التنوع الوراثي لبعض التراكيب الوراثية للقمح الطري استناداً على التحليل المتعدد المتغير تحت الظروف المطرية

Genetic Diversity of Some Bread Wheat Genotypes Based on Cluster and Principal Component Analyses Under Rainfed Conditions

حسام إبراهيم علي فرج[1] [2]

Hossam Farag [1] [2]

hossam_frg@yahoo.com

(1) المركز العربي لدراسات المناطق الجافة والأراضي القاحلة/ أكساد، دمشق، سورية.

(1) The Arab Center for the Studies of Arid Zones and Dry Lands/ACSAD, Damascus, Syria

(2) مركز بحوث الصحراء، المطرية، القاهرة، مصر.

(2) Desert Research Center, El-Matarya, Cairo, Egypt.

الملخص

يعد القمح الطري من أهم محاصيل الحبوب التصديرية والإستراتيجية في العالم والمنطقة العربية من حيث الإنتاج والاستهلاك. قام برنامج تربية الحبوب في أكساد بتحسين تراكيب وراثية من القمح الطري (.Triticum aestivum L) تحت الظروف البعلية. ضمن هذا البحث، تم تقييم عدد 120 سلالة واعدة وصنفين معتمدين لتقدير التنوع الوراثي. أجريت التجارب الحقلية في موسمي 2018/19 و 2019/20 بإستخدام 122 طرزا وراثيا من القمح بإستخدام تصميم القطاعات العشوائية الكاملة في ثلاث مكررات تحت ظروف البعلية في محطة بحوث إزرع للتجارب الزراعية ـ أكساد في محافظة درعا ، سوريا وتم دراسة 14 صفة ؛ تاريخ طرد 50% من السنابل (يوم)، تاريخ النضج (يوم)، مساحة ورقة العلم (سم 2) ، الزاوية القاعدية لورقة العلم (°) ، ارتفاع النبات (سم) ، عدد السنابل / نبات ، طول السنبلة (سم) ، عدد السنيبلات / السنبلة ، عدد الحبوب / السنبلة ، وزن 1000 حبة (جم) ، محصول الحبوب بالسنبلة (جم) ، محصول الحبوب (طن / هكتار) ، محصول القش (طن / هكتار) والمحصول البيولوجي (طن / هكتار).

ـ كشف تحليل التباين عن وجود فروق معنوية ذات دلالة إحصائية (P ≥ 0.05 أو 0.01) بين الطرز الوراثية لجميع الصفات في كل من المواسم وعبر الموسمين مما يشير إلى قدر كبير من التباين بين الطرز الوراثية لكل صفة مدروسة. بالنسبة تاريخ طرد 50% من السنابل و تاريخ النضج ، كانت الطرز الوراثية الستة المحسنة، أكساد 1286 ، وأكساد 1288 ، وأكساد 1226 ، وأكساد 1234 ، وأكساد 1240 ، وأكساد 1282 هي المبكرة. بينما ، أظهرت الطرز الوراثية الثلاثة عشر ، أكساد 1196 وأكساد 1258 وأكساد 1300 وأكساد 1302 وأكساد 1306 وأكساد 1332 وأكساد 1334 وأكساد 1364 وأكساد 1372 وأكساد 1373 وأكساد 1388 وأكساد 1414 وأكساد 1416 أفضل أداء حيث سجلت أعلى متوسط لصفات المحصول ومكوناته.

- لوحظ وجود علاقة ارتباط موجبة معنوية بين محصول الحبوب مع معظم الصفات المدروسة. بينما أظهر معامل المرور المحسوب لصفة محصول الحبوب أن الصفات الأربع؛ مساحة ورقة العلم ، عدد الحبوب / السنبلة ، عدد السنيبلات / السنبلة ووزن 1000 حبة اعلى الصفات الرئيسية المساهمة في محصول الحبوب تحت الظروف البعلية.

- أظهر تحليل التحليل المبدئي للمكونات الأساسية (PCA) انقسام الطرز الوراثية وتقسيمها إلى ثلاث مجموعات تبعا للصفات المختلفة تحت الدراسة وأعطى كل مكون تفسيرا بنسبة (58.61٪ ، 13٪ و 7.23٪ ، على التوالي) من التباين الكلي ، التحليل العنقودي لمجموعة الطرز المدروسة 122 طرزا وراثيا، إلى إنقسامها الى ثلاث مجموعات رئيسية و 11 تحت عنقود ، اشتملت المجموعة الأولى (I) والثانية (II) على العدد الأكبر من الطرز الوراثيّة 27 و 23 طرزا وراثيا (22.13٪ و 18.85٪ من إجمالي من الطرز الوراثيّة ، على التوالي) والتي أظهرت درجة عالية من التنوع الجيني.

- بشكل عام لوحظ وجود تباين عالى بين الطرز الوراثية وأظهرت الطرز الوراثية عالية الإنتاجية ـ أكساد 1196، أكساد 1258 ، أكساد 1300 ، أكساد 1302 ، أكساد 1306 ، أكساد 1332 ، أكساد 1334 ، أكساد 1364 ، أكساد 1372 ، أكساد 1373 ، أكساد 1388 ، وأكساد 1414 ، وأكساد 1416 أكثر قابلية للتكيف، ويمكن توزيعها من خلال تجارب كفاءة الإنتاجية العربية على الدول العربية حتى يمكن انتخاب المناسب منها ومن ثم اعتمادها وتسجيلها وتوزيعها كأصناف تجارية جديدة لبيئات مماثلة تحت الظروف المطرية.

الكلمات المفتاحية: قمح الخبز ، الظروف المطرية، الارتباط المظهري، معامل المرور، تحليل المكونات الأساسية ، التحليل العنقودي.

Abstract

Breed wheat considered to be one of the most important export and strategic cereal crop in the world and Arab region in terms of production and utilization. ACSAD cereal breeding program improved a number bread wheat (*Triticum aestivum* L.) genotypes under rainfed conditions. In the present investigation, 120 promising lines and 2 cultivars were evaluated to estimate the extent of genetic diversity. Field experiments was conducted in 2018/19 and 2019/20 cropping seasons by utilizing 122 wheat genotypes using Randomized Complete Block Design where genotypes were replicated three times under rainfed conditions at Izraa Agricultural Experiment Stations of ACSAD at Daraa governorate, Syria and 14 characters were recorded; heading date (days), maturity date (days), flag leaf area (cm2), basal angle of flag leaf (°), plant height (cm.), number of spikes/plant, Spike Length (cm.), number of spikelets/spike, number of grains/spike, 1000-kernel weight (g.), main spike grain yield(g.), grain yield (t./ha), straw yield (t./ha) and biological yield (t./ha.).

- Analysis of variance revealed highly significant differences (P≤0.05 or 0.01) among genotypes for all traits in both and across seasons indicating considerable amount of variation among genotypes for each trait. For days to heading (50%) and maturity date the six newly genotypes ACSAD 1286, ACSAD 1288, ACSAD 1226, ACSAD 1234, ACSAD 1240 and ACSAD 1282 were the earliest. While, the thirteen genotypes; ACSAD 1196, ACSAD 1258, ACSAD 1300, ACSAD 1302, ACSAD 1306, ACSAD 1332, ACSAD 1334, ACSAD 1364, ACSAD 1372, ACSAD 1373, ACSAD 1388, ACSAD 1414 and ACSAD 1416 showed best performance by producing highest one/or more of yield attributes.

- A significant positive correlation was observed among grain yield with most of studied characters. The computed coefficient for yield showed that the four traits; flag leaf area, no. of grains/spike, no. of spikelets/spike and 1000-kernel weight proved to be the major grain contributors under rainfed conditions.

-The first three principal components based on the Euclidean similarity matrix explained (58.61%, 13% and 7.23%, respectively) of the total variation, Cluster analysis revealed that the 122 genotypes were grouped into three main clusters and 11 intra cluster, the first (I) and second (II) clusters was the largest

and contained 27 and 23 genotypes (22.13% and 18.85% of total genotypes, respectively) which exhibited high degree of genetic diversity.

-Generally, it has been observed the presence of variability among the genotypes and the high yielding genotypes ACSAD 1196, ACSAD 1258, ACSAD 1300, ACSAD 1302, ACSAD 1306, ACSAD 1332, ACSAD 1334, ACSAD 1364, ACSAD 1372, ACSAD 1373, ACSAD 1388, ACSAD 1414 and ACSAD 1416 have more adaptability and could be distributed with the Arab production efficiency trials on the Arab countries for possible selection, registration and release as new commercial cultivars for similar environments under rained conditions.

Key words: Bread wheat, Rained conditions, phenotypic correlation, path analysis, Principle Component Analysis, Cluster analysis.

Introduction

Wheat (*Triticum aestivum* L.) is the principal food source of people globally and occupies a central position in the agriculture sector. It ranks second after rice as a source of calories for consumers in emerging countries (Braun *et al*. 2010). It was reported that, bread wheat grown under a broad range of environmental conditions in terms of water regimes, climatic factors, and soil types. As current changes in global climate have increased variability in precipitation with more frequent episodes of drought (Trenberth, 2011). World cultivation area reached (223.5 million hectare) and production (765.41 million tons) during 2019/2020 growing season (FAO, 2020) As a result of ongoing population growth and climate change, it has been estimated that wheat production must increase by 50% by 2050 (Grassini *et al*. 2013 and Ray *et al*. 2013).

The Arab countries potential of cultivated area with bread wheat especially under rainfed conditions is limited due to lack of improved genotypes, poor management practices, biotic factors (weeds, diseases and insect pests.. etc.) and a biotic factors (drought, heat and salinity stresses), rain fall variability (intensity as well as duration) (Chimdesa *et al*. 2017). Therefore, a challenge for wheat breeders is to combine the stability of grain yield potential to meet the growing demand, and to improve resistance and tolerance to both biotic and abiotic stresses (Winfield *et al*. 2017). Therefore, the improvement of high yielding genotypes and knowledge of specific traits contributing to high yield (as polygenic character) should be influenced by environmental changes as well as drought tolerance, is very importance in the selection of newly promising wheat cultivars in dryland environments. (Farooq *et al*. 2010 and Arain *et al*. 2018)

Genetic variability and heritability knowledge provide dependable tool to wheat breeders for improvement and considered to be indispensable to convene the diversified target of plant breeding such as breeding for increasing yield, wider adaptation, pest and disease resistance (Wani *et al*. 2018). the information of the genetic diversity within a genotypes has a significant impact for crop improvement and vital for development of wheat varieties resilient to climate change and diverse environment. Principal component analysis (PCA) and cluster analysis based on genetic diversity of yield traits can be used to assess genetic variation among plant genotypes to detect significant variation and facilitates the selection procedures of high yielding potential genotypes in wheat breeding programs under rained conditions (Ali *et al*. 2019 and Adilova *et al*. 2020)

The present study was carried out on 120 newly bread wheat genotypes in F_7 to achieve the following objectives; a) Identification and selection of high yielding and promising genotypes under rainfed conditions, b) Estimation of genetic variability, heritability correlation and path analysis for several agro-morphological traits and c) study the genetic diversity of advanced lines by using principal component and cluster analyses.

Materials And Methods

The present experiment was carried out to evaluate the response of 120 derived lines in F_7 which developed from bread wheat breeding program at ACSAD compared with the two cultivar Doma 4 and Doma 6, sources and pedigree/or selection history of tested genotypes are listed in Table (1). The selected genotypes were grown at Izraa Agricultural Experiment Station of ACSAD, Daraa governorate, Syria (32.8449° N, 36.2251° E) semi-dry location under rainfed conditions for two consecutive growing seasons (2018/19 and 2019/20).

The experiment (primary comparing yield trial) was laid out in randomized complete block design with three replications, Sowing dates were Nov. 15 and 18 in the 1st and 2nd season, respectively. Meteorological data and the location receives annual rainfall perception of 215.45 and 354.2 in the 1st and 2nd season respectively are given in Table (2) show that the mean of temperature, and amount of rainfall every month in each season. Experimental plots had six rows of 5 m length, spaced 30 cm apart for each genotype per replicate. The recommended dose of fertilizers $N:P_2O_5$ at 120:60 kg ha^{-1} was applied, N was applied 1/3 of the amount was incorporated in dry soil before sowing, 1/3 was added one week before panicle initiation growth stage 18 and the rest was added at grain filling period growth stage 50 of Zadoks' scale (Zadok *et al* 1974). While, the other agricultural practices recommended for growing bread wheat were followed. Soil Mechanical and chemical analysis are presented in Table (3). Observations from the central four rows were recorded on 10 randomly selected and tagged plants per genotype or line for the following traits: days to heading (50%) (days), maturity date (days), flag leaf area (cm^2), basal angle of flag leaf (°), plant height (cm.), number of spikes/plant, Spike Length (cm.), number of spikelets/spike, number of grains/spike, 1000-kernel weight (g.), main spike grain yield(g.), grain yield (t./ha), straw yield (t./ha) and biological yield (t./ha.) were recorded. Data were subjected to the combined analysis of variance after seasonal homogeneity F test for each environment, as outlined by Steel and Torrie (1984).

All statistical analyses were performed using the program Genes, version 2018.25 (Cruz, 2013). The phenotypic and genotypic variance and coefficient of variation were estimated according to the methods suggested by Burton, and Devane (1953). While, Phenotypic correlation coefficients were also calculated for different pairs of traits according to Snedecor and Cochran (1989). The direct and indirect effect of yield related traits on grain yield per hectare has been analyzed through path coefficient analysis according to Dewey and Lu (1959). The genetic divergence among the wheat genotypes, descriptive statistics, cluster analysis and principal component analysis (PCA) were calculated by canonical (Vector) of divergence estimation using R method (Oksanen, 2010), PAST (Hammer *et al* 2001) and squared Euclidian distance as a measure of dissimilarity according to (Ward, 1963).

Table 1. Name, cross/pedigree and origin of the parental genotypes.

Genotypes	Cross/Pedigree	Genotypes	Cross/Pedigree	Origin
ACSAD 1196	TEVEE7/ SHUHA19/3/ CHILERO-3// TSI/SNB′s′	ACSAD 1318	ACSAD 1123 /4/ RL6043/4*NAC // PASTOR /3/ BABAX	ACSAD*
ACSAD 1198	CMH79.955/3*CNO79//HE1/CNO79/3/MILAN/4/ACSAD901	ACSAD 1320	ACSAD 1123 /4/ RL6043/4*NAC // PASTOR /3/ BABAX	ACSAD
ACSAD 1200	CMH79.955/3*CNO79//HE1/CNO79/3/MILAN/4/ACSAD901	ACSAD 1322	ACSAD1133 /3/ TOBA97 /BAV92 // MILAN /KAUZ	ACSAD
ACSAD 1202	BEZ/TRACHA-2//PREW	ACSAD 1324	CHAM6 / PBW343*2 / KUKUNA	ACSAD
ACSAD 1204	PRINIA/ ACSAD901	ACSAD 1326	SIDS 9 /3/ BOHOUTH -4 // NS732/HER	ACSAD
ACSAD 1206	W462/VEE/KOEL/3/PEG//MRL/BUC/4/	ACSAD 1328	SIDS 9 / RAAD-2	ACSAD
ACSAD 1208	KASYON/GENARO.81/TEVEE/3/HUITES.F95	ACSAD 1330	SIDS 9 / RAAD-2	ACSAD
ACSAD 1210	KASYON/GENARO.81/TEVEE/3/HUITES.F95	ACSAD 1332	SALAMBO // FLORKWA.1 / DHARWAR DRY	ACSAD
ACSAD 1212	KASYON/GENARO.81/TEVEE/3/GIZI44//PNJ′s′/BOW′s′	ACSAD 1334	SALAMBO // FLORKWA.1 / DHARWAR DRY	ACSAD
ACSAD 1214	ACSAD977/4/W462//VEE/KOEL/3/PEG//MRL/BUC	ACSAD 1336	BOUHOTH 116 /4/ MILAN / KAUZ//PRINIA/3/ BABAX	ACSAD
ACSAD 1216	ACSAD977/3/KASYOUN/GENARO.81/TEVEE-1	ACSAD 1338	BOUHOTH 116 /4/ MILAN / KAUZ//PRINIA/3/ BABAX	ACSAD
ACSAD 1218	TSH/DOVE//KAUZ/3/BCN/4/ ACSAD 881	ACSAD 1340	BOUHOTH 116 /5/ PJN /BOW//OPATA /3/PASTOR	ACSAD
ACSAD 1220	KAUZ/FCT/3/OPATA/RAYON//KAUZ	ACSAD 1342	BOUHOTH 116 /5/ PJN /BOW//OPATA /3/PASTOR	ACSAD
ACSAD 1222	KAUZ/FCT/3/OPATA/RAYON//KAUZ	ACSAD 1344	ACSAD 1123 // PASTOR / FLORKWA .1	ACSAD
ACSAD 1224	AALAAL-1/3/VEE/PJN//KAUZ	ACSAD 1346	ACSAD1133 /3/ TOBA97 /BAV92 // MILAN /KAUZ	ACSAD
ACSAD 1226	BOUSHODA-1/ACSAD 903	ACSAD 1348	CHAM6 / PBW343*2 / KUKUNA	ACSAD
ACSAD 1228	MELLAL-1//TEVEE-7/SHUHA-19	ACSAD 1350	CHAM-6/GHURAB′S′//JADIDA-2 /3/ SIDS-9	ACSAD
ACSAD 1230	MELLAL-1//TEVEE-7/SHUHA-19	ACSAD 1352	DYBR1982-83/842ABVD C-50// KAUZ/3/PLK70/ LIRA/4/	ACSAD
ACSAD 1232	SIDS-1/ ACSAD 903	ACSAD 1354	NAC/VEE′S′//TEMMU196.74 /TITO′S′ /4/ CASKOR	ACSAD
ACSAD 1234	GIZA164/SAKHA34//SIEF-7	ACSAD 1356	NAC/VEE′S′//TEMMU196.74 /TITO′S′ /4/ CASKOR	ACSAD
ACSAD 1236	GIZA164/SAKHA34//SIEF-7	ACSAD 1358	NAC/VEE′S′//TEMMU196.74 /TITO′S′ /3/ SIDS-9	ACSAD
ACSAD 1238	GIZA164/SAKHA34//SIEF-7	ACSAD 1360	NAC/VEE′S′//TEMMU196.74 /TITO′S′ /3/ IRQIPAW 183-	ACSAD
ACSAD 1240	GIZA164/SAKHA34//SIEF-7	ACSAD 1362	BOUSHODA-1 / SIDS-9	ACSAD
ACSAD 1242	GIZA164/SAKHA34//HUD-10	ACSAD 1364	SIDS-9 / IRQIPAW 183-S2-98	ACSAD
ACSAD 1244	GIZA164/SAKHA34//HUD-10	ACSAD 1366	IRQIPAW 99-S2-98 // INQALAB91*2/KUKUNA	ACSAD
ACSAD 1246	ACSAD529//GIM/BUC/3/ANGI-4	ACSAD 1368	ACSAD 1097 // BOHOUTH-6/CHIL-1	ACSAD
ACSAD 1248	54/(17+20+21+29)	ACSAD 1370	ACSAD 1097 // BOHOUTH-6/CHIL-1	ACSAD
ACSAD 1250	55/(17+20+21+29)	ACSAD 1372	ACSAD 1069 /4/ KAUZ/LUCO-M//PVN/STAR/3/ FOW-1	ACSAD
ACSAD 1252	HAAMA-11//KARAWAN-1/TALLO-3	ACSAD 1373	PICUS/4/CS5A/5RL-	ACSAD
ACSAD 1254	HAAMA-11//KARAWAN-1/TALLO-3	ACSAD 1374	PICUS/4/CS5A/5RL-1//BUC/BJY/3/ALD/PVN/5/LAJ3302/6/	ACSAD
ACSAD 1258	PRINA// KARAWAN-1/TALLO-3	ACSAD 1375	PICUS/4/CS5A/5RL-1//BUC/BJY/3/ALD/PVN/5/LAJ3302/6/	ACSAD
ACSAD 1260	GIZA168 / ACSAD1081	ACSAD 1376	CHAM-6/GHURAB′S′//MELLAL-1 /3/ OTEIK	ACSAD
ACSAD 1262	CHAM-4//NS732/HER/3/SIEF-7	ACSAD 1377	FOW′S′//NS732/HER/3/CHAM-6//GHURAB′S′ /4/ ACSAD	ACSAD
ACSAD 1264	CHAM-4//NS732/HER/3/SIEF-7	ACSAD 1378	FOW′S′//NS732/HER/3/CHAM-6//GHURAB′S′ /4/ ACSAD	ACSAD
ACSAD 1266	SIEF-7 / CHAM-4	ACSAD 1379	FOW′S′//NS732/HER/3/CHAM-6//GHURAB′S′ /4/ ACSAD	ACSAD
ACSAD 1268	QAFZAH-27/CHAM-4	ACSAD 1380	CHAM-6/FLORKWA-2 // OTEIK	ACSAD
ACSAD 1270	QAFZAH-27/CHAM-4	ACSAD 1382	ACSAD 1115 / GEMMEIZA9	ACSAD
ACSAD 1272	QAFZAH-27/CHAM-6	ACSAD 1384	ACSAD 1115 / GEMMEIZA9	ACSAD
ACSAD 1274	QAFZAH-27/CHAM-6	ACSAD 1386	ACSAD 1115 / SHANDAWEEL1	ACSAD
ACSAD 1276	KAR-1//RMNF12-71/JUP ′S′ /3/ SKAUZ/BAV92//PASTOR	ACSAD 1388	ACSAD 885 / EARLY1	ACSAD
ACSAD 1278	KAR-1//RMNF12-71/JUP ′S′ /4/ KABY/ BAV92 /3/CROC_1/	ACSAD 1390	ACSAD 1135 /3/ PFAU/WEAVER*2//KIRITATI	ACSAD
ACSAD 1280	PASTOR/DHARWAR DRY /4/ RL6043/	ACSAD 1392	ACSAD 1135 /3/ PFAU/WEAVER*2//KIRITATI	ACSAD
ACSAD 1282	PASTOR/DHARWAR DRY /4/ RL6043/	ACSAD 1368	ACSAD 1097 // BOHOUTH-6/CHIL-1	ACSAD
ACSAD 1284	PASTOR/DHARWAR DRY /3/ SKAUZ/BAV92//PASTOR	ACSAD 1370	ACSAD 1097 // BOHOUTH-6/CHIL-1	ACSAD
ACSAD 1286	ATTILA/BABAX//PASTOR /3/ SKAUZ /BAV92//PASTOR	ACSAD 1372	ACSAD 1069 /4/ KAUZ/LUCO-M//PVN/STAR/3/ FOW-1	ACSAD
ACSAD 1288	ATTILA/BABAX//PASTOR /3/ SKAUZ /BAV92//PASTOR	ACSAD 1373	PICUS/4/CS5A/5RL-	ACSAD
ACSAD 1290	CHAM-6/FLORKWA-2 /3/ BOHOUTH-4// NS732/HER	ACSAD 1394	ACSAD 1135 /3/ PFAU/WEAVER*2//KIRITATI	ACSAD
ACSAD 1292	CHAM-6/FLORKWA-2 // DOBUC ′S′/STAR′S′	ACSAD 1396	ACSAD 1135 /3/ WHEAR/KUKUNA//WHEAR	ACSAD
ACSAD 1294	MUNIA//CHEN/ALTAR84/3/CHEN /4/	ACSAD 1398	HIDHAB / QIMMA-8	ACSAD
ACSAD 1296	ACSAD 1139 /3/ NAC/VEE′S′// TEMMU196.74/TITO′S	ACSAD 1400	WIFAK /3/ WHEAR/KUKUNA//WHEAR	ACSAD
ACSAD 1298	ACSAD 901 /4/ MILAN/KAUZ// PRINIA/3/BABAX	ACSAD 1402	ACSAD 1178	ACSAD
ACSAD 1300	ACSAD 901 /3/ NAC/VEE′S′// TEMMU196.74/TITO′S′	ACSAD 1404	ACSAD 1178 // TACUPETO F2001*2/KIRITATI	ACSAD
ACSAD 1302	ACSAD 901 /3/ NAC/VEE′S′// TEMMU196.74/TITO′S′	ACSAD 1406	ACSAD 1194 // KIRITATI/2*WBLL1	ACSAD
ACSAD 1304	ACSAD 901 /3/ NAC/VEE′S′// TEMMU196.74/TITO′S′	ACSAD 1408	ACSAD 1198 // ND643/2*WBLL1	ACSAD
ACSAD 1306	SW89 . 5181 /KAUZ /5/ PJN /BOW// OPATA/3/ PASTOR/4/	ACSAD 1410	ACSAD 1067 /4/ DVERD-	ACSAD
ACSAD 1308	BABAX /PASTOR//AMAD/7/SIDS 10 /CIRCUS /6/	ACSAD 1412	ACSAD 1147 / BERKUT	ACSAD
ACSAD 1310	ACSAD 1123 // PASTOR / FLORKWA .1	ACSAD 1414	ACSAD 1147 /4/ TC870344/GUI//TEMPORALERA M	ACSAD
ACSAD 1312	ACSAD 1123 /4/ RL6043/4*NAC // PASTOR /3/ BABAX	ACSAD 1416	ACSAD 1147 /4/ SAAR/3/C80.1/3*BATAVIA//2*WBLL1	ACSAD
ACSAD 1314	ACSAD 1123 /4/ RL6043/4*NAC // PASTOR /3/ BABAX	ACSAD 1418	ACSAD 1147 /4/ SAAR/3/C80.1/3*BATAVIA//2*WBLL1	ACSAD
ACSAD 1316	ACSAD 1123 /4/ RL6043/4*NAC // PASTOR /3/ BABAX	ACSAD 1420	ACSAD 1147 /4/ SAAR/3/C80.1/3*BATAVIA//2*WBLL1	ACSAD
Doma 4	ACSAD529/4/C182.24/C168.3/3/Cno*2/7C//Cc/Tob	Doma 6	SNB′S′SHI#4414/CROW′S′/3/MON′S′/ CROW′S′	ACSAD

*ACSAD ;The Arab Center for the Studies of Arid Zones and Dry Lands.

Table 2. Monthly average weather data at Izraa research station during two growing seasons 2018/19 and 2019/20.

Month	Season (2018-2019)			Season (2019-2020)		
	T.† (C°)		Amount Rainfall (mm)	T.† (C°)		Amount Rainfall (mm)
	Max.	Min.		Max.	Min.	
November	21.64	11.70	4.17	17.31	9.36	11.5
December	16.90	10.28	11.00	13.52	8.22	17.5
January	11.25	8.14	35.00	9.56	6.92	69.8
February	14.19	3.22	67.28	11.35	2.58	90.2
March	18.63	5.81	45.00	14.90	4.65	82.4
April	23.62	11.15	34.00	21.26	10.04	51.7
May	29.44	15.09	19.00	26.50	13.58	31.1
June	35.65	18.70	0.00	32.09	16.83	0.00
Mean	21.41	10.51	Tot. =215.45	18.31	9.02	Tot. =354.2

†T. = Temperature

Table 3. Mechanical and chemical analysis of soil at Izraa research station.

Depth	pH	Organic matter (%)	Mechanical analysis			Chemical analysis		
			Sand (%)	Silt (%)	Clay (%)	N (mg)	P (mg)	K (mg)
0-30	7.52	0.71	19.70	17.40	62.90	7.42	10.67	390.10

Results And Discussion

Analysis of variance:

The analysis of variance results of the two seasons 2018/19 and 2019/20 revealed that error mean squares are homogeneous and their combined analysis across seasons for 14 characters are presented in Table 3. The results revealed that the mean squares due to seasons (S.) and genotypes (G.) were significant (P≤0.05) for all characters. This indicates that demonstrated the existence of considerable differences among different selected bread wheat lines and would respond positively to selection. Similar findings were reported by Majumder *et al* (2008), Khan *et al* (2015), Arain *et al* (2018) and Muhder *et al* (2020).

Table 4. Mean squares of bread wheat genotypes (G.) for different studied traits in 1st and 2nd seasons (S.) and combined analysis under rainfed conditions.

Season	1st season		2nd season		Combined				
Mean Square	G.	Error	G.	Error	S.	Rep. (R)/S.	G.	G.×S.	Error
d.f.	121	242	121	242	1	2	121	121	486
Days to heading (50%) (days)	258.70**	10.99	269.16**	11.43	849.016**	13.33	527.81**	0.05	11.16
Maturity date (days)	507.05**	21.54	527.53**	22.41	16410.73**	26.14	1034.49**	0.10	21.88
Flag leaf area (cm²)	8.79**	0.91	9.14**	0.95	1519.90**	0.54	17.93**	0.001	0.93
Basal angle of flag leaf (°)	84.28**	5.17	88.01**	5.37	12.24**	1.54	172.28**	0.02	5.25
Plant height (cm.)	141.37**	27.15	147.07**	28.25	513.49**	10.64	348.42**	0.02	27.59
No. of spikes/plant	8.41**	0.70	8.76**	0.73	1.84**	4.42	17.17**	0.001	0.71
Spike Length (cm.)	3.49**	0.43	3.63**	0.45	9.40**	0.45	7.12**	0.01	0.44
No. of spikelets/spike	23.33**	2.51	24.29**	2.61	36.39**	2.35	47.62**	0.04	2.55
No. of grains/spike	427.35**	74.33	444.62**	77.34	699.40**	8.56	951.89**	0.08	75.52
1000-kernel weight (g.)	0.16**	0.04	0.17**	0.05	1.834**	0.11	0.33**	0.01	0.05
Grain yield/ main Spike(g.)	0.93**	0.16	0.97**	0.16	0.64**	1.28	1.90**	0.01	0.16
Grain yield (t. /ha)	3.09**	0.12	3.21**	0.12	0.41**	0.09	6.30**	0.02	0.12
Straw yield (t. /ha)	11.17**	0.86	11.62**	0.90	1.31**	0.80	22.78**	0.05	0.88
Biological yield (t. /ha)	25.53**	1.41	26.56**	1.47	3.16**	0.84	52.09**	0.05	1.44

*, ** denote significance at 0.05 and 0.01 probability levels, respectively.

Phenotypic performance of bread wheat genotypes:

Estimated phenotypic performance off the 122 genotypes of bread wheat for 14characters under rainfed conditions are presented in Table 4. For days to heading (50%) and maturity date the six newly genotypes ACSAD 1286, ACSAD 1288, ACSAD 1226, ACSAD 1234, ACSAD 1240 and ACSAD 1282 were the earliest. Meanwhile, the eleven genotypes were the latest; ACSAD 1342, ACSAD 1358, ACSAD 1364, ACSAD 1368, ACSAD 1376, ACSAD 1354, ACSAD 1370, ACSAD 1372, ACSAD 1416, ACSAD 1418 and ACSAD 1420 recorded the highest values for both traits with no significant differences. While, the 17 genotypes; ACSAD 1206, ACSAD 1250, ACSAD 1288, ACSAD 1290, ACSAD 1298, ACSAD 1332,ACSAD 1366, ACSAD 1368, ACSAD 1370, ACSAD 1372, ACSAD 1380, ACSAD 1382, ACSAD 1396, ACSAD 1414, ACSAD 1416,ACSAD 1418, ACSAD 1420 as well as the two cv. Doma 4 and Doma 6 recorded the highest values for Flag Leaf Area. Furthermore, the two genotypes ACSAD 1372 (22.19 cm^2)and ACSAD 1420 (23.05 cm^2) as well as the two cv. Doma 4 (25.46 cm^2) and Doma 6 (22.67 cm^2) had the highest values for Basal Angel Flag Leaf reflecting high variance of these traits under rainfed conditions.

For plant height the four newly genotype ACSAD 1390, ACSAD 1414, ACSAD 1416 and ACSAD 1418 were the tallest. On the other hand, the three genotypes ACSAD 1230, ACSAD 1232 and ACSAD 1286 had the lowest values (Table, 4). The ten genotypes ACSAD 1196, ACSAD 1198,ACSAD 1332, ACSAD 1366, ACSAD 1368, ACSAD 1370, ACSAD 1372, ACSAD 1416, ACSAD 1418 and ACSAD 1420 as well as the cv. Doma 4 had the highest values for no. of spikes /plant. While, the eleven genotypes; ACSAD 1334, ACSAD 1364, ACSAD 1366, ACSAD 1376, ACSAD 1378, ACSAD 1388, ACSAD 1412, ACSAD 1414, ACSAD 1416, ACSAD 1418, ACSAD 1420 had the highest values for spike length. The nine genotypes; ACSAD 1334, ACSAD 1342, ACSAD 1370, ACSAD 1378, ACSAD 1388, ACSAD 1390, ACSAD 1414, ACSAD 1416, and ACSAD 1418 registered the highest values of no. of spikelets/spike.

For no. of grains/spike the six genotypes showed maximum values ACSAD 1368, ACSAD 1396, ACSAD 1398, ACSAD 1400, ACSAD 1378 and ACSAD 1390. Whereas, thirteen genotypes; ACSAD 1196, ACSAD 1258, ACSAD 1300, ACSAD 1302, ACSAD 1306, ACSAD 1332, ACSAD 1334, ACSAD 1364, ACSAD 1372, ACSAD 1373, ACSAD 1388, ACSAD 1414 and ACSAD 1416 recorded the highest mean values for 1000 grain Weight as well as for the four traits grain yield/ main spike, grain yield /ha, straw yield/ha and biological yield except for ACSAD 1258 genotype.

It was concluded from the previous results that the thirteen genotypes; ACSAD 1196, ACSAD 1258, ACSAD 1300, ACSAD 1302, ACSAD 1306, ACSAD 1332, ACSAD 1334, ACSAD 1364, ACSAD 1372, ACSAD 1373, ACSAD 1388, ACSAD 1414 and ACSAD 1416 showed best performance by producing highest one/or more of yield attributes, and hence highest grain yield kg ha^{-1} under rainfed conditions. These lines possess great genetic potential for further evaluation in the field under different locations (The Arab productive efficiency trial) for development of wheat cultivars under rain-fed environment in the Arab countries. similar findings were obtained by Khan *et al*. (2015), Raza *et al*. (2018), Arain *et al*. (2018), and Muhder *et al* (2020).

Table 5. Mean performance of 122 bread wheat genotypes for combined data across seasons under rainfed conditions at Izraa.

Genotypes	Heading Date (days)	Days to Maturity (days)	Flag Leaf Area (cm²)	Basal Angle Flag Leaf (°)	Plant Height (cm.)	No. of Spikes / Plant	Spike Length (cm.)	No. Spikelets / Spike	No. Grains / Spike	1000 grain Weight (g.)	Grain Yield/main Spike (g.)	Grain Yield (t. /ha)	Straw Yield (t. /ha)	Biological Yield (t. /ha)
ACSAD 1196	105.64	148.79	7.16	18.97	83.93	8.29	11.40	21.40	64.73	5.77	3.71	4.12	5.56	9.68
ACSAD 1198	104.16	145.83	5.99	15.87	84.14	9.01	12.25	19.66	49.98	5.14	2.43	3.06	4.13	7.19
ACSAD 1200	105.58	147.81	5.29	14.03	86.90	6.05	11.50	21.23	59.08	5.13	2.86	3.46	4.67	8.13
ACSAD 1202	106.99	149.79	4.77	12.65	83.00	6.98	11.56	19.83	50.10	5.27	2.44	3.11	4.20	7.31
ACSAD 1204	103.00	144.86	4.34	11.50	85.20	6.91	11.71	19.18	52.31	5.17	2.50	2.99	4.04	7.03
ACSAD 1206	100.00	140.20	7.95	11.61	88.26	6.70	11.30	19.00	41.51	5.03	1.93	2.46	3.32	5.78
ACSAD 1208	101.29	141.55	7.08	10.35	83.21	5.44	11.35	20.33	54.58	4.98	2.51	2.53	3.42	5.95
ACSAD 1210	103.16	143.53	6.61	9.66	87.00	5.00	10.50	19.29	53.98	5.06	2.53	2.36	3.19	5.55
ACSAD 1212	100.39	140.55	6.29	9.20	84.65	4.68	11.12	21.25	56.68	4.99	2.60	2.29	3.09	5.38
ACSAD 1214	99.92	139.89	5.04	10.36	80.95	3.96	11.35	19.00	54.18	5.01	2.54	2.84	3.83	6.67
ACSAD 1216	97.57	136.59	5.74	8.39	84.28	4.68	10.92	19.80	48.13	4.96	2.21	3.92	5.29	9.21
ACSAD 1218	101.87	142.21	5.35	10.82	78.17	4.32	10.70	19.19	52.02	4.90	2.36	2.88	3.89	6.77
ACSAD 1220	103.69	145.17	4.33	8.32	81.41	2.91	10.99	17.65	62.34	4.94	2.86	2.50	3.38	5.88
ACSAD 1222	100.09	139.55	4.17	8.09	80.33	3.24	10.71	18.59	54.70	4.97	2.51	2.42	3.27	5.69
ACSAD 1224	96.15	136.61	4.38	8.33	70.97	2.85	10.63	16.71	48.49	4.73	2.12	2.10	2.84	4.94
ACSAD 1226	93.32	130.75	4.07	10.55	76.01	2.16	10.45	18.30	58.44	4.77	2.58	3.04	4.10	7.14
ACSAD 1228	98.51	137.91	4.33	9.32	74.57	3.96	10.90	18.41	45.17	4.85	2.05	2.47	3.33	5.80
ACSAD 1230	94.38	129.33	3.62	8.91	68.08	2.91	10.91	18.37	51.40	4.57	2.17	2.15	2.90	5.05
ACSAD 1232	98.04	137.15	4.00	12.39	68.44	2.85	9.91	19.59	58.99	4.99	2.71	2.46	3.32	5.78
ACSAD 1234	93.32	130.55	4.13	10.07	72.77	3.24	10.09	21.25	51.70	4.90	2.37	2.34	3.16	5.50
ACSAD 1236	96.04	135.35	3.91	7.17	73.85	2.88	10.45	19.81	40.60	5.07	1.88	2.99	4.04	7.03
ACSAD 1238	99.45	139.23	3.30	8.13	75.65	3.63	10.82	19.00	37.84	4.75	1.67	2.10	2.84	4.94
ACSAD 1240	92.85	129.99	4.56	9.67	78.94	3.96	10.29	22.78	44.32	4.89	2.00	2.47	3.33	5.80
ACSAD 1242	98.98	138.57	5.11	9.47	83.57	3.57	10.25	21.00	53.32	5.01	2.47	3.66	4.94	8.60
ACSAD 1244	95.68	133.95	4.09	9.98	76.37	2.88	10.80	21.50	54.77	4.95	2.52	2.31	3.12	5.43
ACSAD 1246	96.15	134.61	5.04	7.36	80.66	3.60	10.27	22.08	55.59	4.91	2.52	2.69	3.63	6.32
ACSAD 1248	99.92	139.89	6.29	9.20	81.05	4.68	10.99	21.90	52.76	5.16	2.57	2.24	3.02	5.26
ACSAD 1250	96.52	136.27	7.63	11.15	82.49	6.12	11.17	20.50	46.56	4.89	2.11	2.40	3.24	5.64
ACSAD 1252	94.27	131.97	6.06	8.85	79.61	4.68	10.36	22.00	53.35	4.85	2.39	2.06	2.78	4.84
ACSAD 1254	102.28	143.19	7.00	10.23	80.00	5.04	10.90	22.55	47.52	5.14	2.26	2.12	2.86	4.98
ACSAD 1258	100.39	140.55	5.81	15.41	79.61	7.93	11.17	22.83	50.86	5.63	2.51	3.69	4.98	8.67
ACSAD 1260	101.34	142.87	4.81	12.76	79.97	6.00	10.81	21.97	57.68	5.31	2.83	3.20	4.32	7.52
ACSAD 1262	103.87	142.21	5.51	14.60	81.77	6.24	11.71	23.42	61.73	5.17	2.96	3.38	4.56	7.94
ACSAD 1264	101.34	141.87	4.73	12.53	78.80	4.68	10.99	21.97	74.62	5.39	3.72	3.09	4.17	7.26
ACSAD 1266	96.72	134.27	3.60	9.54	82.85	3.96	10.63	20.53	70.89	5.15	3.06	2.45	3.31	5.76
ACSAD 1268	99.45	139.23	3.47	9.20	84.65	3.60	10.09	19.72	65.68	4.93	3.00	2.00	2.70	4.70
ACSAD 1270	98.98	138.57	4.47	11.84	79.00	4.68	10.81	21.15	67.51	5.03	3.15	2.77	3.74	6.51
ACSAD 1272	102.39	142.55	5.73	15.18	79.50	5.44	10.63	19.90	72.87	5.36	3.62	3.65	4.93	8.58
ACSAD 1274	103.42	143.76	6.07	13.45	80.69	5.00	10.99	21.35	71.40	5.31	3.52	3.20	4.32	7.52
ACSAD 1276	102.60	143.30	6.68	10.92	78.53	4.32	10.70	20.74	70.81	4.10	3.28	2.61	3.52	6.13
ACSAD 1278	99.92	139.89	6.19	8.28	81.05	3.24	10.20	18.55	73.50	5.10	3.37	2.94	3.97	6.91
ACSAD 1280	97.57	136.59	7.57	8.01	79.97	2.88	10.27	19.63	73.97	4.91	3.31	2.62	3.54	6.16
ACSAD 1282	93.60	132.27	7.28	10.75	78.19	3.70	10.40	20.53	56.40	4.90	2.55	2.71	3.66	6.37
ACSAD 1284	96.62	135.25	7.07	10.55	76.73	3.96	10.09	18.25	48.25	4.89	2.17	2.35	3.17	5.52
ACSAD 1286	93.99	127.35	8.68	8.05	65.20	3.60	9.73	18.05	56.23	4.58	2.38	2.75	3.71	6.46
ACSAD 1288	90.95	130.35	9.06	8.39	72.05	2.88	9.19	19.09	77.56	4.80	3.47	2.82	3.81	6.63
ACSAD 1290	97.59	136.61	7.69	10.13	73.13	3.90	9.55	17.65	51.05	4.84	2.30	2.66	3.59	6.25
ACSAD 1292	93.80	131.31	4.71	8.88	78.53	4.32	10.70	20.22	60.33	4.76	2.63	2.97	4.01	6.98
ACSAD 1294	99.45	139.23	3.16	10.30	74.57	4.02	10.18	19.81	36.13	4.82	1.61	2.19	2.96	5.15
ACSAD 1296	98.98	138.57	4.00	8.54	78.17	3.60	10.00	19.09	49.10	4.99	2.25	2.50	3.38	5.88
ACSAD 1298	112.18	157.05	7.81	20.40	87.18	7.93	11.51	24.14	69.81	5.11	3.43	3.05	4.12	7.17
ACSAD 1300	109.51	154.09	7.24	19.20	83.00	6.48	11.37	23.30	74.47	5.61	3.65	4.39	5.93	10.32
ACSAD 1302	112.92	157.50	5.66	16.00	87.04	5.76	11.89	23.54	77.73	5.82	3.75	4.00	5.40	9.40
ACSAD 1304	113.91	158.89	7.26	18.26	86.46	6.12	11.70	24.14	75.68	5.01	3.28	3.68	4.97	8.65
ACSAD 1306	110.50	155.28	6.03	15.98	85.98	5.04	11.00	20.55	78.38	5.71	3.92	4.06	5.48	9.54
ACSAD 1308	109.82	153.75	5.16	13.68	88.26	5.76	11.29	21.99	68.82	5.23	3.33	3.49	4.71	8.20
ACSAD 1310	105.74	147.00	6.01	13.22	86.82	5.40	11.05	20.55	62.74	5.08	2.95	2.91	3.93	6.84
ACSAD 1312	107.30	151.26	7.31	11.96	83.93	4.68	10.81	20.37	65.48	5.10	3.09	2.68	3.62	6.30
ACSAD 1314	111.04	153.75	6.68	10.92	85.50	4.47	10.63	22.50	72.51	5.19	3.28	2.53	3.42	5.95
ACSAD 1316	109.60	153.25	6.92	10.35	77.45	3.55	11.60	20.56	63.41	5.24	3.08	2.25	3.04	5.29
ACSAD 1318	107.88	152.43	6.30	10.00	80.33	3.24	11.28	20.00	72.90	5.02	3.39	2.05	2.77	4.82
ACSAD 1320	109.82	154.05	5.69	9.31	82.49	3.50	11.35	21.06	67.19	5.11	3.18	2.11	2.85	4.96
ACSAD 1322	111.71	156.39	5.36	9.08	81.41	3.96	11.17	19.81	58.36	4.28	2.84	2.08	2.81	4.89

Table 5.cont.

ACSAD 1324	110.76	155.07	5.34	8.74	79.25	3.70	12.25	20.91	61.74	5.01	2.86	2.88	3.89	6.77
ACSAD 1326	110.70	153.09	6.89	8.85	78.15	3.50	12.07	21.53	65.80	4.87	2.97	2.97	4.01	6.98
ACSAD 1328	108.00	153.09	6.35	8.16	78.53	3.60	10.81	19.81	62.87	4.83	2.81	2.80	3.78	6.58
ACSAD 1330	111.23	155.73	6.46	12.71	86.82	5.40	12.20	21.25	61.25	4.97	2.83	3.02	4.08	7.10
ACSAD 1332	115.48	161.67	7.81	21.00	97.26	8.29	12.97	25.58	60.85	5.70	3.87	4.76	6.43	11.19
ACSAD 1334	118.36	165.60	6.90	18.28	92.58	7.93	13.51	27.74	63.33	5.53	3.60	4.52	6.10	10.62
ACSAD 1336	112.65	157.71	6.29	16.67	96.18	7.40	12.43	25.58	63.45	5.03	3.00	3.51	4.74	8.25
ACSAD 1338	116.36	163.02	6.16	16.33	94.74	7.56	12.61	26.00	55.39	5.28	2.76	3.89	5.25	9.14
ACSAD 1340	115.01	161.01	5.99	15.87	92.22	7.00	12.99	26.80	58.57	5.24	2.78	3.70	5.00	8.70
ACSAD 1342	120.66	168.93	5.60	14.83	91.50	6.60	12.90	27.02	57.13	5.21	2.86	3.41	4.60	8.01
ACSAD 1344	119.72	167.61	5.33	14.14	93.66	6.36	12.46	26.10	54.12	5.19	2.74	3.32	4.48	7.80
ACSAD 1346	112.65	157.71	4.94	13.11	91.86	6.12	12.69	24.86	58.45	5.05	2.77	3.14	4.24	7.38
ACSAD 1348	119.36	166.50	4.29	11.38	86.10	5.00	11.24	23.50	59.01	4.94	3.05	2.84	3.83	6.67
ACSAD 1350	116.48	162.67	4.25	11.27	90.06	5.08	11.82	23.64	66.44	5.30	3.25	3.03	4.09	7.12
ACSAD 1352	114.36	161.12	4.86	10.23	85.02	5.40	12.30	24.28	51.88	5.06	2.52	2.54	3.43	5.97
ACSAD 1354	123.49	172.89	4.77	10.00	88.62	4.68	11.17	23.42	55.02	5.00	2.86	2.48	3.35	5.83
ACSAD 1356	117.36	164.31	4.64	9.66	86.46	4.20	11.35	21.97	54.88	5.16	2.72	2.19	2.96	5.15
ACSAD 1358	120.45	166.95	4.56	9.43	82.49	4.68	11.98	23.42	57.54	5.14	2.74	2.36	3.19	5.55
ACSAD 1360	114.06	159.69	4.34	8.55	85.62	4.44	11.80	21.50	55.45	4.90	2.51	2.96	4.00	6.96
ACSAD 1362	118.91	166.95	4.00	8.23	85.14	3.96	11.71	21.00	57.65	5.15	2.72	2.86	3.86	6.72
ACSAD 1364	120.19	168.27	7.59	20.12	92.94	6.12	13.26	24.14	65.73	5.63	3.81	4.61	5.28	9.19
ACSAD 1366	116.89	163.65	9.72	19.76	91.55	9.01	13.40	26.80	69.83	5.10	3.00	3.75	5.06	8.81
ACSAD 1368	121.00	170.03	9.41	20.95	93.66	8.29	12.95	25.50	68.81	4.29	3.06	3.16	4.27	7.43
ACSAD 1370	123.02	171.13	9.33	20.72	92.22	8.65	13.04	24.86	72.87	5.21	3.17	3.53	4.77	8.30
ACSAD 1372	123.96	173.54	8.37	22.19	93.61	8.29	13.33	26.35	69.29	5.80	3.82	4.90	6.62	11.52
ACSAD 1373	118.05	167.95	7.46	19.78	91.86	7.20	12.91	23.36	76.62	5.84	3.70	4.58	6.18	10.76
ACSAD 1374	116.93	164.68	6.77	17.94	89.34	6.45	12.95	24.70	73.06	4.92	3.32	3.57	5.36	9.33
ACSAD 1375	123.02	172.23	6.12	16.21	90.06	6.12	12.81	25.02	74.44	4.86	3.34	3.50	5.13	8.93
ACSAD 1376	120.19	168.27	5.64	14.95	87.90	5.40	13.51	24.86	83.77	4.91	3.52	3.78	5.10	8.88
ACSAD 1377	118.78	165.29	5.55	14.72	84.65	4.32	12.79	23.50	80.16	5.01	3.71	2.99	4.04	7.03
ACSAD 1378	119.72	167.61	5.07	13.45	87.54	4.32	13.51	27.25	88.70	4.76	3.33	2.68	3.62	6.30
ACSAD 1379	121.13	169.59	5.51	12.19	83.57	4.68	12.97	25.30	73.45	4.85	3.39	2.93	3.96	6.89
ACSAD 1380	114.59	161.03	7.94	12.99	86.46	3.70	12.50	24.14	77.60	4.49	3.68	2.44	3.29	5.73
ACSAD 1382	117.36	164.31	7.80	12.76	87.18	3.96	12.72	23.42	78.29	4.54	3.29	2.41	3.25	5.66
ACSAD 1384	115.01	161.01	6.04	11.89	80.10	3.50	11.53	22.73	72.67	4.67	3.13	2.07	2.79	4.86
ACSAD 1386	117.30	164.63	5.62	11.20	82.00	3.24	12.07	23.69	74.72	4.95	3.46	2.00	2.70	4.70
ACSAD 1388	112.65	157.71	8.28	21.96	95.82	6.51	13.62	27.50	81.98	5.58	3.97	4.55	6.14	10.69
ACSAD 1390	119.25	166.95	7.20	19.09	100.51	5.82	12.85	27.98	85.42	5.01	3.89	3.92	5.29	9.21
ACSAD 1392	116.85	162.62	6.59	17.48	92.94	5.82	12.14	24.92	78.87	4.80	3.57	3.82	5.16	8.98
ACSAD 1368	114.63	160.06	6.03	15.98	90.42	5.04	12.25	25.58	84.99	4.89	3.65	2.60	4.86	8.46
ACSAD 1370	113.29	157.41	6.07	16.10	96.90	4.68	12.07	27.00	80.61	4.88	3.61	3.13	4.23	7.36
ACSAD 1372	112.55	158.00	4.99	13.22	89.34	4.32	12.79	24.14	79.11	4.90	3.58	2.89	3.90	6.79
ACSAD 1373	115.95	162.33	6.31	11.96	86.10	3.60	11.62	22.71	82.41	5.08	3.87	2.58	3.48	6.06
ACSAD 1394	112.65	157.71	6.83	12.76	85.38	4.32	11.82	24.80	81.09	4.73	3.55	2.86	3.86	6.72
ACSAD 1396	108.88	152.43	7.66	12.53	95.10	3.38	12.61	25.58	88.27	4.70	3.84	2.10	2.84	4.94
ACSAD 1398	116.89	163.65	6.75	11.04	86.31	3.10	11.35	21.97	84.52	5.12	3.84	2.54	3.43	5.97
ACSAD 1400	114.63	160.00	6.54	10.69	82.25	3.20	10.81	23.60	84.15	4.77	3.71	2.24	3.02	5.26
ACSAD 1402	111.23	155.73	6.61	10.81	91.86	3.28	12.43	24.28	79.37	4.74	3.47	2.10	2.84	4.94
ACSAD 1404	111.71	156.39	6.18	10.12	87.18	3.40	11.44	23.08	73.95	4.80	3.31	2.17	2.93	5.10
ACSAD 1406	114.53	160.35	5.76	9.43	86.10	3.70	12.65	23.84	68.65	4.70	3.11	2.00	2.70	4.70
ACSAD 1408	113.59	159.03	6.11	10.00	79.25	3.50	12.07	24.00	69.36	4.90	3.15	2.15	2.90	5.05
ACSAD 1410	112.55	158.06	5.27	8.62	81.77	3.80	11.60	23.24	72.59	4.91	3.29	2.68	3.62	6.30
ACSAD 1412	117.83	164.97	7.28	15.74	87.90	5.70	13.60	25.58	61.56	5.04	2.88	3.22	4.35	7.57
ACSAD 1414	123.79	174.50	9.02	20.22	97.98	7.93	13.87	27.50	81.90	5.79	4.16	4.15	4.72	7.40
ACSAD 1416	123.20	175.48	8.45	20.71	99.06	8.65	14.05	28.46	72.74	5.49	4.12	3.84	5.18	9.02
ACSAD 1418	123.32	173.84	9.63	20.17	97.62	7.93	13.11	27.90	80.18	5.16	3.62	2.59	3.50	6.09
ACSAD 1420	122.89	172.04	8.20	23.05	94.97	8.08	13.70	26.96	78.38	5.29	3.54	3.08	4.16	7.24
Doma 4	118.10	165.34	9.60	25.46	91.25	8.01	12.97	26.24	66.33	4.94	3.29	2.36	3.19	5.55
Doma 6	120.41	168.58	9.15	22.67	93.06	7.52	12.86	26.43	76.86	5.31	3.66	2.82	3.81	6.63
Mean	108.84	152.38	6.11	12.91	84.58	5.05	11.63	22.48	64.62	5.04	3.02	2.94	3.97	6.91
L.S.D 5%														
G.	3.16	5.24	2.33	3.91	3.65	1.07	0.94	1.222	5.79	0.38	0.75	1.06	1.51	1.72

Phenotypic correlation Coefficients:

The present study showed a significant (p ≤ 0.05) and positive correlation among the various attributes (Tab. 6). The highest significant positive correlation coefficients was found between grain yield/ha and straw yield/ha with biological yield (r = 0.902 and 0.894). Positive and significant correlation was found between; days to heading (50%) with each of maturity date, basal angle of flag leaf, plant height, spike length, no. of spikelets/spike, grain yield/ha, straw yield/ha and biological yield across seasons as well as maturity date (days) with each of basal angle of flag leaf, plant height, spike length, no. of

spikelets/spike, grain yield/ main spike, grain yield/ha, straw yield/ha and biological yield, flag leaf area with each of basal angle of flag leaf and straw yield/ha.

Basal angle of flag leaf was positively and significantly correlated with most of studied triats; days to heading, maturity date, flag leaf area, plant height, no. of spikes/plant, spike length, no. of spikelets/spike, grain yield/ main spike, grain yield/ha, straw yield/ha and biological yield ($r = 0.672$, 0.731, 0.833, 0.765, 0.811, 0.742, 0.868, 0.634, 0.756, 0.641 and 0.778, respectively). Plant height showed a highly significant positive correlation with spike length, no. of spikelets/spike, grain yield/ha, straw yield/ha and biological yield as well as no. of spikes/plant with each of grain yield/ha, straw yield/ha and biological yield. Spike length with no. of spikelets/spike, straw yield/ha and biological yield. number of spikelets/spike, and grain yield/ main spike depicted a positive and highly significant correlation with grain yield/ha, straw yield/ha and biological yield, number of grains per spike with grain yield/ main spike and grain yield/ha, 1000-kernel weight showed a positive and significant association with no. of grains/spike, grain yield/ main spike and grain yield/ha. Meanwhile, grain yield/ha developed a strong positive correlation with straw yield/ha and biological yield as well as between straw yield/ha and biological yield.

In general, positive and significant correlation of grain yield with its component appears to reflect the presence of interaction among the characters in which a gene conditioning an increase in one character will also influence another character, Similar result were obtained by Bhushan *et al.* (2013), Gelalcha and Hanchinal (2013), Chimdesa (2017), Singh and Upadhyay (2013), Arain *et al* (2018) and Ullah *et al* (2018).

Table 6. Sperman Coefficients of phenotypic correlation for combined data across seasons for the studied traits under rainfed conditions.

Traits	(X_1)	(X_2)	(X_3)	(X_4)	(X_5)	(X_6)	(X_7)	(X_8)	(X_9)	(X_{10})	(X_{11})	(X_{12})	(X_{13})	(X_{14})
Days to heading (50%) (days)	1.000													
Maturity date (days)	0.845**	1.000												
Flag leaf area (cm².)	0.313	0.316	1.000											
Basal angle of flag leaf (°)	0.672**	0.731**	0.833**	1.000										
Plant height (cm.)	0.776**	0.775**	0.431	0.765**	1.000									
No. of spikes/plant	0.509	0.510	0.417	0.811**	0.405	1.000								
Spike Length (cm.)	0.762**	0.825**	0.396	0.742**	0.806**	0.591	1.000							
No. of spikelets/spike	0.799**	0.740**	0.173	0.868**	0.811**	0.586	0.827**	1.000						
No. of grains/spike	0.519	0.440	0.533	0.530	0.480	0.068	0.482	0.534	1.000					
1000-kernel weight (g.)	0.332	0.270	0.054	0.451	0.334	0.581	0.230	0.155	0.761**	1.000				
Grain yield/ main Spike(g.)	0.579	0.618**	0.455	0.634**	0.547	0.213	0.516	0.587	0.866**	0.163	1.000			
Grain yield/ha(T.)	0.680**	0.641**	0.520	0.756**	0.774**	0.888**	0.528	0.752**	0.686**	0.648**	0.613**	1.000		
Straw yield/ha (T.)	0.705**	0.694**	0.608**	0.641**	0.800**	0.802**	0.724**	0.788**	0.578	0.626**	0.673**	0.759**	1.000	
Biological yield	0.688**	0.675**	0.579	0.778**	0.831**	0.839**	0.766**	0.784**	0.552	0.472	0.659**	0.902**	0.894**	1.000

*, ** denote significance at 0.05 and 0.01 probability levels, respectively.

Path coefficients:

For phenotypic path coefficient analysis the six traits; flag leaf area, basal angle of flag leaf, no. of spikes/plant, no. of spikelets/spike, no. of grains/spike and1000-grain weight were used in path coefficient analysis to detect the relative importance to grain yield/plant under rainfed conditions, the direct and indirect effects of the six yield attributes are shown in Table (7). The greatest positive direct

effect on grain yield/plant was expressed by Flag leaf area (0.941) , No. of spikelets/spike (1.164) and 1000-kernel weight (1.448). The indirect effects Flag leaf area and 1000- kernel weight via other traits were very low. The direct effect of No. of grains/spike seemed to be unimportant to grain yield/plant, such it showed very small value(-1.011) meanwhile , the indirect effects of this trait via Flag leaf area (0.502) and No. of spikelets/spike (0.622) were moderate and via 1000- grain weight were high (1.102) under rainfed conditions.

The components of the total grain yield variation determined directly and jointly by each factor are presented in Table (7). The main sources of plant yield variation in order of importance were the two direct effects of 1000-kernel weight (11.58%) and no. of spikelets/spike (7.48%) their joint effects with no. of grains/spike (12.30% and 6.94% , respectively) as well as the direct effect of no. of grains/spike (5.64%) and flag leaf area (4.89%) and its joint effect with each of basal angle of flag leaf (4.23%) and no. of grains/spike (5.60%). in addition to the joint effect of basal angle of flag leaf with no. of spikelets/spike (5.45%). Other effects ranging from 0.34% to 3.65% were contributed by the rest direct and joint effects. The total contribution of four traits studied was 89.97%, while the residual effect assumed to be about 10.03% of total phenotypic variation.

It is worthy to note that the four traits flag leaf area, no. of grains/spike, no. of spikelets/spike and 1000-kernel weight proved to be the major grain contributors under rainfed conditions. Thus these traits should be considered as selection criteria for screening and identifying the most drought tolerant bread wheat genotypes and could be used effectively for yield improvement in breeding programs under the present specific environments. Similar results were obtained by Iftikhar *et al.* (2012), Bhushan *et al.* (2013), Degewione *et al.* (2013), Gelalcha and Hanchinal (2013) , Singh and Upadhyay (2013) and Chimdesa *et al.* (2017).

Principal component (PCA) and Biplot analysis:

Principal component and biplot analysis was performed for all traits under study (Table 8 and Fig.1). PCA showed existence of a high level of variability among the genotypes and allowed the division of the collection data for different studied traits of genotypes performance into three groups corresponding (components). The three components could justify more than 71% of the whole variance in the original data. The first, second and third components explained (58.61%, 13% and 7.23%, respectively) of the total variance among different traits under Izraa conditions with total cumulative percentage of the whole variance (71.99% and 65.61%) in the original data. Rotate component matrix showed that basal angle of flag leaf, grain yield/ha, straw yield/ha, and biological yield were in the first group (component1), no. of spikes/plant, no. of grains/spike, 1000-kernel weight and grain yield/ main spike were in the second group (component2) and Flag leaf area in the third group (component3). While, The sum of the eigenvalues are often used to determine 12.71 variables or factors to retain.

These findings were confirmed by factor loadings for 9 studied traits of these two Principal component analysis which plotted on Fig. 1 to display the relationship between the 120 genotypes and traits under study. The vectors of trait revealed angles between different traits, angles < 90° refer to a positive correlation between traits, while angles > 90° refer to a negative correlation. Further, angles near 0° and 180° refer to increase in association intensity. Moreover, length of trait vector indicates the extent of variation caused by this trait in PCA. It can be concluded that the traits of each group are correlated. Similar findings were obtained by Khodadadi *et al.* (2011), Shajitha *et al.* (2015) and Adilova *et al.* (2020).

Table 7. Partitioning of phenotypic path coefficients, components (direct and joint effects) in percentage of contribution between grain yield/ha and flag leaf area, basal angle of flag leaf, no. of spikes/plant , no. of spikelets/spike, no. of grains/spike and 1000-kernel weight under rainfed conditions.

Sources of variance	Variation	Coefficient of determination (CD)	Relative importance (RI%)
1- Flag leaf area vs. grain yield/ ha			
Direct effect (r_{y1})	0.941	0.887	4.89
Indirect effect via Basal angle of flag leaf	-0.407	-0.767	4.23
Indirect effect via No. of spikes/plant	-0.186	-0.35	1.93
Indirect effect via No. of spikelets/spike	0.201	0.379	2.09
Indirect effect via No. of grains/spike	-0.539	-1.014	5.6
Indirect effect via 1000-kernel weight	0.078	0.147	0.81
Total (r_{y1})	0.088	-------	-------
2- Basal angle of flag leaf vs. grain yield/ha			
Direct effect (r_{y2})	-0.489	0.239	1.32
Indirect effect via Flag leaf area	0.784	-------	-------
Indirect effect via No. of spikes/plant	-0.362	0.354	1.95
Indirect effect via No. of spikelets/spike	1.010	-0.988	5.45
Indirect effect via No. of grains/spike	-0.536	0.524	2.89
Indirect effect via 1000-kernel weight	0.653	-0.639	3.53
Total (r_{y2})	1.061	-------	-------
3- No. of spikes/plant vs. grain yield/ ha			
Direct effect (r_{y3})	-0.446	0.199	1.11
Indirect effect via Flag leaf area	0.392	-------	-------
Indirect effect via Basal angle of flag leaf	-0.397	-------	-------
Indirect effect via No. of spikelets/spike	0.682	-0.609	3.36
Indirect effect via No. of grains/spike	-0.069	0.061	0.34
Indirect effect via 1000-kernel weight	0.842	-0.752	3.65
Total (r_{y3})	1.004	-------	-------
4- No. of spikelets/spike vs. grain yield/ ha			
Direct effect (r_{y4})	1.164	1.355	7.48
Indirect effect via Flag leaf area	0.163	-------	-------
Indirect effect via Basal angle of flag leaf	-0.425	-------	-------
Indirect effect via No. of spikes/plant	-0.262	-------	-------
Indirect effect via No. of grains/spike	-0.540	-1.257	6.94
Indirect effect via 1000-kernel weight	0.225	0.523	2.88
Total (r_{y4})	0.325	-------	-------
5- No. of grains/spike vs. grain yield/ha			
Direct effect (r_{y5})	-1.011	1.022	5.64
Indirect effect via Flag leaf area	0.502	-------	-------
Indirect effect via Basal angle of flag leaf	-0.259	-------	-------
Indirect effect via No. of spikes/plant	-0.030	-------	-------
Indirect effect via No. of spikelets/spike	0.622	-------	-------
Indirect effect via 1000-kernel weight	1.102	-2.229	12.3
Total (r_{y5})	0.925	-------	-------
6- 1000-kernel weight vs. grain yield/ ha			
Direct effect (r_{y6})	1.449	2.098	11.58
Indirect effect via Flag leaf area	0.051	-------	-------
Indirect effect via Basal angle of flag leaf	-0.221	-------	-------
Indirect effect via No. of spikes/plant	-0.259	-------	-------
Indirect effect via No. of spikelets/spike	0.180	-------	-------
Indirect effect via No. of grains/spike	-0.769	-------	-------
Total (r_{y6})	0.430	-------	-------
Residual		1.817	10.03
Total		1.00	100

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Table 8. The principal component analysis in combined data across seasons for different studied traits under Izraa conditions .

Component[1]	Eigen Value[2]	Cumulative percentage	Days to heading (50%)	Maturity date	Flag leaf area	Basal angle of flag leaf	Plant height	No. of spikes/ plant	Spike Length	No. of spikelets/ spike	No. of grains/ spike	1000-kernel weight	Grain yield/ main Spike	Grain yield/ ha	Straw yield/ ha	Biological yield
1	9.38	58.61	0.277	0.284	0.184	0.406	0.286	0.244	0.283	0.285	0.207	0.138	0.236	0.405	0.556	0.314
2	2.14	71.99	-0.068	-0.041	-0.142	0.089	0.016	0.497	-0.047	-0.050	0.412	0.450	0.504	0.187	0.047	0.096
3	1.19	79.40	-0.420	-0.417	0.600	0.173	-0.133	0.119	-0.270	-0.204	0.148	-0.023	0.159	0.146	0.194	0.176

[1]Component: the axis which explained variance by the k-dimensional ordination.
[2]Eigenvalue: the variance explained by the k-dimensional ordination.
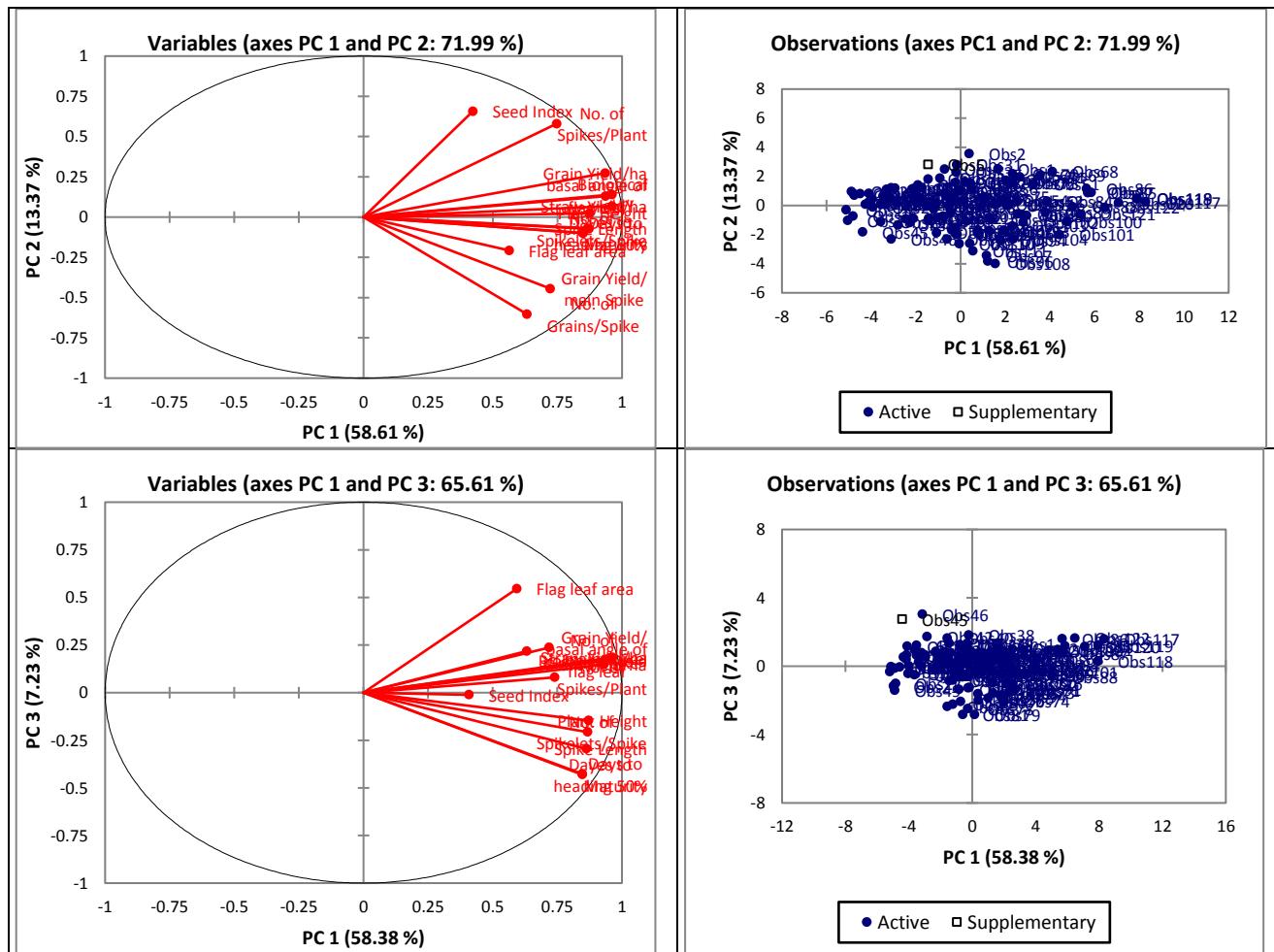
Figure 1. Biplot graphical display of the measured traits in bread wheat cultivars under rainfed conditions.

Genetic divergence and Cluster analysis:

Cluster analysis of Euclidean distances, based on studied traits revealed a high degree of genetic divergence in the present set of genotypes under rainfed conditions were carried out (Table 9) and (Figure 2). Dendrogram classified the 120 lines into three main clusters if the cutting is done on the distance 12. While, 11 intra cluster under Izraa conditions. Amongst these clusters accompanied with hierarchical Euclidean cluster analysis, the first (I) and second (II) clusters was the largest and contained

27 and 23 genotypes (22.13% and 18.85% of total genotypes, respectively) which exhibited high degree of genetic diversity and may be helpful in further wheat breeding and selection programs. The minimum intra cluster distance was observed within clusters VIII, IX, X and XI (Table 9), which exhibited less genetic diversity and thus may be utilized under population improvement of bread wheat genotypes. Ali *et al.* (2008), Degewione and Alamerew (2013), Shajitha *et al.* (2015), Mecha *et al.* (2017) and Adilova *et al.* (2020) they reported that the discrimination of genotypes in to discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the near isogenic lines screened in the present study indicated that this material may serve as good source for selecting diverse lines for hybridization from various clusters which could be useful in future breeding program for bread wheat improvement under rainfed conditions.

Table 9. Distribution and grouping of 122 bread wheat genotypes into different diversity classes based on D2 analysis under Izraa conditions.

| Cluster	Number of genotypes	Name of Lines	Proportions (%)
I	27	7,8,9,10,11,12,14,15,16,17,18,20,21,22,23,24,25,26,27,29,43,44,47,48,49,50,66.	22.13
II	23	57,58,59,60,61,62,63,64,65,67,93,98,99,105,106,107,109,110,111,112,113,114,	18.85
III	8	85,87, 117,118,119,120, Doma 4, Doma 6.	6.56
IV	10	32,33,34,35,37,38,39,40,41,56.	8.20
V	14	53,54,69,71,72,73,74,75,89,90,91,102,103,116.	11.48
VI	12	1, 51,52,55,76,77,78, 79, 80, 81, 82, 83	9.84
VII	10	2,3,4,5,31, 94,96,97,104,108	8.20
VIII	5	88,92,95,100,101	4.10
IX	4	28,30, 68,84	3.28
X	4	19,36,42,46.	3.28
XI	5	6,13,45,70,86.	4.10
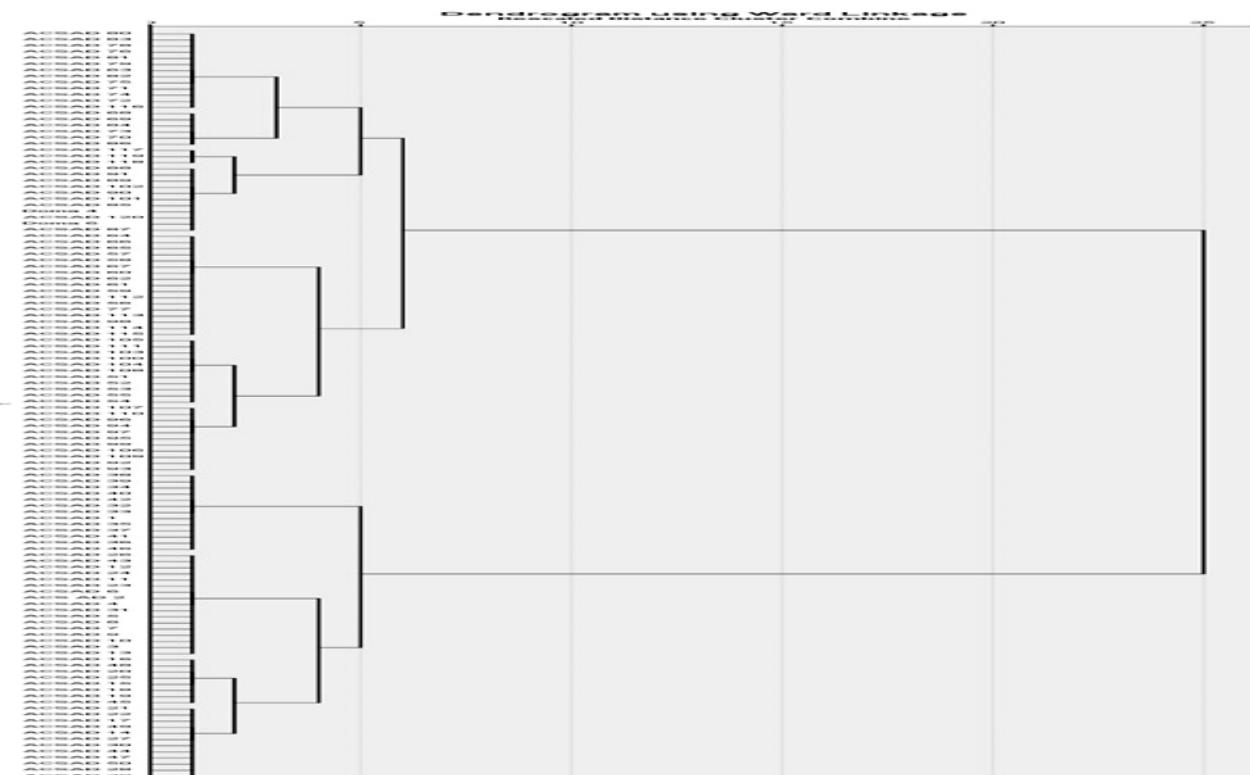
Figure 2. Dendrogram of bread wheat genotypes based on Ward's method based and squared Euclidian distance for studied traits under rainfed conditions.

Conclusion

The present study showed the presence of considerable variability among 122 bread wheat genotypes and the possibility of improving yield and other desirable traits through selection. While, positive and significant correlation of grain yield with its component appears to reflect the presence of interaction among the characters, the four traits flag leaf area, no. of grains/spike, no. of spikelets/spike and 1000-kernel weight proved to be the major grain contributors and should be considered in selection genotypes under rainfed conditions. Moreover, Genetic divergence and Cluster analysis indicated that the first (I) and second (II) clusters was the largest and contained 27 and 23 genotypes which exhibited high degree of genetic diversity and may be helpful in further wheat breeding and selection programs.

The promising genotypes thirteen genotypes; ACSAD 1196, ACSAD 1258, ACSAD 1300, ACSAD 1302, ACSAD 1306, ACSAD 1332, ACSAD 1334, ACSAD 1364, ACSAD 1372, ACSAD 1373, ACSAD 1388, ACSAD 1414 and ACSAD 1416 Exhibited significantly higher grain yield and its components than the two check cultivars Doma 4 and Doma 6 included in the study. Hence, these genotypes can be considered as candidates for multi-environmental variety verification trials (the Arab production efficiency trials) for possible registration and release as new commercial cultivars for similar environments in the Arab region.

RECOMMENDATION

It is highly recommended to use the high adaptability, yielding and promising thirteen bred genotypes; ACSAD 1196, ACSAD 1258, ACSAD 1300, ACSAD 1302, ACSAD 1306, ACSAD 1332, ACSAD 1334, ACSAD 1364, ACSAD 1372, ACSAD 1373, ACSAD 1388, ACSAD 1414 and ACSAD 1416 to be distributed with the Arab production efficiency trials on the Arab countries for possible selection, registration and release as new commercial cultivars for similar environments under rained conditions.

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N° Ref: 1042