ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION AND STABILITY ANALYSIS IN PROMISING RICE (*Oryza sativa* L.) GENOTYPES

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The thesis attached hereto, entitled **"ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION AND STABILITY ANALYSIS IN PROMISING RICE (*Oryza sativa* L.) GENOTYPES"** was prepared under the direction of the chairman of the candidate supervisory committee and has been approved by all members of that committee and board of examiners as a partial fulfillment of the requirements for the degree of **MASTER OF AGRICULTURAL SCIENCE (PLANT BREEDING, PHYSIOLOGY AND ECOLOGY).**

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DECLARATION OF ORIGINALITY

This thesis represents the original work of the author, except where otherwise stated. It has not been submitted previously for a degree at any other University.

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ABSTRACT

In Myanmar, evaluating the genotype × environment interaction (G × E) is essential for rice breeding program because plant breeders use these interaction indicators in determining the stability and sustainability of a crop in wider and different environmental conditions. A study was conducted to evaluate the response of experimental rice genotypes on different planting methods, to estimate the magnitude of G × E interaction effect on yield and yield component characters of experimental rice genotypes and to estimate the yield stability of experimental rice genotypes to ecological conditions. The experiment was conducted using split plot design with three replications in three different locations namely (1) Sein Sar Pin village, Zayar Thiri Township, (2) Tarpet West village, Maubin Township and (3) Katode Phayargyi village, DaikU Township during 2015 dry season. Experimental genotypes served as sub plot and the three planting methods served as main plot. According to additive main effects and multiplicative interaction analysis (AMMI), transplanting method was found to be high yielding environments whereas broadcasting and line sowing methods were found to be low yielding environments in all three locations. The main effects of genotype and environment accounted for 12.67 % and 66.42 % respectively and the interaction effect accounted for 20.90 % for total variation. Therefore, it was found that G × E interaction distinctly existed. Among the five experimental rice genotypes, IR 87707-446-B-B-B (Yeanaelo - 4) produced the highest mean yield (5.42 t ha^{-1}) with below average stability and found to be suited in high yielding environments such as transplanting method at Zayar Thiri, Maubin and DaikU locations. IR 10 T 107 (Pyi Myanmar Sein) had the second highest mean yield (5.25 t ha^{-1}) with above average stability and found to be high yield in broadcasting and line sowing methods at Maubin location. GSR-IR-1-12-D10-S1-D1 had third highest mean yield (5.23 t ha^{-1}) with above average stability and this genotype performed the best yield in broadcasting and line sowing methods at Zayar Thiri and DaikU locations. CSR 36 was found maximum yield (6.50 tha^{-1}) in transplanting method at Maubin location although it was low yield with stable genotype in other tested environments. However, this genotype could be used for specific special quality traits such as long grain, good grain appearance and good grain quality with aromatic. Thee Htat Yin is widely grown variety in Myanmar especially in summer season of lower regions although it had low mean yield (4.63 t ha^{-1}) with stable genotype in all tested environments.

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CHAPTER I
INTRODUCTION

Rice is the most important agricultural commodity in Myanmar; it is a crucial commodity for both the country and the farmers for income and general livelihood. Rice area in Myanmar is about 7. 2 million ha, of which 6.2 million ha was grown in monsoon season and 1.0 million ha was grown in summer season (MOAI 2015). There are many different rice ecosystems in Myanmar such as favorable rice environments including rainfed lowland (48 %) and irrigated lowland (20 %) and unfavorable rice environments including submergence (14 %), salinity (2%), upland (3%), and drought prone areas (13%) (DOA 2014). Myanmar was the largest rice exporter in the world in the early 60's. However rice exports decreased due to many reasons. National average grain yield is 3.94 t ha^{-1}. Total production was 28.2 million MT in 2014-2015. To increase the production of paddy rice, measures are also being undertaken in growing high yielding varieties, including introduction of hybrid rice varieties.

Rice production is dependent to climatic factors and productivity of the crop is determined by soil fertility, planting methods, and other biotic and abiotic factors (Birhane 2013). The method of rice cultivation varies from region to region. There are three major rice establishments, namely, transplanting, wet seeding and dry seeding (Pandey 1994). Transplanting method covers 80 % of the global rice growing areas followed by broadcasting and line sowing methods. In broadcasting method seeds are sown haphazardly and in the line sowing method seeds are sown in line. In rice crop production, the planting methods have an impact on the growth and yield.

The Genotype × Environment (G × E) interaction structure is an important aspect of both plant breeding program and in the introduction of new crop cultivars. The use of stable cultivars over several environments for high yield and quality characteristics is important for many crops (Allard 1960 and Vargas et al. 1998). When cultivars are tested in terms of grain yield at the multi-environmental trials, big differences are commonly observed in yield performance over environments. This different yield response of cultivars from one environment to another is called G × E interaction. In order to decide to restructure the program to minimize the interaction effect, or exploit it to produce varieties with specific adaptation to particular environments, the breeder should be investigated G × E interaction (Eisemann et al. 1990).

Multilocation yield testing of genotypes provides an opportunity to the plant breeders to identify the adaptability of a genotype to a particular environment and also

stability of the genotype over different environments. The adaptability is defined as the ability of a crop variety to perform well over diverse environments (Abeysiriwardana et al. 1991). Genotypes respond to changes in environmental conditions such as temperature, rainfall, soil type, moisture and so on. To be widely accepted, a genotype must show good performance across a range of environments. However it is often difficult to find such cultivars (Robertson 1959; Falconer and Mackay 1995).

Recently, stable and sustainable yields in wider various environmental conditions are important for increased yield only. Plant breeders need to know varietal responses to different environments in selecting adaptive varieties. The development of cultivars, which are adapted to a wide range of diversified environment, is the ultimate aim of plant breeder in a crop improvement program (Muhammad et al. 2003). An ideal variety should have higher mean yield combined with a low degree of fluctuation (Tarakanovas and Ruzgas 2006). Therefore, the yield stability performance is one of the most desirable properties of a genotype to be released as a variety for cultivation.

To reduce the magnitude of G × E interaction, stable genotypes that perform consistently across environments should be selected (Gebeyehu and Assefa 2003). Stability of yield refers to the ability of a genotype to avoid substantial fluctuations in yield over a range of environments (Heinrich et al. 1983). Genotypes differ genetically in their stability across environments.

The promising varieties that are adapted to a wide range of target environments are the eventual goal of plant breeders. Thus, evaluation of genotypes under varying environmental conditions for yield and yield contributing characters is crucial to increase rice production. In this regard, the study was carried out with the following objectives.

(1) To evaluate the response of experimental rice genotypes on different planting methods
(2) To estimate the magnitude of G × E interaction effect on yield and yield component characters of experimental rice genotypes
(3) To determine the yield stability of experimental rice genotypes to different ecological conditions

CHAPTER II
LITERATURE REVIEW

2.1 Rice Varieties in Myanmar

Utilization of suitable varieties in rice cultivation is one of the most effective ways to increase productivity and production. Traditional varieties were widely cultivated until 1960s. There were many rice varieties in the country, many of them identical although called by different names in different localities. More than 2000 cultivars have been recorded in the country. Although improved varieties were introduced since 1965, the adoption was slow due to poor eating quality and average yield was about 1.7 t ha^{-1} up to 1970s. In 1973, Myanmar was involved in IRRI International Rice Testing Program (IRTP) by introducing rice breeding materials (Win 1991).

Continuous effort has been made for identifying some IRRI breeding lines as promising varieties such as IR 24, IR 28, IR 36 and IR 50 which are dwarf, early maturing, fertilizer responsive and high yielding. Since 1980s and after technical supports from international organizations in terms of human resource development and germplasm resource improved rice varieties were released to farmers for different rice environments (Win 1991). It was known that 7729 accessions for cultivated rice and 180 accessions for wild rice were collected in seed bank, DAR, Myanmar at present (DAR 2015).

As achievements, rice division (DAR) already released so many improved varieties nearly 106 varieties which were adapted to different ecological zones to farmers in current. Among them, 17 varieties were released through hybridization and selection method for irrigated and rain fed rice ecosystems from 1975 to 2007, 5 varieties improved by mutation breeding undertaken at Department of Agricultural Research (DAR), Myanmar from 1974 to 2005, 3 varieties through biotechnology and mutation breeding and 2 varieties through hybrid rice technology. With the collaboration between International Rice Research Institute (IRRI) and DAR, Myanmar, 79 varieties were released through introduction for different environments from 1967 to 2015 (DAR 2015).

2.2 Methods of Planting

Rice can be established by four principal methods: dry direct seeded rice (Dry-DSR), wet direct seeded rice (Wet-DSR), water seeding, and transplanting. Dry-DSR, wet-DSR, and water-seeding, in which seeds are sown directly in the main field instead of transplanting rice seedlings, are commonly referred to as direct seeding. Direct seeding is the oldest method of rice establishment. Prior to the 1950s, direct seeding was most

common, but was gradually replaced by puddle transplanting (Grigg1974; Pandey and Velasco 2005; Rao et al. 2007).

In rice, the planting methods have an impact on the growth and yield besides cultivation cost and labor requirements (Rani and Jayakiran 2010). Direct seeding method is early flowering and shorter day maturity because it had better crop establishment, with higher intra competition due to shorter spacing and plant density per unit area, triggering quicker reproductive phase responses. Direct seeded rice matures seven to ten days earlier than transplanted rice. The longer days to flowering and maturity in seedling transplanting could be due to longer period required for crop establishments compared to direct seeded method (Rana et al. 2014).

The mean effects of increasing plant population by different planting methods, is increased competition between adjacent plants which subsequently affect yield. This could be due to varying physiological processes that affect leaf sheath and blade extension and overall development processes under varying planting methods and spacing (Hay and Walker 1989). The higher grain yield of rice was obtained from transplanting method than the grain yield obtained from direct seeding method according to the finding of Anonymous (2004). The same finding also reported by Dingkuhn et al. (1991) that transplanted rice produce significantly higher grain yield than direct seeded. Transplanting method recorded the highest average yield because the planting distance ensure air circulation, water and light which are basic factors necessary for photosynthesis (Baloch et al. 2002).

2.3 Genotype × Environment Interaction

G × E interaction has been important and challenging issues for plant breeders in developing improved varieties (Letta 2007). The interplay between the effects of genotypes and environments is usually known as G × Einteraction (Moll and Stuber 1974). A breeder usually undertakes a series of genotypes evaluation across locations and over years before a new genotype is released.

The phenotype of an individual is determined by both the genotype and the environment; these two effects are not always additive which indicates that G × E interaction is present. The phenotypic response to change in environment is not the same for all genotypes, the consequences of variation in phenotype depend upon the environment. Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year (from season to season) (Dabholkar 1999).

Significant G × E interaction results from the changes in the magnitude of differences between genotypes in different environments or changes in the relative ranking of the genotypes (Falconer 1952 and Fernandez 1991). There are two forms of G × E interaction as qualitative (rank changes) and quantitative (absolute differences between genotypes) (Peto 1982). G × E interaction makes 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 and Yau 1995). The G × E interaction reduces the correlation between genotype and phenotype; and reduces the effectiveness of selection (Flores et al. 1998). It complicates selection and testing of plant genotypes. Measuring G × E is important in order to determine an optimum strategy for selecting genotypes with adaptation to target environments (Ramagosa et al. 1993; DeLacy et al. 1994 and Annicchiriarico 1997).

The mean across environments are adequate indicators of genotypic performance in trials with non-significant G × E interaction. However, when it is significant, these means genotypes differ markedly in relative performance with different environments. Selection form one environment may often perform poorly in another (Fox et al. 1997).

The significant G × E interaction effects demonstrated that genotypes responded differently to the variation in environmental conditions of location which indicated the necessity of testing rice varieties at multiple locations. G × E interaction is the major problem in the study of quantitative traits due to complication of interpretation in genetically experiments and difficult predictions (Tariku et al. 2013).

It can help in identifying traits and environments for better cultivar evaluation and those suitable for cultivation. Varieties that show low G × E interaction have high stable yields are desirable for plant breeders and farmers, because it indicates the lesser effect of environment on the performance of genotypes and their yields are largely due to their genetic composition (Mahalingam et al. 2013). An understanding of environmental and genotypic causes of G × E interaction is important at all stages of plant breeding, including parent selection based on traits, and selection based on yield (Jackson et al. 1998; Yan and Hunt 1998). Contribution of G × E interaction can be utilized to identify ideal test conditions and to formulate extensive genotype evaluation by eliminating unnecessary testing sites and by fine tuning of the breeding program. The presence of a large G × E interaction may necessitate the establishment of additional testing sites, thus increasing the cost of developing commercially important varieties (Kang 1993).

2.3.1 Genotype and Environment

Genotype means the complete set of genes inherited by an individual that is important for the expression of a trait under investigation. It is essentially a fixed character of the organism; it remains constant throughout life and is unchanged by environmental effects (Suzuki et al. 1981).

Phenotypic performance of genotypes in combination with different environments can be analyzed to quality the amount of variation attributable to the effects of the environment, genotype, and G × E interactions. Therefore, the phenotype changes continually and the direction of that change is a function of the sequence of environments which the individual experiences (Suzuki et al. 1981).

The environment means the sum total of the effects of physical, chemical and biological factors of an individual except its genotype. The term environment refers to all biotic and abiotic factors that influence plant growth at that location including weather (temperature, wind, precipitation, heat, cold, drought), impact of planting date, plant stand, disease pressure, soil type, and management factors including items such as irrigation, fertility, use of plant growth regulators, weed control, pressure and practices, insect pressure and control, etc (Kerby et al. 2000).

The environment divided into two categories; (i) Macro (ii) Micro-environments. Macro-environmental variation is caused by fluctuation in variable which have large and easily recognized effects (i.e. years locations, fertility levels, planting dates, etc.), whereas micro-environmental variation arises from plot to plot variability within macro-environments (Comstock and Moll 1963).

The environmental variation can be divided into two groups: predictable and unpredictable (Allard and Bradshaw 1964). The predictable environment includes the regular and more or less permanent features of the environment such as climate as determined by its longitude and latitude, soil type, rainfall and day length. It also includes what are called controllable variables (Perkins and Jinks 1971) e.g. the level of fertilizer applied, sowing date, sowing density, amount of irrigation and others that can be artificially created. The unpredictable or uncontrollable environments include weather fluctuations such as differences between seasons in terms of amount and distribution of rainfall and temperature, and other factors, such as established density of the crop. The absence or low level of interaction will be useful for uncontrollable variables, whereas for the controllable variables a high level of interaction in the favorable direction is desirable to obtain maximal performance (Chahal and Gosal 2002).

2.3.2 Classification of genotype × environment interactions

G × E interaction occurs when differences between genotypes are not the same in all locations within and across seasons/years (Edmeades et al. 1989). It is the inconsistency of relative performance of genotypes over environments (Hill et al. 1998). The G × E interaction is considered as crossover or qualitative if it leads to change in relative ranking of genotypes in different environments. Crossover interactions are of interest in plant breeding because these affect the genotypes to be selected in a given environment. Such interactions also suggest that genotypes are specifically adapted to environments (Allard and Bradshaw 1964).

The non-crossover of quantitative G × E interaction, on the other hand results in differential change of mean but not of ranking of different genotypes and influences the nature and magnitude of components of genetic variances and other related parameters like heritability and genetic advance (Allard and Bradshaw 1964). The cultivar rank changes are of greater importance than scale change interactions in cultivar trials conducted over a series of environments (Becker and Leon 1988).

The breeder is mainly interested in the ranking of genotypes in different environments and in the changing of these rankings (Kang 1993). For plant breeder, large G × E interaction impedes progress form selection and has important implications for testing and cultivar release (Smithson and Grisely 1992). Anyway, breeders are only wanted to know whether the best genotype in one environment is also the best in the other. Hence, G × E interaction is critical only if it involves significant crossover interactions (significant reversal in genotypic rank across environments) (Becker and Leon 1988).

When breeders can do to overcome the problem of G × E interaction depends upon the relative importance of variance components. Moreover, breeding programs aimed to develop stable genotypes also depend upon whether a breeder is dealing with predictable or unpredictable environmental variation. Whenever dealing with predictable environments variation, the first step that should be taken is to identify the differences. There is no difficulty when differences are recognizable, for example, differences in the seasons such as varieties to be developed for the rainy season or post-rainy season. Breeders can develop varieties suitable for both these seasons because the environmental variation is defined (Dabholkar 1999).

Yield trials are tested in the same locations (L) and genotypes (G) and over years (Y), G × E analysis of variance may be partitioned into components due to G × L, G × Y

and G × L × Y. Significance of mean square for G × L generally suggests that the region for which genotypes are being bred comprises of a number of special environments. In such circumstances the geographic region could be subdivided into sub regions which are relatively homogeneous. Varieties should be bred which are specifically adapted to these ecotypes. Implication of G × Y interaction is very different from G × L interaction. This is because year to year fluctuations cannot be predicted in advance and breeders can hardly aim their program to develop varieties suited to particular years (Dabholkar 1999).

In some situations, environmental variation is predictable but can also be corrected. It is relatively easier to develop varieties specifically adapted to predictable environmental situations than to breed for unpredictable environmental variations. The aim of the breeding program should be to develop genotypes that can withstand unpredictable transient environmental fluctuations. In other words, widely adapted genotypes should be bred (Dabholkar 1999).

The G × E interaction and grain yield stability analysis of rice (*Oryza sativa* L.) genotypes evaluated in north western Ethiopia by using AMMI model. They reported that largest proportion of the total variation in grain yield was attributed to environments in this trial and all of the evaluated genotypes were affected by the G × E interaction effects, so that no genotype had superior performance in all environments. Most of the genotypes showed environment specificity. In this study, the AMMI model classified the testing environments into three sections. Accordingly, six of the tested genotypes were found to be best for environments ENV1, ENV2 and ENV3; while the other six genotypes were found best for environments ENV4, ENV5, ENV6, ENV7 and ENV8. However, four of the tested genotypes were not found best to any of the testing environments. Among the tested genotypes, three genotypes were selected and promoted to verification based on their performance for grain yield and other agronomic traits including earliness, medium to tall height, high spikelet fertility percentage, white seed color, big seed size, better disease reaction and farmers' preferences (Tariku et al 2013).

2.4 Concepts of Stability

Stability statistics can be classified into three distinct groups (Types I, II, and III) (Lin et al. 1986).

Type 1: A genotype is considered to be stable if its among-environment variance is small. Becker and Leon (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 Leon (1988) called this stability the dynamic or agronomic concept of stability and this dynamic concept of stability relates to Type II 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 1972) stability variance 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 men at of all the genotypes in all locations. Type 3 is also part of the dynamic or agronomic stability concept according Becker and Leon (1988). Methods to describe type 3 stability are the methods of Eberhart and Russell (1966). All stability procedures based on quantifying GEI effects belong to the dynamic concept (Becker and Leon 1988).

A favorable genotype is one that combines both high mean yield and performance stability making it acceptable over a wide range of environmental conditions (Allard and Bradshaw 1964). Each stability statistic reflects different aspects of yield stability and no single method can adequately explain performance across different environments. Therefore, it is better that a MET's data set is evaluated through different aspects of yield stability for a reliable G × E interaction and effective selection of favorable genotypes (Kang 1998; Flores et al. 1998).

2.5 Statistical Methods to Measure G × E Interaction

A combined analysis of variance procedure is the most common method used to estimate the existence of G × E Interaction from replicated multilocation trials. If GEI variance is found to be significant, different statistical methods have been proposed for estimation and partitioning of the G × E interactions and the stability and can be broadly categorized into four groups: conventional analysis of variance, parametric approach, non-parametric, and multivariate methods (Rahmatollah et al. 2012).

2.5.1 Stability analysis or parametric approaches

Although there is no unanimous concept for the phenotypic stability, several methods, and models have been used to explain the G × E interaction. These include the use of uni-segmented and bi-segmented linear regression (Cruz et al. 1989; Eberhart and Russel 1966; Finlay and Wilkinson 1963; Perkins and Jinks 1971; Perkins and Jinks 1968a, b; Shukla 1972; Toler 1990; Toler and Burrows 1998; Verma et al. 1978), where the basic idea consists of regressing the genotypes performances on the environmental mean yields, expressed by an environmental index, through a linear or a non-linear model in the parameters. Stability analysis provides a general summary of the response patterns of the genotypes to environmental change. Freeman (1973) termed the main type of stability analysis, joint regression analysis or joint linear regression (JLR). It involves the regression of the genotypic means on an environmental index. Joint regression analysis provides a means of testing whether the genotypes have characteristic linear responses to changes in environments. Joint regression analysis was first proposed by Yates and Cochran (1938) and then widely used and reviewed by various authors (Finlay and Wilkinson 1963; Eberhart and Russell 1966; Wright 1971; Freeman and Perkins 1971; Shukla 1972; Hardwick and Wood 1972; Freeman 1973; Hill 1975; Lin et al. 1986; Westcott 1986; Becker and Leon 1988; Baker 1988; Crossa 1990; Hohls 1995).

2.5.1.1 Regression coefficient (b_i) and deviation mean square (S^2_{di})

Simple linear regression provides a conceptual model for genotypic stability and is the most widely used provides in plant breeding (Ramagosa and Fox 1993). This model is also called the Finlay and Wilkinson (1963) approach. The regression of each genotype's mean yield against the mean yields of an environmental is determined and the stability range is determined by the main effects multiplied by the regression coefficients of genotypes. The G × E interaction is divided into two segments; a component due to linear regression (b_i) of the i^{th} genotype on the environment mean and a deviation (d_{ij}). Therefore

$$GE_{ij} = b_i E_j + d_{ij}$$

$$Y_{ij} = \mu + G_i + E_j + (b_i E_j + d_{ij}) + e_{ij}$$

The regression coefficient was determined by regressing the mean of all genotypes on the environmental mean, and plotting the obtained genotype regression coefficients against the genotype mean yields (Finlay and Wilkinson 1963). The genotype

pattern obtained when genotype regression coefficients are plotted against genotype mean yields (Figure 2.1). Regression coefficients approximating 1.0 indicated average stability. When this is associated with high mean yield, varieties have good general adaptability. When associated with low mean yield, genotypes are poorly adapted to all environments. Regression values above 1.0, describe genotypes with increasing sensitivity to environmental change (below average stability) and greater specificity of adaptability to high yielding environments. Regression coefficients below 1.0 provide a measure of greater resistance to environmental change (above average stability) and, therefore, increasing specificity of adaptability to low yielding environment. The model proposed by Eberhart and Russell (1966) is

$$Y_{ij} = \mu + b_i I_i + \delta_{ij} + \varepsilon_{ij}$$

where, Y_{ij} is the mean for the genotype i at location j; μ is the general mean of genotype i; b_i is the regression coefficient for the i^{th} genotype at a given location index, which measures the response of a given to varying location; I_i is the environmental index, which is defined as the mean deviation for all genotypes at a given location from the overall mean; δ_{ij} is the deviation from regression for the i^{th} genotype at the j the location; ε_{ij} is the mean for experimental error. Eberhart and Russell (1966) reported two parameters of stability:

$$\text{Regression coefficient, } b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

where, Y_{ij} is the mean of the i^{th} genotype at j environment; and I_j is the environmental index which is defined as the mean deviation for all genotypes at a given location from the overall mean.

$$I_j = \frac{\sum_i y_i}{t} - \frac{\sum_i \sum_j y_{ij}}{ts}$$

$$I_j = \frac{\text{total of all varieties at } j^{th} \text{environment}}{\text{number of genotype}} - \frac{\text{grand total}}{\text{total number of observations}}$$

$$\text{Mean square deviation from linear regression, } S_{di}^2 = \frac{\sum_j \delta_{ij}^2}{s-2} - \frac{S_e^2}{r}$$

where, δ_{ij}^2 is the deviation from regression of the i^{th} genotype at j^{th} environment and S_e^2 is the estimate of pooled error.

The deviation sums of squares are the sums of variance due to deviation from

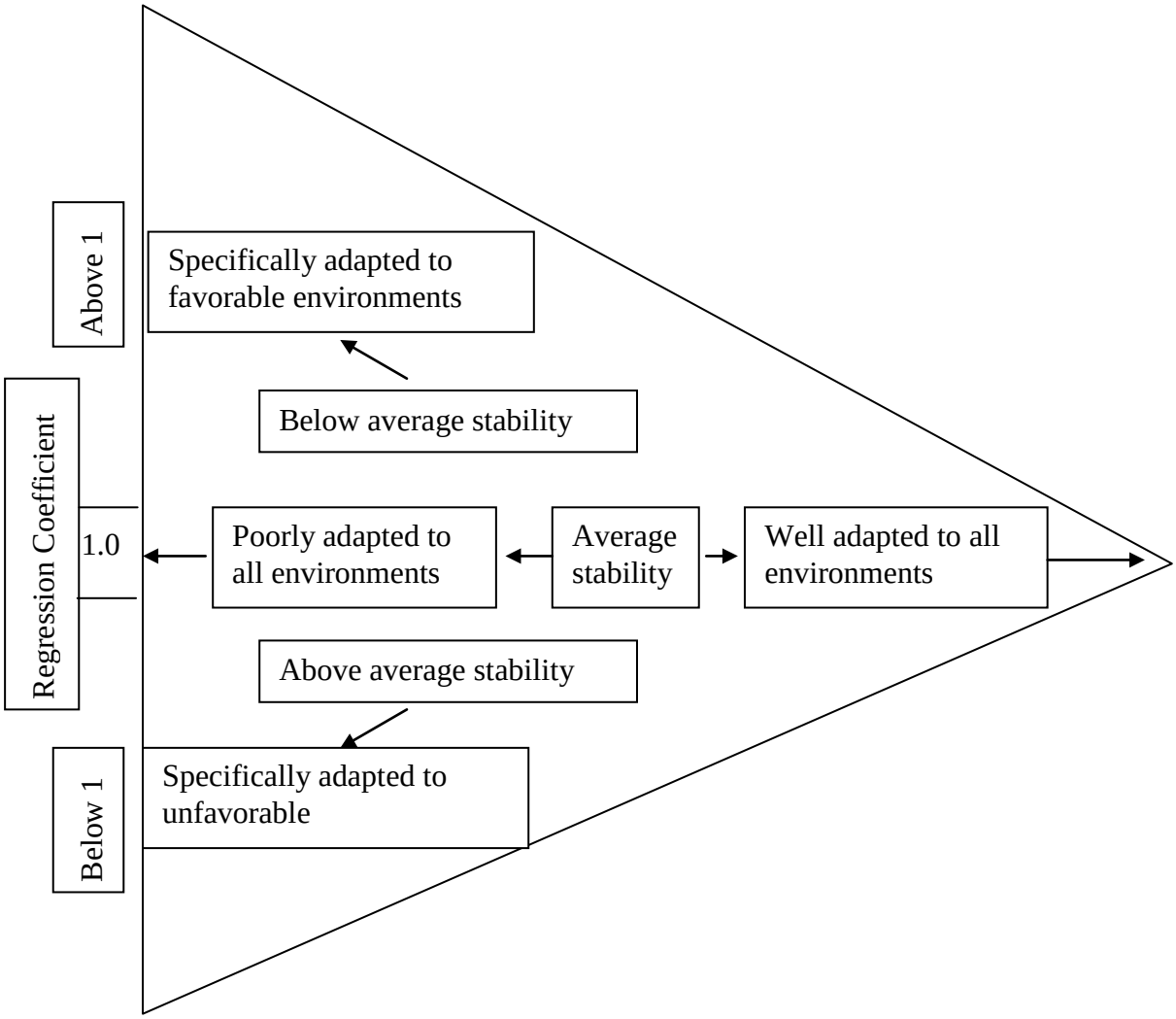

Figure 2.1 A generalized interpretation of the genotype pattern obtained when, genotypic regression coefficients are plotted against genotypic mean, adapted from Finlay and Wilkinson (1963).

regression divided by (S-2), and subtracting pooled error mean square, where S stands for the number of locations for each variety (Eberhart and Russell 1966). Therefore, varieties which have a less predictable response for a given set of environments have a probability of F value to zero and will deviate significantly from linearity.

$$S^2_{di} = \frac{1}{s-2}\left[E_j(X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X}\ldots)^2 - (b_i - 1)^2 E_j(\bar{X}_j - \bar{X}\ldots)^2\right]$$

According to model of Eberhart and Russell (1966), an ideal genotype would have a high mean performance with stability over a wide range of environments. A stable genotype has regression coefficient (b_i) equals to one and deviation from regression (S^2_{di}) equals to zero.

The using of the combination of b_i and S^2_{di} as a stability parameter was suggested by Becker and Leon (1988). Many scientists consider b_i as a response parameter and S^2_{di} as a stability parameter, since additional information on average response of a genotype to favorable environments is given by b_i, this is schematically presented in Figure 2.2. Although many authors and breeders used the regression approach, simultaneous studies emphasized the limitations, biologically and statistically (Freeman and Perkins 1971; Westcott 1986). There are statistical limitations: firstly genotypes mean and marginal means of the environments are not independent form one another. This problem may be overcome by a large number of genotypes used (Freeman and Perkins 1971).

Secondly, errors associated with the slopes of the genotypes are not statistically independent, because the sum of squares for deviation, with (G-1) (E-1) df, can't be subdivided orthogonally among the G genotypes (Crossa 1990) and thirdly, this method assumes a linear relationship between interaction and environmental means, which is not always the case and results may be misleading (Westcott 1986).

Biologically limitation seems to be in the case where only a few low or high yielding sites are included in the analysis and the genotype's position in the range is mostly determined by its performance in a few extreme environments which in turn generated misleading results (Westcott 1986). Regression analysis should be used with caution when the data set includes results from only a few extremely high or low yielding locations (Crossa 1990).

2.5.2 Multivariate analysis techniques

Multivariate analyses are appropriate for analyzing two-way matrices of genotype and environments. Multivariate techniques are widely applied in stability analysis to

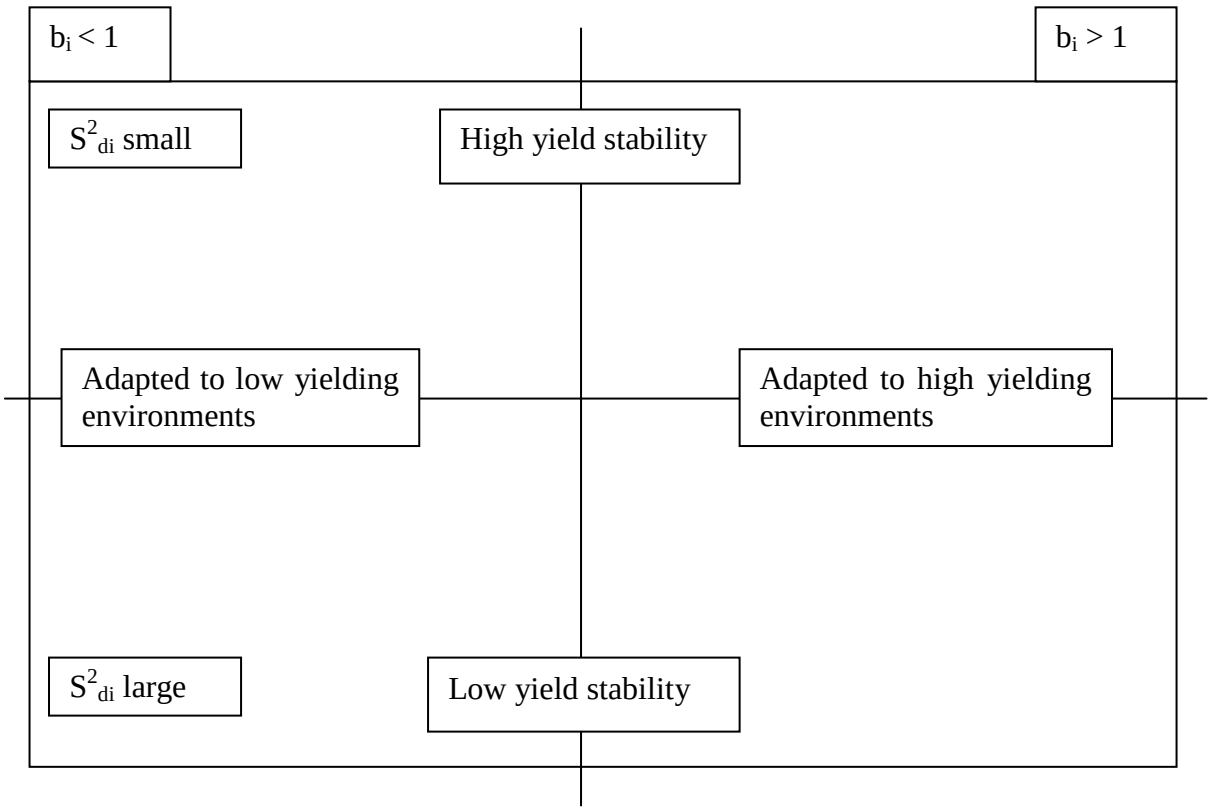

Figure 2.2 Interpretation of the parameters b_i and S^2_{di} of the regression approach (Becker and Leon 1988).

provide further information on real multivariate response of genotypes to environments. The multivariate analysis has three main purposes: to eliminate noise from the data pattern (i.e to distinguish systematic form nonsystematic variation), to summarize the data and to reveal the structure in the data (Becker and Leon 1988).

Two groups of multivariate techniques have been used to elucidate the internal structure of genotype × environment interaction:

1. Ordination techniques, such as principal component analysis, principal coordinate's analysis, and factor analysis, assume that the data are continuous. These techniques attempt to represent genotype and environment relationships as faithfully as possible in al low dimensional space. A graphical output displays similar genotypes' or environments near each other and dissimilar items are farther apart. Ordination is effective for showing relationships and reducing noise (Gauch 1982).

2. Classification techniques such as cluster analysis and discriminate analysis, seek discontinuities in the data. These methods involve grouping similar entities in clusters and are effective for summarizing redundancy in the data (Crossa 1990). Through multivariate analysis, genotypes with similar responses can be clustered, hypothesized, and later tested, and their data can be easily summarized and analyzed (Crossa 1990 and Hohls 1995).

2.5.2.1 Additive main effects and multiplicative interaction (AMMI)

AMMI is a combination of analysis of variance for the main effects of the G × E interaction (Zobel et al. 1988 and Gauch 1988). It can be used to analyze mult0ilocation trials. There are three traditional models, analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and environment main effects, linear regression models account for only a small portion of the interaction sum of squares (Zobel et al. 1988).

The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trial, because it provides and analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch 1988). Secondly, AMMI clarifies the G × E interaction and it summarizes patterns and relationships of genotypes and environments (Zobel et al.1988). The third use is to improve the accuracy of yield estimates. Gains have been obtained in 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 and Crossa 1990). Such

gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments or to improve efficiency in selecting the best genotypes.

The AMMI model combines the analysis of variance of the genotype and environment main effects with principal components analysis of the genotype and environment interaction. It has proven useful for understanding complex GEI. The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments. AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters. The model equation is:

$$Y_{ij} = \mu + G_i + E_i + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

Where Y_{ij} is the mean yield of ith genotype in the jth environment; μ is the grand mean; G_i is the gth genotype effect; E_i is the eth environment deviations from the grand mean; λ_k is the eigen value of IPCA analysis axes k; γ_{jk} are the genotype and environment principal component scores for axes k; n is the number of principal components retained in the model and e_{ij} is the error term.

In the analysis of variance, the total variation is partitioned into three sources, namely genotypes, environment and G × E interactions. In this regard, a review of Purchase (1997) revealed that, in most yield trials, the proportion of sum of squares due to differences among sites ranged from 80 to 90% and the variation due to G × E interactions is often larger than that of the genotypes. Hence AMMI model can produce biplot graphs, which display the variability of genotypes and G × E interactions.

Regarding agricultural problems form G × E interaction, there were two basic options, on aimed at the genotypes and the other at the environments (Ceccarelli 1989; Simmonds 1991 and Zavala et al. 1992). One option is to seek a high yielding, widely adapted genotype that wins throughout the growing region of interest. The other option, particularly relevant when the first fails, is to sub divide the growing region into several relatively homogeneous macro-environments (with little interaction within each microenvironment) and then breed and recommend varieties form each. As explained earlier, AMMI can help with both of these options.

The advantages of the AMMI model are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman 1990). Within limits, any model may be expected to fit the data from which it was derived.

However, the AMMI model has a good chance of being able to predict the performance of cultivars in similar sites and future years (Gauch 1988).

The PCA of AMMI partitions G x E interactions into several orthogonal axes, the interaction principal component analyses (IPCA). Gauch and Zobel (1996) explained that AMMI 1 with IPCA 1 and AMMI 2 with IPCA 1 and IPCA 2 are usually selected and the graphical representation of axes, either as IPCA 1 or IPCA 2 against main effects or IPCA 1 against IPCA 2 is generally informative. When AMMI 3 and higher models are presented for agricultural data, the third and higher IPCA axes are dominated by noise and have no predictive value (Van Eeuwijk 1995).

Since AMMI has the biplot feature, genotypes and environments are plotted on the same diagram, facilitating inference about specific interactions of individual genotypes and environments by using the sign and magnitude of PCA 1 values. Any genotype with a PCA 1value close to zero means general adaptation to the tested environment. A large genotypic PCA 1 scores reflects more specific adaptation to environments with PCA 1 score of the same sign. AMMI provides a better biological explanation of G × E than the regression model and it has been found useful when applied to across years analyses with a higher element of unpredictability (Yau 1995; Gauch and Zobel 1996 and Annicchiarico 1997).

The AMMI model is more efficient in determining the most stable and high yielding genotypes in multi-environment trials compared to earlier procedures (Finlay and Wilkinson 1963; Eberhart and Russel 1966). Biplot analysis is possibly the most powerful interpretive tool for AMMI models. Biplots are graphs where aspects of both genotypes and environments are plotted on the same axes so that interrelationships can be visualized. The AMMI biplot where the main effects (genotype mean and environment mean) in X axis and IPCA1 scores for both genotypes and environments are plotted in Y axis. The effectiveness of AMMI procedure has been clearly demonstrated (Crossa et al. 1991; Das et al. 2009; Tarakanovas and Ruzgas 2006).

The combination of ANOVA and PCA in the AMMI model, along with prediction assessment, is a valuable approach for understanding G × E interaction and obtaining better yield estimates. The interaction is showed in the form of a biplot display where PCA scores are plotted against each other and it provides visual inspection and interpretation of the G × E interaction components. Integrating biplot display and genotypic stability statistics allows genotypes to be grouped based on similarity of performance across diverse environments (Tsige 2002).

AMMI has its weaknesses as other models. The nature of the residuals after fitting the additive main effects inevitably produces the appearance of multiplicative effects. Consequently the sum of square for fitting the multiplicative term, which may be read directly from the latent root proportions of explained variation, will tend to be much larger than the expected value. Therefore, it is not possible to recommend a single model to be used at all times, because these models, depending on the type of data and research purposes, can be complimentary rather than being competitive to each other. However, studies may differ depend on the quality of the data, the different methods applied to an experiment will lead to similar conclusions (Baril et al. 1995).

CHAPTER III
MATERIALS AND METHODS

3.1 Experimental Site

The field experiment were conducted at three locations; Sein Sar Pin village, Zayar Thiri (19° 51' N latitude and 96° 7' E longitude at 297 m of sea level), Tarpet West village, Maubin (16° 73' N latitude and 96° 65' E longitude at 13 m of sea level), Katode Phayarkyi village, DaikU Township (17° 33' N latitude and 96° 48' E longitude at 18 m of sea level) during the dry season 2015.

3.2 Materials

A total of five rice genotypes were used in these experiments (Table 3.1). These experimental rice genotypes were introduced from IRRI through International Network Genetic Evaluation for Rice (INGER) program. DAR released three genotypes namely IR 10 T 107 and CSR 36, and IR 87707-446-B-B-B among the tested genotypes in 2015 as Pyi Myanmar Sein, Shwe Aesan and Yeanaelo - 4 during conducting this experiment.

3.3 Methods

The experimental set-up was a split plot design with three replications. Three planting methods namely broadcasting, line sowing and transplanting method served as main plot. Tested genotypes namely IR 10 T 107, CSR 36, IR 87707-446-B-B-B, GSR - IR-1-12-D10-S1-D and Thee Htat Yin served as sub plot. In this experiment, planting methods served as microenvironments. Therefore, nine different environments were comprised of the following treatments. M1Z (Broadcasting at Zayar Thiri), M2Z (Line sowing at Zayar Thiri), M3Z (Transplanting at Zayar Thiri), M1M (Broadcasting at Maubin), M2M (Line sowing at Maubin), M3M (Transplanting at Maubin), M1D (Broadcasting at DaikU), M2D (Line sowing at DaikU), M3D (Transplanting at DaikU).

In broadcasting method, the plot size was 10 m^2 and seed rate was 155.61 kg ha^{-1}. Row length was 2 m long and the seed were randomly distributed. In line sowing method, the plot size was 10 m^2 and seed rate was 155.61 kg ha^{-1}. Row length was 2 m long and row spacing was 20 cm. Each plot had 10 rows. The seed rate for transplanting method was 155.61 kg ha^{-1}. Nursery was raised for seedling transplanted rice and the seedlings were 25 days old, they were uprooted and transplanted to experimental plots with 2-3 seedlings $hill^{-1}$. The plot size was 10 m^2 and row length was 2 m long. The spacing was 20 cm between rows and 15 cm between plants. Each plot had 10 rows. Plantation of broadcasting and line sowing were done on the day seeds were sown in the nursery for

Table 3.1 List of experimental rice genotypes and their sources

No.	Genotypes	Pedigree	Parental Source	Origin	Organization of Seed Source	Days to Maturity	Distinct Characters
1	IR 10 T 107 (Pyi Myanmar Sein)	IR 83412-B-B-3-1-1-1	(IRRI 126/IRRI 135)	IRRI	DAR	116	Early, tolerance to salinity stress
2	CSR 36 (Shwe Asean)	CSR 36	CSR 13/Panvel 2/ IR 36	India	DAR	115	Early, tolerance to salinity stress
3	IR 87707-446-B-B-B (Yeanaelo-4)	IR 87707-446-B-B-B	IR 77298-14-1-2-10/IR 77298-5-6-11 (IR 64 Nils)	IRRI	DAR	114	Early, tolerance to drought
4	GSR-IR -1-12-D10-S1-D1	GSR-IR -1-12-D10-S1-D1	Pyramided line (Backcross breeding and pyramiding crosses)	IRRI	DAR	115	Early, adaptable for multienvironments
5	Thee Htat Yin (Check variety)	IR13240-108-2-3	IR30 (BPHS)/ BABAWEE//IR36	IRRI	DAR	119	Early, High yielding variety

Source: International Network Genetic Evaluation for Rice (INGER)

transplantation to maintain the same seedling age for all treatments.

3.4 Crop Management

The field was prepared with one stroke of ploughing, three rotary and leveling was done with bullock before broadcasting and seed drilling. Basal application of Triple Super Phosphate (62.738 kg ha^{-1}) was applied at final leveling for all experimental sites. The split application of Urea and Potash (188.21 kg ha^{-1} and 62.74 kg ha^{-1}) were applied for vegetative stage (94.11 kg ha^{-1} and 31.37 kg ha^{-1}), reproductive stage (47.05 kg ha^{-1} and 15.69 kg ha^{-1}) and flowering stage (47.05 kg ha^{-1} and 15.69 kg ha^{-1}). This was recommended by Soil Science Section, Soil Science, Water Utilization and Agricultural Engineering Division, DAR. Cultural practices and control measures for pests and diseases were done as required. Genotypes were harvested at the time of physiological maturity.

3.5 Data Collection

The data were recorded on randomly twelve selected plants from each genotype in each replication for the following characters according to International Rice Research Institute (IRRI) Standard Evaluation System for Rice (SES) descriptor.

(1) Days to Maturity (days): Average days of three replicated plots were counted from sowing to 90% grain maturity on most of the plants.

(2) Plant height (cm): Average height of randomly selected plants was measured from the base of plant to the top of panicle on the main stem from each genotype in each replication.

(3) Number of effective tillers m^{-2}: Number of effective tiller m^{-2} was counted form each genotype in each replications.

(4) Panicle length (cm): Average length of randomly selected panicles was measured from the base of pedicle to the top to panicle in each replication.

(5) Number of spikelet $panicle^{-1}$: Average spikelets $panicle^{-1}$ from randomly selected panicles was accounted from each genotype in each replication.

(6) Filled grain %: Filled grain % was calculated with the following equation.

$$\text{Filled grain } \% = \frac{\text{Filled grain}}{\text{Total grain}} \times 100$$

(7) Thousand grain weight (g): The 1000 randomly selected seeds weigh from each genotype in each replication.

(8) Grain yield (t ha^{-1}): Plot grain yield were recorded in grams and converted into t ha^{-1} from each genotype in each replication.

3.6 Statistical Analysis

Analysis of variance for each environment and combined analysis of variance across the tested environments were calculated by using Statistix (8.0). Additive Main Effects and Multiplicative Interaction and Stability Analysis were processed by using Plant Breeding Tools (PB Tools). Stability parameters: regression coefficient (b_i) and mean square deviation (S^2_{di}) from linear regression were estimated by Finlay and Wilkinson (1963).

CHAPTER IV
RESULTS AND DISCUSSION

4.1 Analysis of Variance for Evaluated Characters in Sein Sar Pin Experiment

Mean squares obtained for yield and agronomic characters of experimental rice genotypes in three planting methods at Sein Sar Pin village, Zayar Thiri are presented in Table 4.1.

4.1.1 Days to maturity

The effect of planting methods on days to maturity were highly significant ($p<0.01$) and this indicated that days to maturity were influenced by different plantings (Table 4.1). Broadcasting and line sowing methods had shorter days to maturity than transplanting method. There were highly significant variations among genotypes for days to maturity. Among the experimental rice genotypes, IR 10 T 107 was significantly the earliest days to maturity (112.22 days) followed by IR 87707-446-B-B-B (112.67 days) while Thee Htat Yin was the late maturing (113.78 days) to reach its physiological maturity (Table 4.1). The interaction effect of genotypes and planting methods was significant and this mean that changes of days to maturity in genotypes were influenced by different planting methods.

4.1.2 Plant height

Plant height was significantly influenced by genotypes (Table 4.1). Among the experimental rice genotypes, IR 87707-446-B-B-B has the maximum plant height (110.10 cm) followed by IR 10 T 107 (109.51 cm) and CSR 36 (109.23 cm) while Thee Htat Yin has the minimum plant height (99.97 cm) (Table 4.1). Plant height was not significantly affected by planting methods. The interaction effect of genotypes and planting methods was not significant and this mean that changes of plant height in genotypes were not influenced by different planting methods.

4.1.3 Number of effective tillers m^{-2}

The effect of planting methods on number of effective tillers m^{-2} were highly significant ($p<0.01$). This showed that numbers of effective tillers m^{-2} were influenced by different plantings (Table 4.1). The highest tiller numbers was obtained under transplanting followed by line sowing and broadcasting methods. There were highly significant variations among genotypes for number of effective tillers m^{-2}. Among the experimental rice genotypes, GSR-IR-1-12-D10-S1-D1 has the highest tillers number

Table 4.1 The Mean performance of yield and yield component characters of experimental rice genotypes at Sein Sar Pin village, Zayar Thiri Township, Nay Pyi Taw in the dry season, 2015

Treatment	DTM	PH	ET/m^2	PL	SPK	FG%	1000 Gwt	Yld
Broadcasting (M1)	110.67 b	105.92 a	241.16 b	21.74 a	103.08 b	81.55 b	23.10 a	4.68 b
Line Sowing (M2)	109.53 c	108.31 a	241.63 b	22.27 a	103.40 b	81.83 b	23.25 a	4.71 b
Transplanting (M3)	118.73 a	106.05 a	260.05 a	22.67 a	110.40 a	89.12 a	23.12 a	5.83 a
LSD 0.05	**1.02**	**3.65**	**5.80**	**1.94**	**2.53**	**4.83**	**0.59**	**0.11**
Genotypes								
IR 10 T 107	112.22 c	109.51 a	249.11 ab	22.55 ab	104.13 b	85.31 a	22.28 b	5.15 c
CSR 36	112.78 bc	109.23 a	235.79 c	22.54 ab	103.78 b	83.11 a	24.38 a	4.97 c
IR 87707-446-B-B-B	112.67 c	110.10 a	246.98 b	23.56 a	109.33 a	83.52 a	24.41 a	5.38 a
GSR-IR-1-12-D10-S1-D1	113.44 ab	106.96 a	256.60 a	20.30 c	106.89 ab	86.02 a	22.36 c	5.26 b
Thee Htat Yin (Check variety)	113.78 a	97.99 b	249.59 ab	22.15 b	104.00 b	82.84 a	21.35 d	4.58 d
LSD 0.05	**0.71**	**3.31**	**8.54**	**1.40**	**4.96**	**3.93**	**0.53**	**0.24**
Pr> F								
Planting Methods	0.00	0.24	0.00	0.46	0.00	0.01	0.77	0.00
Genotypes	0.00	0.00	0.00	0.00	0.12	0.37	0.00	0.00
PltM x Geno	0.00	0.11	0.01	0.18	0.02	0.24	0.54	0.00
CV % (a)	0.89	3.38	2.31	8.61	2.37	5.67	2.53	2.21
CV % (b)	0.65	3.19	3.55	6.50	4.83	4.81	2.39	4.95

In each column, means having a common letter are not significantly different at 5 % LSD

DTM = Days to maturity, PH = Plant height, ET/m^2 = Number of effective tillers m^{-2}, PL = Panicle length, SPK = Number of spikelets $panicle^{-1}$, FG % = Filled grain percent, 1000 Gwt= Thousand grain weight, Yld = Grain yield, PltM= Planting method, Geno = Genotypes

(256.60) followed by Thee Htat Yin (249.59) and IR 10 T 107 (249.11) while CSR 36 (235.79) has the least tillers numbers (Table 4.1). The interaction effect of genotypes and planting methods was significant and this means that variations of number of effective tillers m^{-2} in genotypes were influenced by different planting methods.

4.1.4 Panicle length

Panicle length was not significantly affected by planting methods. Transplanting method produced the longer panicle length (22.67 cm) than broadcasting (21.74 cm) and line sowing (22.27 cm) (Table 4.1). Panicle length was significantly influenced by genotypes. Among the experimental rice genotypes, IR 87707-446-B-B-B produced the longest panicle length (23.56 cm) followed by IR 10 T 107 (22.55 cm) and CSR 36 (22.54 cm) while GSR-IR-1-12-D10-S1-D1 produced the shortest panicle length (20.30 cm) (Table 4.1). The interaction effect of genotypes and planting methods was not significant and this mean that changes of panicle length in genotypes were not influenced by different planting methods.

4.1.5 Number of spikelets panicle^{-1}

The effect of planting methods on number of spikelets panicle^{-1} were highly significant ($p<0.01$). This indicated that number of spikelets panicle^{-1} were influenced by different plantings (Table 4.1). Transplanting method produced the highest number of spikelets panicle^{-1} (110.40) among three planting methods. Number of spikelet panicle^{-1} was not significantly influenced by genotypes. Among the experimental rice genotypes, IR 87707-446-B-B-B has the highest number of spikelets panicle^{-1} (109.33) followed by GSR-IR-1-12-D10-S1-D1 (106.89) while CSR 36 was the minimum spikelets panicle^{-1} (103.78) (Table 4.1). The interaction effect of genotypes and planting methods was significant and this mean that the number of spikelets panicle^{-1} in genotypes were influenced by different planting methods.

4.1.6 Filled grain percent

The effect of planting methods on filled grain percent were significant and filled grain percent were influenced by different planting (Table 4.1). Transplanting method gave higher number of filled grain percent than broadcasting and line sowing methods. There were not significant variations among genotypes for filled grain percent. Among the experimental rice genotypes, GSR-IR-1-12-D10-S1-D1 has the highest filled grain percent (86.02) followed by IR 10 T 107 (85.31) and IR 87707-446-B-B-B (83.52) while Thee Htat Yin has the least filled grain percent (82.84) (Table 4.1). The interaction effect of genotypes

and planting methods was not significant and this mean that changes of filled grain percent in genotypes were not influenced by different planting methods.

4.1.7 Thousand grain weight

Thousand grain weight was significantly differed due to varietal effects (Table 4.1). IR 87707-446-B-B-B produced the highest thousand grain weight (24.41 g) followed by CSR 36 (24.38 g) and IR 10 T 107 (22.28 g) while Thee Htat Yin produced the lowest thousand grain weight (21.35 g). Thousand grain weight was not significantly affected by planting methods. It was observed that the higher thousand grain weight (23.25 g) under line sowing method than transplanting (23.12 g) and broadcasting methods (23.10 g) (Table 4.1). The interaction effect of genotypes and planting methods was not significant and this mean that changes of thousand grain weight in genotypes were not influenced by different planting methods.

4.1.8 Yield performance of experimental rice genotypes in three planting methods

The grain yield was significantly influenced by genotypes (Table 4.1). Among the tested genotypes, IR 87707-446-B-B-B has the highest grain yield (5.38 t ha^{-1}) followed by GSR-IR-1-12-D10-S1-D1 (5.26 t ha^{-1}) and IR 10 T 107 (5.15 t ha^{-1}) which were significantly different among each other while Thee Htat Yin has the lowest grain yield (4.58 t ha^{-1}) followed by CSR 36 (4.97 t ha^{-1}) (Table 4.1).

Planting methods were significantly influenced the grain yield. Transplanting method produced the higher grain yield (5.83 t ha^{-1}) than line sowing (4.71 t ha^{-1}) and broadcasting method (4.68 t ha^{-1}). The interaction effect of genotypes and planting methods was significant and therefore, the genotype × planting methods interaction on grain yield was distinctly existed (Table 4.1).

Comparing the three methods of planting, all of the experimental rice genotypes had higher yield in transplanting method than broadcasting and line sowing methods (Table 4.2). This was due to number of effective tillers m^{-2}, number of spikelets $panicle^{-1}$ and filled grain percent. All of these parameters were high in transplanting method. This yield variation in the method of planting could be due to better establishment or growth of rice plants as a result of lesser competition for water, sunlight and nutrients.

Grain yield obtained from transplanting treatment was higher than grain yield obtained from treatments subjected to broadcasting and line sowing methods (Birhane 2013). The higher number of effective tillers m^{-2} under transplanting might be due to the optimal

Table 4.2 Mean comparison of grain yield (t ha^{-1}) as affected by planting methods and genotypes at Sein Sar Pin village, Zayar Thiri in the dry season, 2015

Genotypes	Grain yield (t ha^{-1})		
	Broadcasting	**Line sowing**	**Transplanting**
IR 10 T 107	4.96 a	4.80 ab	5.70 bc
CSR 36	4.46 b	4.73 ab	5.73 bc
IR 87707-44-B-B-B	4.86 a	4.56 ab	7.23 a
GSR-IR-1-12-D10-S1-D1	4.97 a	4.96 a	5.86 b
Thee Htat Yin	4.13 c	4.50 b	5.13 c
Mean	**4.68**	**4.71**	**5.93**
LSD 0.05		**0.40**	

Means followed by a same letter were not significant at 5 % level

spacing for growth of the plants which will result in higher yield reported by Birhane (2013). Significantly higher in number of spikelets panicle^{-1} and filled grain percent were by transplanting method as compared to direct seeding method and the differences was due to availability of moisture and nutrients to the crop plants at the panicle imitation stage (Pandey et al. 2001).

Grain yield of tested genotypes ranged from 4.13 t ha^{-1} to 4.97 t ha^{-1} in broadcasting system (Table 4.2). GSR-IR 1-12-D10-S1-D1 (4.97 t ha^{-1}) gave the maximum yield followed by IR 10 T 107 (4.96 t ha^{-1}) and IR 87707-446-B-B-B (4.86 t ha^{-1}) which were not significantly differences among each other whereas Thee Htat Yin (4.13 t ha^{-1}) which produced the minimum yield followed by CSR 36 (4.46 t ha^{-1}) which were significantly different from each other.

Grain yield of tested genotypes ranged from 4.50 t ha^{-1} to 4.96 t ha^{-1} in line sowing system (Table 4.2). The maximum yield was observed from GSR-IR 1-12-D10-S1-D1 (4.96 t ha^{-1}) followed by IR 10 T 107 (4.80 t ha^{-1}) and CSR 36 (4.73 t ha^{-1}) which were not significantly different among each other whereas Thee Htat Yin (4.50 t ha^{-1}) gave the minimum yield followed by R 87707-446-B-B-B (4.56 t ha^{-1}) which were not significantly differences from each other.

Grain yield of tested genotypes ranged from 5.13 t ha^{-1} to 7.23 t ha^{-1} in transplanting system (Table 4.2). Genotype 87707-446-B-B-B gave the maximum yield (7.23 t ha^{-1}) followed by GSR-IR 1-12-D10-S1-D1 (5.86 t ha^{-1}) which were significantly difference from each other whereas Thee Htat Yin (5.13 t ha^{-1}) produced the minimum grain yield followed by IR 10 T 107 (5.70 t ha^{-1}) which were not significantly differences from each other. Therefore, the present study revealed that the rank of genotypes for grain yield varied across the planting methods and therefore, genotypes × planting methods interaction on grain yield were distinctly existed.

4.2 Analysis of Variance for Evaluated Characters in Tarpet West Experiment

Mean squares obtained for yield and yield components characters of experimental rice genotypes in three planting methods at Tarpet West village, Maubin are presented in Table 4.3.

4.2.1 Days to maturity

The effect of planting methods on days to maturity were highly significant ($p<0.01$) and this indicated that days to maturity were influenced by different planting (Table 4.3). Broadcasting and line sowing methods had shorter days to maturity than

Table 4.3 The Mean performance of yield and yield components characters of experimental rice genotypes at Tarpet West village, Maubin Township, Ayeyarwadddy region in the dry season, 2015

Treatment	DTM	PH	ET / m^2	PL	SPK	FG %	1000 Gwt	Yld
Broadcasting (M1)	110.80 b	105.11 b	232.55 b	21.76 a	107.13 b	83.04 a	23.28 a	4.66 b
Line Sowing (M2)	110.13 b	105.59 b	235.73 b	20.96 b	109.13 b	80.35 a	23.30 a	4.82 b
Transplanting (M3)	119.13 a	110.14 a	260.60 a	21.91 a	116.60 a	84.84 a	23.21 a	5.83 a
LSD 0.05	**1.08**	**3.31**	**10.57**	**0.28**	**3.38**	**5.31**	**0.29**	**0.35**
Genotypes								
IR 10 T 107	112.56 b	106.06 c	250.11 a	20.40 b	111.67 a	83.47 a	23.52 b	5.58 a
CSR 36	112.89 b	108.87 bc	221.02 b	23.06 a	112.56 a	84.63 a	24.40 a	5.16 b
IR 87707-446-B-B-B	112.89 b	112.51 b	247.47 a	22.48 a	111.22 a	82.55 a	24.46 a	5.61 a
GSR-IR-1-12-D10-S1-D1	114.11 a	118.19 a	247.62 a	21.14 b	111.11 a	81.59 a	22.25 c	5.00 b
Thee Htat Yin (Check variety)	114.33 a	89.11 d	243.57 a	20.68 b	108.22 b	81.49 a	21.68 d	4.65 c
LSD 0.05	**0.51**	**4.80**	**11.55**	**0.86**	**2.57**	**5.32**	**0.43**	**0.26**
Pr> F								
Planting Methods	0.00	0.02	0.00	0.00	0.00	0.17	0.68	0.00
Genotypes	0.00	0.00	0.00	0.00	0.02	0.71	0.00	0.00
PltM x Geno	0.00	0.27	0.09	0.00	0.05	0.00	0.73	0.00
CV % (a)	0.95	3.06	4.29	1.29	3.01	6.33	1.25	6.83
CV % (b)	0.46	4.62	4.89	4.12	2.39	6.62	1.93	5.83

In each column, means having a common letter are not significantly different at 5 % LSD

DTM = Days to maturity, PH = Plant height, ET/m^2 = Number of effective tillers m^{-2}, PL= Panicle length, SPK = Number of spikelets $panicle^{-1}$, FG % = Filled grain percent, 1000 Gwt= Thousand grain weight, Yld = Grain yield, PltM= Planting method, Geno = Genotypes

transplanting method. There were highly significant variations among genotypes for days to maturity. Among the experimental rice genotypes, IR 10 T 107 was the earliest days to maturity (112.56 days) followed by IR 87707-446-B-B-B (112.89 days) and CSR 36 (112.89 days) while Thee Htat Yin (114.33 days) was the late maturing genotype (Table 4.3). The interaction effect of genotypes and planting methods was significant and this mean that changes of days to maturity in genotypes were influenced by different planting methods.

4.2.2 Plant height

The effect of planting methods on plant height were significant ($p<0.05$) (Table 4.3) and this showed that plant height was influenced by different plantings (Table 4.3). The highest plant height was obtained under transplanting method followed by broadcasting and line sowing methods. There were highly significant variations among genotypes for plant height. Among the experimental rice genotypes, GSR-IR-1-12-D10-S1-D1 (118.19 cm) was obtained the maximum plant height followed by IR 87707-446-B-B-B (112.51 cm) and CSR 36 (108.87 cm) while Thee Htat Yin (89.11 cm) produced the minimum plant height (Table 4.3). The interaction effect of genotypes and planting methods was not significant and this mean that changes of plant height in genotypes were not influenced by different planting methods.

4.2.3 Number of effective tillers m^{-2}

The effect of planting methods on number of effective tillers m^{-2} were highly significant and this indicated that number of effective tillers m^{-2} were influenced by different planting (Table 4.3). The highest tiller numbers was obtained under transplanting followed by line sowing and broadcasting methods. There were highly significant variations among genotypes for number of effective tillers m^{-2}. IR 10 T 107 produced the highest tillers number (250.11) followed by GSR-IR-1-12-D10-S1-D1 (247.62) and IR 87707-446-4-12-D10-S1-D1 (247.47) while CSR 36 (221.02) gave the least tillers number (Table 4.3). The interaction effect of genotypes and planting methods was not significant and this means that variations of number of effective tillers m^{-2} in genotypes were not influenced by different planting methods.

4.2.4 Panicle length

Panicle length was significantly affected by planting methods. Transplanting method produced the longest panicle length (21.91 cm) followed by broadcasting

(21.76 cm) and line sowing (20.96 cm) (Table 4.3). Panicle length was significantly influenced by genotypes. Among the experimental rice genotypes, CSR 36 produced the longest panicle length (23.06 cm) followed by IR 87707-446-B-B-B (22.48 cm) and GSR-IR-1-12-D10-S1-D1 (21.14 cm) while IR 10 T 107 produced the shortest panicle length (20.40 cm) (Table 4.3). The interaction effect of genotypes and planting methods was significant and this mean that changes of panicle length in genotypes were influenced by different planting methods.

4.2.5 Number of spikelets panicle^{-1}

The effect of planting methods on number of spikelets panicle^{-1} were highly significant ($p<0.01$) and this indicated that the number of spikelets panicle^{-1} were influenced by different plantings (Table 4.3). Transplanting method produced the higher spikelets panicle^{-1} (116.60) than line sowing (109.13) and broadcasting (107.13) methods. Number of spikelet panicle^{-1} was significantly influenced by genotypes. Among the experimental rice genotypes, CSR 36 gave the maximum spikelets panicle^{-1} (112.56) followed by IR 10 T 107 (111.67) and IR 87707-446-B-B-B (111.22) while Thee Htat Yin gave the minimum spikelets panicle^{-1} (108.22) (Table 4.3). The interaction effect of genotypes and planting methods was significant and this means that variations of number of spikelets panicle^{-1} in genotypes were influenced by different planting methods.

4.2.6 Filled grain percent

The effect of planting methods on filled grain percent was not significant (Table 4.3) and there were not significant variations among genotypes for filled grain percent. Among the experimental rice genotypes, CSR 36 gave the highest filled grain percent (84.63) followed by IR 10 T 107 (83.47) and IR 87707-446-B-B-B (82.55) while Thee Htat Yin gave the least filled grain percent (81.49).(Table 4.1). The interaction effect of genotypes and planting methods was significant and this mean that changes of filled grain percent in genotypes were influenced by different planting methods.

4.2.7 Thousand grain weight

Thousand grain weight was significantly differed due to varietal effects (Table 4.3). IR 87707-446-B-B-B produced the maximum thousand grain weight (24.46 g) followed by CSR 36 (24.40 g) and IR 10 T 107 (23.52 g) while Thee Htat Yin produced the minimum thousand grain weight (21.68 g). Thousand grain weight was not significantly affected by planting methods. The highest thousand grain weight (23.30 g) was observed in line sowing method followed by broadcasting (23.28 g) and transplanting

methods (23.21 g) (Table 4.3). The interaction effect of genotypes and planting methods was not significant and this mean that changes of thousand grain weight in genotypes were not influenced by different planting methods.

4.2.8 Yield performance of experimental rice genotypes in three planting methods

The grain yield was significantly influenced by genotypes (Table 4.3). Among the experimental rice genotypes, IR 87707-446-B-B-B produced the highest grain yield (5.61 t ha^{-1}) followed by IR 10 T 107 (5.58 t ha^{-1}) and CSR 36 (5.16 t ha^{-1}) while Thee Htat Yin gave the lowest grain yield (4.65 t ha^{-1}) (Table 4.3). The grain yield was significantly influenced by planting methods. Transplanting method produced the higher grain yield (5.83 t ha^{-1}) than line sowing (4.82 t ha^{-1}) and broadcasting method (4.66 t ha^{-1}). The interaction effect of genotypes and planting methods was significant and therefore, the genotypes × planting methods interaction on grain yield was distinctly existed (Table 4.3). Comparing the three methods of planting, all of the experimental rice genotypes had higher yield in transplanting method than broadcasting and line sowing methods (Table 4.4). This result was due to number of effective tillers m^{-2} and number of spikelets $panicle^{-1}$. All of these parameters were high in this experiment.

Grain yield of experimental rice genotypes ranged from 4.30 t ha^{-1} to 5.60 t ha^{-1} in broadcasting system (Table 4.4). IR 10 T 107 (5.60 t ha^{-1}) gave the maximum yield followed by GSR-IR 1-12-D10-S1- D1 (4.96 t ha^{-1}) which were significantly differences from each other whereas CSR 36 (4.30 t ha^{-1}) gave the minimum yield followed by Thee Htat Yin (4. 40 t ha^{-1}) which were not significantly different from each other.

Grain yield of experimental rice genotypes ranged from 4. 40 t ha^{-1} to 5.30 t ha^{-1} in line sowing (Table 4.4). The maximum yield was observed from IR 10 T 107 (5.30 t ha^{-1}) followed by IR 87707-446-B-B-B (5.13 ha^{-1}) which were not significant differences from each other whereas Thee Htat Yin (4.40 t ha^{-1}) gave the minimum yield followed by from GSR-IR 1-12-D10-S1-D1 (4.56 t ha^{-1}) and CSR 36 (4.70 t ha^{-1}).

Grain yield of experimental rice genotypes ranged from 5.16 t ha^{-1} to 7.00 t ha^{-1} in transplanting system (Table 4.4). IR 87707-446-B-B-B (7.00 t ha^{-1}) gave the maximum yield followed by CSR 36 (6.50 t ha^{-1}) which were significant differences from each other whereas Thee Htat Yin (5.16 t ha^{-1}) was the minimum grain yield followed by GSR-IR 1-12-D10-S1-D1 (5.46 t ha^{-1}) which were not significantly differences from each other. Therefore, the present study revealed that the rank of genotypes for grain yield varied across the planting methods and therefore, genotypes × planting methods interaction on grain yield were distinctly existed.

Table 4.4 Mean comparison of grain yield (t ha^{-1}) as affected by planting methods and genotypes at Tarpet West village, Maubin in the dry season, 2015

Genotypes	Grain yield (t ha^{-1})		
	Broadcasting	**Line sowing**	**Transplanting**
IR 10 T 107	5.60 a	5.30 a	5.86 b
CSR 36	4.30 c	4.70 bc	6.50 a
IR 87707-44-B-B-B	4.70 bc	5.13 ab	7.00 a
GSR-IR-1-12-D10-S1-D1	4.96 b	4.56 bc	5.46 bc
Thee Htat Yin	4.40 c	4.40 c	5.16 c
	4.79	**4.82**	**6.00**
LSD 0.05		**0.46**	

Means followed by a same letter were not significant at 5 % level

4.3 Analysis of Variance for Evaluated Characters in Katode Phayarkyi Experiment

Mean squares obtained for yield and yield component characters of experimental rice genotypes in three planting methods at Katode Phayarkyi village, DaikU are presented in Table 4.5.

4.3.1 Days to maturity

The effect of planting methods on days to maturity were highly significant ($p<0.01$) and this showed that days to maturity were influenced by different planting (Table 4.5). Broadcasting and line sowing methods had shorter days to maturity than transplanting method. There were highly significant variations among genotypes for days to maturity. Among the experimental rice genotypes, IR 10 T 107 gave the shortest days to maturity (112.22 days) followed by CSR 36 (113.11 days) and IR 87707-446-B-B-B (113.22 days) while Thee Htat Yin was the longest days to maturity (114.78 days) (Table 4.5). The interaction effect of genotypes and planting methods was significant and this mean that changes of days to maturity in genotypes were influenced by different planting methods.

4.3.2 Plant height

Plant height was significantly influenced by genotypes (Table 4.5). Among the experimental rice genotypes, GSR-IR-1-12-D10-S1-D1 showed the maximum plant height (112.16 cm) followed by IR 87707-446-B-B-B (107.81 cm) while Thee Htat Yin gave the minimum plant height (93.48 cm) followed by IR 10 T 107 (100.38 cm) and CSR 36 (100.00 cm) (Table 4.5). Plant height was not significantly affected by planting method. The interaction effect of genotypes and planting methods was not significant and this mean that changes of plant height in genotypes were not influenced by different planting methods.

4.3.3 Number of effective tillers m^{-2}

The effect of planting method on number of effective tillers m^{-2} were highly significant ($p<0.01$) and this showed that number of effective tillers m^{-2} were influenced by different planting (Table 4.5). Transplanting produced higher effective tiller number m^{-2} (251.51) than line sowing methods (232.42) and broadcasting (216.74). There were highly significant variations among genotypes for number of effective tillers m^{-2}. Among the experimental rice genotypes, Thee Htat Yin gave the highest tillers number (247.43)

Table 4.5 The Mean performance of yield and yield component characters of experimental rice genotypes at Katode Phayarkyi village, DaikU Township, Bago region in the dry season, 2015

Treatment	DTM	PH	ET/m^2	PL	SPK	FG%	1000 Gwt	Yld
Broadcasting (M1)	110.27 b	101.46 a	216.74 c	20.80 a	104.73 b	85.05 ab	23.29 a	4.55 b
Line Sowing (M2)	110.60 b	101.16 a	232.41 b	21.06 a	104.93 b	80.17 b	23.30 a	4.56 b
Transplanting (M3)	119.40 a	105.67 a	251.54 a	20.84 a	117.33 a	87.86 a	23.21 a	5.99 a
LSD 0.05	**0.47**	**5.21**	**11.65**	**0.57**	**4.62**	**6.55**	**0.29**	**0.24**
Genotypes								
IR 10 T 107	112.11 d	100.38 c	233.98 b	20.44 b	109.11 a	83.63 b	23.52 b	5.02 bc
CSR 36	113.11 c	100.00 c	216.01 c	23.27 a	110.11 a	83.40 b	24.40 a	4.84 cd
IR 87707-446-B-B-B	113.22 bc	107.81 b	226.12 b	21.04 b	109.33 a	83.17 b	24.46 a	5.08 b
GSR-IR-1-12-D10-S1-D1	113.89 a	112.16 a	244.27 a	18.61 c	110.11 a	90.26 a	22.25 c	5.43 a
Thee Htat Yin (Check variety)	114.78 a	93.48 d	247.43 a	21.13 b	106.33 a	81.34 b	21.57 d	4.66 d
LSD 0.05	**0.67**	**4.27**	**9.05**	**1.10**	**5.16**	**3.74**	**0.43**	**0.21**
Pr> F								
Planting Methods	0.00	0.12	0.00	0.47	0.00	0.07	0.66	0.00
Genotypes	0.00	0.00	0.00	0.00	0.55	0.00	0.00	0.00
PltM x Geno	0.00	0.15	0.00	0.01	0.01	0.24	0.71	0.00
CV % (a)	0.42	5.00	4.92	2.73	4.18	7.66	1.25	4.76
CV % (b)	0.61	4.27	3.98	5.43	4.87	4.56	1.91	4.61

In each column, means having a common letter are not significantly different at 5 % LSD

DTM= Days to maturity, PH = Plant height, ET/m^2 = Number of effective tillers m^{-2}, PL = Panicle length, SPK = Number of spikelets $panicle^{-1}$, FG % = Filled grain percent, 1000 Gwt= Thousand grain weight, Yld = Grain yield, PltM= Planting method, Geno = Genotypes

followed by GSR-IR-1-12-D10-S1-D1 (244.27) while CSR 36 (216.01) gave the least tillers numbers (Table 4.5). The interaction effect of genotypes and planting methods was significant and this means that variations of number of effective tillers m^{-2} in genotypes were influenced by different planting methods.

4.3.4 Panicle length

Panicle length was not significantly affected by planting methods in this experiment (Table 4.5). However, panicle length was significantly influenced by genotypes. Among the experimental rice genotypes, CSR 36 produced the longest panicle length (23.27 cm) followed Thee Htat Yin (21.13 cm) while GSR-IR-1-12-D10-S1-D1 produced the shortest panicle length (18.31 cm) followed by IR 10 T 107 (20.44 cm) (Table 4.5). The interaction effect of genotypes and planting methods was significant and this mean that changes of panicle length in genotypes were influenced by different planting methods.

4.3.5 Number of spikelets panicle^{-1}

The effect of planting methods on number of spikelets panicle^{-1} were highly significant ($p<0.01$) and this showed that number of spikelets panicle^{-1} were influenced by different plantings (Table 4.5). Transplanting method produced the highest spikelets panicle^{-1} (117.33) followed by line sowing (104.93) and broadcasting (104.73) methods. Number of spikelet panicle^{-1} was not significantly influenced by genotypes. Among the experimental rice genotypes, CSR 36 and GSR-IR-1-12-D10-S1-D1 gave the maximum spikelets panicle^{-1} (110.11 cm) while Thee Htat Yin produced the minimum spikelets panicle^{-1} (106.33 cm) (Table 4.5). The interaction effect of genotypes and planting methods was significant and this mean that changes of number of spikelets panicle^{-1} were influenced by different planting methods.

4.3.6 Filled grain percent

The effect of planting methods on filled grain percent was not significant (Table 4.5). Higher number of filled grain percent was obtained under transplanting (87.86) than broadcasting (85.05) and line sowing methods (80.17). There were significant variations among genotypes for filled grain percent. Among the experimental rice genotypes, GSR-IR-1-12-D10-S1-D1 obtained the highest filled grain percent (90.26) followed by IR 10 T 107 (83.63) and CSR 36 (83.40) while Thee Htat Yin gave the least filled grain percent (81.34) followed by IR 87707-446-B-B-B (83.17) (Table 4.5). The interaction effect of genotypes and planting methods was not significant and this mean that changes of filled grain percent

in genotypes was not influenced by different planting methods.

4.3.7 Thousand grain weight

Thousand grain weight was significantly differed due to varietal effects (Table 4.5). IR 87707-446-B-B-B produced the highest thousand grain weight (24.46g) followed by CSR 36 (24.40 g) and IR 10 T 107 (23.52 g) while Thee Htat Yin produced the lowest thousand grain weight (21.57 g) followed by GSR-IR-1-12-D10-S1-D1 (22.25 g). Thousand grain weight was not significantly affected by planting methods. The interaction effect of genotypes and planting methods was not significant and this mean that changes of thousand grain weight in genotypes were not influenced by different planting methods.

4.3.8 Yield performance of experimental rice genotypes in three planting methods

The grain yield was significantly influenced by genotypes (Table 4.5). Among the tested genotypes, GSR-IR-1-12-D10-S1-D1 produced the highest grain yield (5.43 t ha^{-1}) followed by IR 87707-446-B-B-B (5.08 t ha^{-1}) which were significantly different from each other while Thee Htat Yin gave the lowest grain yield (4.66 t ha^{-}) followed by CSR 36 (4.84 t ha^{-1}) which were not significantly differences from each other (Table 4.5). The grain yield was significantly influenced by planting methods. Transplanting method produced the higher grain yield (5.99 t ha^{-1}) than line sowing (4.56 t ha^{-1}) and broadcasting method (4.55 t ha^{-1}). The interaction effect of genotypes and planting methods was significant and therefore, the genotype × planting methods on grain yield was distinctly existed (Table 4.5). Comparing the three methods of planting, all of the tested rice genotypes had higher yield for transplanting method than broadcasting and line sowing methods (Table 4.6). This was due to number of effective tillers m^{-2} and number of spikelets $panicle^{-1}$ and filled grain percent.

The grain yield of experimental rice genotypes ranged from 4.03 t ha^{-1} to 4.90 t ha^{-1} in broadcasting system (Table 4.6). GSR-IR 1-12-D10-S1-D1 (4.90 t ha^{-1}) gave the maximum yield followed by IR 10 T 107 (4.83 t ha^{-1}) and CSR 36 (4.50 t ha^{-1}) which were not significantly differences from each other whereas Thee Htat Yin (4.03 t ha^{-1}) gave the minimum grain yield followed by IR 87707-446-B-B-B (4.20 t ha^{-1}) which were not significantly different from each other.

Grain yield of experimental rice genotypes ranged from 4.26 t ha^{-1} to 4.90 t ha^{-1} in line sowing system (Table 4.6). The maximum yield was observed from GSR-IR 1-12-D10-S1-D1 (4.90 t ha^{-1}) followed by CSR 36 (4.56 t ha^{-1}) and IR 87707-44-B-B-B (4.53 t ha^{-1}) which were significantly different from each other whereas Thee Htat Yin

Table 4.6 Mean comparison of grain yield (t ha^{-1}) as affected by planting methods and genotypes at Katode Phayakyi village, DaikU in the dry season, 2015

Genotypes	Grain yield (t ha^{-1})		
	Broadcasting	**Line sowing**	**Transplanting**
IR 10 T 107	4.83 a	4.46 b	5.76 b
CSR 36	4.50 ab	4.56 b	5.46 b
IR 87707-44-B-B-B	4.20 bc	4.53 b	6.53 a
GSR-IR-1-12-D10-S1-D1	4.90 a	4.90 a	6.50 a
Thee Htat Yin	4.03 c	4.26 b	5.70 b
	4.49	**4.54**	**5.99**
LSD 0.05		**0.37**	

Means followed by a same letter were not significant at 5 % level

(4.26 t ha^{-1}) which gave the minimum yield followed by IR 10 T 107 (4.46 t ha^{-1}) which were not significantly different from each other.

Grain yield of tested genotypes ranged from 5.46 t ha^{-1} to 6.53 t ha^{-1} in transplanting system (Table 4.6). CSR 36 gave the minimum yield (5.46 t ha^{-1}) followed by Thee Htat Yin (5.70 t ha^{-1}) and IR 10 T 107 (5.76 t ha^{-1}) which were not significantly among each other whereas the maximum yield was given from IR 87707-446-B-B-B (6.53 t ha^{-1}) followed by GSR-IR 1-12-D10-S1-D1 (6.50 t ha^{-1}) which were not significantly different from each other. This result means that the rank of genotypes for grain yield varied across the environments. Therefore, the genotypes × planting methods interaction on grain yield was distinctly existed across environments.

4.4 Combined Analysis of Variance for Yield and Yield Component Characters

The mean squares of combined analysis of variance for yield and yield component characters namely days to maturity, plant height, number of effective tillers m^{-2}, panicle length, number of spikelets $panicle^{-1}$, filled grain percent, thousand grain weight and grain yield of five genotypes over nine environments is shown in Table 4.7. The highly significant differences among the tested environments were found in days to maturity, plant height, number of effective tillers m^{-2}, panicle length, number of spikelets $panicle^{-1}$, filled grain percent, and grain yield. This indicated that there were highly significantly differ among tested environments for all evaluated characters except thousand grain weight.

There were highly significant differences among the experimental rice genotypes for all evaluated characters. As regard of G × E interaction, highly significant differences was observed in days to maturity, plant height, number of effective tillers m^{-2}, panicle length, number of spikelets $panicle^{-1}$, filled grain percent and grain yield except thousand grain weight. For significantly different characters namely, number of effective tillers m^{-2}, number of spikelets $panicle^{-1}$, filled grain percent and grain yield found in G × E interaction, varietal trials should be conducted in multi-locations. Multi-location trials were needed because significant effects of genotypes × location interaction indicated the differential genotypic effects across locations. The contribution of genotypic effects was larger than that of G × E interaction effects in all different characters. These results implied limited the crossover G × E interaction with possibility of general adaptation for some genotype across environments or permitted the crossover G × E interaction with the possibility of specific adaptation to specific environment.

Genotype (G), environment (E) and G × E interaction were significant ($P< 0.01$)

Table 4.7 Mean squares for combined analysis of variance for yield and yield components characters of experimental rice genotypes at nine environments in the dry season, 2015

Source of Variation	df	Mean Squares							
		DTM	PH	ET / m^2	PL	SPK	FG %	1000 Gwt	Yld
Environment	8	289.93**	122.28**	3035.39**	6.78**	434.63**	153.88 **	0.08	6.51**
Genotypes	4	17.10**	1439.69**	2781.33**	35.15**	56.63*	60.42*	43.70**	2.48**
Geno × Env	32	2.07**	65.31**	323.41**	4.91**	49.03**	46.64**	0.15	0.51**
Replication within environment	18	5.82	34.87	108.49	7.19	13.54	39.08	0.19	0.11
Residual	72	0.43	18.42	101.57	1.38	20.40	20.39	0.23	0.06
CV %		0.58	4.07	4.18	5.46	4.16	5.39	2.09	4.86

*, ** = significant at 5% and 1% probability levels, respectively

DTM= Days to maturity, PH= Plant height (cm), ET/m^2= Number of effective tillers m^{-2}, PL= Panicle length (cm), SPK= Number of spikelets $panicle^{-1}$, FG %= Filled grain percent, 1000 Gwt= Thousand grain weight, Yld= Grain yield, df = Degree of freedom

for grain yield (Table 4.7). This statistical interaction resulted from the changes in the relative ranking of the genotypes from one environment to another. The significant G × E interaction effects revealed that genotypes responded differently to the variation in environmental conditions which indicated the necessity of testing rice genotypes at multiple locations. The G × E interaction of multi-location trials tend to confound varietal selection and recommendation, indicating a need for investigating stability of genotypes across environments.

4.5 Additive Main Effects and Multiplicative Interactions (AMMI) Analysis for Grain Yield of Experimental Rice Genotypes across Environments

The AMMI analysis of variance for grain yield of experimental rice genotypes tested across environments is presented in Table 4.8. The AMMI model revealed the presence of significant differences between environments that accounted for 66.42 % of the total sum of square (SS). A large sum of squares for environments indicated that the tested environments were diverse, with large differences among environmental means causing most of the variation in rice yield. The genotypes and G × E interactions also accounted significantly and contribute for 12.67 % and 20.90 % respectively of the total SS. This indicated that the existence of a considerable amount of differential responses among the genotypes to change in growing tested environments indicated the substantial differences in genotypic response across tested environments. The degree of G × E interaction sum of squares was larger than that for genotypes indicated the substantial differences in genotypic response across tested environments. Similarly, large contribution of environment was also reported by Dewi et al. (2014) in which they found that environments accounted for the largest proportion followed by G × E interaction and genotypes in rice yield.

The first interaction principal component axis (IPCA 1) was significant, capturing 63.9 % of the total variation in the G × E interaction sum of square and the second interaction principal component axis (IPCA 2) explained a further 20.5 % of sum of square of this G × E interaction. The IPCA 1 component 63.9% of total G × E interaction sum of squares greater than IPCA 2 component 20.5 % and this indicated that there was a differential yield performance among the experimental rice genotypes across environments due to the present of significant G × E interaction effects. Therefore, in order to identify genotypes with specific or relatively broader adaption, studies on the magnitude and patterns of G × E interaction effect of specific genotypes should be an integral part of rice varietal development plotted against their respective means and in

Table 4.8 Additive main effect and multiplicative interaction analysis of variance for rice yield genotypes across environments

Source	df	SS	Contribution of SS (%)	MS	Contribution of G × E interaction SS (%)
Genotype (G)	4	9.94	12.67	2.60**	
Environment (E)	8	52.11	66.42	5.71**	
G × E interaction	32	16.40	20.90	0.28**	
IPCA 1	11	10.54	11.84	0.95**	63.9
IPCA 2	9	3.37	3.95	0.37**	20.5
Error	72	4.44		0.06	
Total	134				

**= significant at 0.01 probability level.

AMMI II biplot, the IPCA 1 and IPCA 2 scores of genotypes and environments were plotted against each other.

The AMMI analysis revealed that mean squares for the IPCA 1 and IPCA 2 were significant at 0.01 level and cumulatively contributed to 84.4 % of the total genotype × environment interactions. Zobel et al. (1988) reported that the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model. According to Gauch and Zobel (1996); Yan and Rajcan (2002) and Khaing (2014) reported that the most accurate model for AMMI can also be predicted by using the first two IPCAs. The interaction of five genotypes with nine environments was therefore best predicted by the first two principal components axes of genotypes and environments.

The AMMI I biplot for yield of experimental rice genotypes at nine environmental conditions is presented in Figure 4.1. The main effects (Genotypes × Environments) accounted for 79.09 % and IPCA I accounted for 11.8 % of total variation in G × E interaction and therefore the AMMI I biplot gave a model fit of 90.89 %. The biplot explains not only the average yield of a genotype but also how it is achieved. Biplot was divided into four quadrants from lower yielding environments in quadrants I and IV to high yielding environments in quadrants II and III. Genotypes and environments on the same parallel line, relative to the ordinate, have similar yields, and a genotype or environment on the right side of the midpoint of the axis has higher yields than those on the left hand side. Regardless of IPCA I scores direction, environments M3Z, M3 and M3D were on the right side of the midpoint of the main effect axis, this indicated that transplanting methods in Zayar Thiri, Maubin and DaikU locations were to be favorable environments for yield of the experimental rice genotypes whereas broadcasting and line sowing methods at Zayar Thiri, Maubin and DaikU locations were to be unfavorable environments.

The M3Z, MP3M and M3D were high potential environments with positive IPCA I values because these fall in quadrant II while low yielding environments (M1Z, M2Z, M1M, M1D and M2D) were found in quadrant IV with negative IPCA I values and M2M was found in quadrant I with positive IPCA I value. Among the tested environments, M3D and M2M showed minimum interaction effect with IPCA I value near to zero and demonstrated as the most stable environments. The greater the IPCA I scores indicates the more specifically adapted these genotypes with certain environments (Zobel et al. 1988 and Crossa et al. 1990). Environments M1M, M2D, M1Z, M2Z, M1M, M2M, M3Z,

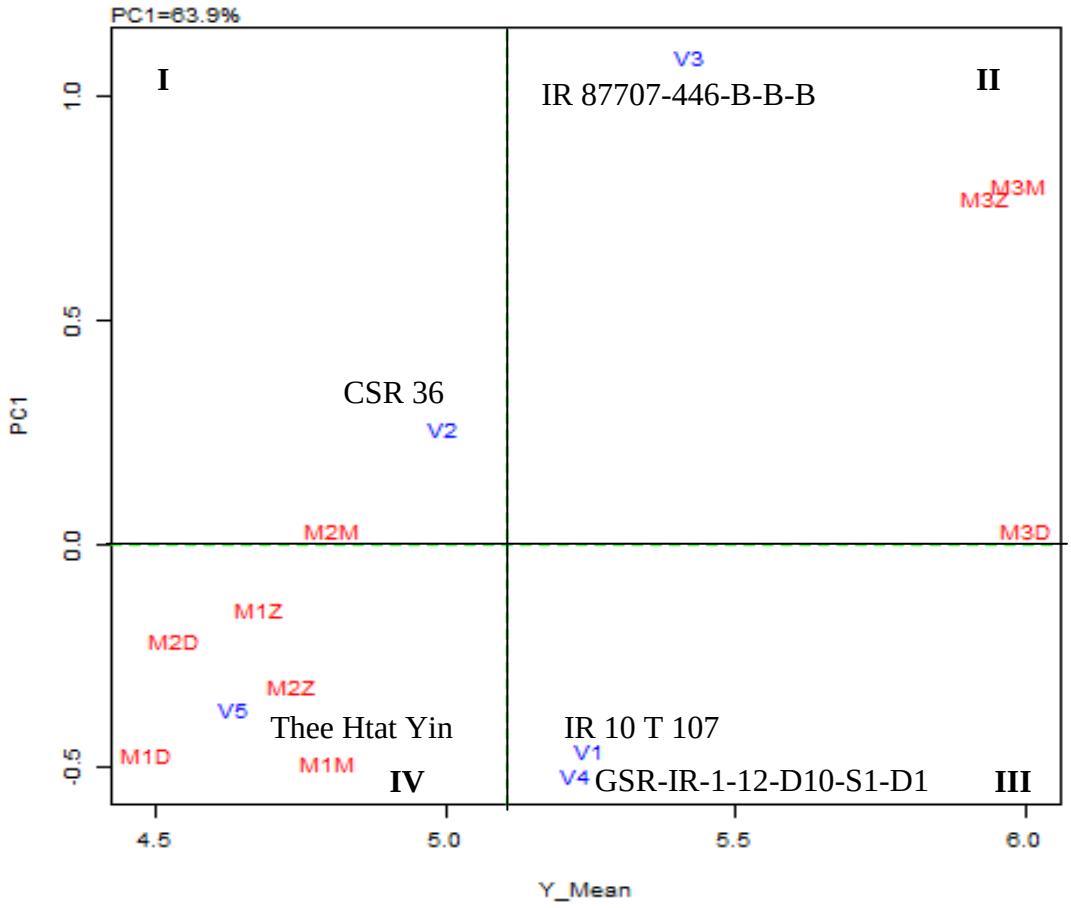

Figure 4.1 AMMI I biplot of main effect and G × E interaction for yield of rice genotypes across environments

M1Z= broadcasting, Zayar Thiri, M2Z= Line sowing, Zayar Thiri, M3Z= Transplanting, Zayar Thiri, M1M= broadcasting, Maubin, M2M= Line sowing, Maubin, M3M= Transplanting, Maubin, M1D= broadcasting, DaikU, M2D= Line sowing, DaikU, M3D= Transplanting, DaikU, V1 = IR 10 T 107, V2 = CSR 36, V3 = IR 87707-446-B-B-B, V4= GSR-IR-1-12-D10-S1-D1, V5 = Thee Htat Yin

M3M, and M3D were ranked 1st, 2nd, 3rd, 4th, 5th, 6th, 7th, 8th, and 9th with respect to rice grain yield. Therefore, high yielding environments M3Z and M3M with greater IPCA I scores were the specific adaptable environments for genotypes evaluated.

In the biplot display, the differences among genotypes in term of direction and magnitude along the X-axis (yield) and Y-axis (IPCA I scores) are important. Genotype with IPCA I scores near zero (either positive or negative) had little interaction across environments and, vice versa for environments (Crossa et al. 1991). As a result, IR 87707-446-B-B-B, IR 10 T 107 and GSR-IR-1-12-D10-S1-D1 were generally high yielding whereas CSR 36 and Thee Htat Yin were generally low yielding genotypes. AMMI I biplot exhibited two groups of genotypes. In group I, IR 87707-446-B-B-B producing above grand mean and CSR 36 having below grand mean with positive IPCA I values interacted positively with unfavorable environments because genotype and environment mean combinations with IPCA I scores of the same sign produced positive specific interaction effects. In group II, genotypes producing above or below grand mean with negative IPCA I scores performed well in favorable environments with similar sign in IPCA I.

The genotypes IR 10 T 107 and GSR-IR-1-12-D10-S1-D1 produced above grand mean of rice yield while Thee Htat Yin had below average rice yield. Among three high yielding genotypes, IR 87707-446-B-B-B was vertically distant apart however they did not fall close to the horizontal line. This implies that this genotype was found to be high yield potential but it showed maximum G × E interaction. Genotypes IR 10 T 107 and GSR-IR-1-12-D10-S1-D1 gave above the mean yield and they fall close to horizontal line as comparison of IR 87707-446-B-B-B.

AMMI II biplot for grain yield per plant of experimental rice genotypes at nine environmental conditions is presented in Figure 4.2. The IPCA 1 component accounted for 63.9 % of G x E interaction, while IPCA 2 accounted for 20.5 %. Distribution of genotypes in the AMMI II biplot revealed that Thee Htat Yin was found to closer or at a lesser distance from the center of the biplot when compared with other genotypes and these was performed as stable genotype. However, Thee Htat Yin was found below the grand mean yield. IR 10 T 107, CSR 36, IR 87707-446-B-B-B and GSR-IR-1-12-D10-S1-D1 was at far distance from the center of the biplot were more sensitive to environmental effect. AMMI II model estimated yield of the genotypes in different environments by the effects of genotype and environment and interaction effects of IPCA1 and IPCA 2. The AMMI II gave a model fit of 94.88 % for grain yield of tested

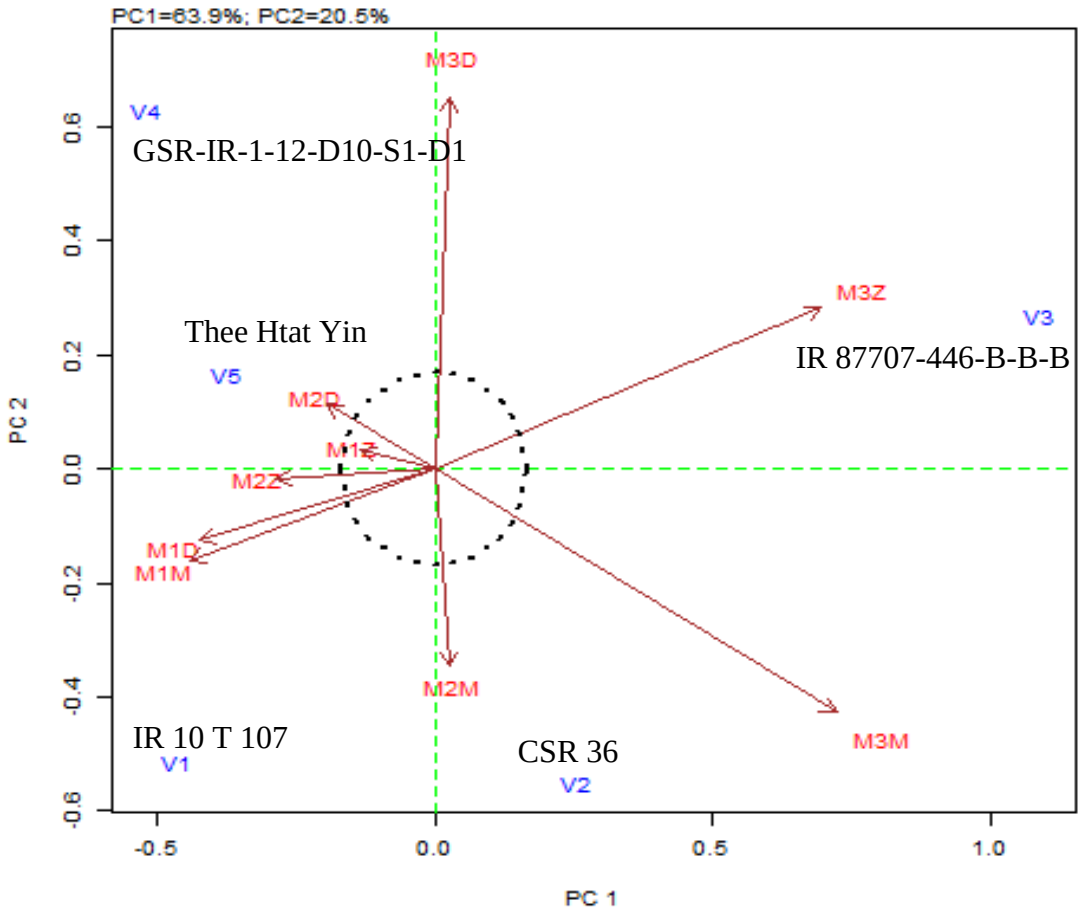

Figure 4.2 AMMI II biplot of main effect and G × E interaction for yield of rice genotypes across environments

M1Z= broadcasting, Zayar Thiri, M2Z= Line sowing, Zayar Thiri, M3Z= Transplanting, Zayar Thiri, M1M= broadcasting, Maubin, M2M= Line sowing, Maubin, M3M= Transplanting, Maubin, M1D= broadcasting, DaikU, M2D= Line sowing, DaikU, M3D= Transplanting, DaikU, V1 = IR 10 T 107, V2 = CSR 36, V3 = IR 87707-446-B-B-B, V4= GSR-IR-1-12-D10-S1-D1, V5 = Thee Htat Yin

rice genotypes. Purchase (1997) also presented that the closer the score to the center of the biplot, the more stable they are.

The best two genotypes in corresponding environments were V1 (IR 10 T 107), and V4 (GSR-IR-1-12-D10-S1-D1) in M1Z, V4 (GSR-IR-1-12-D10-S1-D1) and V1 (IR 10 T 107) in M2Z, V3 (IR 87707-446-B-B-B) and V4 (GSR-IR-1-12-D10-S1-D1) in M3Z, V1 (IR 10 T 107) and V4 (GSR-IR-1-12-D10-S1-D1) in M1M, V1 (IR 10 T 107) and V3 (IR 87707-446-B-B-B) in M2M; V3 (IR 87707-446-B-B-B) and V2 (CSR 36) in M3M, V4 (GSR-IR-1-12-D10-S1-D1) and V1 (IR 10 T 107) in M1D, V4 (GSR-IR-1-12-D10-S1-D1) and V2 (CSR 36) in M2D, and V3 (IR 87707-446-B-B-B) and V4 (GSR-IR-1-12-D10-S1-D1) in M3D. Thee Htat Yin did not include in top two genotypes in all environments (Table 4.9).

According to results, IR 10 T 107 possessed as the best genotype at two environments such as M1M and M2M and also it performed as 2nd highest mean yield in nine environments. GSR-IR-1-12-D10-S1-D1 possessed as the best genotype at four environments such as M1Z, M2Z, M1D and M2D and also it performed as 3rd highest mean yield in nine environments. IR 87707-446- B-B-B was the best genotype in three environments such as M3Z, M3M and M3D and it performed as 1st highest mean yield in nine environments. CSR 36 was below mean yield and not found the best genotype in any environments. Thee Htat Yin did not include the best genotype in all environments and it was more stable with low mean yield than other experimental rice genotypes.

4.6 Stability Analysis of Experimental Rice Genotypes

The result of stability parameters such as regression coefficient (b_i) and mean square deviation from regression (S^2_{di}) for yield of tested rice genotypes are presented in Table 4.9. The mean values for yield of five genotypes across nine environments ranged from 4.63 t ha^{-1} to 5.42 t ha^{-1} with a grand mean of 5.11 t ha^{-1} (Table 4.9). According to the mean ranking for yield, IR 87707-446-B-B-B (5.42 t ha^{-1}) was the top yielding genotype across environments followed by IR 10 T 107 (5.25 t ha^{-1}), GSR- IR-1-12-D10-S1-D1 (5.23 t ha^{-1}) and these three genotypes produced higher mean yield than the grand mean whereas CSR 36 (5.00 t ha^{-1}) and Thee Htat Yin (4.63 t ha^{-1}) produced lower mean yield below the grand mean. Five evaluated genotypes ranged from 0.65 - 1.73 in regression coefficient (b_i) and only three genotypes namely CSR 36, IR 87707-446- B-B-B and Thee Htat Yin were significantly different at 1 % level and two genotypes namely IR 10 T 107 and GSR-IR-1-12-D10-S1-D1 were significant at 5% level. IR 87707-446-B-B-B produced the highest mean yield (5.42 t ha^{-1}) above overall mean and performed very

Table 4.9 Mean performance of grain yield (t ha^{-1}) and stability parameters for experimental rice genotypes estimated by Finlay and Wilkinson (1963) in Zayar Thiri, Maubin and DaikU Townships

Genotypes	Tested Environments											
	M1Z	**M 2Z**	**M 3Z**	**M 1M**	**M 2M**	**M 3M**	**M 1D**	**M 2D**	**M 3D**	**Mean**	**b_i**	**S^2_{di}**
IR 10 T 107	4.96	4.80	5.70	5.60	5.30	5.86	4.83	4.46	5.76	**5.25**^{2}	0.65	0.08
CSR 36	4.46	4.73	5.73	4.30	4.70	6.50	4.50	4.56	5.46	**5.00**^{4}	1.00	0.11
IR 87707-446-B-B-B	4.86	4.56	7.23	4.70	5.13	7.00	4.20	4.53	6.53	**5.42**^{1}	1.73	0.07
GSR-IR-1-12-D10-S1-D1	4.97	4.96	5.86	4.96	4.56	5.46	4.90	4.90	6.50	**5.23**^{3}	0.78	0.12
Thee Htat Yin	4.13	4.50	5.13	4.40	4.40	5.16	4.03	4.26	5.70	**4.63**^{5}	0.81	0.03
Mean	**4.68**	**4.71**	**5.93**	**4.79**	**4.82**	**6.00**	**4.49**	**4.54**	**5.99**	**5.11**		

b_i= Regression coefficient, S^2_{di} =Deviation from regression

(M1Z = broadcasting, Zayar Thiri, M2Z= Line sowing, Zayar Thiri, M3Z= Transplanting, Zayar Thiri, M1M= broadcasting, Maubin, M2M= Line sowing, Maubin, M3M= Transplanting, Maubin, M1D= broadcasting, DaikU, M2D= Line sowing, DaikU, M3D= Transplanting, DaikU

sensitive to changes in the environment (below average stability) (Figure 4.3). Under the most favorable conditions, it becomes one of the highest yielding genotype. Therefore it performed as being specifically adapted to high yielding environments such as transplanting system in all tested environments and is characterized by a regression coefficient greater than 1.0 (b_i =1.73). However, this genotype can be grown not only transplanting methods but also the areas where broadcasting and line sowing methods due to irrigation shortage problem because it yields above 4.0 t ha^{-1} in broadcasting and line sowing methods.

IR 10 T 107 (5.25 t ha^{-1}) and GSR-IR-1-12-D10-S1-D1 (5.23 t ha^{-1}) had the 2nd and 3rd highest mean yield above overall mean with a regression coefficient less than 1.0 (b_i = 0.65) and (b_i = 0.78) and this genotypes performed very little changes in yield despite large changes in the environment (above average stability). Therefore, this genotypes were found to be grown in both of the regions where direct sowing and transplanting methods in all tested environments. Especially, IR 10 T 107 gave high yield under broadcasting and line sowing methods at Maubin location. GSR-IR-1-12-D10-S1-D1 performed the best yield in broadcasting and line sowing methods at Zayar Thiri and DaikU locations. CSR 36 showed average stability with linear regression coefficient (b_i = 1.0) but it produced below average yield (5.00 t ha^{-1}) and this indicated that these genotype was poorly adapted in all tested environments except transplanting method in Maubin location. However, this genotype could be used for specific special quality traits such as long grain, good grain appearance and good grain quality with aromatic. Thee Htat Yin producing low mean yield (4.63 t ha^{-1}) below overall mean with close to unity (b_i = 0.81) and these served as stable genotype which adapted poorly to all environments. Thee Htat Yin is widely grown variety in Myanmar especially in summer season of lower regions although this variety was low mean yield with stable in results of all tested environments in this experiment.

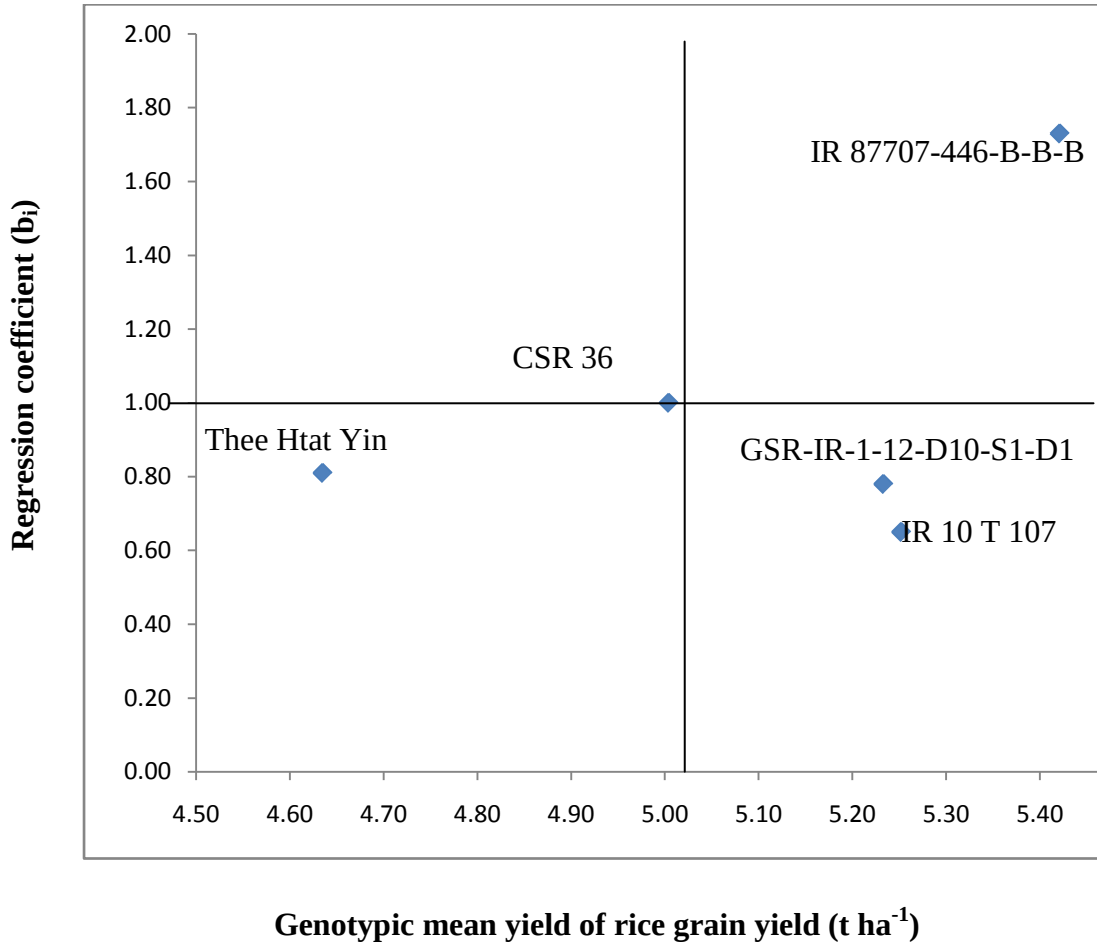

Figure 4.3 The relationship between the regression coefficient (b_i) and genotypic mean of rice grain yield (t ha^{-1}) of five genotypes across environments

CHAPTER V
CONCLUSION

Among the tested genotypes, IR 87707-446-B-B-B produced the highest yield in transplanting method at Zayar Thiri, Maubin and DaikU locations. IR 10 T 107 gave the best yield among the experimental rice genotypes in broadcasting method and line sowing methods at Maubin locations, GSR-IR-1-12-D10-S1-D1 obtained the highest yield in broadcasting and line sowing method at Zayar Thiri and DaikU locations. CSR 36 and Thee Htat Yin (check variety) were not included the highest yield in any tested environments but they were stable with low yield across environments. Among three planting methods, transplanting method was found to be high yielding environments whereas broadcasting systems and line sowing methods were found to be low yielding environments.

The results of analysis of variances for each environment can be concluded that all evaluated genotypes had different variation with varying characters. As the mean performances of all recorded characters among the tested genotypes observed the high variation in ranking patterns from one environment to another, the existence of G × E interaction was distinctly exhibited across tested environments. As the result of AMMI analysis, there were very high environmental variation and high effects of G × E interaction.

Among the experimental rice genotypes, IR 87707-446-B-B-B produced the highest mean yield (5.42 t ha^{-1}) above overall mean and performed very sensitive to changes in the environment (below average stability) and therefore it performed as being specifically adapted to high yielding environments such as transplanting methods in all tested locations. However, it can be grown in low yielding environments such as broadcasting and line sowing methods because it yields above 4.0 t ha^{-1} in these environments according to the results. IR 10 T 107 (5.25 t ha^{-1}) and GSR-IR-1-12-D10-S1-D1 (5.23 t ha^{-1}) had the second and third highest mean yield above overall mean and they performed insensitive to changes in the environment (above average stability) and therefore, these genotypes performed as being specifically adapted to low yielding environments. And also, this genotypes were found to be grown in both of the regions where broadcasting, line sowing, and transplanting methods in all tested environments. CSR 36 showed average stability but it produced below average yield and this indicated that this genotype was poorly adapted in all tested environments except transplanting

method in Maubin location. Thee Htat Yin producing low mean yield with close to unity (b_i=0.81) and therefore, these served as stable genotype which adapted poorly to all environments.

The experimental rice genotypes were not only genetically variable but some of them also exhibited different response to variable environment all factors such as available water or irrigation facilities, temperature, soil type, pests and diseases and cultural management practices. During the conducting of this experiment, three genotypes among the experimental rice genotypes were released as new improved varieties by the collaboration of ACIAR - DAR program. Therefore, all the evaluated data from this experiment will be available to be strongly recommended to do varietal registration as in new varieties.

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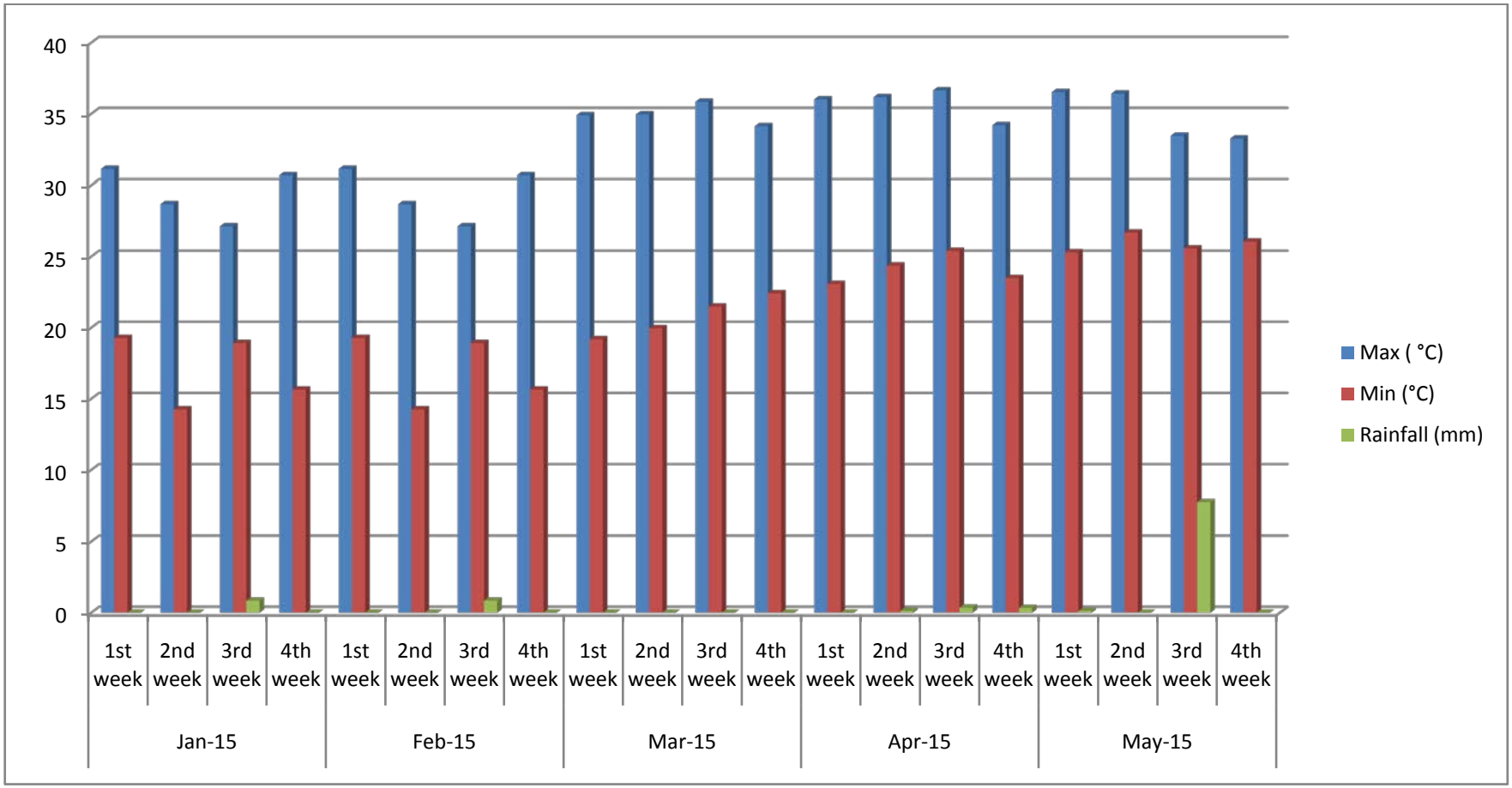
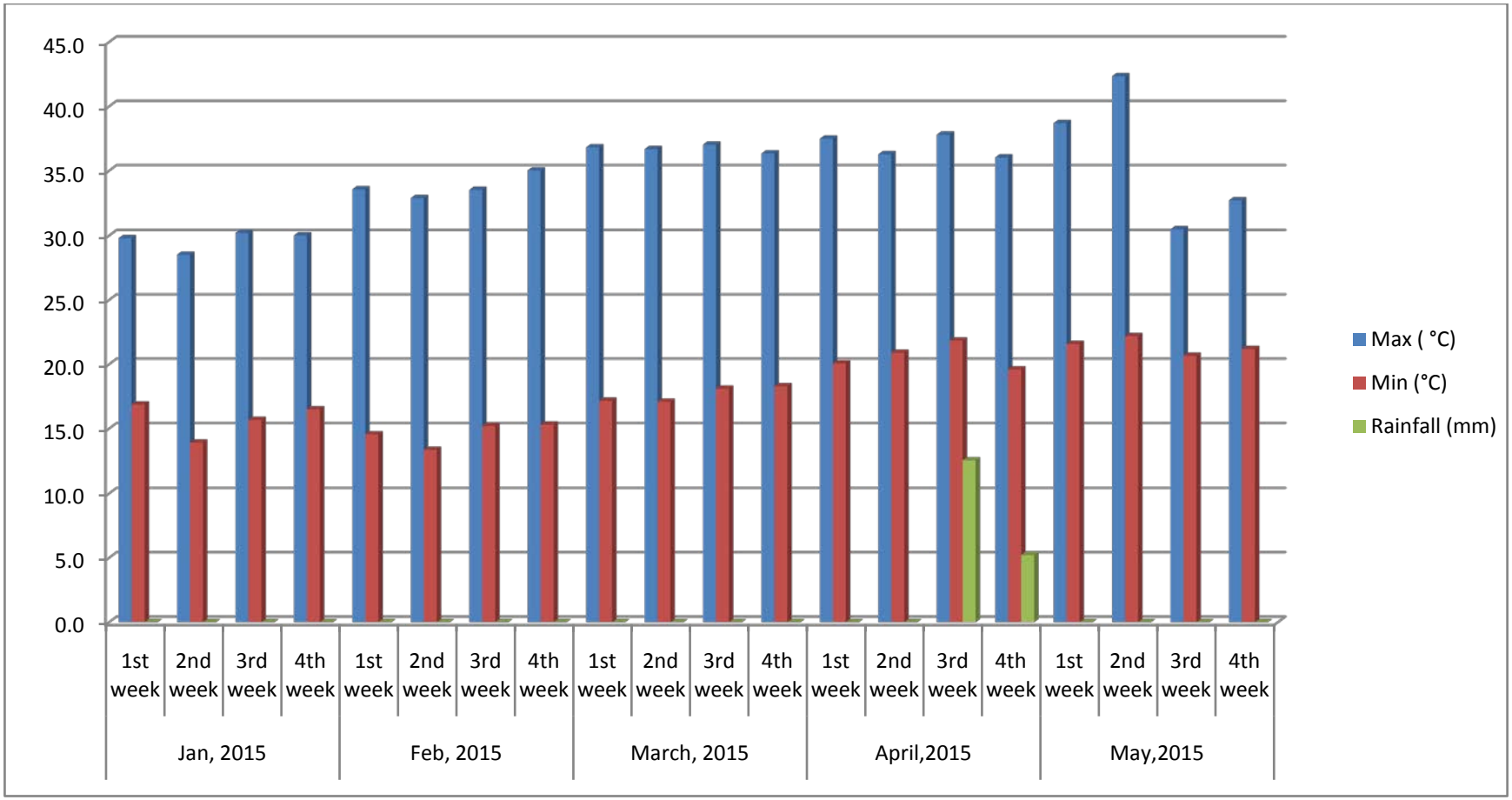
APPENDICES

Appendix 1. Result of soil analysis from experimental sites during the dry season, 2015

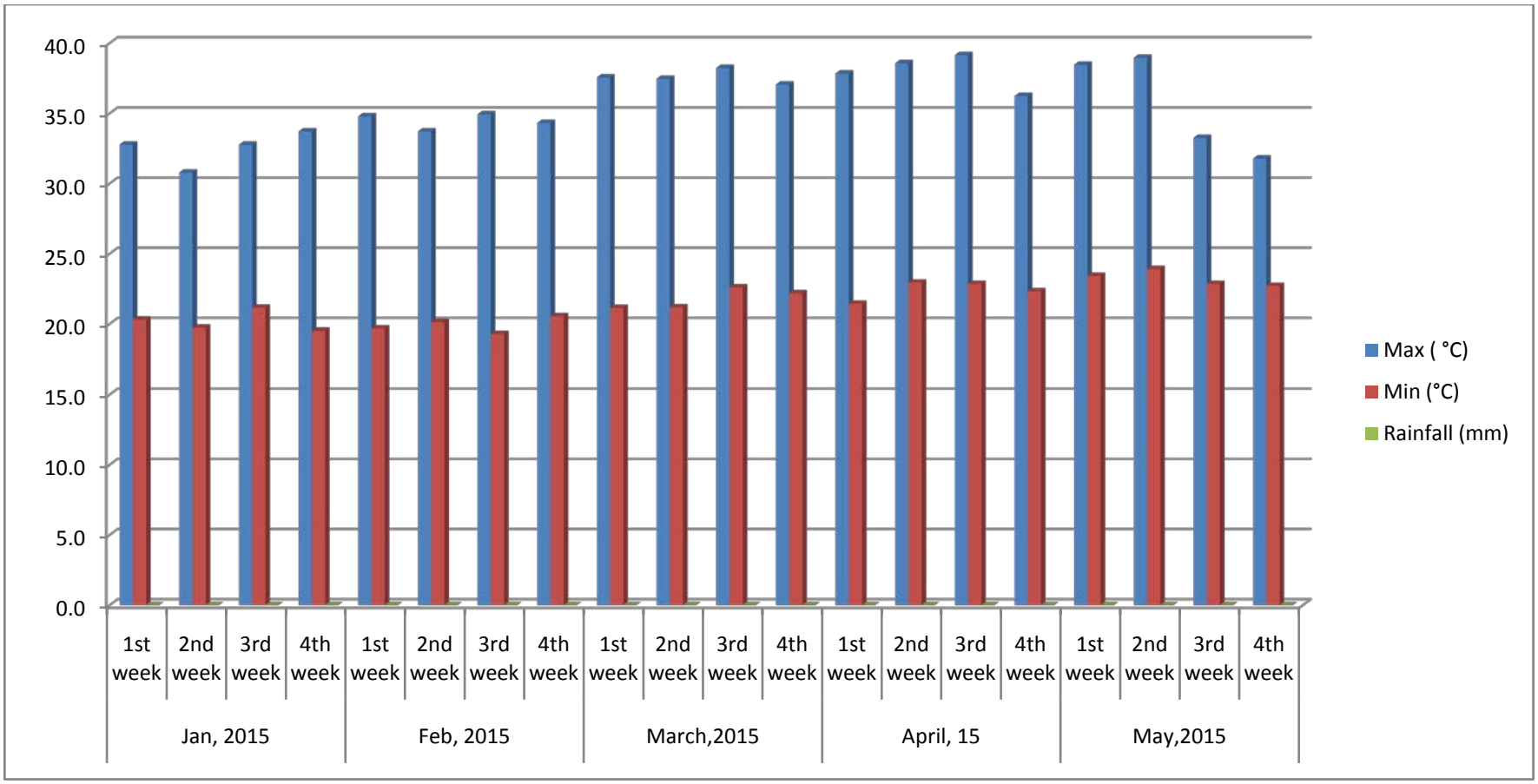
Characteristics	Unit	Zayar Thiri Township		Maubin Township		DaikU Township	
		Result	Rating	Result	Rating	Result	Rating
pH		7.00	Neutral	6.00	Moderately acid	6.90	Neutral
Available N	(mg/kg)	75.80	Medium	65.20	Medium	63.60	Medium
Available P2O5	(mg/kg)	30.60	High	43.70	Excessive	39.30	High
Available K2O	(mg/kg)	177.00	Medium	260.50	High	102.00	Low
Organic Matter	%	1.21	Low	2.27	Medium	1.44	Low
Textural Class	%	Sandy Loam		Silty Loam		Loam	
Sand	%	64.80		3.40		42.40	
Silt	%	24.40		45.30		39.10	
Clay	%	10.70		51.20		18.40	



Appendix 2. Weekly maximum and minimum temperatures (°C) and rainfall (mm) during the experimental period at Sein Sar Pin village, Zayar Thiri, Nay Pyi Taw Region in 2015-2016.



Appendix 3. Weekly maximum and minimum temperatures (°C) and rainfall (mm) during the experimental period at Tarpet West village, Maubin Township, Ayeyarwaddy Region in 2015- 2016



Appendix 4. Weekly maximum and minimum temperatures (°C) and rainfall (mm) during the experimental period at Katode Phayarkyi village, DaikU Township, Bago (East) Region in 2015 -2016.