Identification of drought tolerant Chickpea genotypes through multi trait stability index

Tamoor Hussaina, Zahid Akrama, Ghulam Shabbira, Abdul Manafb, Mukhtar Ahmedb,c,*

a Department of Plant Breeding and Genetics, PMAS Arid Agriculture University, Rawalpindi 46300, Pakistan
b Department of Agronomy, PMAS-Arid Agriculture University, Rawalpindi 46300, Pakistan
c Department of Agricultural Research for Northern Sweden, Swedish University of Agricultural Sciences, 90183 Umeå, Sweden

Abstract

Drought is a major and constantly increasing abiotic stress factor, thus limiting chickpea production. Like other crops, Kabuli Chickpea genotypes are screened for drought stress through Multi-environment trials (METs). Although, METs analysis is generally executed taking into account only one trait, which provides less significant reliability for the recommendation of genotypes as compared to multi trait-based analysis. Multi trait-based analysis could be used to recommend genotypes across diverse environments. Hence, current research was conducted for selection of superior genotypes through multi-trait stability index (MTSI) by using mixed and fixed effect models under six diverse environments. The genotypic stability was computed for all traits individually using the weighted average of absolute scores from the singular value decomposition of the matrix of best linear unbiased predictions for the genotype vs environment interaction (GEI) effects produced by a linear mixed-effect model index. A superiority index, WAASBY was measured to reflect the MPS (Mean performance and stability). The selection differential for the WAASBY index was 11.2%, 18.49% and 23.30% for grain yield (GY), primary branches per plant (PBP) and Stomatal Conductance (STOMA) respectively. Positive selection differential (0.80%/C20 selection differential) were examined for traits averaged desired to be increased and negative (-0.57%/C20 selection differential) for those traits desired to be reduced. The MTSI may be valuable to the plant breeders for the selection of genotypes based on many characters as being strong and simple selection process. Analysis of MTSI for multiple environments revealed that, the genotypes G20, G86, G31, G28, G15, G12, G105, G45, G50, G10, G30, G117, G81, G48, G85, G17, G32, G4, and G37 were the most stable and high yielding out of 120 chickpea genotypes, probably due to high MPS of selected traits under various environments. It is concluded that identified traits can be utilized as genitors in hybridization programs for the development of drought tolerant Kabuli Chickpea breeding material.

1. Introduction

The mean global temperatures have risen to record 1.2 C higher than previous century (Voosen, 2021). Likewise, it has been predicted that in 2100 it will further increase and could go up to 3 C (Schneider et al., 2007). Many scientists projected that drought, higher magnitude of concentration of CO2 and global temperatures will go higher with the passage of time in sub-tropical and semi-arid ecological zones (Araus et al., 2002; Wang et al., 2017). Consequently, due to these variations the rate of crop evapotranspiration will increase which could create more worse scenario for crop production due to lesser water availability to fulfill crop water needs (Abbas et al., 2017; Ahmad et al., 2017; Ahmad et al., 2019; Fatima et al., 2020; Fatima et al., 2020). This will lead to high risk of lesser crop production (Ahmed et al., 2020; Ahmed, 2020; Zampieri et al., 2020) and consequently declined water productivity (Ali et al., 2020; Amiri et al., 2021). Determinantal impact of climate change and drought on food and water security have been reported by Ding et al. (2021). Their results suggested that these
problems could be solved by using different management options through simulation modeling.

Chickpea (Cicer arietinum L.) is the 3rd largely grown pulse crop across the globe with harvested area of 13.72 million hectare and production of 14.25 million tons in 2019. Asia is the largest chickpea producer with production of 90.6% followed by Americas (5.2%), Africa (3.5%), Europe (0.6%) and Oceania (0.1%) (FAOSTAT, 2019). It is the 2nd most important legume crop after common bean (Gaur et al., 2008). The major producer of chickpea includes India, Australia, Canada, Ethiopia, Iran, Mexico, Myanmar, Pakistan, Turkey, and the USA (Dixit et al., 2019). Chickpea have two main types i.e. desi and kabuli and it has been suggested that desi × kabuli introgressions could be used for improving the adaptability and yield stability of Kabulis (Purushothaman et al., 2014). Chickpea is an important source of protein for mankind with protein content of 16 to 28% (Liu et al., 2008; Chibbar et al., 2010). Whole chickpea can tolerate drought stress but significant negative effects on the productivity of chickpea have been reported due to drought (Jha et al., 2014; Rani et al., 2020; Shah et al., 2020). Thus it is essential to have resilient crop cultivars so that crop can have potential to endure water stress period (Massawe et al., 2015). Drought impacts on crop have been further worsen due to climate change (Thomas, 2008; Korres et al., 2016; Tripathi et al., 2016). Since climate change resulted to spatio-temporal variability in the rainfall intensity and distribution thus it is the main cause of water stress across the globe (Vergni and Todisco, 2011; IPCC, 2014; Nicholson et al., 2018; Talchabhadel et al., 2018; Caloiero et al., 2019; Jamro et al., 2019; Ahmed, 2020; Mengistu et al., 2020; Yang et al., 2021). Furthermore, to fulfill the protein demand of increasing human population it is essential to increase the productivity of chickpea on long term basis (Chaturvedi et al., 2018). Major abiotic challenges faced by chickpea production includes drought, low and high temperature at different growth stages (Jha et al., 2014; Garg et al., 2015). Moreover, unpredictable climate change is the top most constraint which leads to climate extreme events with higher frequency of drought and temperatures (Low < 15 °C and High greater than 30 °C) that reduces grain yields significantly (Kadiyala et al., 2016). Hence, it is imperative to identify and develop high-stable yielding varieties of Chickpea to cope abiotic stress which has been main task of this work (Devasirvatham and Tan, 2018).

Drought is a foremost and constantly increasing abiotic stress that limits crop production across the world (Vurukonda et al., 2016). It is the most destructive abiotic stress affecting world's food security. The negative effect of drought appears significantly in the arid and semi-arid regions (Murungweni et al., 2016; El Sayed et al., 2021; Kheir et al., 2021). It has been documented that crop growth at more than 50% of the arable lands will be significantly affected by the drought (Vinocur and Altman, 2005). Drought stress under changing climate and ever-increasing population is serious concern for agriculture. Severe drought has shown negative effects on crop growth, development, and yield (Barnabás et al., 2008; Makonya et al., 2020; Cohen et al., 2021; Jabbari et al., 2021; Waqas et al., 2021). Annually 40–50% reduction in yield across globe is reported due to terminal drought (Ahmad et al., 2005; Thudil et al., 2014). Improvement in drought tolerance is possible by understanding various morphological, physiological and biochemical responses to drought stress (Shah et al., 2020). Similarly, different agronomic managements and development of new plant types are recommended to meet the main challenges of chickpea adaptation to stresses (Vazquez et al., 2021). A significant positive correlation with grain yield, high heritability coupled with high genetic variability and less yield losses under optimal conditions are essential for a character to be expressed as drought tolerance marker (Maqbool et al., 2017; Chandora et al., 2020).

Therefore, a comprehensive multiple enhancement approach is needed for sustainable crop production under drought stress (Arif et al., 2021). Thus, there is dire need to utilize techniques those present adaptability as well as stability to select the most excellent genotypes under different environmental conditions. The different breeding techniques used to enhance the drought tolerance in chickpea would be applied through integration of morphological and physiological systems of drought tolerance from resistant genotypes (Kumar et al., 2020; Singh et al., 2021). Numerous physiological, phenological and morphological characters have been established those play an imperative role in adaptation of a particular crop in adverse environmental conditions (Najan et al., 2018; Sharifi et al., 2018). Multi environment trials (MET) are mostly used to evaluate impact of drought stress on crops could be analyzed by using additive main effect and multiplicative interaction (AMMI) and best linear unbiased prediction (BLUP) methods (Olivoto et al., 2019a, b). AMMI stability and drought tolerance indices were recommended as drought-tolerance evaluation methods particularly in resource poor countries (Arif et al., 2021). The AMMI is good graphical tool, but it lacks linear mixed-effect model (LMM) while BLUP provides good estimates, however, new insights are needed to deal with a random genotype vs environment interaction (GEI). The Weighted Average of Absolute Scores (WAASB) is a new quantitative genotypic stability measure that could be used to address above mentioned issues. This could help agronomists and breeders to make correct decisions for selection and recommendations of specific genotypes. Furthermore, MET analysis is performed on the basis of single trait, mainly keeping in view the grain yield only (Nowosad et al., 2016; Mohammad et al., 2017; Erdemci, 2018; Azam et al., 2020; Shah et al., 2020). Conversely, the more reliable genotypes can be selected when multi traits are considered in MET analysis under different environments. For this purpose, a technique for MET analysis (METAN) allows for the comprehensive selection for MPS of numerous traits into a single index could provide a unique selection process. Multi-trait stability index (MTSI) is valuable to the plant breeders for the selection of genotypes based on several traits as it gives a strong and simple selection process (Olivoto et al., 2019a,b). These tools have been used successfully for the selection of drought and salinity tolerant soyabean genotypes (Zuffo et al., 2020) and determination of quality traits in Brassica spp. Genotypes (Bocianowski et al., 2018). The work of Zuffo et al. (2020), Bocianowski et al. (2018) and Nowosad et al. (2016) successfully selected the crop genotypes on the basis of multi-trait under diverse climatic conditions. Thus, present study was designed with the goal to identify the most stable and high yielding chickpea genotypes by applying popularly recommended multi-trait stability analysis under diverse environmental conditions.

2. Materials and methods
2.1. Multi location experiments

The current research work was conducted by using 120 Kabuli chickpea genotypes including three local checks collected from different Research Institutes in Pakistan (Table 1). To assess the performance and stability simultaneously, these Kabuli chickpea genotypes were evaluated in six environments (E) (E1: Chakwal full irrigated, E2: Chakwal limited irrigation, E3: Chakwal drought...
stress, E4: Chakwal rainfed, E5: Bhakkar rainfed and E6: Fateh Jang rainfed conditions) to select the superior genotypes based on multiple traits during Rabi season 2018–19. The field research was performed in alpha lattice design comprised of two replications at each environment. Chakwal full irrigated (E1), limited irrigation (E2) and drought stress (E3) were developed at Barani Agricultural Research Institute, Chakwal, by managing three complimentary irrigation treatments viz: T1 (Control); a well irrigated treatment, T2 (Limited Irrigation): Irrigation at the field bed preparation, flowering initiation only and pod development, T3 (Drought stress): Irrigation treatments viz: T1 (Control); a well irrigated treatment, T2 (Limited Irrigation): Irrigation at the field bed preparation, flowering initiation only and pod development, T3 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T4 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T5 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T6 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T7 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T8 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T9 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development, T10 (Drought stress): Irrigation at the field bed preparation, flowering initiation only and pod development. The overall grain yield of Kabuli chickpea genotypes ranged from

| Sr. Code | Genotype No. | Origin | Sr. Code | Genotype No. | Origin | Sr. Code | Genotype No. | Origin |
|----------|--------------|--------|----------|--------------|--------|----------|--------------|--------|
| G1       | 17KCC-101    | BARI   | G41      | 13KCC-114    | BARI   | G81      | 6KCC-103     | BARI   |
| G2       | 17KCC-105    | BARI   | G42      | 13KCC-115    | BARI   | G82      | 6KCC-121     | BARI   |
| G3       | 17KCC-106    | BARI   | G43      | 13KCC-116    | BARI   | G83      | 6KCC-124     | BARI   |
| G4       | 17KCC-107    | BARI   | G44      | 12KCC-101    | BARI   | G84      | 6KCC-126     | BARI   |
| G5       | 17KCC-108    | BARI   | G45      | 12KCC-103    | BARI   | G85      | 6KAG-15      | AZRI   |
| G6       | 17KCC-109    | BARI   | G46      | 12KCC-104    | BARI   | G86      | 6KAG-37      | AZRI   |
| G7       | 17KCC-114    | BARI   | G47      | 12KCC-105    | BARI   | G87      | 11AG-38      | AZRI   |
| G8       | 17KCC-115    | BARI   | G48      | 12KCC-106    | BARI   | G88      | 11AG-41      | AZRI   |
| G9       | 17KCC-116    | BARI   | G49      | 12KCC-108    | BARI   | G89      | 11AG-43      | AZRI   |
| G10      | 17KCC-117    | BARI   | G50      | 12KCC-109    | BARI   | G90      | 11AG-48      | AZRI   |
| G11      | 17KCC-118    | BARI   | G51      | 12KCC-110    | BARI   | G91      | Aus Sel-100  | BARI   |
| G12      | 16KCC-101    | BARI   | G52      | 12KCC-111    | BARI   | G92      | Aus Sel-101  | BARI   |
| G13      | 16KCC-105    | BARI   | G53      | 12KCC-112    | BARI   | G93      | Aus Sel-102  | BARI   |
| G14      | 16KCC-106    | BARI   | G54      | 12KCC-119    | BARI   | G94      | 12AG-36      | AZRI   |
| G15      | 16KCC-107    | BARI   | G55      | 12KCC-120    | BARI   | G95      | 12AG-60      | AZRI   |
| G16      | 15KCC-101    | BARI   | G56      | 11KCC-112    | BARI   | G96      | 12AG-61      | AZRI   |
| G17      | 15KCC-106    | BARI   | G57      | 11KCC-113    | BARI   | G97      | 12AG-129     | AZRI   |
| G18      | 15KCC-107    | BARI   | G58      | 11KCC-114    | BARI   | G98      | 12AG-133     | AZRI   |
| G19      | 15KCC-110    | BARI   | G59      | 11KCC-115    | BARI   | G99      | 12AG-230     | AZRI   |
| G20      | 15KCC-112    | BARI   | G60      | 11KCC-119    | BARI   | G100     | 12AG-235     | AZRI   |
| G21      | 15KCC-113    | BARI   | G61      | 11KCC-127    | BARI   | G101     | 12AG-247     | AZRI   |
| G22      | 14KCC-102    | BARI   | G62      | 11KCC-129    | BARI   | G102     | 12AG-248     | AZRI   |
| G23      | 14KCC-103    | BARI   | G63      | 11KCC-130    | BARI   | G103     | CM/731/06    | NIAB   |
| G24      | 14KCC-104    | BARI   | G64      | 10KCC-101    | BARI   | G104     | CM/736/06    | NIAB   |
| G25      | 14KCC-107    | BARI   | G65      | 10KCC-102    | BARI   | G105     | CM/742/06    | NIAB   |
| G26      | 14KCC-108    | BARI   | G66      | 10KCC-111    | BARI   | G106     | CM/762/06    | NIAB   |
| G27      | 14KCC-109    | BARI   | G67      | 10KCC-112    | BARI   | G107     | CM/771/06    | NIAB   |
| G28      | 14KCC-110    | BARI   | G68      | 10KCC-113    | BARI   | G108     | CM/792/06    | NIAB   |
| G29      | 14KCC-111    | BARI   | G69      | 10KCC-114    | BARI   | G109     | CM/813/06    | NIAB   |
| G30      | 14KCC-114    | BARI   | G70      | 9KCC-100     | BARI   | G110     | FS-4        | PRI    |
| G31      | 14KCC-115    | BARI   | G71      | 9KCC-103     | BARI   | G111     | FS-5        | PRI    |
| G32      | 13KCC-101    | BARI   | G72      | 9KCC-163     | BARI   | G112     | FS-6        | PRI    |
| G33      | 13KCC-102    | BARI   | G73      | 9KCC-164     | BARI   | G113     | FS-7        | PRI    |
| G34      | 13KCC-103    | BARI   | G74      | 9KCC-172     | BARI   | G114     | FS-8        | PRI    |
| G35      | 13KCC-105    | BARI   | G75      | 8KCC-151     | BARI   | G115     | FS-9        | PRI    |
| G36      | 13KCC-108    | BARI   | G76      | 8KCC-152     | BARI   | G116     | FS-10       | PRI    |
| G37      | 13KCC-110    | BARI   | G77      | 8KCC-153     | BARI   | G117     | FS-13       | PRI    |
| G38      | 13KCC-111    | BARI   | G78      | 8KCC-154     | BARI   | G118     | CM-2008      | (C)    |
| G39      | 13KCC-112    | BARI   | G79      | 7KCC-154     | BARI   | G119     | TAMMAN (C)   | BARI   |
| G40      | 13KCC-113    | BARI   | G80      | 7KCC-156     | BARI   | G120     | NOOR-2013 (C) | NIAB |

BARI: Barani Agricultural Research Institute, Chakwal, NIAB: (Nuclear Institute for Agriculture and Biology Faisalabad); AZRI: (Arid Zone Research Institute, Bakkhar); PRI: (Pulses Research Institute, AARI Faisalabad)
102 kg ha to 1633 kg/ha while the environments mean yield was 867.50 kg/ha. Others statistical factors such as, mean, standard error of mean (SEM), standard deviation (St dev), 1st and 2nd quartiles for characters in all environments (Table 3). Proximally 82% of the phenotypic variance was due to the genotypic variance. The portion of residual variance was 7.82% and genotype × environment interaction contribution was 9.94% only. For all traits (except for internal CO2), the genotypic variance was higher than residual and GEI variance (Fig. 2). High values of broad sense heritability were calculated for all traits under study except for STOMA, seeds per pods and WUE exhibited low heritability. The genotypic selection accuracy (AS) values ranged from 0.94 (SPP) to 0.99 (GY). The highest CVg was recorded for all traits except for the DTF, DTM and internal CO2, which showed low CVg Table 4.

3.2. Association analysis

High extent of association was noticed between grain yield and TSW, DTF, DTM and CHLOR contents. Positive and highly significant interactions were found between GY and DTF, PPP and TGW (Fig. 3).

4. Genotypes selection based on MTSI and contribution of factors to the MTSI

Nine principal factors were maintained, and the accumulated variance in these factors was 53.85% (Table 5). After proper vari-max rotation, mean communality (h) was 0.82 signifying that higher ratio of each trait variance was influenced by the factors. The 16 attributes were clustered into the nine different factors as: FA1: (GY and TSW); FA2: (DTF, DTM and CHOLOR); FA3: (PHOTO and WUE); FA4: (TRANS and INT CO2), FA5: (PPB); FA6:
Basic descriptive statistic for various morphological and physiological traits of Kabuli Chickpea genotypes under studied evaluated in six environments.

| Traits         | Mean   | SE Mean | St Dev | Minimum | Q1     | Q3     | Maximum |
|----------------|--------|---------|--------|---------|--------|--------|---------|
| PH             | 72.12  | 0.28    | 10.54  | 41.34   | 65.82  | 80.35  | 93.34   |
| DTF            | 139.78 | 0.38    | 14.51  | 101.00  | 139.00 | 149.00 | 159.00  |
| DTM            | 177.82 | 0.37    | 14.13  | 140.00  | 176.00 | 187.00 | 199.00  |
| BY             | 2307.00| 2.23    | 84.70  | 217.00  | 187.00 | 287.00 | 4157.00 |
| PBP            | 1.80   | 0.01    | 0.53   | 1.00    | 1.40   | 2.00   | 3.00    |
| HSW            | 22.23  | 0.10    | 3.78   | 14.67   | 19.48  | 24.33  | 34.65   |
| PPP            | 21.30  | 0.12    | 4.72   | 13.00   | 18.00  | 24.00  | 40.00   |
| HI             | 44.92  | 0.16    | 6.18   | 21.45   | 41.00  | 49.15  | 65.00   |
| PHOTO          | 10.40  | 0.11    | 3.99   | 2.00    | 8.29   | 13.52  | 18.93   |
| STOMA          | 0.22   | 0.00    | 0.05   | 0.14    | 0.19   | 0.25   | 0.37    |
| CHLOR          | 1.66   | 0.01    | 0.26   | 0.99    | 1.48   | 1.81   | 2.77    |
| TRANS          | 4.10   | 0.02    | 0.82   | 2.00    | 3.55   | 4.63   | 5.93    |
| INT CO₂        | 514.14 | 1.41    | 53.40  | 392.00  | 475.12 | 539.00 | 632.00  |
| WUE            | 2.08   | 0.01    | 0.43   | 1.08    | 2.40   | 2.95   | 3.87    |

Table 3

Where PH: Plant height in cm, DTF: Days to fifty percent flowering, DTM: Days to maturity, GY: Grain yield Kg ha⁻¹, BY: Biological yield Kg ha⁻¹, PBP: Number of primary branches per plant, SPP: Number of seeds per pod, HSW: 100 seed weight, PPP: Number of pods per plant, HI: Harvest index %, PHOTO: Photosynthesis rate, μmole CO₂ m⁻² sec⁻¹, CHLOR: Chlorophyll contents, mg g⁻¹ fresh weight, TRANS: Transpiration rate, mmol H₂O m⁻² sec⁻¹, INT CO₂: Internal CO₂ concentration, ppm and WUE: Water use efficiency, S Dev.: Standard deviation, SEM: Standard error of mean, Q1: 1st quartile, Q3: 3rd quartile.

5. Discussion

Multi Trait Stability Index is useful technique to identify the drought resilient genotypes under water stress environments as more than 90% of chickpea is grown under rainfed environment (Kumar and Abbo, 2001). This approach is valuable to plant breeders as in our study we were able to select genotypes out of 120 genotypes into most stable and high yielding genotypes (G20, G86, G31, G28, G116, G12, G105, G45, G50, G10, G30, G117, G81, G48, G85, G17, G32, G4, and G37). Thus it is recommended that identified traits should be utilized as genitors in hybridization programs for the development of drought tolerant Kabuli Chickpea breeding material (Daryanto et al., 2015; Shah et al., 2020). For all traits (except for intercellular CO₂), the genotypic variance was higher than residual and GEI variance; as a result, genotypic variance is more considerable constituent of the phenotypic variance (Fig. 2). Therefore, high values of broad sense heritability were calculated for all traits under study except for STOMA, seeds per pods and WUE exhibiting low heritability. This implies that the expected gain from selection would be high if the traits having high heritability values are used as selection criteria in chickpea breeding program. Our results are in line with earlier studies where they reported highest heritability for pods per plant, days to 50% flowering, hundred seed weight, harvest index and grain...
### Table 4
Deviance analysis, genetic parameters and variance components for 16 Morphological and physiological traits evaluated in 120 Kabuli Chickpea genotypes

| Traits   | PV     | Heritability | GEI R² | h²mg | AS r ge | CVg | CVr | CV ratio |
|----------|--------|--------------|--------|------|---------|-----|-----|---------|
| PH       | 11.227 | 0.989        | 0.009  | 0.998| 0.999   | 0.848| 4.621| 0.189   | 24.452 |
| DTF      | 8.181  | 0.824        | 0.084  | 0.974| 0.987   | 0.480| 1.858| 0.619   | 3.003  |
| DTM      | 6.716  | 0.862        | 0.092  | 0.978| 0.989   | 0.663| 1.353| 0.315   | 4.301  |
| GY       | 672.144| 0.980        | 0.015  | 0.997| 0.998   | 0.777| 24.520| 1.652   | 14.839 |
| BY       | 4293.254| 0.946      | 0.049  | 0.991| 0.995   | 0.902| 26.515| 1.989   | 13.329 |
| PBP      | 0.188  | 0.792        | 0.047  | 0.974| 0.987   | 0.226| 21.399| 9.645   | 2.179  |
| SPP      | 0.078  | 0.535        | 0.290  | 0.895| 0.946   | 0.623| 12.994| 7.427   | 1.749  |
| HSW      | 9.873  | 0.939        | 0.010  | 0.994| 0.997   | 0.166| 13.696| 3.201   | 4.279  |
| PPP      | 17.393 | 0.914        | 0.011  | 0.992| 0.996   | 0.139| 18.715| 5.145   | 3.637  |
| HI       | 30.109 | 0.804        | 0.135  | 0.967| 0.983   | 0.690| 10.950| 3.015   | 3.632  |
| PHOTO    | 1.966  | 0.768        | 0.044  | 0.972| 0.986   | 0.196| 11.812| 5.686   | 2.077  |
| STOMA    | 0.001  | 0.674        | 0.176  | 0.942| 0.970   | 0.539| 9.723 | 4.589   | 2.119  |
| CHLORO   | 0.033  | 0.752        | 0.076  | 0.966| 0.983   | 0.316| 9.508 | 4.440   | 2.141  |
| TRANS    | 0.243  | 0.923        | 0.006  | 0.993| 0.996   | 0.079| 11.549| 3.197   | 3.612  |
| INT_C2   | 234.143| 0.872        | 0.008  | 0.987| 0.994   | 0.064| 2.778 | 1.032   | 2.693  |
| WUE      | 0.075  | 0.559        | 0.199  | 0.913| 0.956   | 0.452| 7.665 | 5.037   | 1.522  |

Where PH: Plant height in cm, DTF: Days to fifty percent flowering, DTM: Days to maturity, GY: Grain yield Kg ha⁻¹, BY: Biological yield Kg ha⁻¹, PBP: Number of primary branches per plant, SPP: Number of seeds per pod, HSW: 100 seed weight, PPP: Number of pods per plant, HI: Harvest index %, PHOTO: Photosynthesis rate, μmol CO₂ m⁻² sec⁻¹, STOMA: Stomatal conductance, mol H₂O m⁻² sec⁻¹, CHLOR: Chlorophyll contents, mg g⁻¹ fresh weight, TRANS: Transpiration rate, mMol H₂O m⁻² sec⁻¹, INT. CO₂: Internal CO₂ concentration, vpm and WUE: Water use efficiency, PV: phenotypic variance, GEI R²: GEI coefficient of determination, h²mg: heritability of genotypic mean, AS: accuracy of genotype selection, rge, association among genotypic values across environments, CVg: genotypic coefficient of variation, CVr: residual coefficient of variation.

---

**Fig. 3.** Pearson’s correlation matrix among 16 Kabuli Chickpea traits evaluated in six environments. Where WUE: Water use efficiency, SPP: Number of Seeds per pod, PBP: Number of primary branches per plant, PPP: Number of Pods per plant, HSW: 100 seed weight, GY: Grain yield, BY: Biological yield, DTF: Days to fifty percent flowering, DTM: Days to Maturity, PH: Plant height, STOMATA: Stomatal conductance, INTERNAL_CO_2: Intercellular CO₂ concentration.
yield per plant (Yücel et al., 2006; Arora and Kumar, 2018; Banik et al., 2018; Hagos et al., 2018; Sharifi et al., 2018; Kumar et al., 2019). Similarly, genetic diversity of 25 chickpea genotypes was studied using multivariate technique. The results showed that first three principal components depicted 69.60% variations. The three factors were phenological traits (33.69%), morphological traits (20.82%) and yield components (15.19%) (Sharifi et al., 2018). Based upon our results and as reported in the previous studies outcomes from these works can be used in the breeding strategies for the classification of diversity among genotypes. Furthermore, it can also be used for yield improvement through hybridization programs. Our results reported high extent of association between grain yield and TSW, DTF, DTM and CHLOR contents. Positive and highly significant interactions were found between CY and DTF, PPP and TGW indicating that these characters had good relationship with grain yield in Kabuli chickpea, therefore, were important characters for bringing genetic improvement in grain yield. Plant breeders can also focus their attention on the traits having strong correlation with grain yield to develop better genotypes of Kabuli chickpea. A strong association between CY with TSW, DTF, DTM and PPP has been reported in previous work (Noor et al., 2003; Arshad et al., 2004; Kumar et al., 2019).

Our selection based on the multi traits may assemble genotypes with a superior adaptability across prevailing weather conditions of immense significance for hybridization programs. Recently it has been proposed that the WAAASB (Weighted Average of Absolute Scores) index could be good indicator for selection of superior genotype on the base of multi-traits in multi-environment (Olivoto et al., 2019a,b). Principally, this index is computed by Non-Impartial Linear Forecast) for the GEI sound effects produced using the single value decomposition of the BLUPs matrix (Best Linear Unbiased Predictions). The genotypes with the lower WAASB index values have been proposed that the WAASB (Weighted Average of Absolute Scores) index could be good indicator for selection of superior genotype on the base of multi-traits in multi-environment scores. So the technique used by Olivoto et al., 2019a has been used for hybridization programs. Similarly, genetic diversity of 25 chickpea genotypes was studied using multivariate technique. The results showed that first three principal components depicted 69.60% variations. The three factors were phenological traits (33.69%), morphological traits (20.82%) and yield components (15.19%) (Sharifi et al., 2018). Based upon our results and as reported in the previous studies outcomes from these works can be used in the breeding strategies for the classification of diversity among genotypes. Furthermore, it can also be used for yield improvement through hybridization programs. Our results reported high extent of association between grain yield and TSW, DTF, DTM and CHLOR contents. Positive and highly significant interactions were found between CY and DTF, PPP and TGW indicating that these characters had good relationship with grain yield in Kabuli chickpea, therefore, were important characters for bringing genetic improvement in grain yield. Plant breeders can also focus their attention on the traits having strong correlation with grain yield to develop better genotypes of Kabuli chickpea. A strong association between CY with TSW, DTF, DTM and PPP has been reported in previous work (Noor et al., 2003; Arshad et al., 2004; Kumar et al., 2019).
permitted for selection of the better advanced lines in the six evaluated environments (RBFI, RBLI, RBDS, BRFC, FRFC, ARFC) on the basis of data collected from a set of sixteen traits. Fig. 5 shows the ranking of genotypes for the MTSI presuming 15% selection intensity, eighteen genotypes were selected viz.: G20, G86, G31, G28, G116, G12, G105, G45, G50, G10, G30, G117, G81, G48, G85, G17, G32, G4, and G37 as the most stable out of 120 genotypes in present research work. The MTSI of 9.90 serves as the cut point (Fig. 5, red circle) considering the selection intensity. The G37 and G4 genotype were in close proximity to this red circle and may possibly possess remarkable characters. Therefore, in further research, it would be attractive to explore the performance of the genotypes near and close to the base cut point (Olivoto et al., 2019a,b).

The selection accomplished in Fig. 3 served as a source to estimate genetic attributes for each analyzed trait considering a selection intensity of 15 (Table-5). For all the investigated attributes, the mean of the genotypes selected (Xs) was greater than the mean of the original population (Xo), comprised of all 120 genotypes except for chlorophyll which mean this attribute was more affected by environmental conditions as compared to others evaluated traits. The extent of this percentage increase varied as a function of the investigated trait and encouraged stress in the genotypes (Table 6). The SD was from 2.37% (DTF) to 23.30% (STOMA) between the six environments evaluated and the various traits under study, which represents the prospect of achieving gain with selection on all traits recorded (Table 6).

There is very meager information available in literature for selection of genotypes on the basis of multi traits multi environment trials. So according to present climate change scenario, the chickpea breeder should focus on this aspect for selection of

| Table 7 | Selection Gain (%) for the mean of 16 Kabuli Chickpea traits |
|---------|----------------------------------------------------------|
| VAR     | Factor | xo     | Xs     | SG     | SG percent | Sense | Goal |
|---------|---------|--------|--------|--------|------------|-------|------|
| GY      | FA 1    | 104.67 | 113.61 | 8.93   | 8.53       | Increase | 100  |
| HSW     | FA 1    | 22.23  | 23.24  | 0.80   | 0.57       | Increase | 100  |
| DTF     | FA 2    | 139.78 | 138.98 | 0.80   | 0.57       | Decrease | 100  |
| DTM     | FA 2    | 177.82 | 177.19 | 0.62   | 0.35       | Decrease | 100  |
| CHLORO  | FA 2    | 1.66   | 1.63   | -0.03  | -0.16      | Decrease | 100  |
| PHOTO   | FA 3    | 10.40  | 10.96  | 0.55   | 3.32       | Increase | 100  |
| WUE     | FA 3    | 2.68   | 2.72   | 0.04   | 1.58       | Increase | 100  |
| TRANS   | FA 4    | 4.10   | 4.25   | 0.15   | 3.67       | Increase | 100  |
| INT CO₂ | FA 4    | 514.14 | 512.29 | 4.16   | 0.81       | Increase | 100  |
| PBP     | FA 5    | 1.80   | 2.04   | 0.23   | 13.00      | Increase | 100  |
| BY      | FA 6    | 240.30 | 268.31 | 28.01  | 11.66      | Increase | 100  |
| HI      | FA 6    | 43.84  | 44.92  | 1.97   | 1.97       | Increase | 100  |
| PH      | FA 7    | 72.12  | 71.95  | -0.17  | -0.23      | Decrease | 100  |
| PPP     | FA 7    | 21.30  | 22.79  | 1.49   | 6.99       | Increase | 100  |
| STOMA   | FA 8    | 0.22   | 0.23   | 0.01   | 6.82       | Increase | 100  |
| SPP     | FA 9    | 1.56   | 1.57   | 0.01   | 0.34       | Increase | 100  |

Where PH: Plant height in cm, DTF: Days to fifty percent flowering, DTM: Days to maturity, GY: Grain yield Kg ha⁻¹, BY: Biological yield Kg ha⁻¹, PBP: Number of primary branches per plant, SPP: Number of seeds per pod, HSW: 100 seed weight, PPP: Number of pods per plant, HI: Harvest index %, PHOTO: Photosynthesis rate, μmoles CO₂ m⁻² sec⁻¹, STOMA: Stomatal conductance, Mol H₂O m⁻² sec⁻¹, CHLOR: Chlorophyll contents, mg g⁻¹ fresh weight, TRANS: Transpiration rate, mMol H₂O m⁻² sec⁻¹, INT. CO₂: Internal CO₂ concentration, vpm and WUE: Water use efficiency. Xo: Mean for traits of the original population, Xs: Mean for traits of the selected genotypes, SG: Selection gain.

Fig. 4. The strengths and weaknesses view of genotypes selected. The y-axis presents the ratio of each factor on the calculated MTSI of the selected genotypes. The minimum the proportions explicated by a factor, the nearer the traits within that factor are to the ideotype. Where G stands for genotypes and FA stands for factor.
superior genotypes which perform better under diverse environmental conditions as the genotypes affected generally by the significant GEI that happens in the majority of the crops including chickpea. In the present era to ensure the food security, agriculture sector must fulfill the demands for food in the changing climate scenario, while mitigating the unfavorable impacts of agriculture on the weather conditions. The solution to achieving this valuable task is to develop breeding material having comprehensive genetic variation at different plant growth stages in reaction to the various abiotic and biotic stresses (Bailey-Serres et al., 2019; Zuffo et al., 2020).

So the most imperative aim is to assess the genotypes under various environmental conditions and to choose those better genotypes which perform superior under changing climatic condition from one region to others. The incorporation of MTSI research permitted us to express scientific solutions to stress experiments. In the present evaluation, genetic stability was computed by using MTSI in six different environments presenting the efficacy of this technique proposed by Olivoto et al. (2019). Drought stress generally reduces different plants growth stages and ultimately grain yield in a broad sense, by altering physiological and morphological changes (Shah et al., 2020). To cope and understand these variations in plants when assessing a comparatively a greater number of genotypes, as well as several stresses concurrently, it is essential to utilize suitable techniques to achieve desirable goals. Techniques such as principal component analysis (Giordani et al., 2019), BLUP (Olivoto et al., 2017), AMMI (additive main effects and multiplicative interaction) (Novosad et al., 2016; Olivoto et al., 2019a,b), the combination of BLUP and AMMI, and MTSI (Olivoto et al., 2019a,b), have been used but the information on MTSI in chickpea is very meager. According to the computed MTSI for multiple environments, genotypes G20, G86, G31, G28, G116, G12, G105, G45, G50, G10, G30, G117, G61, G48, G85, G17, G32, G4, and G37 selected as the most stable and high yielding among the 120 genotypes in present research work. The genotypes selected from the present research are best to be utilized in breeding program for development of superior genotypes to perform better in diverse environmental conditions. The high selection gains explained that character’s variation is mainly owing to genetic makeup and hence probably to be incorporated to potential future fillial generations through breeding techniques. The superior genotypes can be utilized as genitors in future hybridization plans for the development of breeding material of Kabuli chickpea resilient to abiotic stresses.

6. Conclusion

Drought tolerance evaluation in six environments led us to conclude that MTSI could be used to select superior chickpea genotypes with improved yield traits. Genotypes were categorized into groups based on their performance under set of variable environments. We were able to identify genotypes that showed differential response under irrigated and water stress environments while some performed well under both set of environments. The MTSI is estimated based on the genotype ideotype distance projected with values of factor analysis. Accordingly, genotypes G20, G86, G31, G28, G116, G12, G105, G45, G50, G10, G30, G117, G61, G48, G85, G17, G32, G4, and G37 selected as the most stable and high yielding among the 120 genotypes. The MTSI technique presented the selection of most stable genotypes for the traits to be increased with positive selection differentials and negative selection differential for attributes that required to be reduced. The MTSI may be valuable for the plant breeders for the selection of genotypes for MPS based on multiple traits as it gives a strong and simple to understand process of selection. Furthermore in future identified materials can be used as genitors in breeding programs with the aim to have offspring with higher yield and resistance to abiotic stress.

We recommend that breeder should apply MTSI to identify high yielding stable drought tolerant genotypes prior to testing them under various environments which is ultimately required for approving variety in different environments. This technique will be best for the countries where resources are limited as it will save time and cost. This study also provides useful information to policy makers and provides directions for the development of stable drought tolerant resilient chickpea cultivars in the water stress environments.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

Abbas, G., Ahmad, S., Ahmad, A., Nasim, W., Fatima, Z., Hussain, S., Rehman, M.H.U., Khan, M.A., Hasanuzzaman, M., Fahad, S., Boote, K.J., Hoogenboom, G., 2017. Quantification the impacts of climate change and crop management on phenology of maize-based cropping system in pakistan. Agricultural and Forest Meteorology 247, 42–55. https://doi.org/10.1016/j.agrformet.2017.07.012. Available from http://www.sciencedirect.com/science/article/pii/S0168192317302289.

Ahmad, S., Aaur, P., Cresser, J., 2005. Chickpea (cicer arietinum l). Genetic resources, chromosome engineering, and crop improvement-grain legumes 1, 187–217.

Ahmad, S., Abbas, G., Ahmad, A., Nasim, W., Younis, H., Khan, R.J., Nasim, W., Habib Ur Rehman, Ahmad, A., Rasul, G., Khan, M.A., Hasanuzzaman, M., 2017. Quantification of climate warming and crop management impacts on cotton phenology. Plants (Basel) 6 (1), 7. https://doi.org/10.3390/plants6010007. Available from https://pubmed.ncbi.nlm.nih.gov/28208605. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5371766/.

Ahmed, K., Shabbir, C., Ahmad, M., Shah, K.N., 2020. Phenotyping for drought resistance in bread wheat using physiological and biochemical traits. Science of the Total Environment 729, https://doi.org/10.1016/j.scitotenv.2020.139082. Available from http://www.sciencedirect.com/science/article/pii/S0378117720325997.

Ahmed, M., 2020. Introduction to modern climate change. Andrew e. Dessler: Cambridge university press, 2011, 252 pp, isbn-10: 0521172759. Science of the Total Environment, 734: 133937. Available from http://www.sciencedirect.com/science/article/pii/S0048969720329144. DOI 10.1016/j.scitotenv.2020.139082.

Ali, M.G.M., Ibrahim, M.M., El Barouidy, A., Fullen, M., Omar, E.-S.H., Ding, Z., Kheir, A.M.S., 2020. Climate change impact and adaptation on wheat yield, water use and water use efficiency at north nile delta. Frontiers of Earth Science 14 (3), 522–536. https://doi.org/10.1007/s11707-019-00806-4. Available from 10.1007/s11707-019-00806-4.

Amiri, S., H. Eyni-Narghesi, S. Rahimi-Moghaddam and K. Azizi, 2021. Water use efficiency of chickpea agro-ecosystems will be boosted by positive effects of co2 and using suitable genotype × environment × management under climate change conditions. Agricultural Water Management, 252: 106928. Available from https://www.sciencedirect.com/science/article/pii/S0378377421001931. https://doi.org/10.1016/j.agwat.2021.106928.

Asrar, G., I. Slater, G.A., Reynolds, M.P., Royo, C., 2002. Plant breeding and drought in chickpea (cicer arietinum l). Journal of Pharmacognosy and Phytochemistry 7 (2), 2675–2677.

Arshad, M., Bakhsh, A., Ghafoor, A., 2004. Path coefficient analysis in chickpea (cicer arietinum l) under rainfed conditions. Pakistan Journal of Botany 36 (1), 75–82.

Azam, M., Iqba, M., Hossain, M., Hossain, M., 2020. Stability investigation and genotype environment interaction in chickpea genotypes utilizing ammi and gge bplot model. Genetics and Molecular Research 19 (3).
Olivoto, T., A.D.C. Lúcio, J.A.G. da Silva, B.G. Sari and M.I. Diel, 2019. Mean Schneider, S., Semenov, S., Patwardhan, A., Burton, I., Magadza, C., Oppenheimer, M.,
Rani, A., Devi, P., Jha, U.C., Sharma, K.D., Siddique, K.H., Nayyar, H., 2020. Developing
Thomas, R.J., 2008. Opportunities to reduce the vulnerability of dryland farmers in
Talchabhadel, R., R. Karki, B.R. Thapa, M. Maharjan and B. Parajuli, 2018. Spatio-
Sharifi, P., H. Astereki and M. Pouresmael, 2018. Evaluation of variations in chickpea
Purushothaman, R., H.D. Upadhyaya, P.M. Gaur, C.L.L. Gowda and L. Krishnamurthy, Genetica and Molecular Research 16 (1), 1–19.

Tripathi, A., D.K. Tripathi, D.K. Chauhan, N. Kumar and G.S. Singh, 2016. Paradigms of climate change impacts on some major food sources of the world: A review on current knowledge and future prospects. Agriculture, Ecosystems & Environment, 216: 356–373. Available from https://www.sciencedirect.com/science/article/pii/S0167880915300092. DOI https://doi.org/10.1016/j.agee.2015.09.034.

Vader, V., Harrapour, A., Korsh, L.B., Alamgham, M., Pushpavalli, R., Ramirez, M.L., Kashiwagi, J., Kholova, J., Turner, N.C., Sadas, V.O., 2021. Chapter 10 - chickpea. In: Sadas, V.O., Calderini, D.F. (Eds.), Crop physiology case histories for major crops. Academic Press, pp. 342–358.

Vergni, L. and F. Todisco, 2011. Spatio-temporal variability of precipitation, temperature and agricultural drought indices in central italy. Agricultural and Forest Meteorology, 151(3): 301–313. Available from https://www.sciencedirect.com/science/article/pii/S0168192311003060. DOI https://doi.org/10.1016/j.agrformet.2011.11.005.

Vinocur, Basia, Altman, Arie, 2005. Recent advances in engineering plant tolerance to abiotic stress: Achievements and limitations. Current opinion in biotechnology 16 (2), 123–132.

Vooosen, P., 2021. Global temperatures in 2020 tied record highs. American Association for the Advancement of Science. Vurukonda, S.S.K.P., S. Vardharajula, M. Shrivastava and A. Skz, 2016. Enhancement of drought stress tolerance in crops by plant growth promoting rhizobacteria. Microbiological Research, 184: 13-24. Available from https://www.sciencedirect.com/science/article/pii/S0168192310003080. DOI https://doi.org/10.1016/j.micres.2015.12.003.

Wang, J.Y., Turner, N.C., Liu, Y.X., Siddique, K.H.M., Xiong, Y.C., 2017. Effects of drought stress on morphological, physiological and biochemical characteristics of wheat species differing in ploidy level. Functional plant biology : FPB 44 (2), 219–234. https://doi.org/10.1071/fp16082.

Wang, Xiaosheng, Gao, Wensui, Zhang, Jusong, Zhang, Hua, Li, Jiangui, He, Xiaoling, Ma, Hao, 2010. Subunit, amino acid composition and in vitro digestibility of protein isolates from chinese kabuli and desi chickpea (cicer arietinum l.) cultivars. Food Research International 43 (2), 567–572.

Waqas, M.A., X. Wang, S.A. Zafar, M.A. Noor, H.A. Hussain, M. Aher Nawaz and M. Farooq, 2021. Thermal stresses in maize: Effects and management strategies. Plants, 10(2): 293. Available from https://www.mdpi.com/2223-7747/10/2/293.

Yang, W., G. Feng, A. Adeli, H. Tewolde and Z. Qu, 2021. Simulated long-term effect of wheat cover crop on soil nitrogen losses from no-till corn-soybean rotation under different rainfall patterns. Journal of Cleaner Production, 280: 124255. Available from https://www.sciencedirect.com/science/article/pii/S0959652620343006. DOI https://doi.org/10.1016/j.jclepro.2020.124255.

Yucei, D.O., Aalasri, A.E., Yucei, C., 2006. Genetic variability, correlation and path analysis of yield, and yield components in chickpea (cicer arietinum l.). Turkish Journal of Agriculture and Forestry 30 (3), 183–188.

Zampieri, M., C.J. Weissreiner, B. Grottetti, A. Toreti, M. van den Berg and F. Dentener, 2020. Estimating resilience of crop production systems: From theory to practice. Science of The Total Environment, 735: 139378. Available from https://www.sciencedirect.com/science/article/pii/S0048969720328953. DOI https://doi.org/10.1016/j.scitotenv.2020.139178.

Zuffo, A.M., F. Steiner, J.G. Aguilera, P.E. Teodoro, L.P.R. Teodoro and A. Busch, 2020. Multi-trait stability index: A tool for simultaneous selection of soybean genotypes in drought and saline stress. Journal of Agronomy and Crop Science, 206(6): 815-822. Available from https://onlinelibrary.wiley.com/doi/abs/10.1111/jac.12409. DOI https://doi.org/10.1111/jac.12409.