Part 2—Sustainability, Processing, and Applications of Amaranth *Sustainable protein sources* (pp. 257-264): Elsevier.
81. Sarker, U., & Oba, S. (2021). Color attributes, betacyanin, and carotenoid profiles, bioactive components, and radical quenching capacity in selected Amaranthus gangeticus leafy vegetables. *Scientific Reports, 11*(1), 1-14
82. Satterthwaite, F. E. (1946). An approximate distribution of estimates of variance components. *Biometrics bulletin, 2*(6), 110-114
83. Sawadogo, N., Nanema, R., Bationo, P., Traore, R., Nebie, B., Tiama, D., . . . Zongo, J. (2014). Évaluation de la diversité génétique des sorghos à grains sucrés (Sorghum bicolor (L.) Moench) du Nord du Burkina Faso. *Journal of Applied Biosciences, 84*, 7654-7664
84. Schnetzler, K. A. (2018). Food uses and amaranth product research: a comprehensive review. *Amaranth Biology, Chemistry, and Technology*, 155-184
85. Selvan, R. K., Yassin, M. G., & Govindarasu, R. (2013). Studies on genetic parameters in grain amaranthus (Amaranthus hypochondriacus L.) as influenced by plant densities. *Journal of Plant Breeding and Genetics, 1*(1), 34-41
86. Shah, L. R., Afroza, B., Khan, S., & Habib, M. (2018). Morphological characterization of Amaranthus spp. under temperate environment using NBPGR descriptor. *Journal of Pharmacognosy and Phytochemistry, 7*(1), 2716-2718
87. Sharma-Natu, P., & Ghildiyal, M. (2005). Potential targets for improving photosynthesis and crop yield. *Current Science*, 1918-1928
88. Sharma, D., Chaudhary, D., & Chaudhary, V. (1997). Genetic variability, heritability and genetic advance for yield and its contributing traits in pea. *Indian Journal of Horticulture, 54*(3), 242-246
89. Sheikh, S. M., & Singh, O. (2013). Pseudocereals and millets: the lost crops of Kashmir. *Genetic Resources and Crop Evolution, 60*(3), 1191-1199
90. Shongwe, V. D., Magongo, B. N., Masarirambi, M. T., & Manyatsi, A. M. (2010). Effects of irrigation moisture regimes on yield and quality of paprika (Capsicum annuum L). *Physics and Chemistry of the Earth, Parts A/B/C, 35*(13-14), 717-722
91. Showemimo, F., Soyombo, M. A., Amira, J. O., & Porbeni, J. B. (2021). Traits selection criteria for genetic improvement of grain and leafy Amaranth (Amaranthus spp) using Principal Component Analysis. *Egyptian Journal of Agricultural Research, 99*(2), 170-179
92. Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, A., & Singh, S. (2006). Genotypic variability in vegetable amaranth (Amaranthus tricolor L for foliage yield and its contributing traits over successive cuttings and years. *Euphytica, 151*(1), 103-110
93. Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, J., Singh, N., & Singh, S. (2006). Mineral profile and variability in vegetable amaranth (Amaranthus tricolor). *Plant Foods for Human Nutrition, 61*(1), 21-26
94. Singh, Ceccarelli, S., & Hamblin, J. (1993). Estimation of heritability from varietal trials data. *Theoretical and Applied Genetics, 86*(4), 437-441
95. Singh, & Chaudhary, B. D. (1977). Biometrical methods in quantitative genetic analysis. *Biometrical methods in quantitative genetic analysis*.
96. Singh, Sharma, V., Paswan, S. K., Chaudhary, M., Sharma, B., & Chauhan, M. (2016). Study on genetic variability, heritability and genetic advance for yield and its contributing traits in linseed (Linum usitatissimum L.). *Curr Adv Agric Sci Int J*
97. Singh, Singh, S., Kumar, D., & Verma, H. (2001). Studies on Variability, Heritability & Genetic.
98. Singhal, R., & Kulkarni, P. (1988). Amaranths–an underutilized resource: Wiley Online Library.
99. Sivasubramanian, S., & Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agric. J, 60*(7), 1139-1140
100. Smith, D. L., & Hamel, C. (2012). *Crop yield: physiology and processes*: Springer Science & Business Media.
101. Sogbohossou, O. E., & Achigan-Dako, E. G. (2014). Phenetic differentiation and use-type delimitation in Amaranthus spp. from worldwide origins. *Scientia Horticulturae, 178*, 31-42
102. Sokolova, D., Shelenga, T., Zvereva, O., & Solovieva, A. (2021). Comparative characteristics of the amino acid composition in amaranth accessions from the VIR Collection. *Turkish Journal of Agriculture and Forestry, 45*(1), 68-78

103. Sossou, E. B., Achigan-Dako, E. G., Sogbohossou, E. D., & PF, H. (2021). Evaluation of 25 genotypes of Amaranthus cruentus for leaf yield, iron, zinc and carotenoids content.
104. Sravanthi, V., Begum, H., Sunil, N., & Reddy, M. (2012). Variance component analysis for grain yield and agro-economic traits in grain amaranths (Amaranthus spp.).
105. Stevens, J. P. (2012). *Applied multivariate statistics for the social sciences*: Routledge.
106. Temesgen, T., Keneni, G., Sefera, T., & Jarso, M. (2015). Yield stability and relationships among stability parameters in faba bean (Vicia faba L.) genotypes. *The crop journal, 3*(3), 258-268
107. Thapa, R., & Blair, M. W. (2018). Morphological assessment of cultivated and wild amaranth species diversity. *Agronomy, 8*(11), 272
108. Trivedi, A., Kumar, P., Chandra, G., Guleria, H., & Chauhan, S. (2022). Estimation of genetic variability, heritability and genetic advance in grain amaranth (Amaranthus hypochondriacus L.).
109. Upadhyay, S., Mehta, N., & Tiwari, A. K. (2019). Assessment of variability among flax type linseed genotypes (Linum usitatissimum L.) of Chhattisgarh plains. *Int. J. Curr. Microbiol. Appl. Sci, 8*(06), 2633-2637
110. Varalakshmi, B. (2004). Characterization and preliminary evaluation of vegetable amaranth (Amaranthus spp.) germplasm. *Plant Genetic Resources Newsletter*
111. Venkatesh, L., Niranjana, M., & Nehru, S. (2014). Genetic variability, heritability and genetic advance in grain amaranth (Amaranthus spp.). *Asian Journal of Bio Science, 9*(1), 67-70
112. Venskutonis, P. R., & Kraujalis, P. (2013). Nutritional components of amaranth seeds and vegetables: a review on composition, properties, and uses. *Comprehensive Reviews in Food Science and Food Safety, 12*(4), 381-412
113. Vikram, P., Swamy, B. M., Dixit, S., Trinidad, J., Sta Cruz, M. T., Maturan, P. C., . . . Kumar, A. (2016). Linkages and interactions analysis of major effect drought grain yield QTLs in rice. *PLoS One, 11*(3), e0151532
114. Wang, Y., Meng, Y.-L., Ishikawa, H., Hibino, T., Tanaka, Y., Nii, N., & Takabe, T. (1999). Photosynthetic adaptation to salt stress in three-color leaves of a C4 plant Amaranthus tricolor. *Plant and cell physiology, 40*(7), 668-674
115. Yadav, R., Rana, J., & Ranjan, J. (2014). Analysis of variability parameters for morphological and agronomic traits in grain amaranth (amaranthus sp) genotypes. *The bioscan, 9*(4), 1661-1665
116. Yanti, F. (2016). Estimation of variability, heritability and genetic advance among local chili pepper genotypes cultivated in peat lands. *Bulgarian Journal of Agricultural Science, 22*(3), 431-436
117. Yao, Y., Liu, Q., Liu, Q., & Li, X. (2008). LAI retrieval and uncertainty evaluations for typical row-planted crops at different growth stages. *Remote Sensing of Environment, 112*(1), 94-106
118. Yarnia, M., Benam, M. K., & Tabrizi, E. F. M. (2010). Sowing dates and density evaluation of amaranth (cv. Koniz) as a new crop. *Journal of Food, Agriculture & Environment, 8*(2), 445-448

Figures

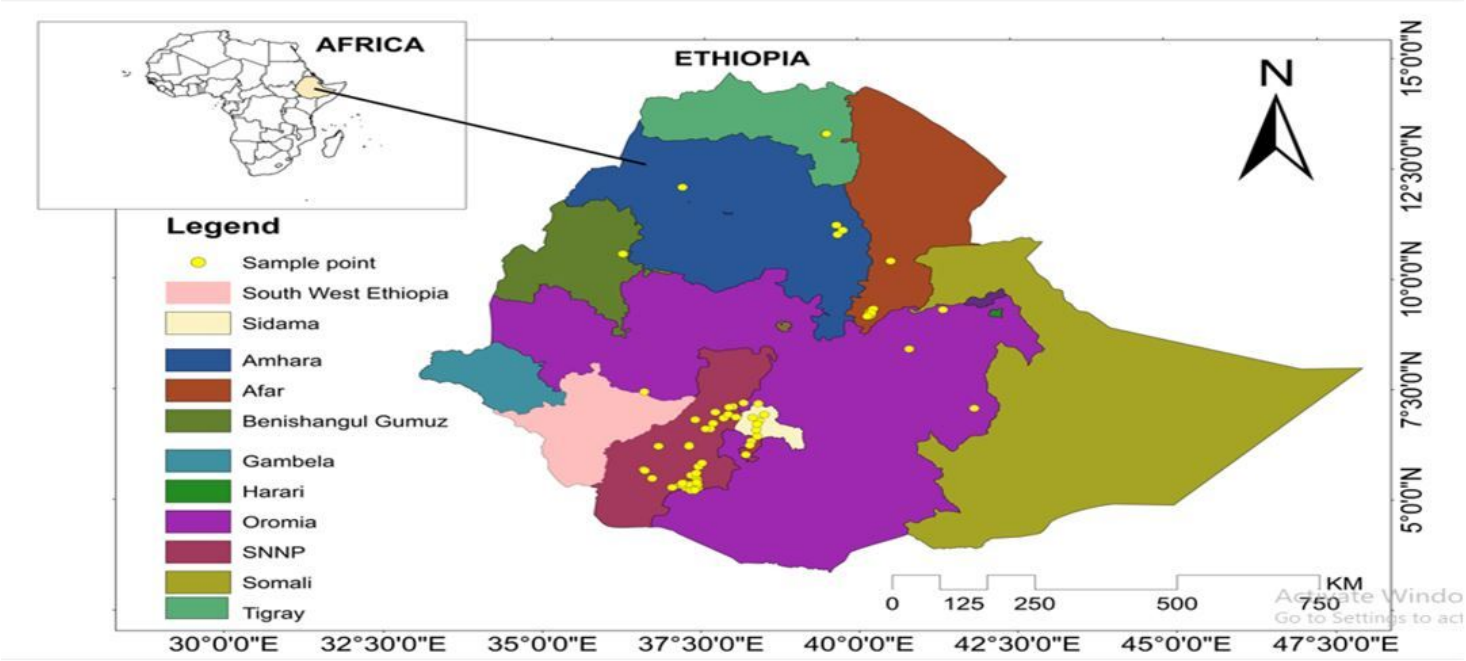


Figure 1

Figure 3. Map of Ethiopia showing the collection site for the different genotypes of Amaranths species from different agro-ecological regions. Maps were generated using QGIS v.3.14.15 Pi, QGIS Development Team. QGIS Geographic Information System. Open Source Geospatial Foundation; 2020. http://qgis.osgeo.org.

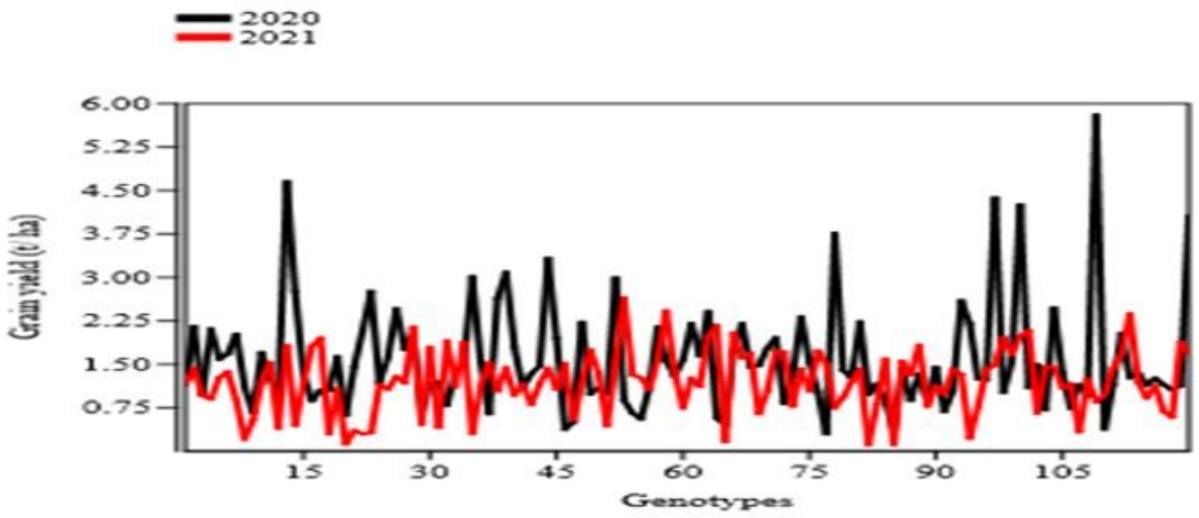


Figure 2

Figure 1. Genotype-by-year interaction (crossover) for grain yield of 120 amaranths genotypes grown at two years in 2020 and 2021 cropping seasons.

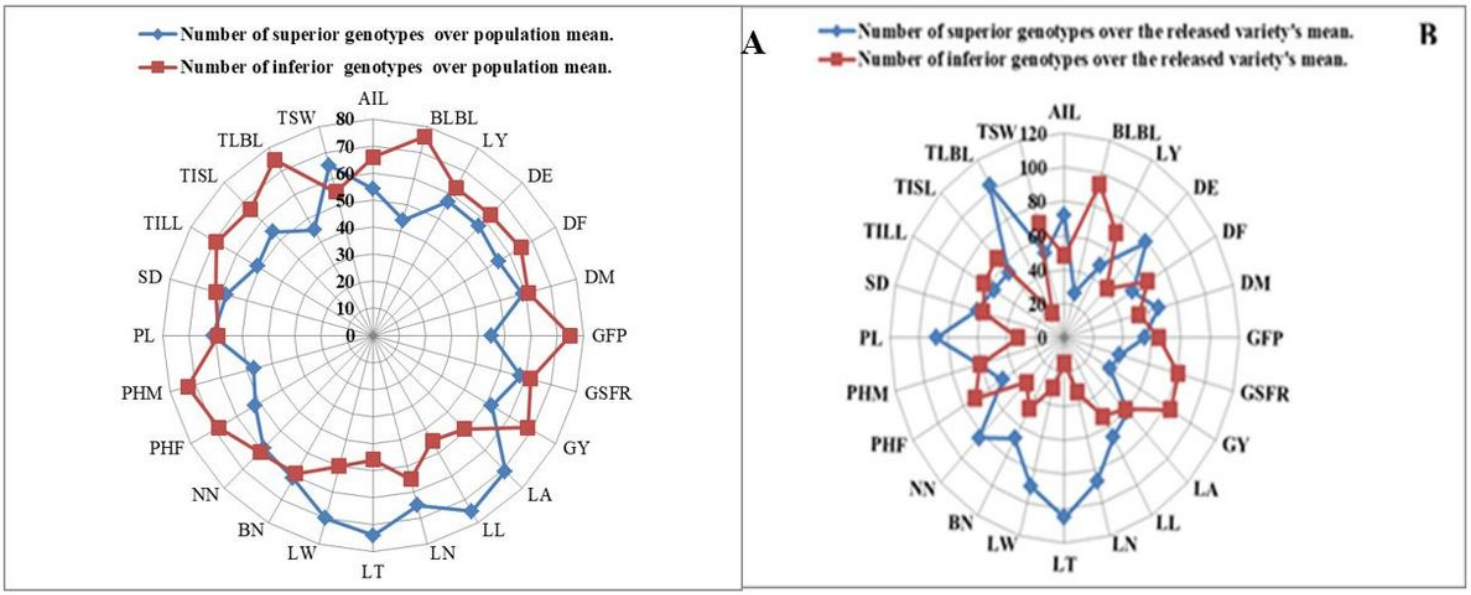
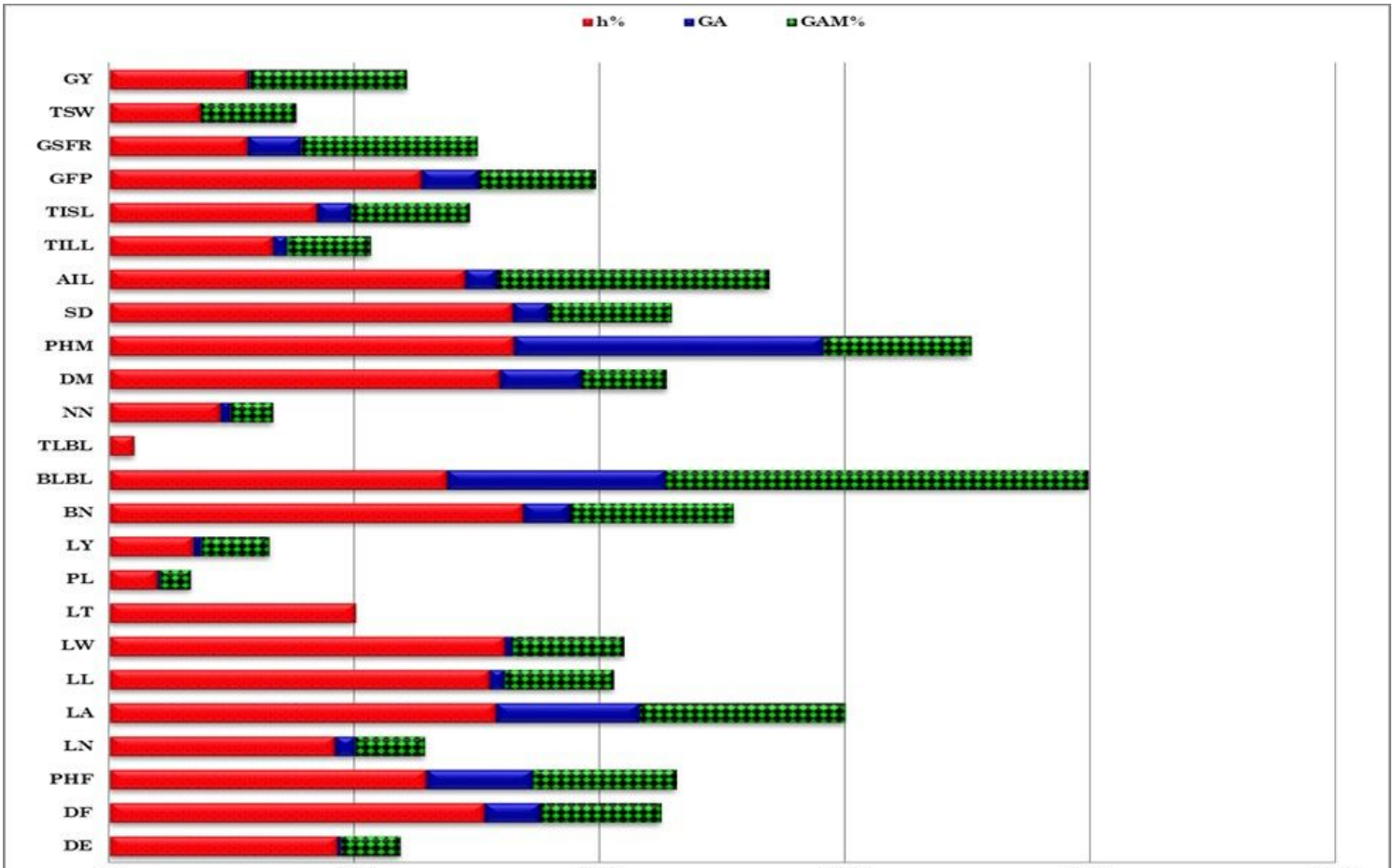


Figure 3

Figure 2: The number of superior and inferior amaranth genotypes over (A) the population means and (B) the mean of released varieties grown at Hawassa University's agricultural research site in 2020 and 2021. Abbreviated names (codes) of different traits see table **1**.



	DE	DF	PHF	LN	LA	LL	LW	LT	PL	LY	BN	BLBL	TLBL	NN	DM	PHM	SD	AIL	TILL	TISL	GFP	GSFR	TSW	GY
h%	46.5	76.3	64.5	45.9	78.7	77.3	80.4	50.0	9.8	17.0	84.0	68.6	4.9	22.5	79	82.3	82.1	72.3	33.2	42.2	63.3	28.1	18.5	28.1
GA	0.79	11.36	21.59	4.20	29.26	3.19	1.61	0.00	0.39	1.45	9.68	44.70	0.00	2.25	16.77	63.00	7.14	6.67	3.03	6.97	11.88	10.85	0.17	0.44
GAM%	11.9	24.6	29.3	14.1	41.8	22.2	22.8	0.0	6.3	14.1	33.4	86.1	0.0	8.5	17.4	30.1	25.2	55.4	16.9	24.1	23.8	36.0	19.2	32.0

Figure 4

Figure 3. Heritability, genetic advance, and genetic advance as percent of the mean for 24 traits of 120 amaranth genotypes grown at Hawassa University's agricultural research site in the 2020 and 2021 cropping seasons. Abbreviated names (codes) of different traits (see Table 1).