



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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www.agronomyjournals.com
2022; 5(2): 95-101
Received: 14-05-2022
Accepted: 19-07-2022

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Review on genetic-environmental interaction (GxE) and its application in crop breeding

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DOI: <https://doi.org/10.33545/2618060X.2022.v5.i2b.115>

Abstract

Interactions between genotype and environment are a crucial component to investigate in plant breeding. In order to identify those with specific or stable adaptability in a specific place, breeders routinely test desirable lines and hybrids in a variety of situations. Most quantitative traits, including yield, plant height, thousand seed weight, and other essential traits, exhibit GXE interactions. GXE conversations are vital to the development and assessment of crop varieties because they lower the requirements for genotypic stability in a variety of environments. In order to identify and advance cultivars, the large percentage of assessments of the impact of the environment on results have relied on multi-environmental field testing that depicts target production environments. Gene-environmental interaction and its Applications are reviewed in this paper. The development of acceptable varieties for the pressures of climate change and numerous other stresses, tolerance/resistance to significant abiotic and biotic factors, and advancement of social ability are the final poignant targets that GXE in crop breeding constantly strives to achieve.

Keywords: Genotypic variation, phenotypic variation, stability, adaptability

Introduction

The term genotype by environment interaction refers to the differences in genotype interactions across sites (Bavandpori *et al.*, 2015) ^[30]. Interactions between genotype and environment (GXE) are an important factor to investigate in plant breeding. The repeatable GXE interactions resulted, change the ranking of genotypes across environments, and are meaningful for the specific breeding strategy (Sabaghnia *et al.*, 2008) ^[31]. Most economically important quantitative traits, such as yield, plant height, and weight, are influenced by genotype-environment interactions. Genotype x environment (GXE) interaction and yield-stability analysis has continued to be important in measuring varietal stability and suitability for cultivation across seasons and ecological zones. The genotype x environment analyses have been focused on identifying stable genotypes for crop production.

Cooper (2001) ^[32] asserts that the magnitude of genotype by environment interaction is greater where there is wide variation in the incidence of the same stress such as climate soil biotic and management factors. Ecological factors can be internal or external, micro or macro, non-organic or organic. Intercellular and extracellular environments both have an impact on plant growth and yield. The majority of the intercellular environments in plants are essentially contained in vacuoles, which encompass waste materials, molecules, and water (like inorganic and organic molecules), while also retaining internal hydrostatic pressure, or turgor, temperature, and an acidic pH.

The changes in pH, osmotic pressure, temperature, etc. brought on by material exchange and signal transduction with external environments have a significant impact on the internal environments. Plants respond completely to particular external conditions through a series of receptors, signal transductions, and responses, which result in ion transmembrane transport, metabolic pathway regulation, cytoskeleton modification, and gene expression regulation (Nicotra *et al.* 2010, Yunbi Xu, 2016) ^[33, 34]. Plant breeding determines the causes of GXE to increase predictability, Distinguishing between what is predictable and what is unpredictable, GXE the GXE Structured models' separate G and E components. To understand how various crops interact with one another and to find the best genotypes, several statistical models have been used (Bose *et al.*, 2014) ^[35]. Therefore, the objective of this paper is to review genotypes - environmental interaction (GXE) and its applications.

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Literature Review

Study of GxE during the early 20th Century

The biometrical genetics conceptualization of GXE was popularized by Ronald Fisher from plant and animal studies for the purposes of optimizing crop yield (an exhaustive summary is provided in Tabrey, 2008) ^[36]. This viewpoint concentrated on the quantity of genetic and environmental variations responsible for population variation. GxE is defined in biometrical genetics as an organism's genotype-specific sensitivity to environmental exposure (Fisher, Immer, & Tedin, 1932) ^[37]. Fisher tested data from carefully crafted plant and animal experiments using ANOVA and predicted to find GXE when, at the functional level, genetic differences were seen as environmental sensitivity. Fisher found that he could frequently eliminate significant GXE by merely changing the scale of the environment, which is interesting because he was not convinced that GXE was a significant influence on traits and treated it as a hindrance.

The Study of GxE during the mid-late 20th Century

Concentrate on Human Research of GXE Some of the constraints of traditional multiple biometric genetics approaches to GXE research have been addressed in recent decades. For instance, the fact that genetic and environmental influences are interdependent has received a great deal of attention in studies of human behavior. Further, either gene-environment correlation (rGE), GXE, or their combination may be responsible for the detection of statistically significant GxE.

The work of Cattell (1960) ^[38] and Loehlin (1965) ^[39] detailed some of the first approaches to detecting and estimating both GxE and rGE simultaneously in humans. Jinks and Fulker (1970) ^[40] later adapted these approaches to fit within the biometrical genetics' framework using data from monozygotic and dizygotic twins. Plomin, DeFries and Loehlin (1977) ^[41] were the first to detail the concept of rGE and summarized study designs and statistical approaches for detection (1977). Scarr and McCartney (1983) ^[42] extended the concept of rGE to a developmental model in order address the role of rGE in human behavior across the lifespan. These papers highlighted the fundamental concepts we currently use to define and categorize GE as either passive, active or evocative. Additionally, Rutter and colleagues continued to consider the dynamic nature of the individual within an ever-changing environment.

Prior breeding studies were unable to test for the effects of specific genetic influences. Additionally, these studies generally did not address the complexity of multiple environmental influences working together as they do for human outcomes. Nevertheless, studies in the biometrical genetics' tradition provided some expectations regarding the nature of gene-environment interplay. Further, they emphasized the need to study many genetic and environmental influences on a trait to understand the mechanisms underlying a trait. These studies identified three specific characteristics on the nature of GXE.

The future of the study of GxE

The Fisher/Hogben debate regarding the detection "true" GXE endures into present-day research (REF-Tabrey book). While such discussion may encourage a researcher to throw their hands up in frustration, it also highlights an opportunity for greater clarity and discussion in this particular area of study. Those who address the study GXE are tasked with a careful balancing act regarding the detection of statistical GXE as well as its interpretation for the purpose of understanding etiology and application. For example, Saccari (1980) ^[79] identified three general definitions GXE: statistical, biological and public health.

We modify these definitions to be generalizable across additional disciplines. In order for the study of GXE in any field to improve the burden of illness, these three perspectives require consideration.

The statistical perspective on GXE focuses on the detection of statistical interactions in general and GxE specifically, which strictly refers to modeling the effect of GxE as the product of two variables each with their own main effects. The presence of GxE is first identified as a statistically significant interaction effect, which may be detected through appropriate study design and statistical tests typically as a departure from only additive main effects.

The conceptual frameworks of GXE as a biological process is the primary focus of the biological viewpoint. This refers to how components of a biological system or components of different systems interact to spread a mechanism. The typical goal of GXE as a physiological interaction is to comprehend how nature and nurture interact. Genetic and environmental influences may only be found as significant additive main effects because the existence of biological GXE does not always require statistical interaction.

GxE and its challenges

GxE and yield stability have long been a source of controversy among breeders and biometricians because they make selecting superior genotypes more challenging by stifling genetic progress. A GxE is essential to minimizing the utility of the genotype implies across locations or environments when choosing and moving superior genotypes to the next stage of selection. (Natalia de Leon *et al.*, 2016 ^[43]; Pham and Kang, 1988) ^[44]. Plant breeders have managed these interactions all across the history of crop domestication, crop improvement, and crop dispersal as well as in more recent times through the formalized processes of plant genetics.

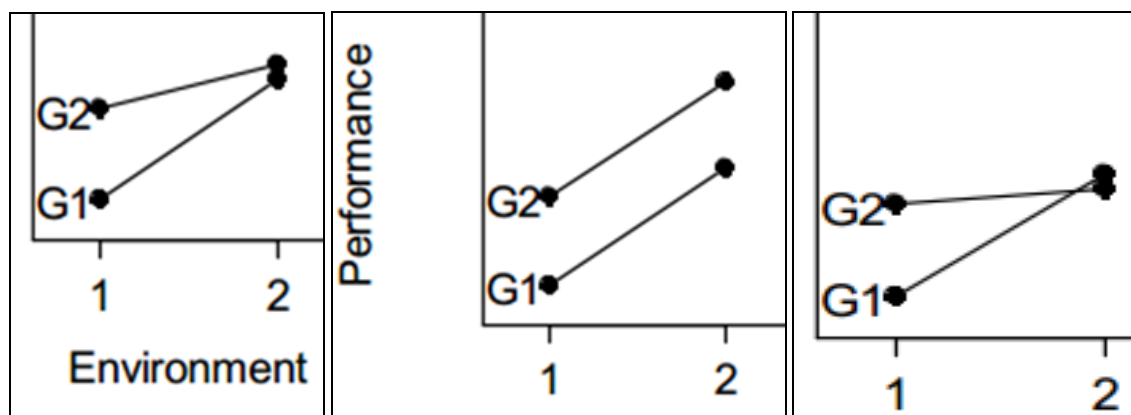
The ecological impact is the highest, but it is insignificant in terms of selection. Because many of the selected activities performed by the conservative technique are performed in on-stations that are good production environments, the association between selection settings and target production environments has been a fundamental problem in Ethiopia (Ceccarelli, S. and S. Grando, 2007, Melkamu Temesgen *et al.*, 2015) ^[8]. Many statistical methods take into account all phenotypic variation (i.e., means across environments), which can be misleading. GXE interaction is both a problem and an opportunity" (Simmonds, 1991) ^[45]. Varietal stability may be jeopardized not only by changes in the test environment, but also by shifts in the planting season for every biosphere (Dagnachew *et al.*, 2014) ^[46]. A few really weather variables are consistent (soil type, soil fertility, plant density), and others are not (rainfall, temperature, humidity etc.).

Importance of studying GXE

GXE interactions are significant in the formation and review of plant varieties since they reduce genotypic-stability values in a range of climates (Hebert *et al.*, 1995) ^[47]. Real progress in crop production may be possible by breeding varieties for yield and yield component stability (Singh *et al.*, 2009 ^[48]; Lal *et al.*, 2010) ^[49]. GxE relationships are statistically detected as a widely differing sequence of responses among genotypes across environments, and biologically, this occurs when the contributions (or level of expression) of the genes regulating the trait differ across environments (Basford and Cooper, 1998) ^[50]. The slope of the line when genotype performance is schemed it against ridgelines is a common way to represent a conceptual

GXE interaction. Lines that are not parallel but just don't intersect prove that cultivar performance ranks remain constant across environments. The ideal cultivar will vary by location, and lines that intersect show a change in cultivar rank across environments. Just about all decision-making mechanisms associated with plant breeding strategies are affected by GXE, including identifying the most suitable testing environments, allocating resources within a breeding program, and selecting the appropriate genetic variability and breeding approach (Natalia de Leon *et al.*, 2016) ^[51]. Agricultural output is

environmental conditions, genetic background, and the interplay of the three. Info on the transition of variety and stability over environments is essential for testing widely adapted and stable genotypes. In locations where environmental fluctuations are noticeable, it is crucial to identify stable genotypes that exhibit the least GE interaction. When genotype performance varies from one environment to another, GE interaction occurs, making the selection and/or recommendation of genotypes more difficult.



Source: Ric Coe (r.coe@cgiar.org), Statistical Services Centre, University of Reading, UK and World Agroforestry Centre, Kenya, 5 April 2012

Fig 1: Examples of different types of interaction between two genotypes and two environments

Types of Variation in Gx E and Components Genotypic Variation

The genetic diversity of the breeding population for a specific feature measures the rate of genetic gain in plant breeding (Hallauer and Miranda, 1981 ^[52], Kai Luo *et al.*, 2016) ^[53]. The degree of genetic diversity in plant populations will enable the creation of breeding plans that will maximize genetic gain (Moll and Stuber, 1974 ^[54], Kai Luo *et al.*, 2016) ^[53]. For instance, based on estimated genetic variation for a variety of morphological and quality traits in switch grass, Jahufer and Casler (2015) ^[55] and Kai Luo *et al.* (2016) ^[53] evaluated the relative advantage in genetic gain using single trait selection, correlated response to selection, and index selection (*Panicum virgatum* L.). Some of the significant forage grasses and legumes have shown genetic variation for important traits: ryegrass (Breese and Hayward, 1972 ^[56], Kai Luo *et al.*, 2016) ^[53], tall fescue (Piano *et al.*, 2007) ^[57], white clover (Jahufer *et al.*, 2002 ^[55], Kai Luo *et al.*, 2016) ^[23], Alfalfa (Riday and Brummer, 2007) ^[58].

There really are 3 kinds of variation: additive genetic (genes that are totally handed down from parent to offspring), dominant gene action, and epigenetic modification gene components (when one gene masks the effect of another gene). These three components are used to create variety. $VP = VG + VE = VD + VH + VI + VE$, where VP = Total phenotypic variance, VG = Genotypic variance, VD = Additive gene, VH = Dominance gene, and VI = Epistatic, $VI = I_j$, and l .

Phenotypic Variation

Genotypes were screened for various yield contributing traits in all environments and seasons using the Basic Evaluation Process (IRRI, 2013, Divya Balakrishnan *et al.*, 2016) ^[22, 14]. Field experiments were used to collect data on yield and morpho-agronomic traits. The plant phenotype (P) is determined not only by the plant's genetic composition (G) and environmental factors (E), but also by their interaction (GXE), which is typically

described by the linear model $P = G + E + GXE$ (Visscher PM *et al.*, 2008 ^[59], Bernardo, R., 2008, Mohamed El-Soda *et al.*, 2014) ^[5]. As a consequence, variety trials in a breeding program are normally performed in multiple environments to minimize the risk of discarding genotypes that may perform well in some but not all environments (Kang MS 1997 ^[60], Ceccarelli, S. *et al.*, 1994, Mohamed El-Soda *et al.*, 2014) ^[9]. In overall, to forecast the germplasm rebuttal to preference all over ecosystems, a trait's slim sense heritable traits (Visscher PM, *et al.*, 2008 ^[59], Holland, J.B. *et al.*, 2003, Eichler EE *et al.*, 2010 ^[61], Mohamed El-Soda *et al.*, 2014) ^[21] is estimated based on main effects, leaving GXE effects within the unexplained phenotypic variance, and thus In other words, missing heritability can be caused by a variety of factors, including epistasis, epigenetic variants, rare variants (such as those found in association mapping studies), small undetected QTL, and GXE (Eichler EE, *et al.*, 2010 ^[61], Manolio TA, *et al.*, 2009 ^[62], cited by Mohamed El-Soda *et al.*, 2014) ^[63].

Determining genetic traits in diverse contexts is vital to understanding the scope of GXE (Bergelson J and Roux F, 2010, Van Eeuwijk FA, *et al.*, 2010, Mohamed El-Soda *et al.*, 2014) ^[4, 26], and it is of considerable interest to harvest genetic improvement to ascertain how much of the selection progress made in one environment can be carried over to other environments (Van Kleunen M, Fischer M 2005 ^[64], Nicotra AB *et al.*, 2010 ^[33], Kang MS 1997 ^[60], Mohamed El-Soda *et al.*, 2014) ^[9].

Stability and Adaptability

Factors relating to a genotype's transition or appropriateness to a variety of locations, but it has been used to identify stable specific genes that are unchanged by climate conditions, whereas versatility is a genotype's better survival over any specific environment (Moorthy *et al.*, 2012, Chandrakanth N *et al.*, 2016) ^[23, 10]. Stability knowledge is essential for crop variety selection as well as breeding programs. Because of the high

annual variation in mean yield, especially in arid and semi-arid areas, yield stability is an intriguing feature of today's plant breeding programs (Mohammadi *et al.*, 2012) ^[65]. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments.

A diversity or genotype is regarded as extra responsive or steady if it has a high mean yield but a reduced amount of yield fluctuations when cultivated in a variety of environments. The idea of stability has been estimated in biometrical methods, including univariate and multivariate ones developed to assess stability (LIN *et al.*, 1986 ^[66]; CROSSA 1990 ^[67], Chandrakanth N *et al.*, 2016) ^[10]. The regression method, which is based on regressing the mean value of each genotype on the environmental index or marginal means of environments, is the most widely used (Moorthy *et al.*, 2012, Chandrakanth N *et al.*, 2016) ^[23, 10]. Finlay and Wilkinson (1963) ^[68] proposed a good method for measuring stability, which was later improved by (Eberhart and Russell 1966 ^[69], Chandrakanth N *et al.*, 2016) ^[10]. Moorthy *et al.* (2012) ^[23] applied successfully Eberhart and Russell's (1966) ^[69] method to determine index in 46 silkworm breeds in environments. This method was also used in many crops (Akcira *et al.*, 2005; DEWDAR, 2013, Chandrakanth N *et al.*, 2016) ^[11, 12, 10].

Methods of Measuring GXE

The adverse consequences of GXE Interplay in collection, selection, and variety advancement have been identified by plant breeders, who have concentrated on creating breeding tools and resources to mitigate those effects and maximize the benefits of Interaction (Freeman, 1973 ^[70]; Cooper, 1999 ^[71]; Cooper *et al.*, 2014 ^[72]; Sadras and Richards, 2014 ^[73], Natalia de Leon *et al.*, 2016) ^[51]. Cultivars are frequently chosen for use in a particular environment (Cooper *et al.*, 1997 ^[74]; Chapman *et al.*, 1997, Natalia de Leon *et al.*, 2016) ^[11]. G X E was used to handle stress trials in order to highlight the impact of specific sources of abiotic stress on genotype performance and to know the implications of specific environmental disruption on phenotypes. To innovate and implement cultivars, most estimations of the effects of global climate change on performance have relied on non - linear and non-field testing that represents target production environments (Comstock, 1977 ^[75], Natalia de Leon *et al.*, 2016) ^[51]. These multi-site studies provide two-way tables of means for various genotypes in various environments.

Models that incorporate the effects of the genotype, the environment, and also divide the remaining variation into the effects of the interaction between environments and genotypes and the residual experimental error can be used to initially analyze data from such two-way tables (pooled error). This gives an indication of how much of the variance is due to genotype's main effect as opposed to GXE, but it does not give much information about the nature of the interaction. In the context of plant breeding, a lot of that descriptive information was modified by others and built on the work of Finlay and Wilkinson (1963) ^[68], Natalia de Leon *et al.* (2016) ^[51], and others (Eberhart and Russell, 1966) ^[69] which qualified GXE based on the slope of the regression of the performance of particular genotypes across an environmental gradient. The simplest models use the average performance of all genotypes in that environment to calculate the quality gradient. As long as the settings fall within the range of the differential in tested locations, this methodology allows extrapolation of the quality of a particular genotypes under inquiry across untested environments. Because it provides a single evaluation of the

slope of the genotype-environment gradient regression line, which can be used as the entry phenotype for genotypic-phenotypic associations, for example, to understand the genetic architecture of plasticity itself, this conventional idea of stability is useful for the study of phenotypic plasticity. Other useful techniques for evaluating environmental stability include stability variance from Natalia de Leon *et al.* (2016) ^[43] and mean-CV analyses from Francis and Kannenberg (1978) ^[76] and Shukla (1972) ^[77].

Incorporating multidimensional environmental characterizations into statistical models is crucial to GXE's significance. One of the earliest applications of this strategy was the additive main effects and multiplicative interaction (AMMI) model (Gollob, 1968; Gauch, 1988, Natalia de Leon *et al.*, 2016) ^[19, 18]. In this situation, GXE is modelled as the result of a genotype's specific sensitivity to an unobservable latent environmental variable. The variation explained by the products of the resulting genotype sensitivities by environmental variables is maximized by a principal components strategy (Gabriel, 1978 ^[78], Natalia de Leon *et al.*, 2016) ^[43]. The development of modelling strategies that included not only the GXE variation but also the combined effect of the genotypic main effect and the GXE as a sum of the multiplicative terms gave rise to another variation of this overall strategy. "Genotype main effects and GXE" or "GGE model" are the names given to this general group of techniques (Natalia de Leon *et al.*, 2016) ^[43]. Because these multiplicative strategies offer insightful graphical representations of performance, it is possible to directly interpret the relationship between various environments and various genotypes, and, in the case of GGE, the impact of various genotypes on various environments.

Another development came from the explicit quantification of environmental components being included in statistical models as explanatory variables, which improved the interpretation of the impact of specific environmental effects on performance. These so-called factorial regression models link the varying sensitivity of genotypes to noted environmental variables (such as rainfall in May), which could be selected based on what is required for crop growth (Van Eeuwijk *et al.*, 1996) ^[26]. Since breeders are primarily concerned with overall performance, this kind of analysis makes it easier to directly interpret performance from a biological perspective and consequently has immediate value for actual breeding programs. In addition, a number of mixed model applications, primarily for multi-environment analysis involving a large number of genotypes, have been proposed to analyze and interpret GXE. In this context, genotypes can be modeled as random effects and their potential heterogeneity of variances (and co-variances) can be interpreted as an indication of differential genotypic sensitivity to certain environmental cues.

Summary and Conclusion

According to these the information of this review, the overall purpose of plant breeders in a crop improvement program is the development of varieties with high yield potential in order to maintain high agricultural productivity. A new cultivar should have stable performance and broad adaptation over a variety of environments in addition to high yield potential. Since large interactions can reduce selection benefits and make it more difficult to identify superior cultivars, the presence of genetic background by ecosystem interaction is of utmost importance for crop breeders because genotypes differ in how their phenotypic responses to environmental change. Moreover, since it is inspired by biotic and abiotic natural conditions, observable traits rebuttal may not be the same in various environments.

GXE to reduce the genotype means across various environments, interaction is crucial. As a measure of the genotypes' plasticity to the expression of particular phenotypes in diverse areas, it is a continuing challenge of plant breeders due to environmental fluctuation across various locations and over time. The main goals of multi-environment trials are to identify superior genotypes, monitor genotype stability across environments, and find the location that most closely resembles the production environment's target environment.

Future GXE Interaction in Plant Breeding's main areas of focus includes: GXE throughout Plant Biotechnology pursues consistently trying to shift specific goals in developing the appropriate varieties for pressures from climate change and many other stresses (tolerance/resistance to major abiotic stresses like drought, salinity, etc., and biotic factors like diseases and pests), as well as by providing better mastery.

References

1. Akcura M, Kay YA, Taner S. Genotype-environment interaction and phenotypic stability analysis for grain yield of Durum wheat in the Central Anatolian region. *Turkish Journal of Agriculture and Forestry*. 2005;29(50):369-375.
2. Allard RW, Bradshaw AD. Implication of genotype-environmental interaction in applied plant breeding. *Crop Science*. 1964;5:503-506.
3. Amjad AM, Nobel NN, Amjad A, Zulkiffal M, Sajjad M. Evaluation of selection criteria in *Cicer arietinum* L. using correlation coefficients and path analysis. *Australian Journal of Crop Science*. 2009;3(2):65-70.
4. Bergelson J, Roux F. Towards identifying genes underlying ecologically relevant traits in *Arabidopsis thaliana*. *Nature Reviews Genetics*. 2010;11(12):867-879.
5. Bernardo R. Molecular markers and selection for complex traits in plants: Learning from the last 20 years. *Crop Science*. 2008;48(5):1649-1664.
6. Bnejdi Fethi, El Gazzeh Mohamed. Impact of Epistasis in Inheritance of Quantitative Traits in Crops; c2012.
7. Ceccarelli S. Wide adaptation: How wide. *Euphytica*. 1989;40:197-205.
8. Ceccarelli S, Grando S. Growing Areas of Tigray Region, northern Ethiopia. Decentralized-participatory plant breeding: An example of demand driven research. *Euphytica*. 2007;155(3):349-360.
9. Ceccarelli S *et al.* Genotype by environment interaction and international breeding programmes. *Experimental Agriculture*. 1994;30(2):177-187.
10. Chandrakanth N *et al.*, Stability and path analysis for yield and related traits in silkworm, (*Bombyx mori* L.) reared under stress conditions – *Genetika*. 2016;48(1):271-284.
11. Chapman SC, Crossa J, Edmeades GO. Genotype by environment effects and selection for drought tolerance in tropical maize: I. Two mode pattern analysis of yield. *Euphytica*. 1997;95(1):1-9. DOI: 10.1023/A:1002918008679
12. Dewdar MDH. Stability analysis and genotype x environment interactions of some Egyptian cotton cultivars cultivated. *African Journal of Agricultural Research*. 2013;8(14):5156-5160.
13. Ding M, Tier B, Yan W. Application of GGE biplot analysis to evaluate genotype (G), environment (E) and GxE interaction on *P. radiata*: A case study. Paper presented to Australasian Forest Genetics Conference Breeding for Wood Quality, 11-14 April 2007, Hobart, Tasmania, Australia; c2007.
14. Divya Balakrishnan. Genotype × Environment Interactions of Yield Traits in Backcross Introgression Lines Derived from *Oryza sativa* cv. Swarna/*Oryza nivara*. Crop Improvement Section, ICAR - National Professor Project, ICAR - Indian Institute of Rice Research, Hyderabad, India. 2016;7:1530.
15. Ezatollah Farshadfar *et al.*, GGE biplot analysis of genotype × environment interaction in wheat-barley disomic addition lines. College of Agriculture, Razi University, Kermanshah, Iran. Seed and Plant Improvement Institute, Karaj, Iran. Department of Plant Breeding, Islamic Azad University, Kermanshah branch, Kermanshah, Iran. 2012;6(6):1074-1079.
16. Falconer DS. The problem of environment and selection. *American Naturalist*. 1952;86(830):293-298. DOI: 10.1086/281736.
17. Farshadfar E, Sutka J. Locating QTLs controlling adaptation in wheat using AMMI model. *Cereal Research Communications*. 2003;31(3-4):249-255.
18. Gauch HG. Statistical analysis of yield trials by AMMI and GGE. *Crop science*. 2006;46(4):1488-1500.
19. Gollob H. A statistical model which combines features of factor analysis and analysis of variance techniques. *Psychometrika*. 1968;33(1):73-115. DOI: 10.1007/BF02289676
20. Hallauer AR, Miranda JB. Quantitative Genetics in Maize Breeding. Ames: IA State University Press; c1981.
21. Holland JB *et al.* Estimating and interpreting heritability for plant breeding: An update. In *Plant Breeding Reviews* (Janick J., Edition.), John Wiley & Sons, Include. 2003;22:9-112.
22. IRRI. Standard Evaluation System (SES) for Rice, 5th Editions. Philippines: RRI. Islam MR, Sarker MRA, Sharma N, Rahman MA, Collard BCY, Gregorio GB, *et al.* Assessment of adaptability of recently released salt tolerant rice varieties in coastal regions of South Bangladesh. *Field Crops Res*. 2013;190:34-43. DOI: 10.1016/j.fcr.2015.09.012
23. Moorthy SM, DAS NK, Mandal K. Genotype x Environment interaction and stability analysis in bivoltine silkworm genotypes of *Bombyx mori* L. *IJBPAS*. 2012;1(10):1443-1449.
24. Morgan M. A gene controlling difference osmoregulation in wheat. *Australian Journal of Plant Physiology*. 1991;18:294-257.
25. Technow F, Messina CD, Totir LR, Cooper M. Integrating crop growth models with whole genome prediction through approximate Bayesian computation. *PLOS One*. 2015;10(6):1-20. DOI: 10.1371/journal.pone.0130855.
26. Van Eeuwijk FA, Denis JB, Kang MS. Incorporating additional information on genotypes and environments; c1996. p. 15-50
27. Yan W. Singular value partitioning in biplot analysis of multi-environment trial data. *Agronomy Journal*. 2002;94(5):990-996.
28. Yan W, Kang MS. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists. 1st Edn., CRC Press LLC., Boca Raton, Florida; c2003. p. 271.
29. Zobel RW, Wright MJ, Gauch HG. Statistical analysis of a yield trial. *Agronomy Journal*. 1988;80(3):388-393.
30. Bavandpori F, Ahmadi J, Hossaini SM. Yield stability analysis of bread wheat lines using AMMI model. *Agricultural communications*. 2015;3(1):8-15.
31. Sabaghnia N, Dehghani H, Sabaghpour SH. Graphic

- analysis of genotype by environment interaction for lentil yield in Iran. *Agronomy Journal*. 2008;100(3):760-4.
32. Hoel H, Cooper CL, Faragher B. The experience of bullying in Great Britain: The impact of organizational status. *European Journal of Work and Organizational Psychology*. 2001;10(4):443-65.
 33. Nicotra AB, Atkin OK, Bonser SP, Davidson AM, Finnegan EJ, Mathesius U, *et al.* Plant phenotypic plasticity in a changing climate. *Trends in Plant Science*. 2010;15(12):684-92.
 34. Xu Y. Envirotyping for deciphering environmental impacts on crop plants. *Theoretical and Applied Genetics*. 2016;129(4):653-73.
 35. Bose J, Rodrigo-Moreno A, Shabala S. ROS homeostasis in halophytes in the context of salinity stress tolerance. *Journal of Experimental Botany*. 2014;65(5):1241-57.
 36. Njoh AJ, Ananga EO, Ngyah-Etchutambe IB, Tabrey HT, Tassang CF, Asafor-Mangheh J. Effects of macro-economic factors on women's formal land ownership status in Cameroon. In *Women's Studies International Forum* 2017;63:1-10.
 37. Fisher RA, Immer FR, Tedin O. The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics*. 1932;17(2):107-124.
 38. Cattell RB, Baggaley AR. The salient variable similarity index for factor matching. *British Journal of Statistical Psychology*. 1960;13(1):33-46.
 39. Loehlin JC. Interpersonal experiments with a computer model of personality. *Journal of Personality and Social Psychology*. 1965;2(4):580-584.
 40. Jinks JL, Fulker DW. Comparison of the biometrical genetical, MAVA, and classical approaches to the analysis of the human behavior. *Psychological bulletin*. 1970;73(5):311-349.
 41. Plomin R, DeFries JC, Loehlin JC. Genotype-environment interaction and correlation in the analysis of human behaviour. *Psychological bulletin*. 1977 Mar;84(2):309-322.
 42. Scarr S, McCartney K. How people make their own environments: A theory of genotype → environment effects. *Child Development*. 1983;54(2):424-435.
 43. Stelpflug, Scott C, Rajandeep Sekhon S, Brieanne Vaillancourt, Candice Hirsch N, Robin Buell C. An expanded maize gene expression atlas based on RNA sequencing and its use to explore root development. *The Plant Genome*. 2016;9(1):1-16.
 44. Pham HN, Kang MS. Interrelationships among and repeatability of several stability statistics estimated from international maize trials. *Crop Science*. 1988;28(6):925-928.
 45. Murray RJ, Simmonds I. A numerical scheme for tracking cyclone centres from digital data. *Australian Meteorological Magazine*. 1991;39(3):155-66.
 46. Inglingstad RA, Steinshamn H, Dagnachew BS, Valenti B, Criscione A, Rukke EO, *et al.* Grazing season and forage type influence goat milk composition and rennet coagulation properties. *Journal of Dairy Science*. 2014;97(6):3800-14.
 47. Wolfe F, Ross K, Anderson J, Russell IJ, Hebert L. The prevalence and characteristics of fibromyalgia in the general population. *Arthritis & Rheumatism: Official Journal of the American College of Rheumatology*. 1995;38(1):19-28.
 48. Singh B, Sharma DK, Kumar R, Gupta A. Controlled release of the fungicide thiram from starch-alginate-clay based formulation. *Applied Clay Science*. 2009;45(1-2):76-82.
 49. Lal S, Link S, Halas NJ. Nano-optics from sensing to waveguiding. *Nanoscience and Technology: A Collection of Reviews from Nature Journals*. 2010;1:213-220.
 50. Basford KE, Cooper M. Genotype × environment interactions and some considerations of their implications for wheat breeding in Australia this review is one of a series commissioned by the Advisory Committee of the Journal. *Australian Journal of Agricultural Research*. 1998;49(2):153-74.
 51. Stelpflug, Scott C, Rajandeep Sekhon S, Brieanne Vaillancourt, Candice Hirsch N, Robin Buell C, *et al.* An expanded maize gene expression atlas based on RNA sequencing and its use to explore root development. *The Plant Genome*. 2016;9(1):1-16.
 52. Hallauer AR, Miranda JB. Quantitative genetics in maize breeding. Iowa State Univ Press, Ames, IA. Jenkins, JN, WL Parrott, JC McCarty Jr & RL Shepherd, 1988a. Registration of three noncommercial germplasm lines of upland cotton tolerant to tobacco budworm. *Crop Science*. 1981;28(5):869-869.
 53. Li Q, Luo KH, Kang QJ, He YL, Chen Q, Liu Q. Lattice Boltzmann methods for multiphase flow and phase-change heat transfer. *Progress in Energy and Combustion Science*. 2016;52:62-105.
 54. Moll RH, Stuber CW. Quantitative genetics—empirical results relevant to plant breeding. *Advances in Agronomy*. 1974;26:277-313.
 55. Jahufer MZ, Casler MD. Application of the Smith-Hazel selection index for improving biomass yield and quality of switchgrass. *Crop Science*. 2015;55(3):1212-1222.
 56. Breese EL, Hayward MD. The genetic basis of present breeding methods in forage crops. *Euphytica*. 1972;21(2):324-336.
 57. Caranti DA, De Mello MT, Prado WL, Tock L, Siqueira KO, De Piano A, *et al.* Short-and long-term beneficial effects of a multidisciplinary therapy for the control of metabolic syndrome in obese adolescents. *Metabolism*. 200;56(9):1293-1300.
 58. Riday H, Brummer EC. Narrow sense heritability and additive genetic correlations in alfalfa subsp. *falcata*. *Journal of the Iowa Academy of Science: JIAS*. 2007;114(1-4):28-34.
 59. Visscher PM, Hill WG, Wray NR. Heritability in the genomics era—concepts and misconceptions. *Nature reviews genetics*. 2008;9(4):255-266.
 60. Rhee S, Lee KH, Kwon H, Kang MS. NF-κB activation by disruption of microtubule array during myogenesis of L6 cells. *Korean Journal of Biological Sciences*. 1997;1(1):63-69.
 61. Eichler EE, Flint J, Gibson G, Kong A, Leal SM, Moore JH, Nadeau JH. Missing heritability and strategies for finding the underlying causes of complex disease. *Nature Reviews Genetics*. 2010;11(6):446-450.
 62. Manolio TA, Collins FS, Cox NJ, Goldstein DB, Hindorf LA, Hunter DJ, *et al.* Finding the missing heritability of complex diseases. *Nature*. 2009;461(7265):747-753.
 63. El-Soda M, Malosetti M, Zwaan BJ, Koornneef M, Aarts MG. Genotype × environment interaction QTL mapping in plants: lessons from Arabidopsis. *Trends in plant science*. 2014;19(6):390-398.
 64. Van Kleunen M, Fischer M. Constraints on the evolution of adaptive phenotypic plasticity in plants. *New Phytologist*. 2005;166(1):49-60.

65. Mohammadi AH, Eslamimanesh A, Gharagheizi F, Richon D. A novel method for evaluation of asphaltene precipitation titration data. *Chemical Engineering Science*. 2012;78:181-185.
66. Lin CS, Binns MR, Lefkovitch LP. Stability analysis: where do we stand? 1. *Crop science*. 1986;26(5):894-900.
67. Crossa J. Statistical analyses of multilocation trials. *Advances in agronomy*. 1990;44:55-85.
68. Finlay KW, Wilkinson GN. The analysis of adaptation in a plant-breeding programme. *Australian journal of agricultural research*. 1963;14(6):742-754.
69. Eberhart ST, Russell WA. Stability parameters for comparing varieties 1. *Crop science*. 1966;6(1):36-40.
70. Freeman RB, Gordon RA, Bell D, Hall RE. Changes in the labor market for black Americans, 1948-72. *Brookings Papers on Economic Activity*. 1973;1973(1):67-131.
71. Cooper R. *Coordination games*. Cambridge University Press; c1999.
72. Blumberg B, Cooper D, Schindler P. *EBOOK: Business Research Methods*. McGraw Hill; c2014.
73. Sadras VO, Richards RA. Improvement of crop yield in dry environments: benchmarks, levels of organisation and the role of nitrogen. *Journal of Experimental Botany*. 2014;65(8):1981-1995.
74. Cooper MC, Lambert DM, Pagh JD. Supply chain management: more than a new name for logistics. *The International Journal of Logistics Management*. 1997;8(1):1-4.
75. Comstock GW, Helsing KJ. Symptoms of depression in two communities. *Psychological Medicine*. 1977;6(4):551-563.
76. Francis TR, Kannenberg LW. Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. *Canadian Journal of Plant Science*. 1978;58(4):1029-1034.
77. Shukla GK. Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity*. 1972;29(2):237-245.
78. Gabriel KR. Least squares approximation of matrices by additive and multiplicative models. *Journal of the Royal Statistical Society: Series B (Methodological)*. 1978;40(2):186-196.
79. Scheffer RP, Livingston RS. Sensitivity of sugarcane clones to toxin from *Helminthosporium sacchari* as determined by electrolyte leakage. *Phytopathology*. 1980;70(5):400-4.