

**APPLICATION OF AMMI MODEL FOR G X E INTERACTION IN
BREAD WHEAT**

A THESIS

By

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18.04.11

URMI TABASSUM

Student No. 0905025

Registration No. 0905025

Session: 2009-2010

Semester: March- August 2010



**MASTER OF SCIENCE (M.S)
IN
GENETICS AND PLANT BREEDING**

**DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHOMMAD DANESH SCIENCE AND TECHNOLOGY
UNIVERSITY, DINAJPUR**

AUGUST 2010

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**Submitted to the
Department of Genetics and Plant Breeding
Hajee Mohammad Danesh Science and Technology University
Dinajpur**

In partial fulfillment of the requirement for the degree of

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Approved as to style and content by



Dr. Md. Hasanuzzaman

Associate Professor

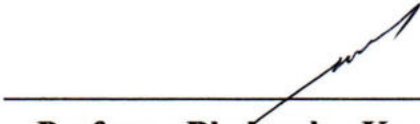
Supervisor



Dr. Dinabandhu Pandit

Principal Scientific Officer, BARI

Co-Supervisor



Professor Bhabendra Kumar Biswas

Chairman

Department of Genetics and Plant Breeding

Hajee Mohammad Danesh Science and Technology University, Dinajpur

AUGUST 2010

**DEDICATED
TO MY
BELOVED PARENTS**

ACKNOWLEDGEMENTS

Firstly the authoress gives her praises and thanks to the one above, things are possible. Who gave her the wisdom and strength to carry on and helped in making her thesis a great success.

The authoress is glad to express high gratefulness to her supervisor, Associate Prof. Dr.Md. Hasanuzzaman, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, for his constant inspiration, affectionate care, critical review and precious suggestions in preparing manuscript.

This work would not been possible without the initiation of her co-supervisor, Dr. Dinabandhu Pandit, Principal Scientific Officer, Wheat Research Centre, BARI, Dinajpur. The authoress thanks him for giving the opportunities, being patient with her, believing her, for his guidance, support and assistance in making this a success. The authoress also thanked to the Wheat Research Centre of Dinajpur, Jessore, Jamalpur, Joydevpur, and Rajshahi where she conduct her research especially Dinajpur for all the support and opportunities provided during the course of her studies.

The authoress expresses her profound gratitude to her respectable teachers Professor Bhabendra Kumar Biswas, Md. Abul Kalam Azad, Associate professor and Md. Arifuzzaman and Farhana Sharmeen, Assistant professors, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur for their cordial valuable help and suggestions during the entire course of the study.

The authoress is also thankful to all stuff members of the Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, for their cordial co-operation during the whole period of this study.

Authoress would further extend her thanks to Mehrab who had to put up with her frustrations during the study. Lastly, she gives her sincere gratitude to her whole family, Father, mother, brothers and sister for their motivations, patience and understanding throughout her studies. The authoress thanks God for having you all in her life.

The authoress

ABSTRACT

Eight advance wheat genotypes including two check varieties BARI Gom 21 (Shatabdi) and BARI Gom 24 (Prodip) were tested in 10 environments under five locations of different WRC stations of BARI during 2009-10. There were significant variations against environments, genotypes and genotype x environment interactions for yield, heading days, grain filling duration and rate. The sum of squares for yield, heading days and grain filling duration were attributed by environments followed by genotype x environment interaction and then genotypes. The environments were diverse and there were substantial differences in genotypic response for all the characters. Interactions of ten genotypes of wheat for yield and heading days with ten environments were predicted by first four principal components of genotypes and environments. Grain filling duration was predicted by first two principal components and grain filling rate by first principal components. The genotypes BAW 1118, BAW 1122, BAW 1140 and BAW 1141 were the most stable genotypes for yield as estimated by both AMMI stability value (ASV) and regression method. All late seeding environments were closer to each other than any optimum environments and vice versa with some variations. Influence of genotypes was the highest in determining grain filling rate of the tested genotypes followed by environments. So, there was less differences in genotypic response for the characters across the environments. The hierarchical classification revealed that, stable genotypes BAW 1118, BAW 1140 and BAW 1141 were closer to each other. Rajshahi optimum environment was different than other optimum environments as well as Jamalpur late environment was also different from other late environments, for attaining higher yield in the tested wheat genotypes.

SYMBOLS AND ABBREVIATIONS

AMMI	= Additive Main Effect and Multiplicative Interaction
ANOVA	= Analysis of Variance
ASV	= AMMI Stability Value (ASV)
BARI	= Bangladesh Agricultural Research Institute
BAW	= Bangladesh Advanced Wheat
bi	= Regression coefficient
CV	= Coefficient of Variation
df	= Degrees of Freedom
E	= Environment
G	= Genotype
GEI, G x E, gxe	= Genotype- Environment Interaction
GFD	= Grain Filling Duration
GFR	= Grain Filling Rate
HD	= Heading Days
IPCA 1	= Interaction Principal Component Axis 1
IPCA 2	= Interaction Principal Component Axis 2
J	= Journal
MS	= Mean Square
PCA	= Principal Component Analysis
SS	= Sum of Square
S^2_{di}	= Deviation from Regression

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INTRODUCTION

CHAPTER I

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the second most important cereal crop in Bangladesh. Although the country is still a small producer of wheat, it made spectacular progress in increasing production during post independence to 1985 indicating that the climatic and soil condition of Bangladesh is suitable for wheat cultivation (Swaminathan, 1986). The wheat area and production in the country was further increased and reached to the highest peak of 0.85 million hectares in 1999. The production in that year was 1.9 million ton (Anonymous, 1999). After that, wheat area started decline due to strong competition with high yielding boro rice, potato, maize and vegetable crops. In 2009-10, 1.07 million tons of wheat was produced from an area of 0.37 million hectares, and the yield was the ever highest 2.9 t/ha (Anonymous, 2010). Current requirement of wheat in the country is 3.0-3.5 million tons; moreover, wheat consumption is increasing @ 3% year⁻¹ (Sufian, 2005). In this situation, it is very important to increase wheat production in the country to reduce huge import costs. In India, improvement in its productivity has played a key role in making the country self-sufficient in wheat production. However, in the past decade there has been marginal increase in the productivity of wheat, particularly under environments relatively favorable for growth and development of wheat (Nagarajan, 2005; Joshi *et al.*, 2007).

Wheat is one of the major sources of carbohydrate. It covers about 4% of the total cropped areas of Bangladesh. Its productivity has prevented widespread food shortage and stabilized the food security of Asia, Latin America and to some extent, Africa. The unique of wheat in contrast to other cereals, except rye, is that its kernel contains a protein called gluten, which along with other quality attributes provides a wide away of end products. It provides more calories to human diet than any other crop. There is a considerable archaeological evidence for the long and close association between wheat and man.

Yield is a quantitative character that is controlled by a number of genes and thus it is considered as a complex trait. It is determined by a number of components with a growth developmental sequence (Grafius, 1978). Thus components produced earlier have an influence on those that are produced later in the plant's growth cycle.

Multilocation trials play an important role in plant breeding and agronomic research. Data from such trials have three main agricultural objectives: a) to accurately estimate and predict yield based on limited experimental data; b) to determine yield stability and the pattern of responses of genotypes or agronomic treatments across environments; and c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years and at new sites (Crossa, 1990).

Analysis of variance of multilocation trials is useful for estimating variance components related to different components for different sources of variation, including genotypes-environment interaction. Variance components have been widely used in genetics and plant breeding (Comstock and Moll, 1964; Cockerham, 1964; Gardner, 1964).

Plant breeders' aim is to develop new wheat cultivars that consistently have high yield in a variety of environments. The adaptability of a variety is usually tested by the degree of its interaction with different environments. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield with low degree of fluctuation in yielding ability grown over diverse climatic conditions. Genotype x Environment interaction does exist when phenotype made changes in the environment is not the same for all genotypes (Comstock and Moll, 1963).

The term GE interaction commonly refers to yield variation that cannot be explained by the genotype main effect (G) and the environment main effect (E). For cultivar evaluation, however, both G and GE must be considered

simultaneously. Using a sites regression model (SREG), Yan *et al.*, (2000) combined G and GE, denoted as G + GE or GGE, and repartitioned this into non crossover GE interaction and crossover GE interaction. The term GE interaction will be hereafter used to denote this combination. Understanding the causes of non crossover and crossover GE interaction would help develop an understanding of the genotypic characteristics that contribute to a superior cultivar, and the environmental factors that can manipulate to facilitate selection for such cultivars.

Genotype-environment interaction (GEI) is of great interest when evaluating the stability of breeding plants under different environmental conditions. The reliability of genotype performance across different environmental conditions can be an important consideration in plant breeding. Breeders are primarily concerned with high yielding and stable cultivars as much possible since cultivar development is a time consuming endeavor. A successfully developed new cultivar should have a stable performance and broad adaptation over a wide range of environments in addition to high yielding potential. Evaluating stability of performance and range of adaptation has become increasingly important for breeding programs. Hence, if cultivars are being selected for a large group of environments, stability and mean yield across all environments are important than yield for specific environments (Piepho, 1996).

Scientists define yield stability in many different ways and also use various stability measures to determine it. Blum (1980) defined yield stability as a measure of variation between potential and actual yield of genotypes across different environments. Fehr, (1987) stated that yield stability of a cultivar is influenced by the genotype of individual plants and the genetic relationship between plants. It can be measured through analysis of variance procedures and regression analysis. Domitruk *et al.*, (2001) indicated that the analysis of variance procedure is a useful tool for estimating the existence and magnitude of $g \times e$ interactions; however, the components of variances do not provide satisfactory explanation of the interaction. There are a number of suggested or proposed

methods that can be used for stability measurement. Yates & Cochran (1938) proposed a purely statistical analysis, which was later used by Finley & Wilkinson (1963) and Eberhart & Russell (1966). They used the analysis to detect and measure the magnitude of $g \times e$ interactions in barley and maize respectively.

Several biometrical methods including univariate and multivariate ones have been developed to assess stability. Between them the most widely used are the regression coefficient, the environmental variance, the Shukla's stability variance and Wricke's ecovalence. More recently, Purchase, (1997) developed the AMMI Stability Value (ASV) based on the AMMI (Additive Main Effect and Multiplicative Interaction) model's PCA1 and PCA2 (Principal Components Axis 1 and 2 respectively) scores for each cultivar. This ASV is in effect the distance from the coordinate point to the origin in a two dimensional scatter gram of PCA1 scores against PCA2 scores.

The practical interest of combining high levels of mean yield and yield stability has led to the development of the yield reliability concept, where a reliable genotype is characterized by consistently high yield across environments. The use of a yield reliability index facilitates genotype selection or recommendation, as the mean yield and the yield stability are combined into a unique measure of genotype merit.

The additive main effect and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach (Gauch, 1988). According to Gauch and Zobel (1988); Zobel *et al.* (1988) and Crossa *et al.* (1990), it can be used to analyze data of multilocation trials.

AMMI-analysis first fits the additive main effects of genotypes and environments by the usual analysis of variance, and then describes the non-additive part of genotypes- environment interaction by principle component analysis.

The AMMI method is used for three main purposes. The first is model diagnosis. AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool for diagnosing other models as sub cases when these are better for a particular data set (Bradu and Grabriel, 1978; Gauch, 1985). The second use of AMMI is to clarify genotype-environment interactions. AMMI summarizes pattern and relationships of genotypes and environments (Kempton, 1984; Zobel *et al.*, 1988; Crossa *et al.*, 1990). The third use is to improve the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al.*, 1988; Crossa *et al.*, 1990). Such gains may be used to reduce costs by reducing the number of replications, to include more treatments in the experiment, or to improve the efficiency in selecting the best genotypes. This last benefit has obvious implications for breeding programs and particularly for Maize hybrid testing systems, in which designs with fewer replicates per location are used (Bradley *et al.*, 1988).

The results can be graphically represented in an easily interpretable and informative biplot that shows both main effects and GEI. The AMMI model has been used extensively with great success over the past few years to analyze and understand various crop genotypes x environment interaction (Crossa, 1990; Yan, 1995; Yan and Hunt, 1998).

Gauch (1992) compared different methods of analyzing multilocal yield trial data. He describes the ANOVA, linear Regression, PCA, AMMI and shifted multiplicative model (SHMN). AMMI is the only model that distinguishes clearly between the main and interaction effect and this is usually desirable in order to make reliable yield estimations.

Different authors worked on wheat in Bangladesh (Sufian *et al.*, 1982, Parh and Khan, 1985, Sarker *et al.*, 1990, Barma *et al.*, 1994). But nobody performed stability analysis using AMMI model. This study with AMMI (Additive Main Effect and Multiplicative Interaction) model, in an analysis of wheat reveals a

highly significant interaction component that has clear agronomic meaning. It offers a more appropriate statistical analysis that may have a Genotypes x Environment interaction. In the present study experiments were conducted to evaluate the yield stability of 10 wheat genotypes in 10 different environments of 5 Wheat Research Stations of Bangladesh Agricultural Research Institute and to determine the nature of G x E interaction.

Objectives of this study

1. To identify the genotypes suitable all over the locations.
2. To know the appropriate locations and climate conditions to achieve higher yield in wheat.
3. To recommend the outstanding genotypes with wide or specific adaptation.

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

The terms phenotypic stability, yield stability and adaptation are often used in quite different senses. Different concepts and definitions of stability have been described over the years (Lin *et al.*, 1986; Becker and Léon, 1988). The first authors to conceptualize the stability analysis were Yates & Cochran (1938). They understood the potential to differentially recommend varieties based on their performance in different environments. Using environments that are of extreme conditions may be of value when evaluating genotypes for yield stability.

Lin *et al.* (1986) identified three concepts of stability:

Type 1: A genotype is considered to be stable if its among-environment variances small. Becker and Léon, (1988) called this stability a static, or a biological concept of stability. A stable genotype possesses an unchanged performance regardless of any variation of the environmental conditions. This concept of stability is useful for quality traits, disease resistance, or for stress characters like winter hardiness. Parameters used to describe this type of stability are coefficient of variability (CV_i) used by Francis and Kannenburg (1978) for each genotype as a stability parameter and the genotypic variances across environments (S_i^2).

Type 2: A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial. Becker and Léon, (1988) called this stability the dynamic or agronomic concept of stability. A stable genotype has no deviations from the general response to environments and thus permits a predictable response to environments. A regression coefficient (b_i) (Finlay and Wilkinson, 1963) and Shukla's (1972) stability variance (σ^2_{2i}) can be used to measure type 2 stability.

Type 3: A genotype is considered to be stable if the residual MS from the regression model on the environmental index is small. The environmental index implicates the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. Type 3 is also part of the dynamic or agronomic stability concept according Becker and Léon (1988). Methods to describe type 3 stability are the methods of Eberhart and Russell (1966) and Perkins and Jinks (1968). Becker and Leon (1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance, procedures using the regression approach such as proposed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968), as well as non-parametric stability analyses.

Stability of quality attributes is important in terms of changing ranks of genotypes across environments and affects selection efficiency (Rharrabti *et al.*, 2003a; Korkut *et al.*, 2007). For end users, such as millers and bakers, consistency in quality performance of genotypes is very important, regardless of changing genotype ranks (Korkut *et al.*, 2007).

Stability of raw material quality is a desirable feature, since it guarantees consistent procedures and reduces product loss during processing (Grausgruber *et al.*, 2000).

Stability of quality characters is also important in increasing variety selection efficiency According to Eberhart & Russell (1966), to obtain useful information for stability parameters, cultivars must be grown in various localities. Assessing a cultivar's suitability for a given environment is based on its yield stability at the environment, yielding ability/potential; days to maturity etcetera are a number of measures that are used for studying the stability of genotypes in the presence of $g \times e$ interaction.

Becker and Léon (1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance, procedures using the regression approach such as proposed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968), as well as non-parametric stability analyses.

Lin *et al.* (1986); Becker and Léon (1988), Crossa (1990) and Hohls (1995) discussed a wide range of methods available for the analysis of GEI and stability and it can be divided into four groups: 1) the analysis of components of variance, 2) stability analysis, 3) qualitative methods and 4) multivariate methods. Plant breeders generally agree on the importance of high yield stability, but there is less accord on the most appropriate definition of "stability" and the methods to measure and to improve yield stability (Becker and Léon, 1988).

The genotype of an individual is determined by its genotypes and its surrounding environment. Environment includes physical, chemical and biological factors, which control the growth and development of an individual (Dabholkar, 1992). The phenotypic response to different environments may be different for all the genotypes, therefore, the consequences of variation in phenotype being dependent upon environment.

The interplay of genetic and non genetic factors on development was termed by Comstock and Moll (1963) as "genotype-environment interaction".

Dixon *et al.* (1994) stated that $g \times e$ interaction is the change in a cultivar's relative performance over environments, which results from differential response of the cultivar, to various edaphic, climatic and biotic factors. $G \times E$ interaction occurs in two ways. Firstly the difference between genotypes vary without alteration in their rank i.e. $G \times E$ interaction is present because one cultivar yields more than another cultivar in all the environments, and secondly the ranking

between cultivars changes across environments i.e. one cultivar will be more productive in one environment, while the other cultivar is more productive in another environment.

The phenotype of an individual is determined by both the genotype and the environment, these two effects are not always additive which indicates that genotype x environment interactions (GEI) are present. The GEI result in inconsistent performances between the genotypes across environments. Significant GEI results from the changes in the magnitude of differences between genotypes in different environments or changes in the relative ranking of the genotype (Falconer, 1952; Fernandez, 1991).

A genotype is therefore considered to be economically stable if its contribution to the genotype x environment interaction (GEI) is low (Rharrabti *et al.*, 2003a).

GE interaction can be an outcome of genotype rank changes from one environment to another, a difference in scale among environment, or a combination of these phenomena (Mohamadi *et al.*, 2007). If the relative performances are highly different, then GE interaction becomes a major challenging factor to crop breeding programs (Zobel and Talbert, 1984). In such cases, the breeder is faced either with developing specific breeding populations for each environment and/or with selecting genotypes that generally perform well across many environments (Isik and Kleinschmit, 2005) some genotypes are adapted have been widely used. Genotype with low co-efficient (b_i) either show, specific adaptation on little variation with environment; those genotypes with high slopes (b_i) are more responsive to environments (Lin *et al.*, 1986; Simmonds, 1991).

GEI makes it difficult to select the best performing and most stable genotypes and is an important consideration in plant breeding programs because it reduces the progress from selection in any one environment (Hill, 1975; Yau, 1995).

The genotype x environment interaction is important for plant breeding because it affects the genetic gain and recommendation and selection of cultivars with wide adaptability (Deitos *et al.* 2006, Souza *et al.* 2009). On the other hand, different genotypes have different performance in each region that can be capitalized to maximize productivity (Souza *et al.* 2008). Eberhart and Russell (1966) developed a methodology for identifying cultivars with greater adaptability and stability that has been widely used in the identification of genotypes for this purpose (Miranda *et al.* 1998, Grunvald *et al.* 2008). However, other methods for identifying cultivars with adaptability and stability have been developed and many multivariate techniques are available such as GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative Interaction) with new information for cultivars, environmental stratification and cultivar x environment interaction (Miranda *et al.* 2009).

Gauch (1985,1988) emphasized the model's success in predicting validation data (prediction criteria). Because multilocation trials are used for selecting in fitting its own data (post diction criteria). Because multilocation trials are used for selecting genotype or agronomic treatments for farmer's fields in new environments, model evaluation should measure predictive success. Gauch proposed that AMMI analysis be used with prediction criterion.

The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure (Shafii *et al.* 1992; Shafii and Price 1998). The AMMI biplot analysis is considered to be an effective tool to diagnose the GEI patterns graphically. In AMMI, the additive portion is separated from interaction by analysis of variance (ANOVA). Then the principal components analysis (PCA), which provides a multiplicative model (Gabriel 1971; Zobel *et al.* 1988), is applied to analyze the interaction effect from the additive ANOVA model.

The AMMI model has a good chance of predicting yield for new sites and years, giving a real advantage (Gauch, 1988). It is a multivariate analysis that is effective for many yield trials. These analyses partition the treatment degrees of freedom into model and residual. The model selectively recovers pattern while the residual selectively recovers noise (Gauch, 1988; 1990), resulting in adjusted treatment means that are predicatively more accurate than the unadjusted means (Gauch & Zobel, 1988; 1989). The AMMI addresses the treatment design and does not require any kind of experimental design; therefore it can be collected under any design and used for on going decisions. It gives more accurate results than any other methods used for stability analysis. With this model, researchers can extract between environments.

The AMMI model combines regular analysis of variance for additive effects with principal component analysis (PCA) for multiplicative structure within the interaction. AMMI also provides a visual representation of patterns in the data through a biplot that makes use of the first interaction principal component axis (IPCA1) and the mean yields of both the genotypes and environments (Nachit *et al.*, 1992).

Additive Main Effect and Multiplicative Interaction (AMMI) effective for understanding the $G \times E$ interaction, improving the accuracy of yield estimates, increasing the probability of successfully selecting genotypes with the highest yields, imputing of missing data and increasing the flexibility and efficiency of experimental designs (Dixon and Nukenine, 1997).

An algorithm for inputting missing values and the fitting the additive main effect and multiplicative interaction (AMMI) model has recently been developed (Gauch and Zobel, 1990).

Hugh G. and Gauch, Jr. (2006) described the Additive Main effects and Multiplicative Interaction (AMMI) model, Genotype main effects and Genotype x Environment interaction (GGE) model, and Principal Components Analysis (PCA) are singular value decomposition (SVD) based statistical analyses often applied to yield-trial data. Agricultural researchers using the analysis face two inevitable choices. First is the choice of a model for visualizing data. AMMI is decidedly superior, not for statistical reasons, but rather for agricultural reasons. AMMI partitions the overall variation into genotype main effects, environment main effects, and genotype x environment interactions. These three sources of variations present agricultural researchers with different challenges and opportunities, so it is best to handle them separately, while still considering all three in an integrated manner. Second is the choice of a member of a given model family for gaining predictive accuracy. AMMI, GGE, and other SVD-based model families are essentially equivalent, but best practices require model diagnosis for each individual dataset to determine which member is most predictively accurate. Making these two choices well allows researchers to extract more usable information from their data, thereby increasing efficiency and accelerating progress.

Some studies on Sunflower have also been done. Fick and Zimmer (1976) found that the stability of yield performance of cultivar is under genetic control. They also found that some inbred lines tend to contribute more to the stability of hybrids than other, which shows that the genotype contributes to some extent to yield stability.

Kempton (1984) used AMMI analysis for Summarizing the pattern of genotype responses across environments with different levels of nitrogen. The first principal component is the axis that maximizes the variation among genotypes. The second principal component is perpendicular to the first and maximizes the remaining variation. The display of the genotypes and the environments along the first two principal component axes for the interaction table of residuals is called the biplot (Gabriel, 1971, 1981).

Baker (1988) studied on G x E interactions of crossover type in particular, are considered to have a negative impact on the success of breeding programs, because breeders search for a few widely adapted cultivars. GEI become important when the rank of breeding lines changes in different environments.

Zobel *et al.* (1988) and Crossa *et al.* (1990) used the AMMI model to analyze a series of soybean and maize trials, respectively. Additive main effect for genotype and environments are first fitted by the analysis of variance. Then, multiplicative effects for genotype interaction are calculated by principal components analysis. The biplot of the model helps to visualize the overall pattern of response as well as specific interactions between genotypes and environments.

Zobel *et al.* (1988) presented analysis of variance and principal component analysis for seven soybean genotypes yield-tested in 35 environments. The genotype by environment interaction sum of squares of the analysis of variance was large but not significant. The principal components analysis with the first three principal axes accounting for 76% of the variation is found to be statistically efficient but undesirable for describing the additive main effects.

Anderson and Smith (1990) found that in May sowing, harvest indices were greatest for the semi-dwarf cv. Aroona, but for June sowing the harvest indices for tall cultivars equaled or exceeded those of semi-dwarf cultivars.

Baker (1990) reported that significant crossover genotype x environment interactions were observed for yield and days to maturity, after study with 4 semi-dwarf Wheat cultivars.

Misra & Panda (1990) reported that inconsistent yield performance of cultivars in different environments may be a contributing factor to productivity due to large g x e interaction

Crossa *et al.* (1991) investigated procedures for improving predictive success of a yield trial, grouping environments and genotypes into homogeneous subsets, and determining the yield stability of 18 CIMMYT bread wheat genotypes evaluated at 25 locations. They reported that Additive Main effects and Multiplicative Interaction (AMMI) analysis gave more precise estimates of genotypic yields within locations than means across replicates. This precision facilitated formation by cluster analysis of more cohesive groups of genotypes and locations for biological interpretation of interactions than occurred with unadjusted means. Locations were clustered into two subsets for which genotypes with positive interactions manifested in high, stable yields were identified. The analyses highlighted superior selections with both broad and specific adaptation.

Xu *et al.* (1991) found that sowing between 24 Oct. and 17 Nov., the yield was highest at 275 kg/mu with sowing on 1 Nov. and lowest 257 kg with the latest sowing date. [1 mu=0.067 ha].

Stability for yield and yield components were studied by Liu (1992) with six varieties of rice in 1990. Jhingua-101 gave the highest yield and had the best adaptability, but there was no correlation between yield and stability indicating that the genes controlling yield and yield stability are independent. The result suggests that in breeding for yield stability, the priority should give to grain number per panicle and the second 1000-grain weight.

Nachit *et al.* (1992) observed that multilocation testing produces significant genotype-environment (GE) interaction that reduces the accuracy for estimating yield and selecting appropriate germplasm. The sum of squares (SS) of GE interaction was partitioned by linear regression techniques into joint, genotypic, and environmental regressions, and by Additive Main effects and the Multiplicative Interactions (AMMI) model in to five significant Interaction Principal Component Axes (IPCA). The AMMI model was more effective in partitioning the interaction SS than the linear regression technique. The SS contained in the AMMI model was 6 times higher than the SS for all three

regressions. Postdictive assessment recommended the use of the first five IPCA axes, while predictive assessment AMMI1 (main effects plus IPCA1). After elimination of random variation, AMMI1 estimates for genotypic yields within sites were more precise than unadjusted means.

Additive Main effect and Multiplicative Interaction (AMMI) model (Gauch, 1993) was used for testing the stability of the bean lines. This model is more efficient in determining the most stable and high yielding genotypes in multi-environment trials compared to other methods.

May and Kozub (1993) did research in Canada on barley to establish whether the selection of genotypes based on $G \times E$ interaction main effects would differ from those made on main effects alone. They found no single genotypes were superior over all nine test sites used, and the grouping of genotypes for similarity of response at locations was not consistent over years. This indicated that genotypes selected on main effects alone, may differ from those selected when the $G \times E$ interaction is taken into account.

Royo *et al.* (1993) studied adaptation of seven complete and twelve substituted triticale to specific soil types based on a series of twenty trials carried out in 1989 and 1990 across Spain. The percentage of the variability explained by the first principal component axis of the AMMI model was 72 and 65 % for the two years, suggesting a specific pattern of adaptation. Soil pH was the single most important environmental factor to explain the adaptation of complete and substituted types. Complete triticale out yielded substituted genotypes in the majority of sites. Complete triticale seem better adapted to the acid soils, whereas substituted types are, in general, more suited to alkaline soils.

Barma, *et al.* (1994) conducted an experiment on twenty genotype of bread wheat were evaluated at three locations. Genotype $\times$ location interaction vis-à-vis stability was studied for days to maturity and grain yield. Genotypes, location and

G x E interactions were found significant for both traits. Significant genotypes x environment (linear) interactions also occurred for maturity and yield indicating different response among the genotypes. Estimated stability parameters (b_i and S^2d_i) for days to maturity indicated that the lines BAW-80, BAW-109, and BAW-166 with least response to environment ($b_i=1.0$) and minimum deviation from regression ($S^2d_i=0$) were found stable over locations. However, high yielding genotypes, BAW-78, BAW-87, BAW-106, BAW-121 and Kanchan were highly sensitive ($b_i>1.0$) to location changes having minimum environment. Only two genotypes (BAW-86 & BAW-189) were found stable with poor adaptability having positive slope close to unity ($b_i=1.0$) and non-significant deviation from regression ($S^2d_i=0$) were found suitable only for unfavorable environments.

Linnemann *et al.* (1995) stated that GE interaction is important to understand crop development in relation to biophysical conditions and changes in season when selecting well-adapted genotypes and correct planting date. Varieties that show low gxe interaction and have high stable yields are desirable for crop breeders and farmers, because that indicates that the environment has less effect on them and their higher yields are largely due to their genetic composition. Therefore, introduction of bambara groundnut varieties That have a high yield and are stable over a wide range of environments will be a bonus to scientists and farmers (Tai, 1971).

Sing *et al.* (1995) evaluated 20 rice genotypes under 3 sowing dates and found significant differences due to genotypes, environments and their interaction for days to 50% flowering , plant height , grain weight and grain yield. The linear component of G xE interaction was important for grain weight and grain yields, whereas the non linear component was significant for all traits. The genotype IET 7970 showed general stability for grain yield and earliness with a high level of performance and suitability for grain yield and earliness with a high level of performance and suitability for rainfed lowland condition.

Iriki (1998) reported the genotype x environment interaction predominantly affected protein content suggesting that several cycles of selection would be required for the improvement of protein content.

Moustafa *et al.*, (1998) reported that 18 selected genotypes, including 10 F3 and 3 lines were evaluated for 8 characters under 2 sowing dates and it was found that delayed sowing had amore pronounced effect on grain filling than vegetative period and had an overall stronger influence on grain yield.

Nerozzi *et al.* (1998) reported that sensitivity analysis showed for Wheat that a delay in sowing had little effect on days of spike development or physiological maturity.

Karim *et al.* (1999) reported that in a field trial in Gazipur, Bangladesh, Wheat sown on 4 December 1995 or 4 January 1996 and it was found that grain yield and grain weight reduced by delay sowing. Similar result was observed by Sanjeev *et al.*, (1999) in India.

Lathwal and Thakral (1999) found that plant height ,grain yield, straw yield, and harvest index decreases with the delay sowing .An increase of 48 and 39% in grain yield was observed from 5 and 15 November sowing compared with 5 December. They also proposed that the differences were not statistically significant.

In South Africa, Laubscher, *et al.*(2000) found that minimum night temperature, which determines the rate of development of certain physiological stages in Maize, was a major contributor to G x E interaction .G x E interaction in potatoes (Steyn, *et al.*1993) Lucerne (Smith and Smith,1992)and Soybean (Smith and de Been, 1991) have been found . G x E interaction in Wheat in South Africa was reported by purchase, *et al.* (2000 a & b). They found that the wheat hybrids and long growth period purchase cultivars had a superior adaptation to high yield

potential conditions .While the short & medium growth period of pureline cultivars were better adapted to lower yield potential conditions.

Ragastis (2000) found that the sowing date significantly affected the grain yield more than the grain quality which was also found by Calderin *et al.* (1999).

Thakar *et al.* (2000) found that the sowing date significantly affected the grain yield and other ancillary characters of Wheat .The highest grain yield (52.0q/ha) was obtained by sowing on 1 December. A significant reduction of 34.4% in grain yield was observed upon delay in sowing from 1 December to 10 January. Reduction in the number in the grain per ear, 1000 grain weight and straw yield of late sown Wheat was observed.

Qayyum *et al.* (2000) performed stability analysis of six rice genotypes, tested five locations. They found the while genotype x location interaction was insignificant the regression coefficient (b_i) and small deviation from regression (S^2_{di}) were significant for all genotypes except Pak-4554 and Basmati-385. Basmati-385 performed best at all locations with average stability.

In an experiments conducted during 1998 and 1991 in Japan, spike development was evaluated in early sown winter Wheat 'Iwainodaichi' , and its relationship with spike traits , such as spikelets number , florets number , grain number, mean grain weight and grain per spike were compared with those in late sown 'Iwainodaichi' and spring Wheat 'Chikugoizumi'. Grain number per spike was found to be smaller in the earlier sowing reported by Fukushima *et al.* (2001).

Babar, *et al.* (2001) evaluated fourteen bread wheat genotypes were evaluated in four different environmental locations viz., Dinajpur, Joydebpur, Jessore and Jamalpur in 1997-1998 to study their genotype x location interaction and stability for grain yield and 1000 grain weights (TGW).Significant differences were observed for genotypes, location genotype x location interaction. Dinajpur

location was the most favorable one for grain yield and TGW, Whereas, Jessore location was the most unfavorable one. Based on phenotypic indices (π), regression coefficient (b_i) and deviation from regression (s^2_{di}); Kanchan and BAW 904 were found most stable and desirable genotypes; the highest yielder BAW 936 and BAW 926 were suitable for better environment and BAW 918 for poor environment. There was a negative relationship between better mean performance and stability.

Mardariya *et al.* (2001) studied with fifty Wheat genotypes under three sowing conditions in Junagadh, Gujarats, India and observed that linear and nonlinear components of genotype x environment interaction were significant for grain yield per plant, number of spikelets per spike, number of grains per spike and 1000-grain weight. For the number of effective tillers per plant, only the linear component was significant.

Duration of grain filling in 16 bread wheat cultivars grown in nine environments was studied by Robert *et al.* (2001). They reported that there were significant cultivar, environment and cultivar x environment effects for duration of grain filling, yield, grain protein concentration, kernel weight and nitrogen amount in the grain.

Yan and Hunt (2001) found that understanding of the causes of genotype x environment (GE) interaction can help identify traits that contribute to better cultivar performance and environments that facilitate cultivar evaluation. Through subjecting environment-centered yield of a multi-environment trial data to singular value decomposition, the portion of yield variation that is relevant to cultivar evaluation is partitioned into non crossover and crossover GE interaction, quantified by the first two principal components (PC), respectively. Each PC is a set of genotypic scores multiplied by a set of environmental scores. By relating the PC scores to genotypic and environmental covariates, GE interaction represented by each PC can be interpreted in terms of trait x factor interactions. This strategy

was employed in analysis of the 1992 to 1998 Ontario winter wheat (*Triticum aestivum* L.) performance trial data. Results indicated that plant height and maturity were the major genotypic causes of GE interaction, whereas cold temperature in the winter and hot temperature in the summer were the major environmental causes of GE interaction. Positive interactions were found between earlier maturity vs. warmer winters or hotter summers, and between shorter plant height vs. warmer winters or cooler summers. The results of this study should help in determining breeding objectives and for selecting test sites or environments for winter wheat breeding in Ontario.

Kaya, *et al.*, (2002) carried out this study to determine the yield performances of 20 bread wheat genotypes across six environments in Central Anatolia, Turkey, in the 2000-2001 growing season. The experimental layout was a randomized complete block design with four replications. Additive main effects and multiplicative interactions analysis (AMMI) indicated that the yield performances of genotypes were under the major environmental effects of genotype by environmental interactions. The first two principal component axes (PCA 1 and 2) were significant ($p < 0.01$) and cumulatively contributed to 78.64% of the total genotype by environment interaction. A biplot generated using genotypic and environmental scores of the first two AMMI components also showed that genotypes with larger PCA 1 and lower PCA 2 scores gave high yields (stable genotypes), and genotypes with lower PCA 1 and larger PCA 2 scores had low yields (unstable genotypes), as in the sites tested.

Ten Wheat cultivars were evaluated for stability in Jammu and Kashmir, India, by Mondal and Khajuria (2002). Results indicated significant genetic variation in terms of genotype-environment interaction for yield and other characters.

Mahak *et al.* (2002) conducted an experiment in Uttar Pradesh, India and found that mean yield differences between genotypes and genotype x environment interaction were highly significant for all the characters (days to reproductive

phase, flag leaf area, plant height, biological yield per spike, number of grains per spike, weight of grains, 1000-grain weight, economic yield and harvest index). The linear component of interaction was significant for all traits. High magnitude of environmental effects in the genotype-environment interaction was recorded.

Nurminiemi *et al.* (2002) analyzed the genotype-by-environment interaction of spring barley. Combined analysis of variance across locations indicated that both environments and genotype by environment interactions influenced significantly the cultivar phenotypes for all characteristics, irrespective of their type (row number) or earliness. The first two interaction principal component axes of the additive-main-effects-and-multiplicative-interaction (AMMI) model accounted together between 35% and 75% of the total genotype-by-environment interaction for all characteristics. Grain yield was, on average, higher in 2-row than in 6-row cultivars, which were significantly earlier in heading and grain maturity than the former. The genotype by location interaction variance accounted by each genotype was significantly associated to the deviation from regression, while the coefficient of regression was significantly correlated to the IPCA1 and IPCA2 of the AMMI model.

Durum Wheat (*Triticum durum*) genotypes were evaluated for stability and significant genotype- environment interaction was found for yield by Ozberk and Ozberk (2002).

Munyuli (2002) found that the differences between environments, genotypes and cropping season were significant for grain yield. The effects of genotype-environment interaction on grain yield were significant.

Patil *et al.* (2003) conducted an experiment during Rabi 1999-2000 in Akola, Maharashtra, India, involving 6 early Wheat cultivars and 5 sowing dates. The total biomass at maturity, grain number per spike, 1000-grain weight and yield/m² decreased significantly with delay in sowing.

Narendranath and Mohanty (2003) conducted an experiment using late sowing practice in two Wheat cultivars to examine the effects on grain yield and found that the grain weight declined in late sown plants of both cultivars, but the number of grains p decreased drastically.

Shanmuganathan *et al.* (2004) analyzed stability for yield in rice hybrid by AMMI model. Combined analysis of variance showed that environment, genotype and G x E interaction were highly significant, suggesting a broad range of genotypic diversity and environmental variation. The AMMI showed that CORH1, KRRH1 and PHB71 have general adaptability, while PSD1, ADTRH1 and KRH2 have specific adaptability. The AMMI model also identified the environment at the Agricultural College and Research Institute in Madurai during Kharif 2000 as the ideal environment.

Madry *et al.* (2006) studied performance of advanced winter wheat lines for grain yield across environments by AMMI analysis. The AMMI analysis was useful and efficient to study stability of genotypes, their adaptation (adaptive response) and grouping locations and genotypes with similar GE interaction effects. Genotypes MOB3926/99 and MOB3191 were specifically adapted to environment in Szelejewie (SZD), in Polanowice (POB) genotypes HRSM91 and KOC1437/01 were preferred, genotypes POB654/95, STH5338, AND418/99 and CHD342/98 were well adapted to environment in Strzelce (STH); genotype POB654/95 was locally adapted to Polanowice (POB), genotypes MOB3977/99 and STH1427 were specifically high productive in Kobierzyce, (KOC), in mega-environment consisted of DED, SMH and NAD genotypes POB126/00 and SMH6847 were locally relatively best yielding.

Rosella Motzo *et al.* (2006) carried out a Multi Environmental Trial with 14 lines of spring triticale ($\times$ *Triticosecale* Wittmack) was in a Mediterranean environment. Yield, yield components and heading date were used to perform an Additive Main effects and Multiplicative Interaction (AMMI) analysis.

Correlations between Interaction Principal Component Axis (IPCA) scores and environmental and genotypic variables showed that genotype by environment interaction for yield and kernels per m² are related to interaction for phenology but not to the yield level. Yield level was significantly correlated with the water availability. Genotype by environment interaction for yield is mainly determined by thermal conditions in the pre-anthesis period, genotypic photoperiodic sensitivity and sowing time.

Tarakanovas and Ruzgas (2006) worked on stability of winter wheat (*Triticum aestivum* L.) varieties across 4 locations and 2 years with respect to grain yield were tested in Lithuania. The analysis of variance of the 13 varieties in 8 environments shows that genotype (G) location (L), crop year (Y) and their interaction were significant ($p < 0.01$) for winter grain yield. Highly significant G x L effects indicated the necessity for testing wheat varieties in Lithuania at multiple locations. It shows that AMMI (Additive Main Effect Multiplicative Interaction) model was effective for studying winter wheat genotype – environment interaction (GEI).

W. Li, *et al.* (2006) studied to estimate the genotype (G), environment (E) and genotype x environment (GE) interaction on the grain yield of Chinese spring wheat genotypes in 2000-2001 by additive Main Effects and Multiplicative interaction (AMMI) model and to evaluate the relationships between yield and its components by correlation and path analysis. Grain yield varied from 3.9 to 5.2 t/ha, among which SW8188 had the highest yield performance, followed by 58769-6 and Chuannong 16. Three interaction principal components (IPC) accounted for a total of 79.99% and 72.96% of the interaction with 41.05% and 52.08% for the corresponding degrees of freedom in 2000 and 2001, respectively. When IPCA3 was significant, the stability coefficient D_i was more 1.804 to 14.665 and 2.497 to 12.481 in 2000 and 2001 respectively. The suitable locations (environment) for all genotypes were characterized. These would be useful for improving the Chinese spring wheat cultivation and improvement.

Lavoranti *et al.* (2007) evaluated phenotypic stability of 20 *Eucalyptus grandis* progenies from Australia that were planted in seven environments in the Southern and Southeastern regions of Brazil. The results showed distinct behaviors of genotypes and environments and the genotype x environment interaction was significant (p value <0.01). The bootstrap coefficient of stability based on the squared Mahalanobis distance of the scores showed that genotypes and environments can be differentiated in terms of their stabilities. Graphical analysis of the AMMI biplot provided a better understanding of the interpretation of phenotypic stability. The proposed AMMI bootstrap eliminated the uncertainties regarding the identification of low scores in traditional analyses.

Maric *et al.* (2007) worked on selection of testing environments for winter wheat breeding. The main effects due to year, location, year x location, genotypes, genotypes x year, genotype x location, genotype x year x location were all highly significant for grain yield. Average wheat yield and coefficient of variation through trial locations indicate stability of Zupanja. Osijek had highest variability for yield while Nova Gradiska had high variability and lowest yield. Stability estimate with AMMI model identified Nova Gradiska as the location with highest stability, while Kutjevo showed the lowest stability. There were no significant correlations between stability parameters and average yield on the test locations.

Rao *et al.* (2007) conducted a study to determine the nature and magnitude of genotype x environment interaction effect on the seed yield of pigeon pea in diverse production environments to identify high yielding and stable genotypes. AMMI analysis indicated highly significant variance for genotypes, environments and G x E interactions. Out of the total variation, the proportion of variance due to differences in environmental factors was largest (78.43%), followed by variance due to G x E interaction (20.70%) and genotypes (0.87%). Variance due to G x E interaction was partitioned into three PCA axes, with contribution of 31.05%, 21.24% and 16.95% to the total G x E interaction variance. According to the

AMMI model, genotypes which are characterized by mean greater than the grand mean and the PCA scores nearly zero are considered as generally adaptable to all the environments. However, genotypes with high mean performance and large value of IPCA scores are considered as having specific adaptability to the environments.

Hugo Ferney *et al.* (2007) was carried out an investigation to determine the stability and adaptability patterns of a set of 40 promising spring wheat genotypes from Kazakhstan and Siberia evaluated in a multi-environment yield trial across 22 environments. Some of the most widely known parametric stability parameters were used as well as the less frequently cited reliability index (I). Grain yield correlated significantly and positively with the stability parameters b and S2 and the reliability index (I); but did not correlate with AMMI ASV. However, the stability parameters failed in detecting adaptability patterns. In contrast, the reliability index (I) was probed to be more useful in supporting practical decisions. With regard to the genotypes, cultivars Lutescens 54, Lutescens 30-94, Lutescens 29-94, Tertsia, Omskaya 35, and Shortandynskaya 95 showed to be the widest adapted and the most reliable cultivars.

Reza Mohammadi, *et al.* (2007) studied an experiment on winter wheat to explore the effect of genotype and genotype x location interaction on the grain yield, data of 20 winter wheat genotypes selected from Iran/ICARDA joint project grown in six locations via GGL (genotype plus genotype x location) biplot methodology. The results of this study indicate the possibility of improving progress from selections under diverse location conditions by applying the GGL biplot methodology.

Mulusew Fikere *et al.* (2008) worked on grain yield of 16 faba bean (*Vicia faba L.*) genotypes tested in a Randomized Complete Block Design (RCBD) with four replications across 12 environments during 2004-2006 growing season of South Eastern Ethiopia was analyzed using parametric stability measures. The objectives

were to assess the genotype environment interactions (GEI), determine stable genotypes, and compare mean yield with the parametric stability parameters. To quantify yield stability seven stability statistics were calculated (ASV, CVi, S2di, Wi2, σ^2 , S2di and bi). EH 94050-2 and EH 9200-ov 4-2-1 were more stable genotypes which has 7 out of 7 stability statistics used in the study. Moreover, the stability analysis identified genotype EH 94050-2 (genotype 7) and EH 9200-ov 4-2-1 (genotype 12) as most stable genotypes and recommended for commercial production in the South East Ethiopia. Highly significant correlations were found among stability parameters implying their closer similarity and effectiveness in detecting stable genotypes and they are equivalent in measuring stability. Hence, any one of these stability parameters could be used to describe genotypes stability.

Admassu *et al.* (2008) tested fifteen maize genotypes at nine different locations in 2005 under rainfed condition to determine stable maize genotypes for grain yield and determine genotypes with high yield and form homogenous grouping of environments and genotypes. Stability was estimated using the Additive Main Effects and Multiplicative Interactions (AMMI). Based on the stability analysis, genotypes 30H83, BH-540, Ambo Synth-1, AMH-800 and BHQP-543 were found to be stable for grain yield. The first two Interaction Principal Component axis (IPCA1 and IPCA2) were significant ($p < 0.01$) and cumulatively contributed 70.27% of the total genotype by environment interaction. The coefficient of determination (R^2) for genotypes 30H83 was as high as 0.92, confirming its high predictability to stability.

Zali *et al.* (2008) carried out an investigation to determine the stability and adaptability of grain yield of 17 chickpea genotypes across environments. The genotype x environment interaction effect analyzed using the additive main effects and multiplicative interaction (AMMI) statistical model was significant at 1% level of probability. The sum of squares of G x E interaction was partitioned by AMMI model into four significant interaction principal component axes

(IPCA). The first four principal component axes (IPCA 1, 2, 3 and 4) cumulatively contributed to 94% of total genotype by environment interaction. A biplot generated using genotypic and environmental scores of the first two AMMI components also showed that genotypes FLIP 97-79, X95TH1 and FLIP 97-114 were selected as stable genotypes, among which the genotype FLIP 97-114 was outstanding for high yield stability.

Sayyed Saeid Pourdad and Reza Mohammadi (2008) conducted an experiment on some phenotypic stability parameters; ecovalence (W^2_i) regression coefficient (b_i), coefficient of determination (R^2_i), coefficient of variation (CV_i), stability variance (S^2_i) AMMI stability value (ASVi) and TOP (proportion of environments in which a genotype ranked in the top third), were used to select among 17 spring Safflower genotypes for yield performance and stability simultaneously across 26 environments under rainfed conditions of Iran during growing seasons 2004-2006. The results of AMMI analysis showed that 83.78% of the total sum of square (SS) was attributable to environments effects, only 1.37 and 14.85% to genotype and GE interaction effects, respectively. The results showed none of the parametric statistics per se was useful for selecting high yielding and stable genotypes. G9, G10 and G11 were the best whereas the G1 and G17 with the highest yield performance were the most instable. In conclusion, both of yield and stability should be considered simultaneously to exploit the useful effect of GE interaction and to make selection of the genotypes more precise and refined.

Misra *et al.* (2009) conducted multilocation yield trials on late duration (106-125 days) finger millet genotypes under early and late transplanting at Bhubaneswar and early direct-sown condition at Berhampur for three years 2004-2006, during *Kharif* season. $G \times E$ interaction analysis of grain yield in AMMI (Additive Main and Multiplicative Interaction) model showed differential interaction of the genotypes in the 3 planting conditions. IPCA-1 explained 93% of $G \times E$ interaction. AMMI $G \times E$ interaction study showed that OEB 56, OEB 71 and VR 822 had high mean and positive interaction, while PES 110 had high mean and very low interaction. On basis of AMMI II predicted yield, the genotypes OEB 56

and OEB 71 were better suited for early transplanting at Bhubaneswar and early direct-sown condition at Berhampur. The genotype PES 110 showed better adaptation to both early and late transplanting conditions at Bhubaneswar. Six other genotypes showed specific adaptation to single environment only, of which Chilika ranked first under late transplanting at Bhubaneswar and VR 822 ranked first under early direct sown condition at Berhampur, indicating specific adaptation.

Heraldo Namorato, *et al*, (2009) was studied to compare the multivariate methods GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative Interaction) with the method of Eberhart and Russell for interpreting genotype x environment interaction. The AMMI and GGE analysis explained around 50% of the sum of squares of the genotype x environment interaction, whereas the method of Eberhart and Russell explained only 9.1 and 15.8% each year. The cultivars classified as minor contribution to the genotype x environment interaction by methods of AMMI and GGE were also the same classification method of Eberhart and Russell. The AMMI and the GGE biplot analyses are more efficient than the Eberhart and Russell. The GGE biplot explains a higher proportion of the sum of squares of the GxE interaction and is more informative with regards to environments and cultivar performance than the AMMI analysis.

Anandan, *et al*. (2009) evaluate their germplasm in multi-environment to study the performance and adaptation for specific or general environment. The objective of the present investigation was to analyze the pattern of Genotype x Environment (G x E) interaction for grain yield of 46 genotypes by Additive Main effects and Multiplicative Interaction (AMMI) model using the data generated from three saline stress environments of east coastal region of Tamil Nadu, India. The results showed highly significant genotypic and G x E interaction. The G x E interaction influenced the relative ranking of the genotypes across saline stress environment condition. Among the genotypes tested, G45, G26, G27 G35 and G34 showed low

interaction effect, with score nearest to zero with above average yield. While two genotypes, G36 and G19 exhibited high positive interaction effect, gave the highest mean grain yield and is better suited to favorable environment. Similarly, AMMI characterized the environments and identified E2 as a favorable environment for the better expression of the trait studied.

Zenebe Mekonnen *et al.* (2009) conducted an experiment on seed yield stability of twenty sesame genotypes of different sources. Combined analysis of variance showed highly significant ($p < 0.01$) difference for the main and interaction effect for the trait studied. AMMI stability analysis methods were used to further shed light on the GEI of seed yield. Two IPCA of AMMI were significant ($P < 0.01$) and captured the largest portion of variation of the total GEI for the trait studied, which indicated that the AMMI model 2 was the best for the data set. Genotypes Temax (1), Acc 051 02 sel 6 (7), Clusu 5 (13), Kelafo 74 (20), NN 0136 sel 2 (6), Acc 212 332 4 (8), Addi (9), and Acc 051 02 sel 10 (11) were the only genotypes showed relatively little GxE interaction in terms of both IPCA1 and IPCA2 axes and therefore stable. The high-yielding genotypes Tatte, Mehado-80 and E were unstable and specifically adapted to high-yielding environments (Goffa, Arbaminch, and Derashie).

Mohammadi and Amri (2009) analyzed GE interactions on grain yield of one bread wheat (*Triticum aestivum* L.) and 19 durum wheat [*T. turgidum*) genotypes by the additive main effects and multiplicative interaction (AMMI) model to evaluate genotype (G), environment (E), and GE interactions with the statistical parameters of AMMI statistic coefficient (D), AMMI stability value (ASV), regression coefficient (b) and ecovalence (W2). Main effects due to E, G, and GE interaction as well as first three interaction principal component axes (IPCA 1 to 3) were found to be significant ($P < 0.01$). The AMMI biplot distinguished genotypes with wide and specific adaptation and environments with high and low genotype discrimination ability. Ranking the statistical parameters indicated that they are similar in general, especially for the genotypes with similar responses and also for the environments with similar discrimination ability. The results show

that the statistical parameters as well as the AMMI model are useful for analyzing GE interaction. Based on the AMMI model, the recommended genotypes had more grain yield improvement in favorable than unfavorable environments. The genotypes selected based on stability of grain yield combined high stability and high-yielding performance.

Sanni *et al.* (2009) used the Additive Main Effects and Multiplicative Interaction (AMMI) to evaluate the effects of GEI in NERICA rice genotype and their adaptation in two years at three locations. Twenty two rice genotypes were grown in 2005 and 2006 under upland condition, using randomized complete block design with three replications. Main effects due to environments (E), genotypes (G) and GE interaction (GEI) were significant ($p < 0.01$), with the highest variation of 43.1% accounted for by environmental effects. The first four Interaction Principal Component Axes (IPCA1, 2, 3 and 4) were significant ($p < 0.01$) and cumulatively contributed 98.5% of the total GEI. AMMI biplot accounted for 91.4% of the total sum of squares. The stability study indicated that NERICAs 3, 10, 11 and 18 could be considered stable in any of the environments, due to their low interactions. However, NERICA 11 was the most promising of the genotypes, with high yield (5.15 t ha^{-1}) and a broad environmental adaptation.

Xi Yuan *et al.* (2009) conducted a study to determine different stability analysis models in assessing the performance of crop varieties. Data from different regional crop trials were analyzed using 5 main stability analysis models, i.e. stability variance model, Finley and Wilkinson regression model, Eberhart-Russell regression model, AMMI model and environmental variance model. Analyzing all data sets showed that the models used differed in both goodness of fitting data, ranking stability and statistical testing mean value of crop varieties and that no model was the best for all data sets. Different models suited to different data sets. Model selection remarkably affected performance assessment of crop varieties.

Aminzadeh (2010) evaluated eighteen advanced winter and intermediate cold hardy wheat genotypes and two advanced genotypes of Toos and Alvand as checks to compare their tolerance to the late season drought stress. The analysis of variance showed that genotypes x environments x regressions interaction and AMMI component 1 were significant. Results show that 10(5002), 2(4016), 15(5034), 1(4002) and 6(4034) the high seed yield in all of sites and all of environment conditions and two years (2007-2008).

Mulusew Filkere, *et al.*(2010) studied on sixteen field pea (*Pisum sativum* L.) genotypes for yield stability across 12 environments during 2004-2006 at highlands of Bale, South eastern Ethiopia. The stability parameters; Shukla's stability variance (σ^2_i), Wricke's ecovalence (W_i), Eberhart & Russell's deviation from regression (S^2_{di}) and Additive main Effect and multiplicative Interaction stability value (ASV) had a significant correspondence over the studied environments .Furthermore , genotype IFPI-1523 and IFPI-2711 genotypes were agronomic performance , reaction for diseases and the most stable genotypes across locations and year so that these genotypes were recommended for large scale production. Generally, whenever new varieties are proposed for release information on agronomic performances, reaction for disease and yield stability should be availed for end user. On the other hand, it can be suggested more conclusive that the use of appropriate biometrics techniques is necessary for identifying the most adapted, responsive and stable genotypes in the final phases of the plant breeding program, where the high cost and the time spent in assays are powerful justifications to search for improved methods.

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted with 8 advance genotypes of Wheat and 2 check varieties BARI Gom 21 (Shatabdi) and BARI Gom 24 (Prodip) in 10 environments of five research stations viz. WRC; Dinajpur, RARS, Jessore and Jamalpur and RWRC, Rajshahi and Joydebpur. Five environments were timely seeding conditions in five stations and other five were late seeding conditions in those stations.

3.1 Description of the Experimental Sites:

Location 1

The experimental farm of the Wheat Research Center, Nashipur, Dinajpur is located at 15 kilometer north of Dinajpur district head quarter. It is situated at 25° 38' N latitude, 88° 41' E longitude and 38.2m above sea level. The land belongs to the Old Himalayan Piedmont Plain (AEZ-1) (FAO and UNDP, 1988). The soil of the experimental field was sandy loam in texture with a p^H of 6.2.

Location 2

Regional Agricultural Research Station (RARS), Jessore, one of the six regional stations of Bangladesh Agriculture Research Institute (BARI) has the responsibility to conduct research activities with BARI mandate crops in the southern part of the country. The station is located 3 kilometer west side of Jessore district head quarter and 271 km westward from Dhaka city at 23° 11' N latitude and 89° 14' E longitude. The elevation is 6.7m from sea level. Jessore agricultural research station belongs to Gopalganj, Khulna Flood Plain (AEZ-14). The soil is classified as calcareous brown flood plain, with p^H ranges from 7-8, and silt to silty-clay loam in texture. The coolest month is January with a mean temperature of about 18°C and total annual rainfall is 1650 mm.

Location 3

Regional Agricultural Research Station (RARS), Jamalpur is located at $24^{\circ} 56'$ N latitude and $89^{\circ} 55'$ E longitude with an elevation of 19m above the sea level. It is about 170 km northwest from Dhaka city. Jamalpur RARS is belongs to the agro ecological zone -9 (AEZ-9) and the soil is Old Bhramaputra Flood Plain.. The soil type is sandy loam to silty clay loam. The p^H of the soil ranges from 5.5 to 7.0.

Location 4

Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur is located at $23^{\circ} 46'$ N and $90^{\circ} 23'$ E longitude with elevation of 8m above sea level. It is about 35 km north from Dhaka city. The soil of the station is belongs to Madhupur tract and Agro Ecological Zone is 28 (AEZ 28). It has silty clay soil of chhiata series and grey terrace type.

Location 5

The regional wheat research Centre (RWRC), BARI, Rajshahi is situated about 250 km North West of Dhaka and 8 kilometer east of Rajshahi city. The station is located at $24^{\circ} 22'$ N and $88^{\circ} 39''$ E longitude 20 meter above sea level. The station is located in AEZ-11). The soil is calcareous alkaline with p^H of 7.5. The station experiences low rainfall 1200-1600 mm (Pandit, 2006) accompanied with severely hot weather during summer and sufficiently cool temperature during winter.

Table 3.1.1: Climatic parameters of the environments where experiments were conducted

Sl #	Environments	Geographical position			Temperature (°C)			Rainfall (mm)
		Longitude	Latitude	Altitude	Maximum	Minimum	Mean	
1	Dinajpur optimum seeding	88° 41'E	25° 38'N	38.2m	33.0	9.7	20.4	1.0
2	Dinajpur late seeding	88° 41'E	25° 38'N	38.2m	33.0	9.7	20.4	1.0
3	Jessore optimum seeding	89.14°E	23.11° N	6.7m	33.0	7.00	25.02	28.5
4	Jessore late seeding	89.14°E	23.11° N	6.7m	33.0	7.00	25.02	54.3
5	Jamalpur optimum seeding	89° 55' E	24° 56' N	19m	36.53	9.69	22.53	00
6	Jamalpur late optimum seeding	89° 55' E	24° 56' N	19m	36.53	9.69	22.53	00
7	Joydebpur optimum seeding	90° 23' E	23° 46' N	8m	28.42	15.62	13.51	37
8	Joydebpur late seeding	90° 23' E	23° 46' N	8m	28.42	15.62	13.51	45
9	Rajshahi optimum seeding	88°39'E	24°22'N	20m	35.94	9.38	24.88	00
10	Rajshahi late seeding	88°39'E	24°22'N	20m	35.94	9.38	24.88	00

3.2 Materials used

Two released varieties and eight advance lines viz. BARI Gom 21 (Shatabdi), BARI Gom 24 (Prodip), BAW 1140, BAW 1137, BAW 1118, BAW 1125, BAW 1122, BAW 1129, BAW 1130 and BAW 1141 were used for the experimentation. Two varieties were used as checks. Sources of all these genotypes were Wheat Research Centre, Bangladesh Agricultural Research Institute, Nashipur, Dinajpur. Bangladesh Advanced Wheat (BAW) number, parentage and their source are shown in Table 2.

Table 3.2.1: BAW number, parentage and sources of 10 wheat genotypes used in the experiment

Sl #	BAW #	Parentage	Source
1	BAW 936	MRNG/BVC//BLO/PVN/3/PJB-81 (BARI Gom 21-Shatabdi)	WRC, BARI
2	BAW1008	G. 162/BL 1316//NL 297 (BARI Gom 24-Prodip)	WRC, BARI
3	BAW 1140	SOURAV/GOURAB	WRC, BARI
4	BAW 1137	GARUDA//BAW 970/NL 297	WRC, BARI
5	BAW 1118	BAW 969/SHATABDI	WRC, BARI
6	BAW 1125	KAN//IAS 63/ALDAN	WRC, BARI
7	BAW 1122	GARUDA//BAW 970/NL 297	WRC, BARI
8	BAW 1129	GOURAB/FANG 60	WRC, BARI
9	BAW 1130	GOURAB/PAVON 76	WRC, BARI
10	BAW 1141	V01078	WRC, BARI

3.3 Land Preparation and Fertilization

The experimental plot was prepared well by ploughing and cross-ploughing with harrow followed by laddering. Weeds and stubbles were removed from the field. In the final land preparation following basal dose fertilizers and manures were applied.

Table 3.3.1: Rate of manures and fertilizers used in the experiment

Sl #	Manures and fertilizers	Rate(kg/ha)	
		Basal	Top dress
1	Cowdung	8000	
2	Urea	150	75
3	Triple super phosphate (TSP)	132	
4	Muriate of potash (MP)	100	
5	Gypsum	120	

All fertilizers and manures except $1/3^{\text{rd}}$ urea of recommended dose were applied at the time of final preparation. Remaining $1/3^{\text{rd}}$ urea was applied as top dress at crown root initiation stage of the crop at 18 days after seeding (DAS).

3.4 Experimental Design and Layout

The experimental plot was laid out in Randomized Complete Block Design (RCBD) with three replications in each environment. Seeds were continuously sown in line in unit plot of 8m^2 ($5\text{m} \times 1.6\text{m}$) with row spacing of 20cm. Block to block and plot to plot distances were 1 meter and 60cm., respectively. The total number of experimental plots per environments was 30. So, the total experimental area per environment was $17\text{m} \times 23.4\text{m}$. The genotypes were randomly distributed to each plot within the block. A pre-sowing irrigation was given in the plot. When moisture comes to field capacity, seeds of the experiments of timely seeded condition were seeded during 20-25 November and those of late seeded condition during 20-25 December 2009 by hand continuously in lines.

3.5 Intercultural Operation

First irrigation was done lightly at 18 DAS at crown root initiation (CRI) stage of the crop. After irrigation, remaining $1/3^{\text{rd}}$ urea was top dressed. Weeding was done by hand when the crop field came in zoe condition after irrigation. Second irrigation was done at the booting stage of the crop at 55 DAS. Third irrigation was provided at the early grain filling stage. Signboard was also placed in the experiments so that visitors can identify it.

3.6. Data Collection

Data on five characters were collected from randomly selected and tagged ten plants from the middle rows excluding borders and from plot basis. Those ten plants were harvested by uprooting.

1. **Heading days:** Days required from seeding date to the date of emergence of spikes of 50% plants of the plots.
2. **Anthesis days:** Days required from seeding date to the date of anthesis in 50% spikes of the plants of the plots.
3. **Maturity days:** Days required from seeding date to the physiological maturity (when peduncle of 50% plants of the plot became yellow).
4. **Thousand grain weight:** Weight in grams of one thousand clean sun dried randomly selected grains from each plots.
5. **Grain yield:** Weight of the moisture adjusted total harvested grains of individual plots in gram and then converted into ton per hectare. Yield was adjusted as follows:

$$Y_{\text{adj}} = Y_{\text{AC}} \times \frac{(100 - M_{\text{AC}})}{(100 - M_{\text{ST}})}$$

Where

Y_{adj} = Adjusted yield

Y_{AC} = Yield at actual moisture percent

M_{AC} = Actual moisture percent

M_{ST} = Standard moisture percent

6. **Grain filling duration:** Days required from anthesis date of 50% plants of a plot to physiological maturity of 50% plants of the plot.
7. **Grain filling rate:** It is the grain weight gain per day and calculated as follows:

$$\text{Grain filling rate} = \frac{\text{Thousand grain weight}}{1000 \times \text{grain filling duration}} \times 100$$

3.7. Statistical Analysis

Analyses of variance for the collected data for single and combined environments were done by F-test using MSTAT-C program.

3.7.1 AMMI Analysis

Stability analysis in AMMI model was performed in CROPSTAT version 7.0 programs using the following formula:

The AMMI model for T genotypes and S environments is given as

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

Where,

Y_{ij} is the mean yield of i^{th} genotype in J^{th} ;

μ is the general mean;

g_i is the i^{th} genotypic effect;

e_j is the J^{th} location effect;

λ_n is the eigen value of the PCA axis n;

α_{in} and γ_{jn} are the i^{th} genotype, J^{th} environment PCA scores for the axis n;

θ_{ij} is the residual;

n' is the number of PCA axes retained in the model.

AMMI Stability Value (ASV)

Purchase, et al. (2000b) tested for yield stability in wheat in the Orange Freestate province in South Africa, using various test. Because AMMI does not make a provision for a quantitative stability measure, they developed their own test based on the AMMI model's IPCA 1 and IPCA 2 values for each cultivar. They called it the AMMI Stability Value (ASV). This ASV is in effect the distance from the co-ordinate point to the origin in a two dimensional scatter gram of IPCA 1 score against IPCA 2 score contribute more o the G x E sum of squares, a weighted value is needed. This weight is calculated according to the relative contribution of IPCA 1 to IPCA 2 to the interaction SS.

$$ASV = \sqrt{\left[\frac{IPCA1SumofSquares(IPCA1score)}{IPCA2Sumofsquare} \right]^2 + (IPCA2Score)^2}$$

Where, ASV = AMMI's stability value, SS = sum of squares, IPCA1 = interaction of principal component axis one, IPCA2 = interaction of principal component axis two.

Cluster Analysis

Hierarchical cluster analysis was performed using SPSS programme.

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The combined of analysis of variance and principal component analysis in the Additive Main effect and Multiplicative Interaction (AMMI) model, along with prediction assessment, is a valuable approach for understanding genotype environment interaction (GEI) and obtaining better yield estimates. The interaction is explained in the form of a biplot display where, Principal Component Analysis (PCA) scores are plotted against each other and it provides visual inspection and interpretation of the genotype-environment interaction (GEI) components. Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of the performance across diverse environments.

Combined analysis of variance for four characters of ten bread wheat (*Triticum aestivum* L.) genotypes presented in Table 4.1 revealed that, there was significant genotypic variation for grain yield (GY), heading days (HD), grain filling duration (GFD) and grain filling rate (GFR). Highly significant ($P \leq 0.01$) mean square due to environment indicated that variations among the tested environments were also significant. This reveals that significant variability was present both among genotypes and environments. The mean square for G x E interaction was also highly significant ($P \leq 0.01$) for all the characters studied.

4.1 Grain Yield

The pooled analysis of variance for grain yield (tons/ha) of 10 wheat genotypes tested in 10 environment showed that 85.1% of the total sum of squares was attributable to environment effects, while only 4.5% and 10.4% of the sum of squares were contributed genotypic and GEI effects, respectively (Table 4.1.1).

Table 4.1: Combined analysis of variance for four characters of 10 bread wheat genotypes, tested in 10 environments at five WRC, BARI stations

Sources of variation (SV)	Degrees of freedom	Mean squares (MS)			
		Grain yield	Heading days	Grain filling	
				Duration (GFD)	Rate (GFR)
Environment (E)	9	14.529**	213.092 **	911.248 **	0.543 **
Error	20	0.172	2.373	3.91	0.009
Genotype (G)	9	0.766**	161.9 **	34.47 **	0.569 **
G x E	81	0.197**	4.373 **	6.891 **	0.019 **
Error	180	0.078	0.673	1.358	0.008

** = $P \leq 0.01$

Table 4.1.1: Analysis of variance for Additive Main Effect and Multiplicative Interaction (AMMI) for grain yield of 10 wheat genotypes tested in 10 environments of different WRC, BARI stations

Sources of variation	DF	SS	MS	F-value	Probability	Percent contributed
Genotypes (G)	9	2.29612	0.255125			4.5
Environment (E)	9	43.5902	4.84335			85.1
G x E	81	5.30862	0.0655386			10.4
AMMI component 1	17	2.08443	0.122614	2.434**	0.006	39.3
AMMI component 2	15	1.38346	0.0922310	2.455**	0.009	26.0
AMMI component 3	13	0.783600	0.0602769	2.053*	0.044	14.8
AMMI component 4	11	0.566436	0.0514941	2.624*	0.022	10.7
G x E Residual	22	0.490689				9.2
Total	99	51.1949				

CV (%) = 6.18, ** = $P \leq 0.01$, * = $P \leq 0.05$

A large sum of square indicates that the environments were diverse and the most of the differences in grain yield was due to the effects of environments. The magnitude of GEI sum of square was 2.3 times larger than that of genotype, indicated that there were substantial differences in genotypic response across environments. This variability was mainly due to the temperature during growing period and inherent soil fertility which varied greatly from environment to environment.

The results of AMMI analysis also showed that the first principal component axis (IPCA 1) of the interaction captured 39.3% of the interaction sum of squares in 20.9% of the interaction degrees of freedom (df). Similarly, the second, third and fourth principal component axis (IPCA 2-4) explained a further 26.0, 14.8 and 10.7% of the GEI sum of square, respectively. These factors cumulatively captured 90.8% of the total GEI Sum of square, using 69.1% of the interaction degrees of freedom (df). This implied that the interaction of the 10 genotypes of wheat with 10 environments was predicted by the first four principal components of genotypes and environments, which is in agreement with the recommendation of Sivapalan *et al.* (2000). This is also in concordance with the results of Van Oosterom *et al.* (1993), where as much as the first five IPCAs were significant. However, this contradicted with the findings of Gauch and Zobel (1996; Mulusew *et al.*, 2008; Yan *et al.*, 2002 etc., which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. These results indicate that the number of the terms to be included in an AMMI model cannot be specified a prior without first trying AMMI predictive assessment (Kaya *et al.*, 2002). In general, factors like type of crop, diversity of the genotypes and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa, 1990).

Finlay and Wilkinson (1963) and Eberhart and Russel (1966) stated that genotypes with high mean yield, regression coefficient equal to unity ($b_i = 1$) and deviation from regression is as small as possible ($S^2 d_i \approx 0$) are considered stable.

Table 4.1.2: Summary of overall mean (t/ha), Additive Main effect and Multiplicative Interaction (AMMI), joint regression and their rank for grain yield of 10 wheat genotypes tested in 10 environments of different WRC, BARI stations

Genotypes	Yield	b_i	S^2_{di}	IPCA1	IPCA2	ASV
Shatabdi	4.01 (8)	1.199	0.10	-0.58	-0.56	1.04
Prodip	4.11 (6)	1.215	0.09	-0.37	0.74	0.93
BAW 1140	4.34 (2)	0.982 (2)	0.05	0.13 (3)	-0.24	0.32 (3)
BAW1137	4.12 (5)	1.162	0.03	-0.21	0.39	0.50 (4)
BAW1118	4.34 (3)	0.984 (1)	0.03	0.04 (1)	0.24 (4)	0.25 (1)
BAW1125	4.00 (9)	1.152 (4)	0.03	-0.37	0.09 (2)	0.57
BAW1122	4.18 (4)	1.088 (3)	0.05	-0.07 (2)	0.28	0.29 (2)
BAW1129	3.95 (10)	0.704*	0.03	0.51	0.02 (1)	0.77
BAW1130	4.00 (7)	0.675*	0.03	0.66	0.18 (3)	1.00
BAW1141	4.37 (1)	0.839 (5)	0.03	0.26	-0.30	0.50 (4)

Printed bold figures in mean yield indicate higher yields than average. Values within parentheses indicate rank.

This method is one of the most widely used stability model that consider both linear and non linear components of GE interaction in judging the stability of genotypes. According to this method, genotypes BAW 1118, BAW 1140, BAW 1122 and BAW 1141 were the most stable (Table 4.1.2) since the regression coefficients of those were close to unity, deviations from regressions were close to zero and also had the higher mean yields than average.

The greater the absolute IPCA scores, the more specifically adapted a genotype is to a certain environment. The closer the IPCA scores to zero, the more stable the genotype is over the tested environments. The absolute value of IPCA 1 scores of BAW 1118 was the lowest (0.04) followed by BAW 1122 (0.07) and BAW 1140 (0.13), and hence, these were the most stable genotypes. On the other hand, BAW 1130 was the most responsive genotype followed by Shatabdi, Prodip and BAW 1125. BAW 1141 had medium responsiveness. On the other hand, when IPCA 2 is considered, BAW 1129 was the most stable genotype followed by BAW 1125, BAW 1130 and BAW 1118. This means that the two IPCAs have different values and meanings. Therefore the other better option is, to calculate AMMI Stability Value (ASV) using a principle of the Pythagoras theorem and to get estimated values between IPCA 1 and IPCA 2 scores. ASV was reported to produce a balanced measurement between the two IPCA scores.

Quantitative stability measurement is essential in order to quantify and rank genotypes according to their yield stability. However, the AMMI model does not provide measure for quantitative stability. For this ASV was proposed by Purchase (1997). According to ASV value the most stable genotype was BAW 1118 followed by BAW 1122, BAW 1140, BAW 1141 and BAW 1137. The most responsive genotype was Shatabdi followed by BAW 1130 and Prodip (Table 4.1.2). The stability estimate using ASV and regression method was almost similar. In both the methods, BAW 1118 was the most stable followed by BAW 1122, BAW 1140 and BAW 1141; and the responsive was BAW 1130, Shatabdi and Prodip.

Figure 4.1.1 is extremely informative, showing both main and interaction effects for both genotypes and environments. In this graph, distances in the direction of abscissa show main effect difference, whereas, the ordinate shows interaction effect differences. The highest differences between BAW 1130 (9) and Shatabdi (1) were mainly due to interaction effect of genotype and environment as their scores along abscissa was almost similar.

According to IPCA 1 score, genotypes that are around origin were considered as stable. The most stable genotype was BAW 1118 (5), BAW 1122 (7) and BAW 1140 (3) (Fig 4.1.1). The genotypes BAW 1137 (4) and BAW 1141 (10) were also stable, but BAW 1137 (4) had lower yield than the average. The remaining 5 genotypes scattered away from the origin, indicating that the genotypes were more sensitive to environmental interactive forces, however, BAW 1130 (9) and BAW 1129 (8) can perform well in late seeding, but their mean yield was lower than average.

As shown in the Fig 4.1.1, five late seeding environments of five locations were located in the same quadrate, indicating that late seeding environments were closer to each other than any optimum seeding environments. However, there were some variations among the late environments and that variations were mostly due to main effect of the environment. The highest variation in late environments were found between Dinajpur and Jamalpur whereas, Jessore was the closest to Dinajpur. Five optimum environments were also located in the same quadrate indicating closer relationship among those than any late environment.

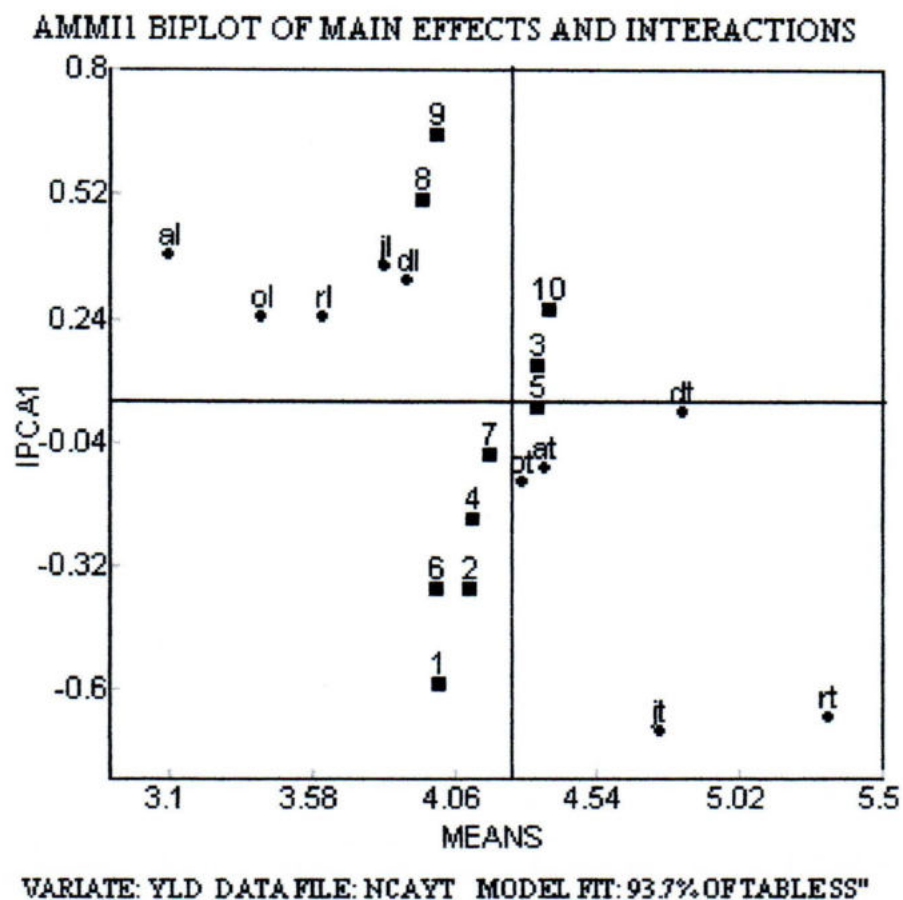


Fig 4.1.1: Biplot of grain yield and interaction principal component axis (IPCA) scores of 10 wheat genotypes tested in 10 environments. (Large square indicate 10 genotypes as: 1-Shatabdi, 2-Prodip, 3-BAW 1140, 4- BAW 1137, 5- BAW 1118, 6- BAW 1125, 7- BAW 1122, 8- BAW 1129, 9- BAW 1130 and 10- BAW 1141 and small square indicate 10 environments as: dt-Dinajpur timely seeding, dl= Dinajpur late seeding, jt=Jessore timely seeding, jl= Jessore late seeding, at- Jamalpur timely seeding, al- Jamalpur late seeding, ot- Joydebpur timely seeding, ol- Joydebpur late seeding, rt- Rajshahi timely seeding and jl-Rajshahi late seeding).

Jessore and Rajshahi optimum seeding were more responsive to environment change, but Dinajpur had the least response followed by Joydebpur and Jamalpur.

The IPCA 2 score was also important (26.0% of G x E SS) in explaining GEI in the experiment, therefore, the biplot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Fig 4.1.2). The IPCA scores of genotypes in the AMMI analysis is an indication of stability or adaptation over environments (Gauch and Zobel, 1996). The greater the IPCA scores, the more specifically adapted is a genotype to a certain environments (Admassu, *et al.*, 2008). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled. A biplot of the first two IPCA show that BAW 1118 (5) was the most stable genotype followed by BAW 1137 (4), BAW 1122 (7), BAW 1140 (3) and BAW 1141 (10) due to their lower IPCA score. BAW 1118 (5), BAW 1140 (3) and BAW 1141 (10) were also best adapted to late seeding conditions of Dinajpur and Rajshahi; BAW 1129 (8) and BAW 1130 (9) at Dinajpur optimum seeding, and late seeding conditions of Joydebpur, Jessore and Jamalpur. BAW 1122 (7) was the best for timely seeding conditions of Joydebpur and Jamalpur. BAW 1125 (6) and BAW 1137 (4) were also suitable for these environments but their yield was lower than the average.

The remaining genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. However, when IPCA 2 are taken into consideration, Shatabdi (1), Prodip (2) and BAW 1130 (9) show considerably more G x E interaction due to the factor or factors explained by IPCA2.

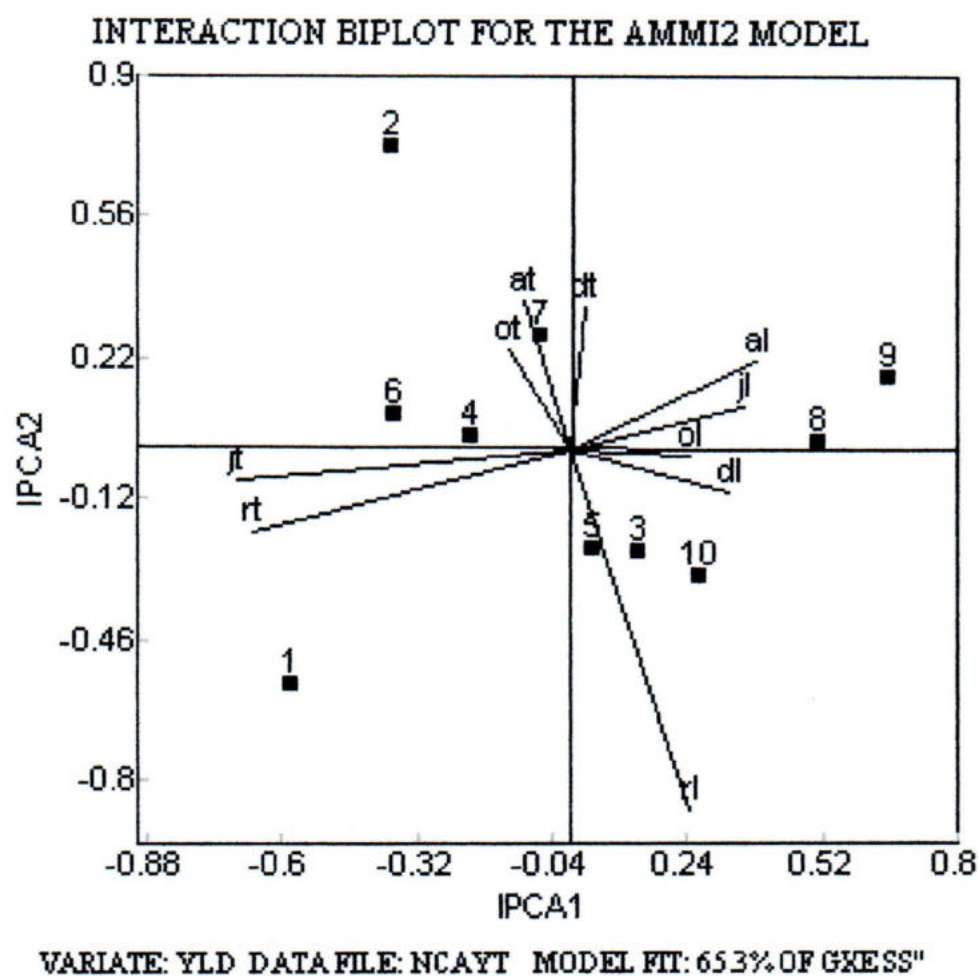


Fig 4.1.2: Biplot of the second interaction principal component axis (IPCA 2) against the first interaction principal component axis (IPCA 1) scores for grain yield of 10 wheat genotypes in 10 environments of different WRC, BARI stations

When looking at the environments, it was clear that there was a good variation in the different environments sampled, ranging from the lower yielding environments in quadrants 3 and 4 and the high yielding environments in quadrants 1 and 2. With respect to the test sites, Rajshahi late seeding environment was the most discriminating as indicated by the longest distance between its marker and the origin (Fig 4.1.2). Due to its large PCA2 score, genotypic differences observed at Rajshahi optimum seeding environment may not exactly reflect the genotypes in average grain yield of overall sites. Timely seeding of Jessore was also discriminating, but genotypic differences at these environments should be consistent with those averaged over sites, because these had near zero PCA2 scores compared to the others. Both seeding of Dinajpur and Joydebpur were the most favorable environments for all genotypes.

4.2 Heading Days

The pooled analysis of variance for heading days of 10 wheat genotypes tested in 10 environments showed that 51.20% of the total sum of squares was attributed to environment effects, while only 39.02% and 9.59% of the sum of squares were contributed to genotypic and GEI effects, respectively (Table 4.2.1). A large sum of squares for genotypes indicates that the genotypes were diverse. The most of the differences in heading days was due to the effects of genotypes. The magnitude of GEI sum of square was 4 times smaller than that of genotype indicated that there were small differences in genotype across environments.

The results of AMMI analysis also showed that the first principal component axis (IPCA 1) of the interaction captured 48.67% of the interaction sum of squares in 20.98% of the interaction degrees of freedom (df). Similarly, the second, third and fourth principal component axis (PCA 2-4) explained a further 24.48, 13.78 and 8.20% of the GEI sum of square, respectively. These factors cumulatively captured 95.13% of the total GEI SS, using 48.2% of the interaction degrees of freedom (df). This implied that the interaction of the 10 genotypes of wheat with 10 environments was predicted by the first four principal components of genotypes and environments, which was in agreement with the recommendation of Sivapalan *et al.* (2000). This is also in concordance with the results of Van Oosterom *et al.* (1993), where as much as the first five IPCAs were significant. However, this contradicted with the findings of Gauch and Zobel (1996; Mulusew *et al.*, 2008; Yan *et al.* 2002 etc., which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. These results indicate that the number of the terms to be included in an AMMI model cannot be specified a prior without first trying AMMI predictive assessment (Kaya *et al.*, 2002). In general, factors like type of crop, diversity of the genotypes and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa, 1990).

Table 4.2.1: The analysis of variance table for AMMI for heading days (HD) for the 10 Wheat genotypes tested over 10 environments of different WRC, BARI stations

Sources of variation	DF	SS	MS	F value	Probability	Percent contributed
Genotypes (G)	9	478.508	53.1676			39.02
Environment (E)	9	627.787	69.7541			51.20
G x E	81	117.528	1.46910			9.59
AMMI component 1	17	57.2056	3.36503	3.514**	0.000	48.67
AMMI component 2	15	28.7700	1.91800	2.918**	0.003	24.48
AMMI component 3	13	16.1958	1.24583	2.839**	0.007	13.78
AMMI component 4	11	9.63369	0.875790	3.673**	0.004	8.20
G x E Residual	24	5.72333				
Total	99	1226.15				

CV (%) = 1.86, ** = $P \leq 0.01$

Table 4.2.2: Summary of overall mean heading days (HD), additive main effect and multiplicative interaction (AMMI), joint regression and their rank for heading days of 10 wheat genotypes tested in 10 environments of different WRC, BARI stations

Genotypes	HD	bi	S ² di	IPCA1	IPCA2	ASV
Shatabdi	69.8(10)	1.38	2.43	-1.47	-1.24	3.18
Prodip	64.2(3)	1.11	0.77	0.41(5)	-0.88	1.19(5)
BAW 1140	63.5(2)	0.83	1.11	0.81	0.57(5)	1.70
BAW1137	65.9(8)	0.92(3)	0.47(4)	-0.31(3)	0.53(4)	0.82(4)
BAW1118	61.6(1)	0.80	1.43	0.70	0.87	1.64(6)
BAW1125	68.1(9)	1.03(1)	2.71	-1.45	0.79	2.99
BAW1122	64.9(6)	0.96(2)	0.29(1)	0.30(2)	0.30(3)	0.66(2)
BAW1129	64.2(4)	1.11(5)	0.34(2)	0.06(1)	-0.25(2)	0.28(1)
BAW1130	64.3(5)	1.08(4)	0.59(5)	-0.35(4)	0.22(1)	0.73(3)
BAW1141	64.9(7)	0.38	-0.42(3)	1.29	-0.94	2.73

Printed bold figures of mean indicate lower heading days than average. Values within parentheses indicate rank.

Finley and Wilkinson (1963) and Eberhart and Russel (1966) stated that genotypes with high mean value, regression coefficient equal to unity ($b_i = 1$) and deviation from regression is as small as possible ($S^2_{di} \approx 0$) are considered stable. But in case of heading days, the genotype with lower mean is expected in our climatic condition as the late varieties face more heat stress in grain filling period resulting poor grains and yields. So, the lowest heading days was ranked first and so on.

The data revealed that, BAW 1122, BAW 1137 and BAW 1130 and BAW 1129 were the most stable genotypes for heading days as their b_i values were close to unity and deviations from regression differed insignificantly from zero. Though, their mean values were not lower than over all mean, still all of them headed earlier than check variety Shatabdi (Table 4.2.2). BAW 1125 had also b_i value close to unity but S^2_{di} value was large and the most responsive genotypes were Shatabdi and BAW 1125.

The greater the absolute IPCA scores, the more specifically adapted a genotype is to a certain environment. The closer the IPCA scores to zero, the more stable the genotypes is over the tested locations. The absolute value of IPCA 1 scores of BAW 1129 was the lowest (0.06) followed by BAW 1122 (0.30) and BAW 1137 (-0.31), and hence, these were the most stable genotypes. On the other hand, Shatabdi was the most responsive one followed by BAW 1125, BAW 1141 and BAW 1140. BAW 1118 had medium responsiveness. On the other hand, when IPCA 2 is considered, BAW 1130 was the most stable genotype followed by BAW 1129, BAW 1122 and BAW 1137. This means that the two IPCA have different values and meanings. Therefore the other better option was to calculate AMMI Stability Value (ASV) using a principle of the Pythagoras theorem and to get estimated values between IPCA 1 and IPCA 2 scores. According to ASV value the genotypes BAW 1129 followed by BAW 1122, BAW 1137 and BAW 1130 had stable heading days.

Figure 4.2.1 is extremely informative, showing both main and interaction effects for both genotypes and environments. In this graph, distances in the direction of abscissa show main effect difference, whereas, the ordinate shows interaction differences. The differences in heading days of BAW 1137 (4) and BAW 1130 (9) were due to main effect as their IPCA1 score is almost similar. On the other hand differences between heading days of Prodip (2) and that of BAW 1129 (8) and BAW 1130 (9) was due to interaction effects. The heading days of BAW 1118 (5) and BAW 1125 (6) differed both by main and interaction effects. According to IPCA 1 score, genotypes that are around origin were considered as stable. The most stable genotype was BAW 1137 (4), BAW 1122 (7), BAW 1129 (8) and BAW 1130 (9) (Fig 4.2.1). The genotype Prodip (2) was moderately stable. The remaining 5 genotypes scattered away from the origin, indicating that the genotypes were more sensitive to environmental change.

Four late seeding environments of five locations were located in the same quadrante, indicating that these environments were closer to each other than any optimum seeding environments. However, there were some variations among the late environments and that variations were due to main and interaction effects. Among the late environments the highest variation was found between Dinajpur and Joydebpur whereas, Rajshahi, Jessore, Jamalpur were the closest. Three optimum environments were also located in the same quadrante indicating their closer relationship (Fig 4.2.1).

The IPCA 2 score was also important (24.48% of G x E SS) in explaining GEI in the experiment, therefore, the biplot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Fig 4.2.2). The greater the IPCA scores, the more specifically adapted a genotype is to a certain environment (Admassu *et al.*, 2008). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled.

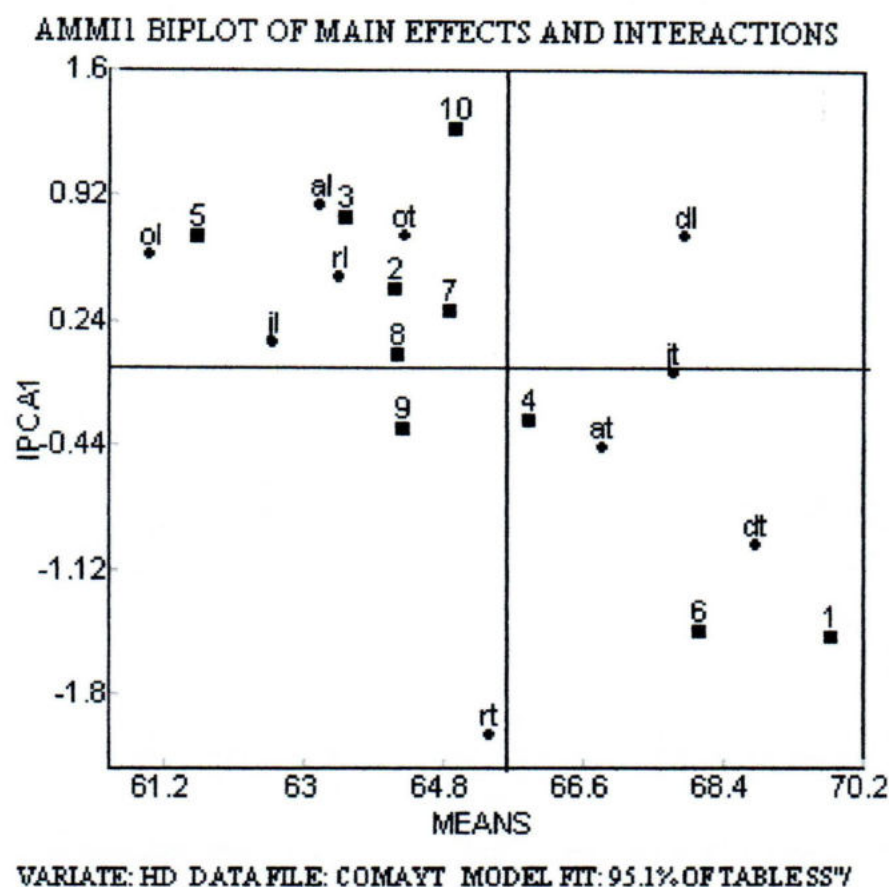


Fig 4.2.1: Biplot of heading days and interaction principal component axis (IPCA) scores of 10 wheat genotypes tested in 10 environments. (Large square indicate 10 genotypes as: 1-Shatabdi, 2-Prodip, 3-BAW 1140, 4- BAW 1137, 5- BAW 1118, 6- BAW 1125, 7- BAW 1122, 8- BAW 1129, 9- BAW 1130 and 10- BAW 1141 and small square indicate 10 environments as: dt-Dinajpur timely seeding, dl= Dinajpur late seeding, jt=Jessore timely seeding, jl= Jessore late seeding, at- Jamalpur timely seeding, al- Jamalpur late seeding, ot- Joydebpur timely seeding, ol- Joydebpur late seeding, rt- Rajshahi timely seeding and jl-Rajshahi late seeding.)

A biplot of the first two IPCA show that BAW 1129 (8) was the most stable genotype followed by BAW 1130(9) and BAW 1137 (4) due to their lower IPCA score. BAW 1122 (7) and BAW 1140 (3) were best adapted to late seeding conditions of Joydebpur, Jessore, Dinajpur and Jamalpur and optimum seeding condition of Joydebpur. BAW 1129 (8), Prodip (2) and BAW 1141 (10) were best adapted to Rajshahi late seeding condition.

The remaining genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. However, when IPCA 2 are taken into consideration, Shatabdi (1), BAW 1141 (10), BAW 1125 (6) and BAW 1118 (5) show considerably more G x E interaction due to the factor or factors explained by IPCA2.

When looking at the environments, it was clear that there was a good variation in the different environments sampled, ranging from the lower yielding environments in quadrants 3 and 4 and the high yielding (lower heading days) environments in quadrants 1 and 2. With respect to the test sites, Rajshahi optimum seeding environment was the most discriminating as indicated by the longest distance between its marker and the origin (Fig 4.2.2). Due to its large PCA2 score, genotypic differences observed at Rajshahi optimum seeding environment may not exactly reflect the genotypes in average heading days of overall sites. Timely seeding of Jessore was also discriminating, but genotypic differences at these environments should be consistent with those averaged over sites, because these had near zero PCA1 scores compared to the others.

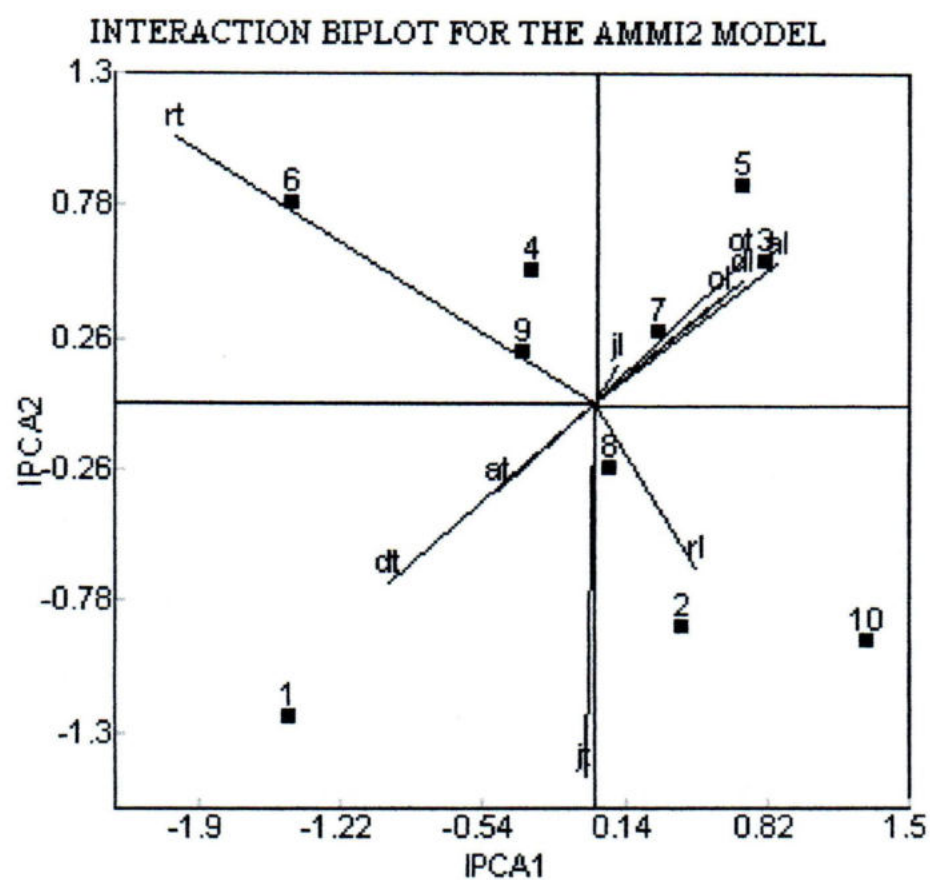


Fig 4.2.2: Biplot of the second interaction principal component axis (IPCA 2) against the first interaction principal component axis (IPCA 1) scores for heading days of 10 wheat genotypes in 10 environments of different WRC, BARI stations

4.3 Grain Filling Duration (GFD)

For grain filling duration (GFD), the pooled analysis of variance of 10 wheat genotypes tested in 10 environments showed that 87.82 % of the total sum of square was attributable to environment effects, while only 4.39 % and 8.68 % of the sum of square were contributed by genotypic and GEI effect respectively (Table 4.3.1). A large sum of squares environments indicates that the environments were diverse, with large differences among environmental means. The most of the differences in grain filling duration was due to the effects of environments. The magnitude of GEI sum of square was 1.97 times larger than that of genotype indicated that there were substantial differences in genotypic response across environments. This variability was mainly due to the temperature during growing period and inherent soil fertility which varied greatly from environment to environment.

From the results of AMMI analysis the first principal component axis (IPCA 1) of the interaction captured 46.78% of the interaction sum of squares in 20.9 % of the interaction degrees of freedom (df). Similarly, the second principal component axis (PCA 2) explained a further 24.14% of the GEI sum of square, respectively. These two factors cumulatively captured 70.9% of the total GEI SS, using 39.5% of the interaction degrees of freedom (df). Therefore, the post-dictive evaluation using an F-test at $P < 0.01$ suggested that two principal component axes of the interaction were highly significant for the model with 32 degrees of freedom. Further, interaction principal component axes were mostly non-significant and therefore did not help to predict validation observations. Thus, the interaction of the 10 wheat genotypes with ten environments was best predicted by the two principal components of genotypes and environments. The most accurate model for AMMI can be predicted by using the first two IPCAs (Mulusew *et al.*, 2008; Yan *et al.*, 2002). Conversely, Silvapan *et al.* (2000) recommended a predictive AMMI model with the first four IPCAs. This is also in concordance with the results of Van Oosterom *et al.* (1993), where as much as the first five IPCAs were significant. These results indicate that the number of the terms to be included in

Table 4.3.1: The analysis of variance table for AMMI of grain filling duration (GFD) for the 10 wheat genotypes tested over 10 environments of WRC, BARI stations

Sources of variation	DF	SS	MS	F value	Probability	Percent contributed
Genotypes (G)	9	128.472	14.2746			4.39
Environment (E)	9	2569.39	285.488			87.82
G x E	81	253.873	3.17342			8.68
AMMI component 1	17	118.767	6.98628	3.258**	0.000	46.78
AMMI component 2	15	61.2848	4.08565	2.657**	0.005	24.14
AMMI component 3	13	25.6264	1.97126	1.432ns	0.194	10.09
AMMI component 4	11	19.4608	1.76917	1.478ns	0.204	7.67
G x E Residual	24	28.7347				
Total	99	2925.65				

CV (%) = 5.4, ** = $P \leq 0.01$ and ns = not significant

Table 4.3.2 Summary of overall mean, additive main effect and multiplicative interaction (AMMI), joint regression and their rank for grain filling duration of 10 wheat genotypes tested in 10 environments of different WRC, BARI stations

Genotypes	GFD	bi	S ² di	IPCA1	IPCA2	ASV
Shatabdi	34.60(1)	1.02(2)	2.49	0.96	0.64(3)	1.97
Prodip	35.53(3)	1.10(5)	3.27	-0.69	1.36	1.90
BAW 1140	37.47(8)	1.01(1)	1.764(4)	-0.15(2)	-0.28(1)	0.40(1)
BAW1137	36.63(6)	0.97(3)	2.16	-0.80	-0.97	1.83
BAW1118	37.37(7)	1.246*	2.76	-1.21	1.23	2.64
BAW1125	34.63(2)	0.95(4)	1.77	-0.06(1)	-0.93	0.92(3)
BAW1122	37.30(9)	1.18	1.72(5)	-0.69(5)	0.65(4)	1.49(5)
BAW1129	36.30(4)	0.855*	0.42(1)	-0.18(3)	-0.72(5)	0.80(2)
BAW1130	36.50(5)	0.87	1.24(3)	-0.47(4)	-1.08	1.41(4)
BAW1141	38.13(10)	0.41	-0.70(2)	2.58	0.29(2)	5.00

Printed bold figures in mean indicate lower grain filling duration than average Values within parentheses indicate rank.

An AMMI model cannot be specified a priori without first trying AMMI predictive assessment (Kaya *et al.*, 2002). In general, factors like type of crop, diversity of the genotypes and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa, 1990).

According to Finlay and Wilkinson (1963) and Eberhart and Russel (1966) considering genotypes with high mean, regression coefficient ($b_i = 1$) and deviation from regression is ($S^2_{di} \approx 0$). The smaller the grain filling duration, the less stress will face the genotype during grain filling stage. So, shorter GFD is expected in Bangladesh condition; therefore, mean was ranked accordingly. The regression value of BAW 1140 ($b_i = 1.01$), Shatabdi ($b_i = 1.02$), BAW 1137 ($b_i = 0.97$) and BAW 1125 ($b_i = 0.95$) was close to unity and their mean GFD was close to average (36.48) except BAW 1140 (mean is 37.470). But deviation from regression of Shatabdi and BAW 1137 was large. So, considering overall performance BAW 1140 and BAW 1125 was treated as stable according to regression model.

The IPCA score is closer to zero, the more stable the genotype is over the tested locations. The absolute value of IPCA 1 scores of BAW 1125 was the lowest (IPCA 1 = 0.06) followed by BAW 1140 (0.15) and BAW 1129 (0.18), and hence, these were the most stable genotypes. On the other hand, BAW 1141 was the most responsive genotype followed by BAW 1118, Shatabdi and BAW 1137. BAW 1122 had medium responsiveness. On the other hand, when IPCA 2 is considered, BAW 1140 was the most stable genotype followed by BAW 1141, Shatabdi and BAW 1122. This means that the two IPCA have different values and meanings. So, ASV (AMMI Stability Value) was calculated using a principle of the Pythagoras theorem and to get estimated values between IPCA 1 and IPCA 2 scores.

According to ASV the most stable genotype was BAW 1140 followed by BAW 1129, BAW 1125, and BAW 1130 and BAW 1122. The most responsive was

BAW 1141 followed by BAW 1118 and Shatabdi .The stability estimate using ASV and regression method was almost similar. In both the methods, BAW 1140 was the most stable and the BAW 1118.

Figure 4.3.1 is extremely informative, showing both main and interaction effects for both genotypes and environments. In this graph, distances in the direction of abscissa show main effect difference, whereas, the ordinate shows interaction differences. Main effect difference from the highest was grain filling duration was the highest between BAW 1140 (3) and BAW 1125 (6) as their IPCA 1 scores was almost same whereas, it was the lowest with BAW 1129 (8) by BAW 1140 (3). According to IPCA 1 score, genotypes that are around origin were considered as stable. The most stable genotype was BAW 1129 (8), BAW 1140 (3) and BAW 1130 (9) (Fig 4.3). The genotypes BAW 1137 (4) and BAW 1122 (7) were also stable and their grain filling duration had lower than the average. The genotype Prodip (2) and BAW 1125 (6) were also stable and had lower grain filling duration.

Three optimum seeding environments of Rajshahi, Dinajpur and Joydebpur were located in the same quadrate, indicated that the environments are closer to each other. On the other hand environments of late seeding of Dinajpur, Jessore and Rajshahi were close to each other (Fig 4.3.1). However, there were some variations among the late environments and optimum environments that variations were due to both main and interaction effect. The highest variations in late seeding environments were found between Joydebpur and Rajshahi and that variation was mainly due to interaction effect and it was the lowest with Jamalpur and Jessore late environment. The highest main effect difference was found between Jamalpur late and Dinajpur optimum seeding and the lowest was found between Joydebpur and Rajshahi optimum seeding.

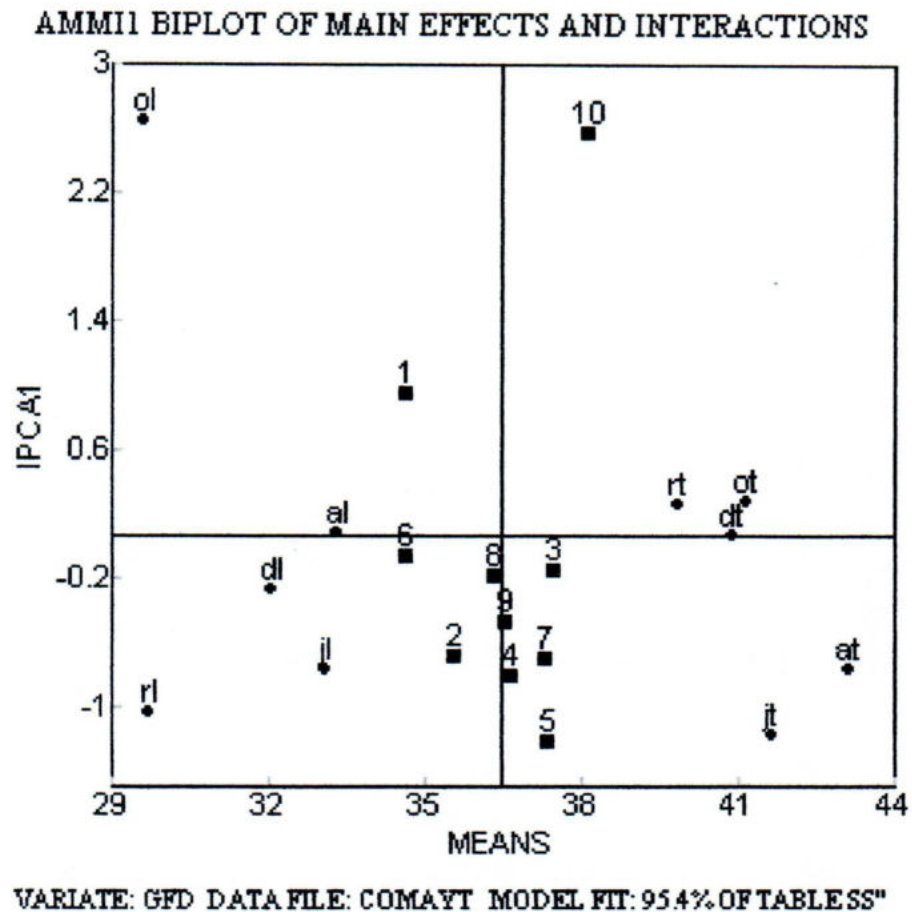


Fig 4.3.1: Biplot of grain filling duration and interaction principal component axis (IPCA) scores of 10 wheat genotypes tested in 10 environments. (Large square indicate 10 genotypes as: 1-Shatabdi, 2-Prodip, 3-BAW 1140, 4-BAW 1137, 5- BAW 1118, 6- BAW 1125, 7- BAW 1122, 8- BAW 1129, 9- BAW 1130 and 10- BAW 1141 and small square indicate 10 environments as: dt-Dinajpur timely seeding, dl= Dinajpur late seeding, jt=Jessore timely seeding, jl= Jessore late seeding, at- Jamalpur timely seeding, al- Jamalpur late seeding, ot- Joydebpur timely seeding, ol- Joydebpur late seeding, rt- Rajshahi timely seeding and jl-Rajshahi late seeding.)

The highest variation were also present among Joydebpur late and optimum seeding condition of Jessore and Jamalpur due to both main and interaction

As IPCA 2 score was important (24.14% of G x E SS) in explaining GEI in the experiment, therefore, the biplot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Fig 4.3.2). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is. The biplot of the first two IPCA show that BAW 1140 (3) was the most stable genotype followed by BAW 1129 (8), BAW 1125 (6) due to their lower IPCA score. BAW 1140 (3) and BAW 1137 (4), BAW 1129 (8), BAW 1130 (9), BAW 1125 (6) were best adapted to late seeding conditions of Jessore, Dinajpur and optimum condition of Jessore.

The remaining genotypes scattered away from the origin in the biplot indicating that those were more sensitive to environmental interactive forces. However, when IPCA2 are taken into consideration, BAW 1141 (10), Shatabdi (1), BAW 1118 (5) and Prodip (2) show considerably more G x E interaction due to the factors explained by IPCA 2.

There was a good variation in the different environments sampled, ranging from the lower yielding environments in quadrants 3 and 4 and the high yielding environments in quadrants 1 and 2. With respect to the test sites, Joydebpur late seeding environment was the most discriminating as indicated by the longest distance between its marker and the origin (Fig 4.3.2). Due to its large PCA2 score, genotypic differences observed at Joydebpur late environment may not exactly reflect the genotypes in average grain filling duration of overall sites. Timely seeding of Rajshahi was also discriminating and had difference in interaction effects with Joydebpur and Dinajpur. Both optimum seeding of Dinajpur and Joydebpur were the most favorable environments for all genotypes with nearly similar grain filling duration but slight difference in interaction.

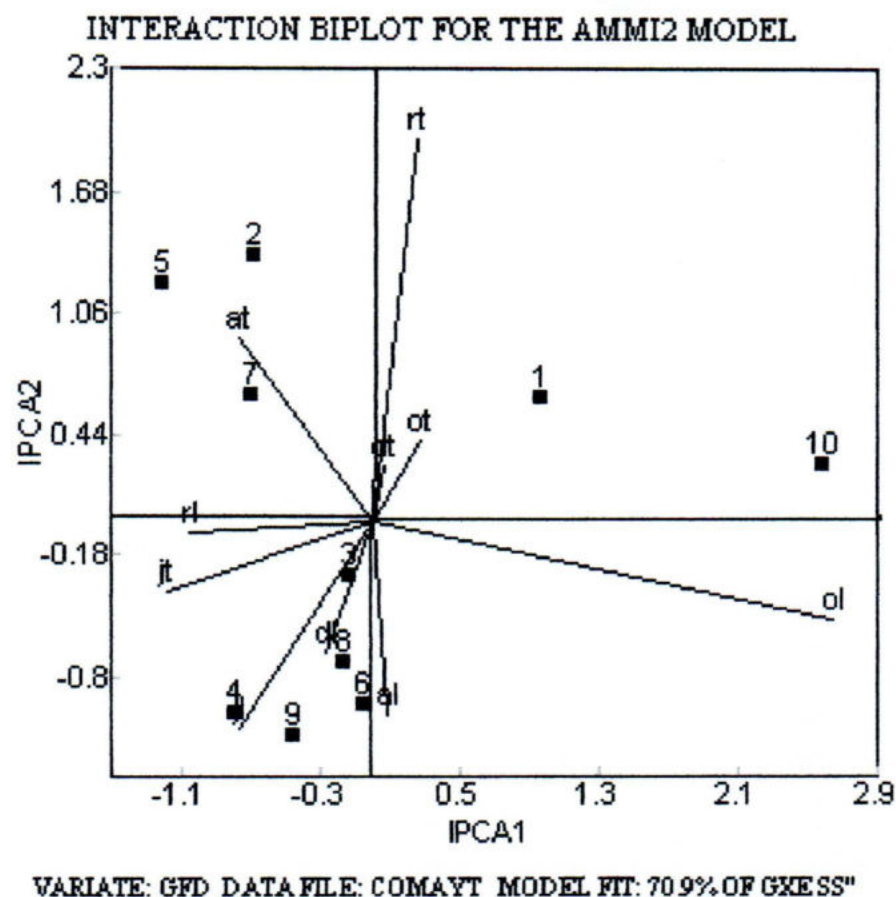


Fig 4.3.2: Biplot of the second interaction principal component axis (IPCA 2) against the first interaction principal component axis (IPCA 1) scores for grain filling duration of 10 wheat genotypes in 10 environments of different WRC, BARI stations

4.4 Grain Filling Rate (GFR)

The pooled analysis of variance for grain filling rate of 10 wheat genotypes tested in 10 environments showed that 37.42% of the total sum of squares was attributable to environmental effects, while 48.53% and 14.42% of the sum of squares were contributed to genotypic and GEI effects, respectively (Table 4.4.1). A large sum of squares for genotypes indicates that the genotypes were diverse. The most of the differences in grain filling rate was due to the effects of genotypes. The magnitude of GEI sum of square was 3.36 times smaller than that of genotype indicated that there were less differences in genotype response across environments.

The AMMI analysis for grain filling rate showed that the first principal component axis (IPCA 1) of the interaction captured 38.05% of the interaction sum of squares in 20.9% of the interaction degrees of freedom (df). The effect of other AMMI components for the character was not significant. The post-dictive evaluation using an F-test at $P < 0.01$ suggested that only first principal component axes of the interaction were highly significant for the model with 17 degrees of freedom. Further, interaction principal component axes captured mostly non-significant (at $P < 0.05$) therefore did not help to predict validation observations. Thus, the interaction of the 10 bread wheat genotypes with ten environments was best predicted by the first Principal Component of genotypes and environments.

The study of Zobel *et al.*, 1988 reported that, the prediction assessment with two interaction principal component axes were the best predictive model. The most accurate model for AMMI can be predicted by using the first two IPCAs (Mulusew *et al.*, 2008; Yan *et al.*, 2002). However, Sivapalan, 2010 reported that 11 IPCAs were significant for this study. These results indicate that the number of the IPCAs to be included in an AMMI model cannot be specified a priori without first trying AMMI predictive assessment (Kaya *et al.*, 2002). In general, factors like type of crop, diversity of the genotypes and range of environmental

conditions will affect the degree of complexity of the best predictive model (Crossa, 1990).

Finlay and Wilkinson (1963) and Eberhart and Russel (1966) stated that genotypes with high mean, regression coefficient equal to unity ($b_i = 1$) and deviation from regression is as small as possible ($S^2_{di} \approx 0$) are considered stable. According to this method, genotypes BAW 1130 and BAW 1129 were the most stable (Table 4.4.2) since, the regression coefficients of those were close to unity, had insignificant deviations from regression and also had the higher mean grain filling rate than average. BAW 1122 and BAW 1118 had also b_i value closer to unity, but their grain filling rate was lower than mean value.

The closer the IPCA score to zero, the more stable the genotype is. The absolute value of IPCA 1 scores of BAW 1125 (6) was the lowest (0.06) followed by BAW 1118 (0.11) and Prodip (0.12), and hence, these were the most stable genotypes. On the other hand, BAW 1141 was the most responsive genotype followed by Shatabdi (1) and BAW 1130. BAW 1129 had medium responsiveness. On the other hand, when IPCA 2 is considered, BAW 1137 was the most stable genotype followed by BAW 1140, BAW 1122 and Prodip. This means that the two IPCA have different values and meanings. So, ASV (AMMI Stability Value) was calculated to get estimated values between IPCA 1 and IPCA 2 scores.

ASV value showed that the most stable genotype was Prodip followed by BAW 1140, BAW 1122, BAW 1129 and BAW 1118. The most responsive genotype was BAW 1141 followed by Shatabdi and BAW 1130 (Table 4.4.2). The stability estimate using ASV and regression method was almost similar. In both the methods, BAW 1129 was the most stable and the responsive were Shatabdi and BAW 1118.

Table 4.4.1: The analysis of variance table for AMMI for grain filling rate (GFR) for the 10 wheat genotypes tested over 10 environments of WRC, BARI stations

Sources of variation	DF	SS	MS	F value	Probability	Percent contributed
Genotypes (G)	9	1.39692	0.155213			48.53
Environment (E)	9	1.07702	0.119668			37.42
G x E	81	0.414940	0.00518675			14.42
AMMI component 1	17	0.157902	0.00928837	2.777**	0.010	38.05
AMMI component 2	15	0.0707747	0.00471831	1.216ns	0.293	17.06
AMMI component 3	13	0.0541325	0.00416404	1.103ns	0.389	13.05
AMMI component 4	11	0.0517523	0.00470476	1.405ns	0.233	12.47
G x E Residual	24	0.0803781				
Total	99	2.87820				

CV (%) = 5.9, ** = $P \leq 0.01$ and ns = not significant

Table 4.4.2: Summary of overall mean with rank, additive main effect and multiplicative interaction (AMMI), joint regression and their rank for grain filling rate of 10 wheat genotypes tested in 10 environments of different WRC, BARI, stations

Genotypes	GFR	bi	S ² di	IPCA1	IPCA2	ASV
Shatabdi	0.00124(5)	1.37	0.00	-0.29	-0.13	0.66
Prodip	0.00139(2)	1.22	0.00	0.12(3)	0.03(4)	0.27(1)
BAW 1140	0.00107(9)	0.68	0.00	0.13(4)	-0.01(2)	0.28(2)
BAW1137	0.00110(8)	1.12(5)	0.00	0.18	0.00(1)	0.40
BAW1118	0.00112(7)	0.91(3)	0.00	0.11(2)	-0.24	0.35(5)
BAW1125	0.00114(6)	0.67	0.00	-0.06(1)	0.42	0.44
BAW1122	0.00105(10)	1.07(2)	0.00	-0.14	-0.02(3)	0.31(3)
BAW1129	0.00135(3)	0.89(4)	0.00	0.14(5)	0.06	0.33(4)
BAW1130	0.00134(4)	1.05(1)	0.00	0.23	-0.09	0.51
BAW1141	0.00142(1)	1.87	0.00	-0.38	-0.05(5)	0.84

Printed bold figures in mean indicate higher grain filling rate than average. Values within parentheses indicate rank.

Figure 4.4.1 showing main and interaction effects for both genotypes and environments. In this graph, distances in the direction of abscissa showed main effect difference, whereas, along ordinate shows interaction differences. The highest differences between BAW 1140 (3) and Prodip (2) was mainly due to main effect of genotypes and environments as their IPCA scores is almost similar. On the other hand, the differences between BAW 1118 (5) and BAW 1141 (10) were due to interaction effect, because their IPCA 1 score varied greatly but mean value were closer. The differences between BAW 1130 (9) and BAW 1141 (10) were due to main and interaction effect. According to IPCA 1 score, genotypes that are around origin were considered as stable. The most stable genotype was BAW 1125 (6) and BAW 1118 (5) (Fig 4.4.1).

Three optimum seeding environments (Rajshahi, Jamalpur and Joydebpur) were located in the same quadrate, indicated that the environments are closer to each other. On the other hand environments of late seeding of Dinajpur and Rajshahi were close to each other (Fig 4.4.1). However, there were some variations among the late environments and optimum environments and that variations were due to both main and interaction effect. The highest variation between the late seeding environments was between Jamalpur and Rajshahi due to main effect as their IPCA score was almost similar. The highest variation was between Jessore late and Jessore timely seeding condition was due to interaction effect. Both main and interaction effects were present between Joydebpur late and Jessore timely seeding.

In explaining GEI in the experiment, the IPCA 2 score was also important (17.06% of $G \times E$ SS) therefore, the biplot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Fig 4.4.2). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is. This biplot of the first two IPCA showed

that Prodip was the most stable genotype followed by BAW 1140 (3), BAW 1122 (7), BAW 1129 (8) and BAW 1137 (4) due to their lower IPCA score.

The remaining genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. BAW 1125 (6) performed better in Joydebpur timely seeding, Shatabdi at late seeding of Dinajpur and Jamalpur and BAW 1118 (5) at optimum and late seeding of Joydebpur.

There was a good variation in the different environments sampled, ranging from the lower yielding environments in quadrants 3 and 4 and the high grain filling environments in quadrants 1 and 2. With respect to the test sites, Jessore optimum seeding environment was the most discriminating as indicated by the longest distance between its marker and the origin (Fig 4.4.2). Due to its large PCA2 score, genotypic differences observed at Jessore late environment may not exactly reflect the genotypes in average grain filling rate of overall sites. Late seeding of Dinajpur and Jamalpur timely seeding was also discriminating.

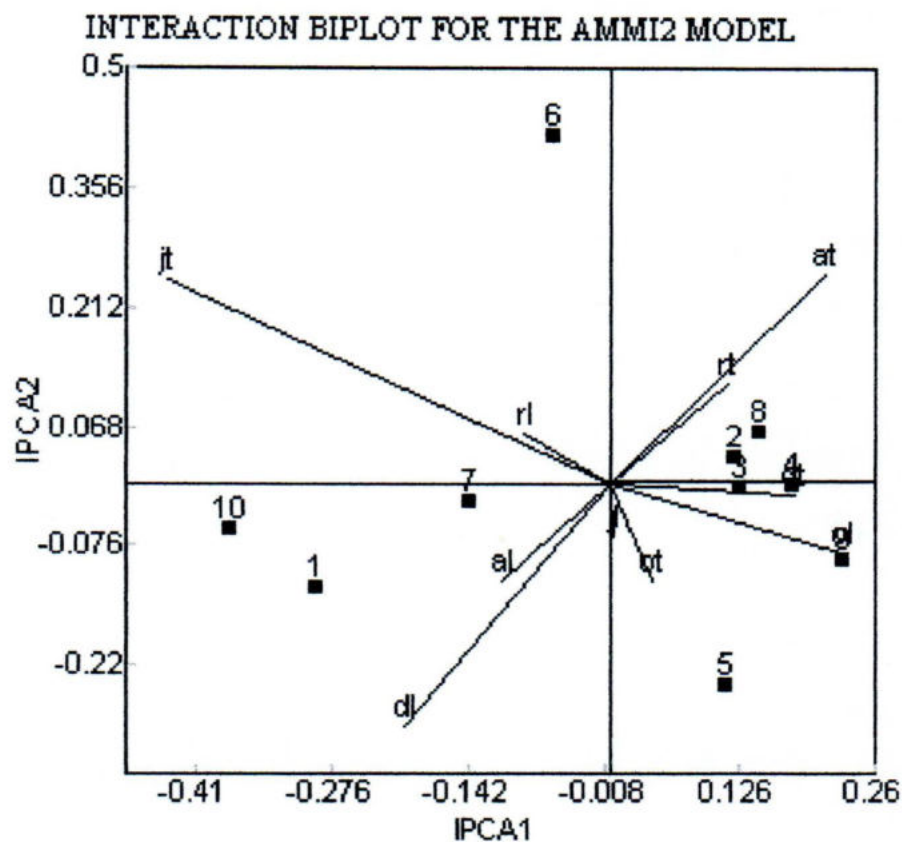


Fig 4.4.2: Biplot of the second interaction principal component axis (IPCA 2) against the first interaction principal component axis (IPCA 1) scores for grain filling rate of 10 wheat genotypes in 10 environments of different WRC, BARI stations

4.5 Cluster Analysis

The dendrogram from a hierarchical cluster classification of 10 genotypes based on AMMI adjusted yield data across 10 environments (using mean and standard deviation of all 10 genotypes was truncated at the 5-grouped level where the similarity and distance level between clusters changed in the amalgamation steps (Fig 4.5.1). Group composition varies from 1 to 3 genotypes. Check variety Shatabdi was closer to BAW 1125, BAW 1130 and BAW 1129. Prodip was close to BAW 1137. The three stable genotypes BAW 1118, BAW 1140 and BAW 1141 were closer to each other.

The dendrogram from the classification of 10 environments based on AMMI adjusted data of 10 genotypes was also truncated into 5-group level where the similarity and distance level between clusters changed noticeably different amount from gradual change in the amalgamation steps (Fig 4.5.2). Late environments were closer to each other with some variation than optimum environments. Similarly optimum environments were also closer to each other except Rajshahi. Jamalpur late environment was also situated in different group.

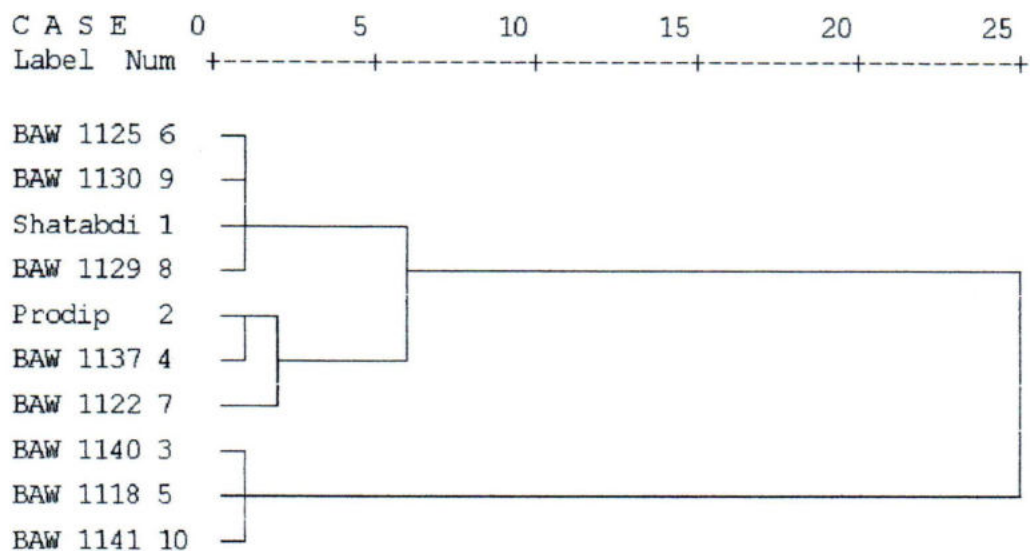


Fig. 4.5.1: Dendrogram using average linkage (between groups) for genotype

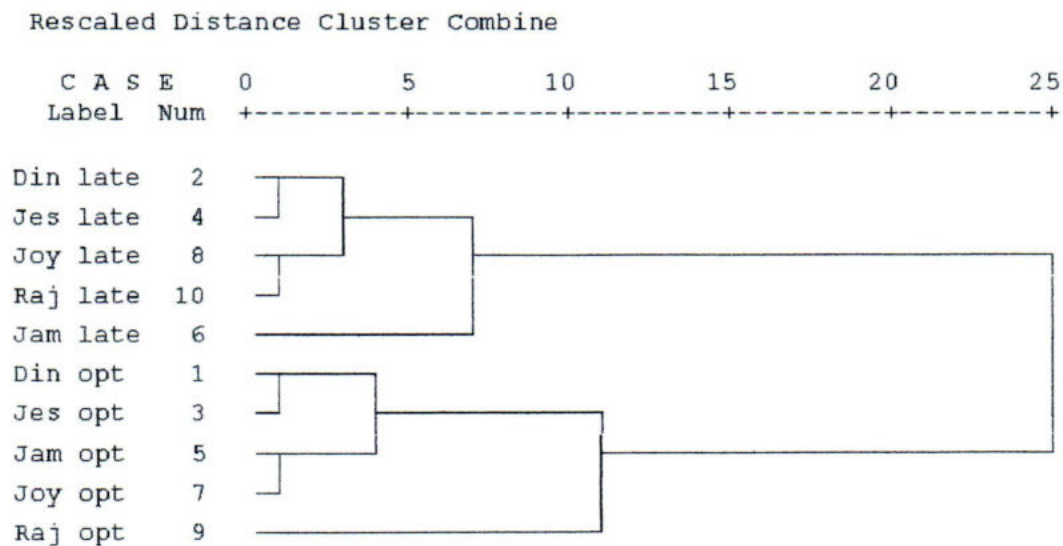


Fig. 4.5.2: Dendrogram using average linkage (between groups) for environment

SUMMARY AND CONCLUSIONS

CHAPTER V

SUMMARY AND CONCLUSIONS

Wheat is second most important cereal crop in Bangladesh. Its consumption in the country is increasing day by day but production is decreasing due to area reduction. The main cause of area reduction is strong competition with high yielding boro rice, maize, potato and other vegetable crops. In this situation yield increase in wheat is very important to reduce huge import cost. For that development of wheat variety with wide or specific adaptation is very important. Different methods are being used to study the stability of crop varieties. Among those regressions method proposed by Eberhart and Russel (1966) are widely used. But it has some limitations. Additive Main effect and Multiplicative Interaction (AMMI) model overcomes many limitations of previous methods. It integrates analysis of variance and principal component analysis into a unified approach. It fits the additive main effects of genotypes and environments by the usual analysis of variance and describes the non-additive part, genotype-environment interaction by principal component analysis. Eight advance wheat genotypes and two check varieties BARI Gom 21 (Shatabdi) and BARI Gom 24 (Prodip) were tested in ten environments of five wheat research stations viz. WRC, Dinajpur; RARS, Jessore and Jamalpur and RWRC, Joydebpur and Rajshahi to study their stability over tested locations by AMMI model. Stability was studied for four important characters viz, grain yield, heading days, grain filling duration and grain filling rate.

Combined analysis of variance revealed that there were significant variations for environments, genotypes and genotype x environment interaction for all the four characters studied. Most of the sum of squares for grain yield was attributed by environments (85.1%) followed by GEI (10.4%) and genotype (4.5%). The results revealed that the environments were diverse and there were substantial differences in genotypic response across environment for yield.

The results of AMMI analysis also showed that the interaction of ten genotypes of wheat for yield with 10 environments was predicted by the first four principal components of genotypes and environments. The stability estimate using AMMI stability value (ASV) and regression method was almost similar. The most stable genotype for yield was BAW 1118 followed by BAW 1122, BAW 1140 and BAW 1141. The most responsive genotypes were BAW 1130, Shatabdi and Prodip. Biplot of mean yield and interaction principal component axis confirmed the above result. Variation between BAW 1130 and Shatabdi was the highest for yield and that variation was mainly due to interaction effect of genotype and environment. All the late seeding environments were closer to each other than any optimum seeding environments. The difference between late and optimum seeding environments was due to both main and interaction effects. Biplot of IPCA1 and IPCA 2 were in agreement with other methods in respect of stability. Both seeding of Dinajpur and Joydebpur were the best for all genotypes, Rajshahi late seeding environment was the most discriminating.

Most of the sum of squares for heading days was attributed to environment (51.2%) followed by genotypes (39.02%) and G x E (9.59%). The result revealed that the influence of environments on heading days was the highest followed by genotypes. There were small differences in heading days across environments. According to both AMMI and regression methods heading days of BAW 1122 was the most stable followed by that of BAW 1137, BAW 1130 and BAW 1129. Biplot of heading days and IPCA 1 confirmed the stability of genotypes as found in regression and ASV method. Like yield, late seeding environments were closer to each other than optimum seeding environments for heading days. Rajshahi optimum seeding environment was the most discriminating due to its large PCA 1 and PCA 2 absolute score, whereas, Jessore late environment was the best for consistent heading days followed by Jamalpur timely seeding.

Influence of environment on grain filling duration was also the highest followed by genotype x environment interaction and then genotype itself. The interaction of

the ten wheat genotypes in 10 environments for grain filling duration was best predicted by the first two principal component axes of genotypes and environments. Further, interaction principal component axis captured mostly noise. Grain filling duration of BAW 1140 was the most stable according to regression and ASV methods. Rajshahi timely seeding and Joydebpur late seeding environments were the most discriminating in explaining the average grain filling duration of all sites. Both seeding of Dinajpur and optimum seeding of Joydebpur were the best in explaining the GFD of overall locations.

Influence of genotype was the highest in determining grain filling rate of the tested materials followed by environment. There was less differences in genotypic response for the character across environments. Grain filling rate of the genotypes in ten environments was best predicted by the first principal component axis of genotypes and environments. Stability of grain filling rate in two methods varied slightly mainly due to mean value, however, stability of BAW 1129 was the best in both methods. The most responsive was Shatabdi followed by BAW 1118. Biplot of grain filling rate and interaction principal component axis indicated that most of the genotypes were scattered around except BAW 1125 indicating that there were more interactive forces for determining grain filling rate of the genotypes. According to biplot of first two IPCAs, Prodip was the most stable followed by BAW 1140, BAW 1129, BAW 1122 and BAW 1137. Jessore timely seeding environment was the most discriminating followed by Dinajpur late and Jamalpur timely seeding environments in explaining the grain filling rates of the genotypes. Late seeding of Jessore and optimum seeding environments of Joydebpur, Dinajpur and Rajshahi and late environments of Rajshahi and Jamalpur were the best for explaining the grain filling rate of the tested genotypes.

Hierarchical classification of the 10 genotypes on the basis of data of 10 environments revealed that the stable genotypes BAW 1118, BAW 1140 and BAW 1141 were closer to each other. The check variety Shatabdi was closer to

BAW 1125, BAW 1129 and BAW 1130. However, Prodip was closer to BAW 1137.

Hierarchical classification of 10 environments on the basis of 10 genotypes indicated that late environments were closer to each other than any optimum environments and vice versa except some variations, Rajshahi optimum environment was different from other optimum and Jamalpur late was different from other late environments.

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