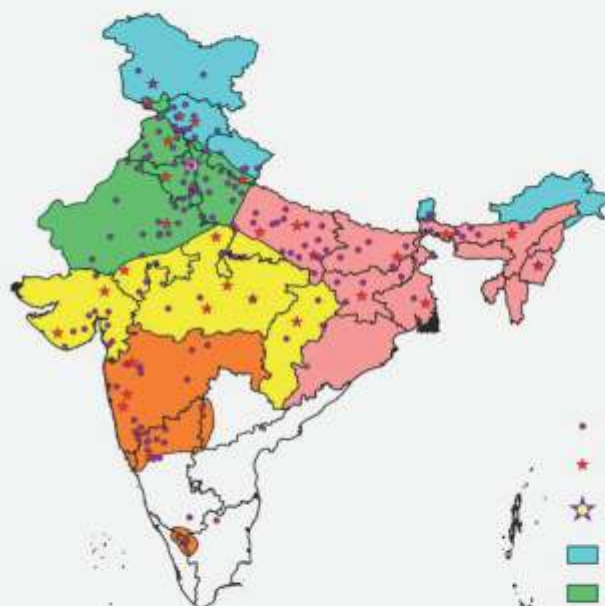# BLUP of Wheat Genotypes under Coordinated System : **Zone Wise Analysis**

ICAR-Indian Institute of Wheat and Barley Research
Karnal-132001, Haryana

AICRP (WHEAT & BARLEY)

LEGEND
- Voluntary Centre
- Funded Centre
- ICAR-IIWBR (HQ)
- Northern Hills Zone
- North-Western Plains Zone
- North-Eastern Plains Zone
- Central Zone
- Peninsular Zone

500 0 500 1000 1500 2000 km

BLUP of Wheat Genotypes
under Coordinated System :
Zone Wise Analysis

'Main objective of a series of trials is to identify,
with minimum selection error,
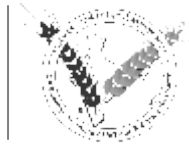the best varieties for cultivation and use.'
Patterson & Silvey

Ajay Verma

Jose Crossa

Mateo Vargas

Arun Kumar Joshi

Gyanendra Pratap Singh

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Acknowledgements

Preface

Wheat (Triticum aestivum) is one of the most important cereal crops that contributed significantly for human survival and adapted widely across different regions with altitude levels ranging from sea level to 4570 in Tibet. Such wide cultivation of wheat across all continents led to the harvest of good wheat crop around the world. Bread wheat covers more than 95% of the wheat production at global level. Goal of wheat breeding is to develop improved genotypes for yield along with other traits. The initial breeding trials use small un replicated plots or with limited replications. As selection continues for desired traits this practice reduces the size of the population. Researchers commonly use replicated multi-environment trials in the final stages of the selection process.

Phenotypic data are generated at each stage evaluation in which the genotypes are tested. The data may be analyzed for different purposes i.e. parent selection, ranking of genotypes and comparing performance of genotypes in different environments. Data generated can be used to recommend the most appropriate strategies to maximize improvement towards short and long term breeding goals. Because the genotypes often derived from different stages of selection, the amount and precision of the data may dramatically vary. Improved estimates of trait means are often obtained with some form of an additive linear model. Such models adjust observed values for non-genetic effects to obtain better estimates of the genetic effects. A classic method of obtaining genetic effects is by combining data across locations and considering all effects in the model as fixed. Unfortunately, cross appraisal are typically incomplete and unbalanced, which creates theoretical concerns about the fixed linear model prediction. Mixed models provide alternative analytical approaches that may overcome limitations of the fixed analytical approach. Best Linear Unbiased Prediction (BLUP), in a mixed linear model framework, has been used for prediction and estimation of genetic merit of tested material in plant breeding research trails. This method demonstrates better prediction accuracy than that obtained by using a fixed linear model.

CONTENTS

Introduction

Since ancient times, wheat has played an important role to feed the world population. Wheat fulfill 19% of calories and 21% of proteins of human beings . Number of consumable food types such as bread, chapati, biscuits, pasta, macaroni, injera, and porridges are prepared by wheat flour alone or in mixture with other cereals flour. An increase in urbanization accompanied with the change in food habits, the demand for wheat is rising every year across the all regions of the world. Wheat production has increased significantly over the years at global level. This appreciable increase in wheat production is attributed to the adoption of improved technology packages, viz. the adoption of high yielding and disease resistant varieties with better response to inputs, machineries and better management practices, coupled with conducive policies and strong institutions linkage. Although there have been impressive increments in wheat production across the years but still a big gap mentioned by policy planners between the demand and annual harvest of wheat. In the face of climate change with continued water shortage both in irrigated and rained environments, it is important to develop high yielding wheat genotypes with high water use efficiency which combines both high yield potential and resistance to drought and heat stresses along with resistance to the major biotic stresses. To this end, it is important to formulate efficient breeding methods and strategies that enable to increase genetic gain while utilizing the depleting resources efficiently.

The challenge now is to maintain the improvement of crops at a rate that will meet a rapidly increasing world population (projected to be 8.3 billion people in 2025). Borlaug mentioned the important point to achieve more production both conventional breeding and sophisticated recent methodologies will be combined accordingly. Further suggested that 'While recent research tools offer much promise, it is also important to recognize that conventional plant breeding methods are continuing to make significant contributions to improved food production and enhanced nutrition'. It is, therefore, vital that the statistical methods used to design and analyse data from breeding and evaluation programmes are as accurate, efficient and informative as possible.

Modern statistics and its application to the analysis of agricultural research experiments can be traced back about 90 yr when British statistician Sir Ronald Aylmer Fisher was hired in 1919 by Rothamsted Experimental Station to analyze field experiments. It was the analysis of these experiments that led Sir Fisher to invent and utilize the techniques known as analysis of variance (ANOVA) and experimental designs. These techniques have revolutionized field and laboratory experimentation in modern agriculture, providing ways to minimize or avoid bias, improve precision and secure valid conclusions. While these conventional techniques remain widely used, new statistical methods that take advantages of the increased computing power have an increasing role in agricultural research.

The development and implementation of general linear models and mixed models are two major advancements that had a great impact on agricultural research. The results of experiments are influenced by two kinds of factors. First, the treatment factors are often chosen intentionally for answering a research question. Second, many factors are not of direct relevance to the objectives of the experiments but cause extraneous variations (collectively known as experimental errors) which tend to mask the effects of the treatments. The experimental errors are either due to inherent variability in experimental materials and across growing seasons and soils or to lack of uniformity in the physical conduct of the experiment. Many experimental designs are available in the literature for minimizing or controlling the experimental errors. The presence of the two kinds of factors in most experiments has posed the need for determining whether or not a factor should be considered a fixed or random effect. Many experiments are carried out using a complete or incomplete block design with a few replications at multiple sites and over several years. These multi-environmental experiments are needed to infer the treatment performance for future years over a wide region. In such experiments, treatments are fixed effects as reasoned above, but the extraneous factors may be fixed or random, depending on whether or not they are subject to randomization.

Examples of random extraneous factors include randomly selected sampling units (e.g., plants, soil samples or quadrants in pest surveys) or randomization units (e.g., rows, columns, and plots). However, blocking units or replications may not necessarily be involved in randomization. For example, the choice of blocks, sites and years is often dictated by the availability of land and time constraints for completing experiments. Sometimes, even if a factor should be considered random, it may have too few levels to allow for a reliable estimate of its variance and a more pragmatic approach is to consider the factor fixed. Thus, to determine if an effect is fixed or random is not always a clear-cut decision.

Classification of effects as Fixed vs. Random

Most agricultural traits of cereal crops are quantitative in nature, are controlled by poly genes with various kinds of genetic effects and are affected by the environment. Replicated yield trials at several environments are often used in final stages of breeding programs to select genotypes based on yield and other economically important traits. Each genotype is commonly tested in more than one environment represented by locations or years or their combinations. A usual feature of all multi environment trials (MET) is the attempt to represent a relatively large target population of environments by a number of representative locations. In multi environment trials, environments might be reasonably assumed as random effects. However, the genotype effects might be treated as fixed since only a few selected genotypes are usually involved in late breeding stages.

Evaluating the genotype performance is the main aim of multi-environment trials in wheat coordinating trials. Broadly two types of inference are of interest (1) general performance of a genotype known as broad inference, and (2) environment specific or narrow inference - the performance of a genotype within a specific environment.

The traditional analytical approach for broad inference considers genotype average across environments that are subjected to multiple pair wise comparisons. Narrow inference from multi environment trials relies on comparisons of genotypic means in specific environments. Unfortunately, this procedure does not use all the available information. It is only possible to infer about performance in a specific environment for genotypes that have been tested in that environment. A random approach for environment and genotype-by-environment interaction effects allows the modeling of correlation structures throughout their associated variance components.

The lack of clear distinction between fixed versus random effects has generated a huge amount of confusion and uncertainty with the mixed-model analysis. Statistically speaking, there is only one criterion used in modern linear model theory for distinguishing fixed and random effects. If the effect levels reasonably represent a probability distribution, then the effect is random; if, on the other hand, effect levels do not represent a probability distribution, then the effect is fixed. For fixed effects, the main objective remains the same: to estimate treatment means and/or test treatment differences. For random effects, in addition to the major focus on modeling and estimating variance or covariance among random factor levels, interest may sometimes be in estimation and statistical inference about specific levels of a random factor. Best Linear Unbiased Prediction (BLUP) of a random effect is a shrinkage estimator to adjust for uncertainty arising from its probability distribution. The BLUP is devised to maximize the correlation between estimates of the realized values of the random

effects and the "true" realized values of the random effects. Based on this statistical criterion, some statisticians have made a pragmatic suggestion that there should be enough information in the data to estimate variance and covariance parameters of random effects with sufficient precision. It had been suggested that a factor should have more than 10 levels before it is considered random. In discussing the mixed-model analysis of regional cultivar trials. Researchers argued that cultivar effects should be random because selection of best genotypes through rankings rather than comparisons is the main goal either in the early "breeding" phase or in advanced "evaluation" phase. Plant breeders would usually consider that years and their interactions with genotypes are random, but debate considerably about how locations should be viewed. Part of the location effect would be "fixed" because it represents known physical properties (e.g., soil type of a location) or long term average (e.g., precipitation or other agro-climatic patterns) of the same location at some future time. However, the goal of most crop improvement programs is to infer future performance at many untested locations. Thus, it appears more appropriate that location effects and their interactions with genotypes should be considered as random.

These discussions may be summarized in a two-step approach for distinguishing fixed from random effects. The first step is to declare the factor to be random and consider two options (i) Is it physically possible for these particular levels of this factor to be repeated at some future time or in some other place? (ii) If the answer to (i) is yes, would it be reasonable for one to choose the same levels for repetition of this research at some future time or in some other place? If the answers to questions (i) and (ii) are both yes, the factor can be considered as fixed. The second step is to modify the declaration for statistical reasons. If a fixed factor is represented by a large number of levels (more than 10) and there is no structure to those levels, it may be best to declare the factor random and use BLUP to predict treatment mean values. The use of BLUP allows for shrinkage of the extreme treatment means. On the other hand, if a random factor has too few levels (less than 10), the estimate of the variance for this factor may be highly unreliable and it may be more practical to consider as fixed factor.

Understanding mixed-model analysis

One of the major impediments to appropriate use and correct interpretation of mixed models is the lack of understanding or appreciation of features and properties that mixed models offer. There are several reasons for choosing mixed models. The first and foremost reason is to avoid consequences of inappropriate models and statistical tests. While rarely recognized or acknowledged, both fixed and random effects are present in many commonly used experimental designs for field trials including randomized complete and incomplete block designs, nested designs, split-plot designs and repeated measures designs. Generally used procedure mixed would be an appropriate analysis of these designs, producing correct results including correct standard errors of differences between treatment means. However, general linear model analysis of these designs would often produce incorrect results. For example, general linear model may give erroneous denominator for F-test and incorrect SE of a treatment due to the presence of additional random effects and/or heterogeneous error variances. Thus, uncritical or inappropriate applications of general linear model, when its required assumptions are not supported by the data or the nature of the experiment may lead to unexpected or incorrect conclusions or may simply fail to achieve the fundamental objective of the experiment.

The second reason is that procedure mixed is better able to handle unbalanced data than general linear model. In the past, all general linear model users would face a difficult choice of which of the four types of sums of squares should be used for appropriate F-tests of fixed effects when analyzing an unbalanced data set. There is no clear-cut guideline in textbooks or user's guide to select Type I or Type III SS from analysed outputs. Moreover, since general linear model treats all effects, fixed and random, as if they were fixed, it is sometimes unable to estimate least squares means for unbalanced data. These problems associated with general linear model would disappear if procedure mixed was used. The third reason is that procedure mixed is able to analyze a wide variety of experimental designs and thus offers the flexibility of identifying the most appropriate design for a given research experiment. The continued trust in and use of general linear model analysis restricts the choice of experimental designs. Consequently, more elaborate and efficient experimental designs are either inaccessible or unknown to the researchers because they are too complicated to be handled by general linear model. The fourth reason is that agricultural researchers may soon be required to clearly show if statistical analysis employs the correct use and interpretation of mixed models. Well established periodicals has a more stringent policy as it "will not normally accept papers reporting the use of the general linear model procedure to analyze data-sets that include random effects or repeated measurements on the same experimental unit where the data show heterogeneous variances and/or unequal within subject time dependent correlations."

Unbalanced Data treated as random effects

The original intent of almost all designed experiments is to obtain a balanced data set, but data imbalance may arise from unforeseen circumstances. Data imbalance refers to having different numbers of observations in individual levels of a factor or combinations of levels of different factors in the experiments. Statistical analysis and hypothesis testing for mixed models remain valid if the missing-completely-at-random (MCAR) assumption is true. In other words, if the MCAR assumption is satisfied, then the missing data pattern is independent of the design. It is not always easy to determine the validity of the MCAR assumption. Following two examples are quite illustrative. In the first example, three sub-samples per plant are analyzed in the lab for a plant nutrient. A test tube is accidently dropped in the lab, causing missing data. Since this accident occurs randomly (i.e., dropping a particular test tube has nothing to do with the treatment or randomization units corresponding to the test tube), the MCAR assumption is satisfied. In the second example, a pot experiment is carried out to evaluate three different fertilizers. Each pot consists of 10 plants at the start of the experiment. One of the fertilizers has a harmful effect on some plants, causing them to die during the experiment. This missing data pattern does not support the MSCAR assumption because whether or not plants die depends on the treatment. With unbalanced data, general linear model produces approximate F-statistics for tests of hypotheses. However, there are no definitive guidelines for selecting a particular type of sum of squares for the numerator of the F-statistics. General linear model analysis often is unable to provide estimates of least squares (LS) means, differences between LS means and estimable functions from the unbalanced data, and even if estimable, the standard errors of these estimable functions are generally undependable. Mixed model analysis based on the true mixed-model methodology builds the parameters for the random effects into the linear model through the covariance structure. Test statistics, estimates of fixed effects, and standard errors of the estimates are computed using the generalized least squares (GLS) method. For unbalanced data, it is not easy to determine degrees of freedom but mixed model offers several options for obtaining approximate degrees of freedom even for unbalance data.

Consideration of genotypes as fixed or random

The adoption of mixed model analyses approach especially for multi environment trials data raise the considerations about variety effects as fixed or random. Some believe the choice depends on the aim of the analysis and consideration of the properties of the two types of estimation procedures, namely best linear unbiased prediction (BLUP) for random effects and best linear unbiased estimation (BLUE) for fixed effects. If the aim of the analysis is selection (that is, to identify the best varieties of those under consideration) then the rankings of the estimated variety effects are required to be as close as possible to the rankings of the true variety effects. In more exact terms, a set of estimates of variety effects is required that best predict the true effects. By definition, this implies the use of BLUP so that variety effects should be regarded as random. The optimality properties of BLUP are based on the assumption that the variance parameters in the model are known. In general, this is not the case and the parameters are estimated from the data. The only question that remains, therefore, is whether the estimates of the variance parameters are sufficiently precise to ensure that the optimality of BLUP. If the aim of the analysis is to determine the difference between specific pairs of varieties, then the use of BLUP as an estimation method is inappropriate since the BLUP of a specific difference is biased. Thus, in this case variety effects should be regarded as fixed. The key issue, therefore, is a clear definition of the aim of the analysis. In order to pursue this, common practice is followed with differentiating between breeding and evaluation programmes, although the distinction is sometimes hazy. Breeding programmes are concerned with the early stages of varietal evaluation phase in which large numbers (often greater than 1000) of new breeding lines are grown in small numbers (usually less than 3) of field trials.

The 'best' lines are selected to continue to the next stage of testing, in which fewer lines are evaluated in more locations. The process culminates in the testing of a small number (usually less than 40) of elite breeding lines, together with commercial standard varieties, in a large number of trials that span a wide range of geographic locations and several growing seasons. On the basis of these trials, a new genotype may be recommended for commercial use on farmer fields. These trials are usually the domain of crop variety evaluation programmes. It is clear that the aim of the analysis of breeding data is selection so that the use of random variety effects is appropriate. Some statisticians advocate the use of random effects in this setting because the varieties themselves are a random sample from a population. After some unspecified number of stages of selection, this ceases to be a reasonable assumption so that at this point variety effects are regarded as fixed.

If environments or genotypes are considered random, effects may be estimated by BLUP. A factor is commonly taken as random if the observed levels may

reasonably be regarded as a random sample from a population. The assumption of a truly random sample is often debatable for both environments and genotypes. Nevertheless, it is frequently assumed that environments are random, mainly to allow inferences which are not restricted to the observed environments. Reports showed that assuming random genotypes may be preferable in terms of predictive accuracy even when genotypes would be considered fixed by conventional standards.

The conventional general linear model coupled with ordinary least squares estimation procedures (OLS), useful as it is in many experiments in agriculture, are too restrictive to perform satisfactory data analyses for the typical data structure of most breeding programs. Error structure in "real world" experiments is often more complex than used in standard linear models for conventional data analysis. In contrast, the general linear mixed model can accommodate covariance structure among observations. Standard linear models usually assume independence. The mixed model handles these correlations with random effects and their associated variance components, modeling variability over and above the component associated with residual error. Mixed linear model approaches can circumvent the troublesome ANOVA for handling unbalanced data and complex models.

Mixed model analysis applies particularly to research involving factors with a few levels that usually can be controlled by the researcher (fixed) as well as factors with levels that are beyond the researcher's control (random). These random factors vary from experiment to experiment, and may be interpreted in the context of a symmetric probability function. Most breeding trials have some mixed model aspect.

The prediction value of unobserved or future performance is an important consideration in plant breeding. Prediction of random variable outcomes, in general, is a fundamental problem in statistics. Assuming that there is a priori knowledge about the distribution of the parameters defining the variable to be predicted, predictions are obtained by finding the posterior distribution of the variable, given the data, from a Bayesian point of view.

Besides the Bayesian approach to the prediction problem, the general mixed model allows prediction in a frequentist framework via the concept of conditional expectation without using a priori distribution. The conditional expectation of the random effects, given the observed data, is the BLUP of those random effects, and is also a Bayes estimator under normal priors. Theoretically, BLUPs have the smallest mean squared error of prediction among all linear unbiased predictors, provided the assumed model holds and the parameters of the model are known.

REML for BLUP

By specifying a normal distribution for the random effects, the estimation of the unknown parameters is usually obtained using likelihood-based procedures. A restricted maximum likelihood method (REML) is usually preferred for estimating the variance components in a mixed model. For unbalanced data, REML can offer significant advantages over ANOVA - based estimators as REML estimates are unique, nonnegative, and have maximum likelihood along with number of sample statistical properties. The asymptotic standard errors of the estimated variance components can be derived readily as part of the estimation procedure. In many plant breeding situations, a normal distribution for the data can be realistically assumed, so REML approaches are mostly appropriate. Nevertheless, REML estimates of variance components are robust to violations of this assumption. The REML procedure of estimating variance components maximizes the residual likelihood function, which is the likelihood function of a set of linear combinations of observed values whose expectations are zero. Those values are usually obtained by transforming the observations. The error contrasts are free of any fixed effects in the model. Thus, the residual likelihood function depends only on the unknown parameters that belong to the variance-covariance structure. The maximization of this function requires numerical procedures. Computation may be extensive with many variance-covariance parameters. Over-parameterized models may be avoided by an appropriate experimental design in relation to the number of parameters to be estimated.

To do model selection in the mixed model framework, a log likelihood-ratio test criterion can be used. In statistics, the likelihood-ratio test assesses the goodness of fit of two competing statistical models based on the ratio of the likelihoods, specifically one found by maximization over the entire parameter space and another found after imposing some constraints. The procedure demands the evaluation of the restricted log-likelihood (LLR) for the reduced model (model with smaller number of parameters) and for the full model (model with higher number of parameters). The test criterion for the likelihood ratio test is, L = -2{ LLR (reduced model) - LLR (full model)}.

Under normality for the null hypothesis that the reduced model is not different from the full model, the likelihood ratio statistic is distributed as a chi square with degrees of freedom equal to the difference in the number of parameters of both models. If the fixed part of the two mixed models under comparison is the same, the test is comparing the covariance structure models.

Procedures to find BLUP's

Linear mixed models have been very well recognized and widely used for analyzing METs data. These models are especially useful in the analysis of incomplete data complex variance-covariance structures for describing the G×E interaction effects.

The most realistic one is unstructured (UN) variance-covariance matrix. This variance-covariance matrix is the most liberal. Each variance or covariance in the matrix is different and is estimated uniquely from the data. The disadvantage of the UN structure in comparison to other structures is the large number of parameters to estimate. This can contribute to complexity of numerical calculations.

On the other end of the spectrum, the compound symmetry (CS) structure, which is the most restrictive variance-covariance matrix for linear mixed model. This structure assumes equal variances and equal covariances.

Recently, researchers more and more often suggest using factor-analytic (FA) structure for the METs data. That variance-covariance matrix also offers the flexibility comparable to the UN structure but with a lower number of parameters to estimate.

Factor analysis is concerned with identifying the common factors which give rise to correlations between variables. This involves fitting a latent variable model. In contrast, principal component analysis aims at identifying factors which explain a maximum amount of variation, and does not imply any underlying model. FA model can be regarded as the mixed model equivalent of the additive main effects and multiplicative interaction model with similar fixed-effects as genotype main effects and G×E interaction effects. AMMI model is based on principal components analysis via singular value decomposition, the factor-analytic model is based on factor analysis with a Cholesky factorization. The factor-analytic model depends on the decomposition of an unstructured variance-covariance matrix. In case of the analysis of the METs data with linear mixed models, it is always recommended to carry out a comparison of the models with different variance-covariance structures first. The second step is to use the selected model for proper analysis and evaluation of the cultivars. More recently, direct estimation enforcing a FA structure has been proposed and suitable algorithms for both restricted maximum likelihood (REML) and Bayesian estimation have been described, and mixed model software packages available, such as ASReml or WOMBAT, readily accommodate such analyses. The underlying concept is that only the most important principal components or common factors need to be estimated, while those explaining little variation can be ignored with negligible loss of information. This reduces the number of parameters to be estimated and thus sampling errors. Provided any bias due to the factors that are ignored is relatively small, this is also expected to reduce mean square errors. Furthermore,

eliminating unnecessary parameters is likely to make estimation more stable and efficient. For instance, omitting factors with corresponding eigen values close to zero reduces problems associated with estimates at the boundary of the parameter space, and can improve convergence rates in iterative estimation schemes. Factor analytic models, which separate genetic effects into common and specific components, provide a natural framework for modeling G × E interaction and related problems. Moreover, these models can substantially reduce computational requirements of mixed model analyses compared to standard multivariate models, both in variance component estimation and genetic evaluation schemes.

Number of studies have evaluated the models with different variance-covariance structures (including FA) and concluded that the FA variance covariance structure is more accurate than the classical ANOVA and numerically less complicated than the UN structure.

The popular method used to choose the best variance- covariance structure is based on information criteria, such as Akaike's information criterion (AIC) or Bayesian information criterion (BIC). It depends on evaluating the predictive accuracy of the effects. AIC is a commonly used criterion to choose the best variance-covariance structure in linear mixed model for METs. The AIC was obtained using the following formula: AIC = $-2 \times \text{Log L} + 2p$, where Log L is the logarithm of maximum restricted likelihood of the model; and p is the number of estimated variance-covariance parameters in the model. The smaller AIC values, the better fit of the variance covariance structure. The expression "$-2 \times \text{LogL}$" is called "deviance" and is also used in calculating other information criteria (e.g. BIC) and likelihood ratio tests.

Change in wheat genotypes as compared to checks

Traditionally in usual coordinated system, the performance of a new genotypes at each site-year has been expressed as a percentage of a chosen "check" cultivar (or the average of several chosen check cultivars), and then relatively simplistic statistical analyses are conducted on this % of check data. This approach has been followed very long for testing of genotypes for several crops. In contrast, the results of genotypes yield as actual values. Individual site-year yield data is presented in publications as a summary column based on overall arithmetic mean from number of years of testing and presented for each genotype. The relatively small number of years of testing reflected in this overall arithmetic mean could be problematic, in that results from an anomalously high or low yield-year could substantially skew the calculated arithmetic mean and possibly reduce the accuracy of crop genotype yield rankings. The check cultivar in the traditional crop MET is grown at all site-years and "occupies" one of a limited number of entries in MET (potential entries in MET obviously are limited due to resource constraints). The rationale underlying this traditional statistical approach was to minimize the influences of location and year on the ultimate ranking of genotype performance.

A complicating factor in the statistical analysis of MET data is that long term, multi-year data tends to be highly unbalanced – that is, not all genotypes are present in all trials in all years. This is understandable as genotypes are introduced, evaluated for several years at a number of sites, and then replaced in the trials by newer genotypes. Expressing genotype performance at each site as a percentage of a long term check cultivar essentially ignores the statistical complications arising from a highly unbalanced data set.

This traditional statistical approach using a check cultivar has several drawbacks: (1) Identification and selection of an appropriate, representative check cultivar may be problematic. The identification and selection of an appropriate check cultivar is usually undertaken by a committee of "experts" after consideration of existing information. One of the considerations is the "popularity" of the check cultivar, or how widely grown. However, this process may still be considered at least somewhat arbitrary, and the selected check cultivar may prove to be unrepresentative / deficient in certain environments. (2) Over time with continual breeding efforts and introduction of new genotypes, the check cultivar may become unrepresentative and inappropriate, and a new check cultivar will need to be chosen. Since MET data has been expressed as a % of check, changing the check makes valid comparisons to historical data very difficult – essentially the percentage based historical database is rendered useless. (3) In certain years over the majority of trial locations, the check cultivar may perform quite

differently than its long term average. For example, this may occur if the check cultivar is susceptible to a specific disease that is exacerbated by weather experienced during the growing season. Newer genotypes in the MET may be resistant or partially resistant to this disease, and this anomalous performance of the check cultivar may lead to predictions of superior newer genotype performance that will not be achieved in the long term. Because newer genotypes are often only evaluated for two or three years in MET, this check under-performance in a specific year can substantially influence predicted genotype performance.

As an alternative to the traditional genotype MET statistical approach using % of check data and relatively simple analysis, linear mixed model analysis had been applied to MET data from mid-1990's onward. Mixed model analysis has a much greater capability to accommodate highly unbalanced data as compared to traditional ANOVA procedures. The use of mixed model analysis with actual yield data has resulted in genotype performance predictions that are more realistic, and farmers are able to harvest substantially lower than those predicted by MET results. Furthermore, an additional advantage to using actual yield data is that a long-term check cultivar in MET is not required which opens up an entry "slot" in the trials reducing the cost associated with growing the same check cultivar in multi-site trials year after year.

One/two stages of analysis for coordinatated system

Multi-environment trials are essential, due to the presence of genotype x environment interaction, as genotypes respond in differently to variable environmental conditions. GxE interaction reduces the overall progress from selection process confined to any one environment and decreases the response to selection for average genetic performance due to the difficulty in selecting the best-performing and most stable genotypes. Multi-environment trial data are commonly analyzed using linear mixed models in either one-stage or two-stage analyses. A one-stage analysis is usually considered the gold standard, as it is more efficient than a two-stage analysis. However, it is computationally expensive when applied to analyze many environments, especially when different types of models are needed to characterize variability for each of individual environment.

In contrast, a two-stage analysis is computationally efficient and can handle a larger amount of data or more complex models as compared to one-stage analysis. A two-stage analysis can be used to model any specific randomization layout and within-environment error for each individual environment in the first stage, then use the adjusted genotype mean for the across-environment at second-stage of analysis. In the analysis of plant breeding MET data, a spatial model is usually fitted for each environment to produce a spatially adjusted genotype mean in each environment. The spatially adjusted genotype means are then combined as the data for the second stage, across-environment analysis. The loss of efficiency in a two-stage analysis is reduced by weighting the adjusted means according to the predicted accuracy of the value in the individual environment analysis.

All the genotypes in the same field are normally grown under the same field management, although genotypes are from different sets, so an overall experimental design that minimizes the estimated error within a field should be used. Moreover, a spatial analysis for a field can be conducted using all available data in that field. For annual crops, genotype performance is usually evaluated on a single phase and single cycle of data across locations, hence a single-year analysis. The results from the analysis of any single year's data have been shown to overestimate the genotypic variance.

Approaches to highlight genotypes performance

Three different methods were used to find yield increases in cereal crops. The first one is based on the use of historical data on annual production at the level of country, state or region; it provides a measure of production increase but does not indicate proportion attributable to genetic gain, as the farm yield is influenced by several non-genetic factors like fertilizer, irrigation, protection against stresses and the intensity of other crop management practices adopted.

The second method is to use the historical set of data on performance of genotypes in national or international trials to derive the genetic gain achieved in yield. The third method to estimate genetic yield gain is to conduct yield trials with an array of generated breeding lines and cultivars, checks or standards using a set of standardized agronomical practices. These trials are often restricted to experiments for a few seasons and years, and ignore the effects of a wide range of environmental conditions and ever-changing crop production practices used in testing older genotypes. Retrospective physiology on genetic progress in tropical rice is also hampered by concerns over the validity of side-by-side comparisons of historic sets of cultivars. This publication is limited to BLUP analysis of coordinated wheat trials carried out at different centers for major wheat growing zones of the country.

During the time period 2008-09 to 2017-18, as many as 1336 promising genotypes were evaluated across major locations of country for wheat crop under coordinated system. Nearly 425 check varieties were considered in multi environmental tests (METs) at coordinated centers. Data sets on wheat yield of genotypes and checks in irrigated timely sown, irrigated late sown, restricted irrigated and rained conditions were analysed as per BLUP/REML procedures. These advanced varietal trials were performed at major locations in 05 zones for wheat cultivation. The same research field trials were laid out in same zone along with recommended crop management practices to harvest good yield. Individual trial data were scrutinized and analysed and data from experiments or locations registered more than 20% of coefficient of variation (CV) were rejected.

Estimation of the variance parameters carried out by using residual maximum likelihood (REML) along with estimation / prediction of the fixed as well as random effects. Quite popular and widely cited ASReml-R package was exploited to fit models which uses the average information algorithm for REML estimation of variance parameters. The implementation for FA models in ASReml-R package handles the situations of where rank of interaction matrix is of less than full rank.

Under coordinated system g genotypes are evaluated in e environments and analysed as per model

$$y_{ijk} = m + t_i + d_j + (td)_{ij} + g(d)_{jk} + e_{ijk}$$

y_{ijk} yield of k replication of ith genotype in j environment	m overall mean	t_i Effect of genotype	d_j Effect of environment	$(td)_{ij}$ Interaction effect	$g(d)_{jk}$ Effect of k-th replication in j-th environment	e_{ijk} Random error

i= 1,2,3,…g; j=1,2,3,…e; k=1,2,3,…r

Possible three versions of equation are : (i) Random model with all effects being random except μ ;(ii) fixed model with all effects being fixed except $g(d)_{jk}$ and e_{ijk} ; (iii) mixed model with genotypic effect is fixed whereas the others are random. When it is considered that the genotypic effect is fixed and the environmental effect is random, and i are fixed effects whiles d_j , $(td)_{ij}$ $g(d)_{jk}$ are independently and normally distributed with zero mean and variances s^2_d, s^2_{dt} and $s^2_{g(d)}$ s^2_e respectively.

The basic idea is to estimate the effects in the linear model and then to weight some or all of the effects by an estimate of the pattern-to-noise ratio associated with the respective effect. The BLUPs of the ij-th cell means from a balanced data set is

$$\text{BLUP}(m_{ij}) = \text{BLUE}(m) + \text{BLUP}(d_j) + \text{BLUP}[(td)_{ij}]$$

$$\text{BLUE}(m) = \text{Mean of the i-th genotype}(\bar{Y}_{i..}),$$
$$\text{BLUP}(d_j) = \frac{rg\sigma^2_d}{E\ MS_d}(\bar{Y}_{.j.}-\bar{Y}_{...})$$

$$\text{BLUP}[(td)_{ij}] = \frac{r\sigma^2_{td}}{E(MS_d)}(\bar{Y}_{-.j.}\ \bar{Y}_{...}) + \frac{r\sigma^2_{td}}{E(MS_{td})}(\bar{Y}_{ij.}-\bar{Y}_{i..}-\bar{Y}_{.J.}+\bar{Y}_{...})$$

$$E(MS_d)= \sigma^2_e + g\sigma^2_{y\ d} + r\sigma^2_{td} + rg\sigma^2_d \quad \text{and}$$

$$E(MS_{td}) = \sigma^2_e + r\sigma^2_{td} .$$

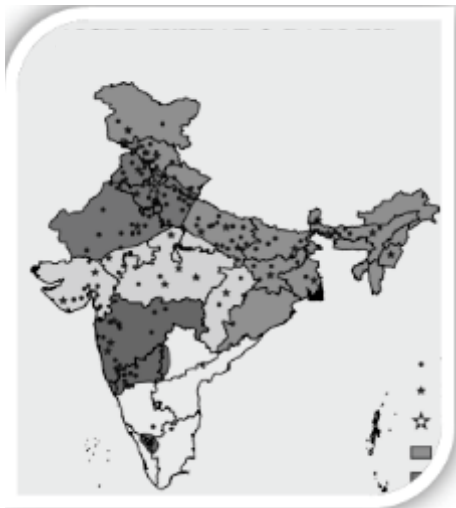$E(MS_d)$ & $E(MS_{td})$: Expected mean squares for environment and GxE interaction

$$\text{BLUP}(m_{ij}) = \bar{Y}_{i..}+f_{id}(\bar{Y}_{.j.}-\bar{Y}_{...}) +f_{itd}(\bar{Y}_{ij.}-\bar{Y}_{i..}-\bar{Y}_{.j.}+\bar{Y}_{...})$$

$f_{id} =[rg\sigma^2_d + r\sigma^2_{td}] /(MS_d)$ & $f_{itd}= r\sigma^2_{td} / (MS_{td})$: shrinkage factor for environment and GxE interaction

BLUP of wheat genotypes : Zone wise analysis

Advantages of BLUP over BLUE had been established in research studies, so BLUP of wheat genotypes were estimated over the years to highlight the increase in wheat production in all major wheat growing zones of the country. All India Coordinated Research Project on Wheat and Barley (AICRP) is coordinating multidisciplinary and multi location testing of varietal, newly developed improved genotypes, crop management and crop protection technologies across the diverse ecosystems for increasing and stabilizing the wheat production. As a nodal agency for wheat research of the country, ICAR-IIWBR facilitates planning, exchange of experimental material, monitoring the field trials / nurseries, data compilation and documentation. Presently, there are 29 funded centres and more than 100 voluntary centres that are carrying out the very systematic planned activities of different production conditions of the five agro-ecological zones of the country.
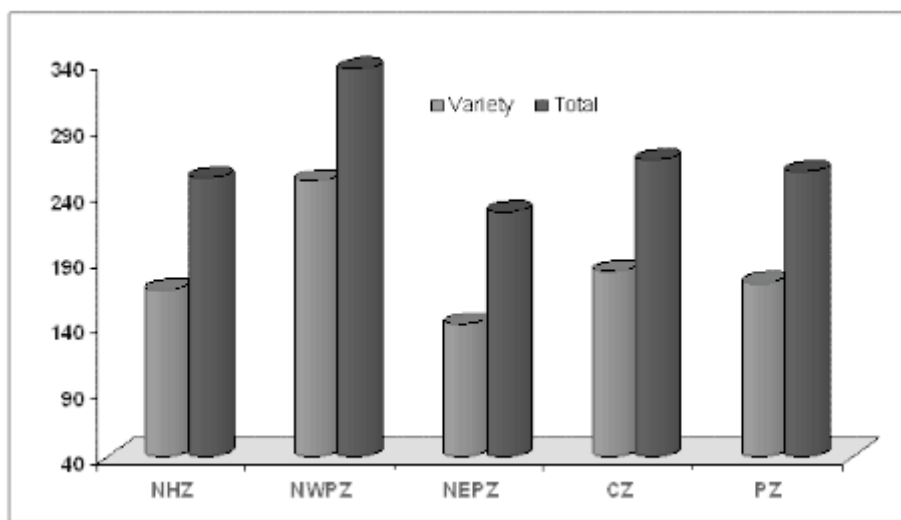

Total wheat genotypes and checks evaluated under coordinated system across zones

Zone wheat area (mha)	Area Covered	Funded centres	Non Funded centres
NHZ (0.82)	Western Himalayan regions of J&K (except Jammu and Kathua distt.); H.P. (except Una and Paonta Valley); Uttaranchal (except Tarai area); Sikkim and hills of West Bengal and N.E. States	CSK-HPKVV, Palampur CSK-HPKVV, Bajaura CAU, Imphal SKUAST-K, Srinagar	**Himachal Pradesh** - Bajaura, Kangra, Bara, Kukumseri, Berthin, Akrot, Dhaulakuan, UNA KVK, Shimla **Uttarakhand -** Almora **Manipur –** Imphal **Jammu & Kashmir** – Khudwani, Wadura
NWPZ (12.33)	Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions) and Western UP (except Jhansi division), parts of J&K (Jammu and Kathua distt.) and parts of HP (Una dist. And Paonta valley) and Uttaranchal (Tarai region)	PAU, Ludhiana CCSHAU, Hisar GBPUAT, Pantnagar RAU, Durgapura SKUAST-J, Jammu	**Haryana –** Bawal, Rohtak, Hisar, CSSRI, Karnal **Uttarakhand -** RRS,Majhera, Pantnagar , KVK, Dhakrani, Sugarcane Research centre, Kashipur, Pantnagar **Punjab –**Gurdaspur, Bathinda, Faridkot, Kapurthala, Balachaur, Rauni, Muktsar **New Delhi -** IARI, New Delhi **Uttar Pradesh -** Bulandshahr, Pilibhit (New), Sahajahanpur, Nagina , Ujhani, KVK-Rampur, Deegh, Araul, Bareilly, Agra **Jammu & Kashmir –**Rajouri **Rajasthan –**Tabiji, Navgaon, Alwar, Diggi, Sri Ganganagar
NEPZ (8.85)	Eastern UP, Bihar, Jharkhand, Orissa, West Bengal, Assam and plains of NE States	CSAUAT, Kanpur NDUAT, Faizabad BHU, Varanasi BAU, Sabour BAU, Ranchi BCKVV, Kalyani UBKV, Coochbehar AAU, Shillongani	**Assam –**Shillongani **Uttar Pradesh –**Varanasi, Kanpur, Faizabad, Chandauli, Ghaghraghat, Mirzapur, Ghazipur, KVK – Amethi (New), KVK – Basti, KVK – Mahrajganj, Gorakhpur, Agra **West Bengal** – Kalyani, Burdwan, Coochbehar, Kharibari, Malda, Manikchak, Majhian, Kalimpong **Bihar-** Sabour, Purnea, Banka, Rohtash, IARI, RS, Pusa, ICAR, Research Complex , Eastern Region, Patna **Jharkhand –**Ranchi, Dhumka, Chianki, Gumla
CZ (6.84)	Madhya Pradesh, Chhattisgarh, Gujarat, Kota and Udaipur divisions of Rajasthan and Jhansi division of Uttar Pradesh	IGKVV, Bilaspur SDAU, Vijapur JAU, Junagarh MPUAT, Udaipur JNKVV, Jabalpur JNKVV, Sagar JNKVV, Powerkhera RVSKVV, Gwalior	**Gujarat** –Vijapur, SK Nagar, Anand, Amreli, Junagarh, Sanosara, Bardoli **Madhya Pradesh** –Gwalior, Jabalpur, Powarkheda, Indore, Bhopal, Sagar, Shahdol, Ujjain, Ratlam, Morena, Tikamgarh, Rewa **Chhattisgarh** – Bilaspur, Ambikapur, Jagdalpur, NIBSM- Raipur, IGKVV-Raipur **Rajasthan –** Kota, Udaipur, Banswara, Mandor
PZ (0.71)	Maharashtra, Karnataka, Andhra Pradesh, Goa, plains of Tamil Nadu Hilly areas of Tamil Nadu and Kerala comprising the Nilgiri and Palni hills of southern plateau.	UAS, Dharwad MPKVV, Niphad MPKVV, Mahabaleshwar ARI, Pune	**Maharashtra** - Rahuri, Niphad, Mahableshwar, Karad, Kolhapur, Pune, Akola, Washim, Parbhani **Karnataka -** Dharwad, Arbhavi, Kalloli, Nippani, Mudhol, Bagalkot, Bailhongal

Northern Hills Zone

Wheat is cultivated in the hills at different altitude under various crop rotations adapted at different elevations. In NHZ, sowing is generally done under rainfed conditions in months of October/November with residual moisture and harvesting takes place in May/June months of the year. In higher hills of Leh (J&K) and Lahaul and Spiti (HP), the winter is severe, causing the crop is to be raised at congenial weather between May to September. Development of high yielding varieties for moisture stress condition is the major objective of wheat improvement programmes in NHZ. Region encompasses the hilly terrain of Northern region extending from Jammu & Kashmir to North Eastern States. The NHZ comprises J&K (except Jammu and Kathua distt.); Himachal Pradesh (except Una and Paonta Valley); Uttarakhand (except Tarai area); Sikkim, hills of West Bengal and North Eastern states (Figure 1). The wheat grown in the NHZ generally has productivity of 15-16 q/ha. Moisture stress is the major factor responsible for low productivity besides soil fertility, soil depth, frost damage, small and fragmented holdings, low and imbalanced use of fertilizers. High incidences of weeds and diseases, particularly yellow rust, brown rust and loose smut etc. are the other factors that limit the productivity.
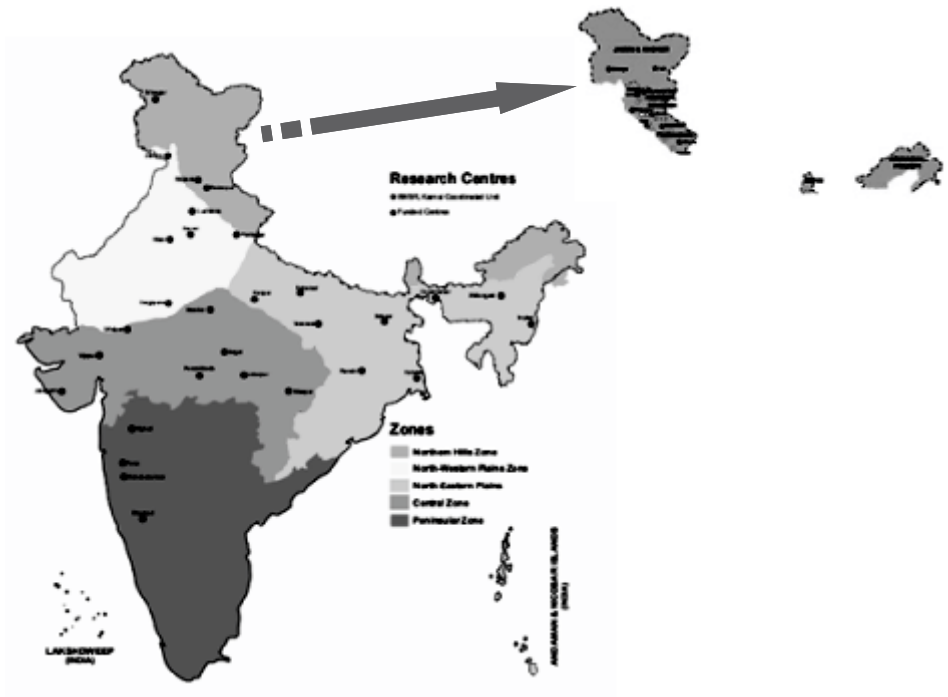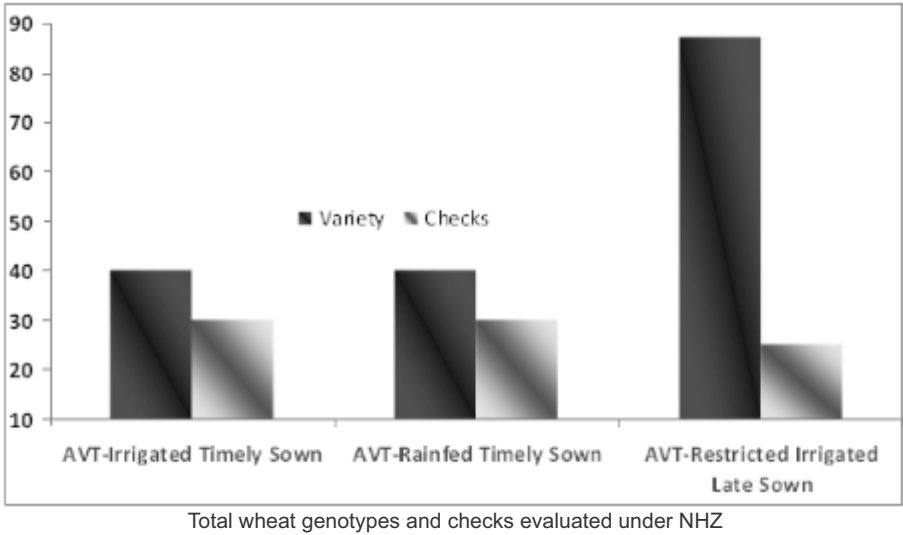
Total wheat genotypes and checks evaluated under NHZ

Table 1: ANOVA for irrigated timely sown conditions

Source	SS	MSS	F value	Pr > F	Root MSE	R-Square	Coeff Var	Std Error	t value	Pr > |t|
Model	92.19014	92.19014	6.84	0.0133	3.67051	0.1717	8.08448			
Error	444.59620	13.47261								
Total	536.78634									
Parameter	Estimates									
Intercept								1.38732	30.39	<.0001
Year								0.31021	2.62	0.0133

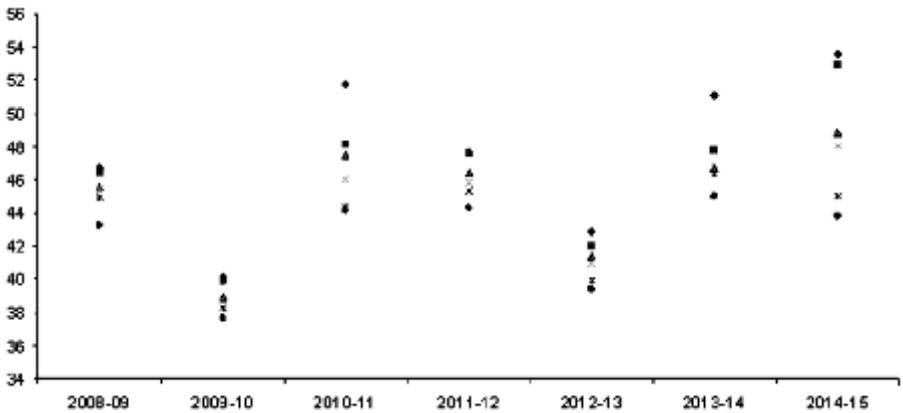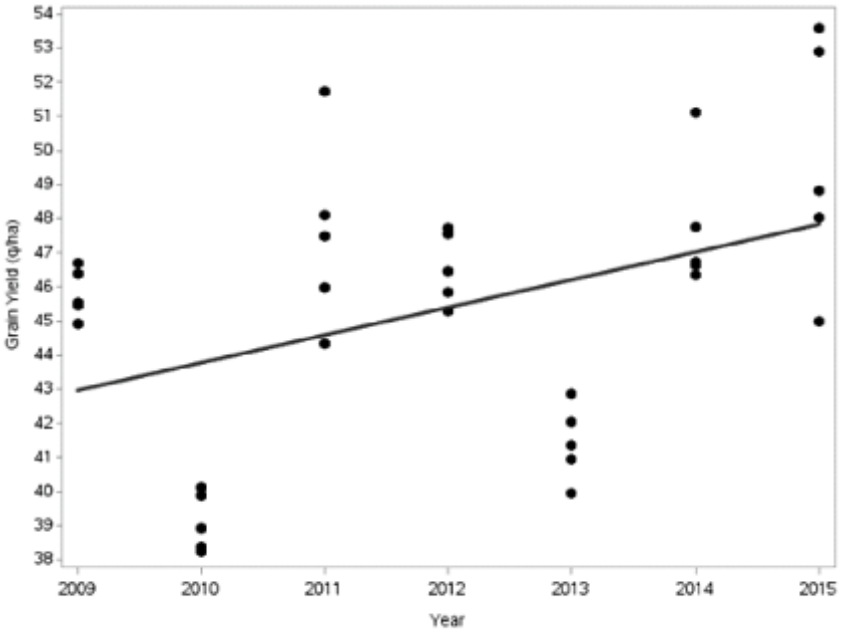Figure 2: Best Linear Unbiased Predictors for promising genotypes for timely sown conditions

Regression Equation:
qy = 42.15598 + 0.811481*Year

Figure 3 Regression analysis of BLUP's for promising genotypes for irrigated timely sown

Table 2: ANOVA for restricted irrigated late sown conditions

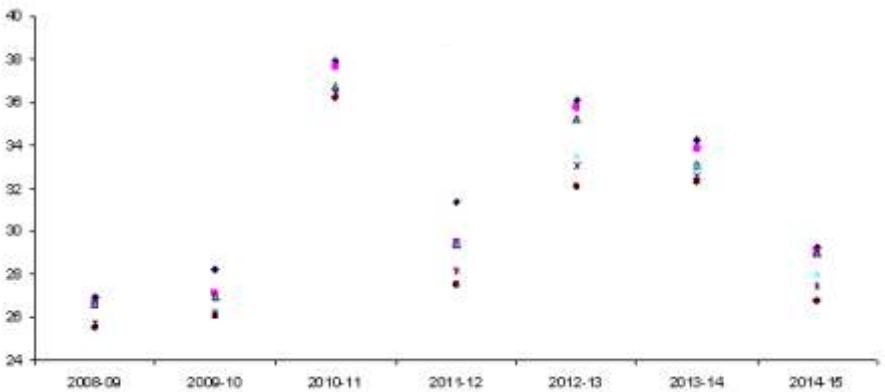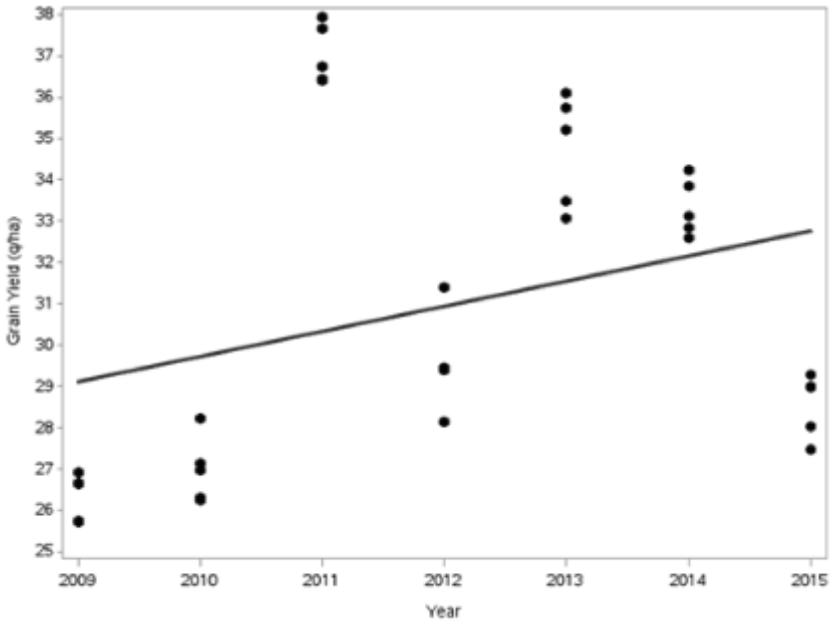| Source	SS	MSS	F Value	Pr > F	Root MSE	R-Square	Coeff Var	Std Error	t Value	Pr > |t|
Model	51.72836	51.72836	3.56	0.0680	3.81224	0.0974	12.32533			
Error	479.59523	14.53319								
Total	531.32359									
Parameter	Estimates									
Intercept								1.44089	19.78	< .0001
Year								0.32219	1.89	0.0680

Figure 4: Best Linear Unbiased Predictors for promising genotypes for late sown conditions

Regression Equation:
gy = 28.49871 + 0.607855*Year

Figure 5: Regression analysis of BLUP's for promising genotypes for irrigated late sown

Table 2: ANOVA for rainfed timely sown conditions

Source	SS	MSS	F value	Pr > F	Root MSE	R-Square	Coeff Var	Std Error	t Value	Pr > |t|
Model	597.85537	597.85537	29.67	< .0001	4.48904	0.4734	15.95091			
Error	664.99925	20.15149								
Total	1262.85462									
Parameter	Estimates									
Intercept								1.69670	11.72	< .0001
Year								0.37939	5.45	< .0001

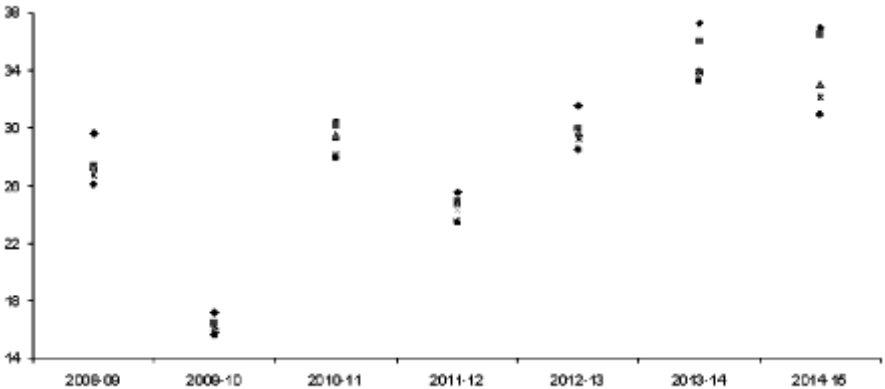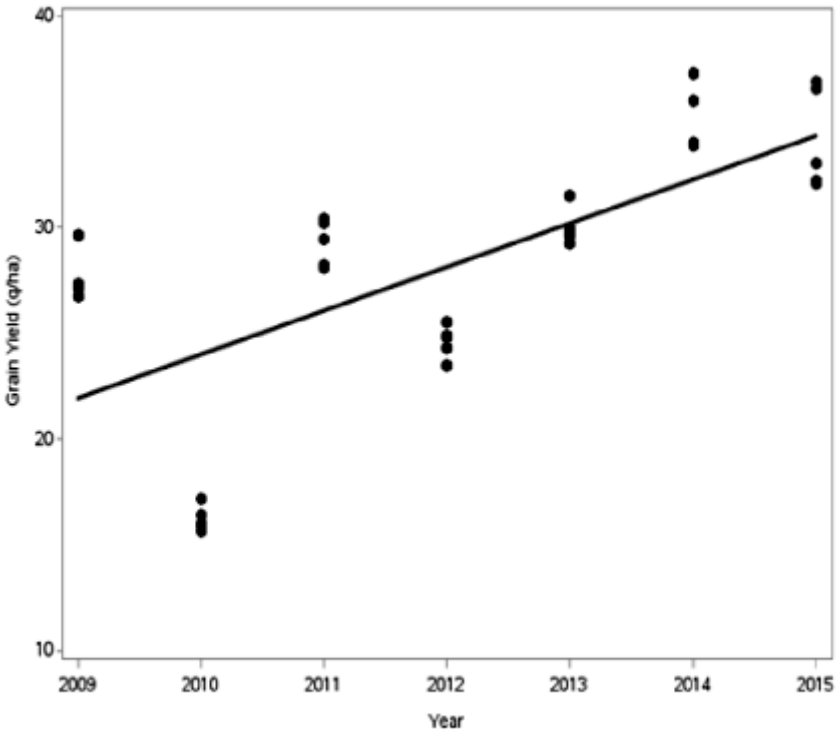
Figure 6: Best Linear Unbiased Predictors for promising genotypes for rainfed timely sown conditions

Regression Equation:
gy = 19.87688 + 2.066494*Year

Figure 7: Regression analysis of BLUP's for promising genotypes for rainfed timely sown

Highly significant change in wheat production had been observed during the studied time period span for irrigated timely sown, late sown and rainfed timely sown conditions trials in Hilly Zone of country as reflected in ANOVA tables (1,2 and 3). Highly significant values of intercept for three conditions along with highly significant slope for rainfed timely sown conditions observed. Significant values of slope for irrigated timely and late sown conditions also seen.

Scatter plots of BLUP's of wheat production versus year were plotted to examine the coefficient of determination (R^2) and linear trend for assessing progress in wheat production for irrigated timely, irrigated late & rainfed timely sown conditions. Regression analysis for production revealed that under rainfed timely-sown condition, the R^2 value was highly significant (P<0.01). Under the rain fed timely-sown conditions, area under cultivations had decreased in zone so trials were discontinued for 2015-16, 2016-17 years though yield improvement was highly significant. Advanced varietal trials were also discontinued for 2015-16 and 2016-17 due to shortage of promising genotypes to next levels. Significant improvement was also visible in rainfed timely-sown conditions of the zone.

Linear trend in the year-wise wheat production in different conditions revealed an increase in average production of promising genotypes in zone by the end of 2015. The production figures elevated to the level of 53q/ha (Fig. 2) for irrigated timely, of 30q/ha (Fig. 4) for irrigated late sown and 36q/ha (Fig. 6) for rainfed timely sown trials. However, in 2008-09, average production was 46q/ha 41q/ha 20q/ha and by the end of period 0.81, 0.61 and 2.06 quintal yield respectively could be added in subsequent trials. Although highest yield levels of 53 q/ha (2014-15), 38 q/ha (2010-11) and 38 q/ha (2013-14) were obtained in irrigated timely, late and rainfed timely sown trials but low values of R^2 for irrigated timely and late sown conditions suggested high variability in production values. More over consistent improvement observed in rainfed timely sown trials as justified by highly significant value of R^2.

Study revealed that during studied period of seven years the wheat production had   progressed nicely in this zone. Fitted straight-line equations by SAS software displayed in corresponding figures indicate that the linear growth was observed under all sown conditions of the zone. During the year 2008-09, the base yield level was 4216, 2849 and 1987 kg/ha respectively (as reflected by intercept of the equation). Rainfed sown conditions of the zone expressed significant yield increase over years (R^2=0.4734**) was registered and the linear trend was noticed from the base yield level of 1987 kg/ha with annual increment of 206 kg/ha. Comparatively large values of CV reflected consistent yield improvement under rainfed timely conditions as compared to other considered situations. BLUP analyses of wheat trials showed continuous increase in the grain yield of the genotypes developed by Indian coordinated Wheat Program. This finding also corroborates with studies on coordinated wheat production estimated by BLUE approach . More over in present study FA structure of the variance–covariance matrix of GxE was considered to estimate the BLUP of wheat yield.

North Western Plains Zone

This zone consists of the parts of sub-humid Sutlej-Ganga Alluvial Plains and arid western plains, which comprises Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions), Western Uttar Pradesh (except Jhansi division and hilly areas), parts of Jammu and Kashmir (Jammu and Kathua districts) and parts of Himachal Pradesh (Paonta Valley and Una districts).Wheat is cultivated for three broad cultural conditions, viz timely sown irrigated, late sown irrigated and timely sown restricted irrigation in major wheat zone. The experimental design was randomized blocks in three replicates. The advanced varietal trials under irrigated timely and late sown with restricted irrigated timely sown conditions were considered during the period 2012-13 to 2017-18 growing seasons in the major locations of the zone.
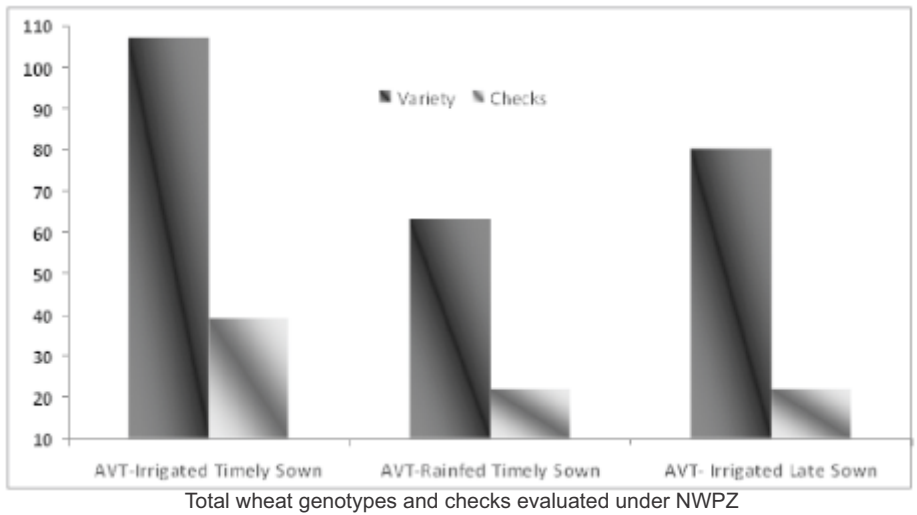
Total wheat genotypes and checks evaluated under NWPZ

Table 1: ANOVA for irrigated timely sown conditions

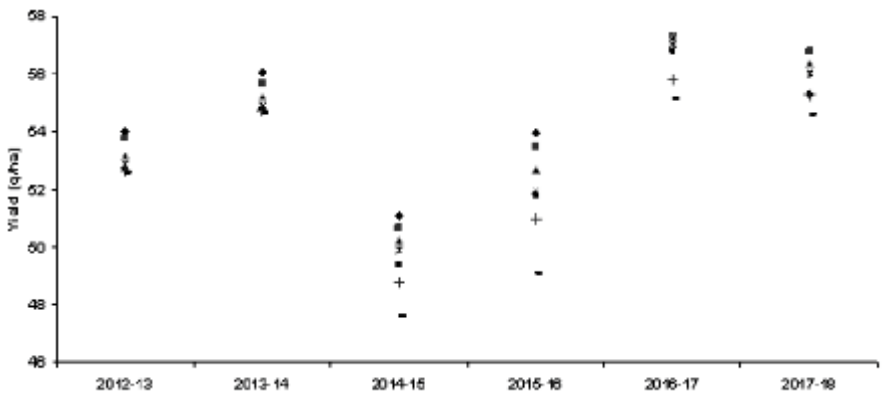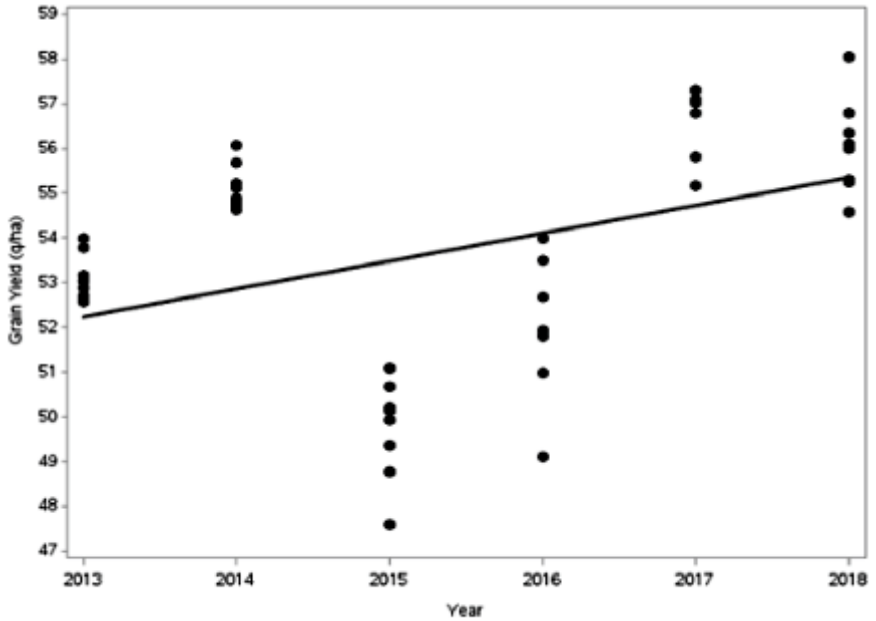| Source	SS	MSS	F value	Pr > F	Root MSE	R-Square	CV	Std Error	t value	Pr > |t|
Model	54.21	54.21	9.11	0.0041	2.4395	0.1653	4.5359			
Error	273.76	5.95								
Total	327.97									
Parameter	Estimates									
Intercept								0.8029	64.27	< .0001
Year								0.2062	3.02	0.0041

Figure 1: Best Linear Unbiased Predictors for promising genotypes for irrigated timely sown conditions

Regression Equation:
qy= 51.6045 + 0.622286*Year

Figure 2: Regression analysis of BLUP's for promising genotypes for irrigated timely sown

Table 2: ANOVA for irrigated late sown conditions

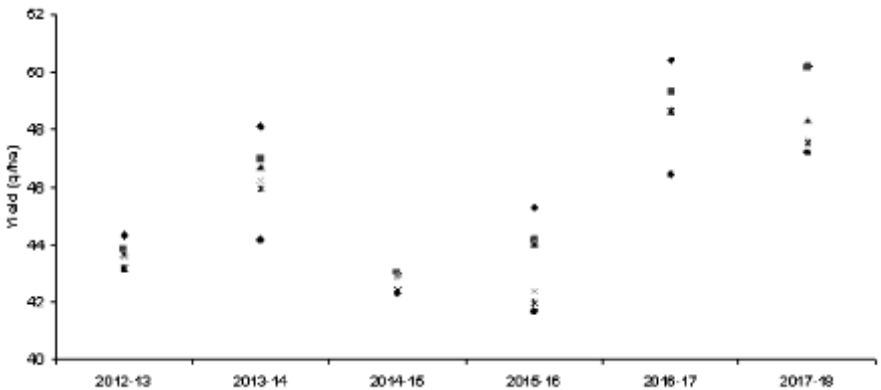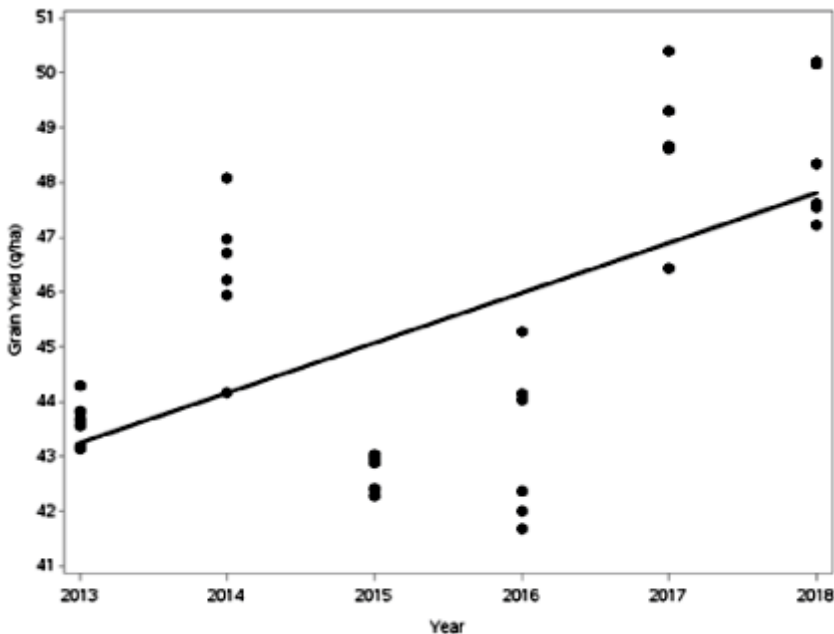| Source	SS	MSS	F Value	Pr > F	Root MSE	R-Square	CV	Std Error	t Value	Pr > |t|
Model	87.58	87.58	17.92	0.0002	2.2105	0.3452	4.8553			
Error	166.15	4.89								
Total	253.73									
Parameter	Estimates									
Intercept								0.8402	50.39	< .0001
Year								0.2157	4.23	0.0002

Figure 3: Best Linear Unbiased Predictors for promising genotypes for irrigated late sown conditions

Regression Equation:
gy = 42.33267 + 0.913286*Year

Figure 4: Regression analysis of BLUP's for promising genotypes for irrigated late sown

Table 3: ANOVA for restricted irrigated timely sown conditions

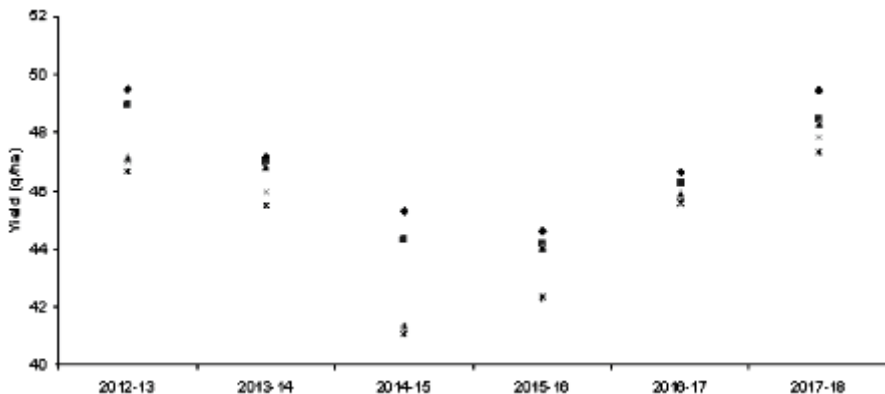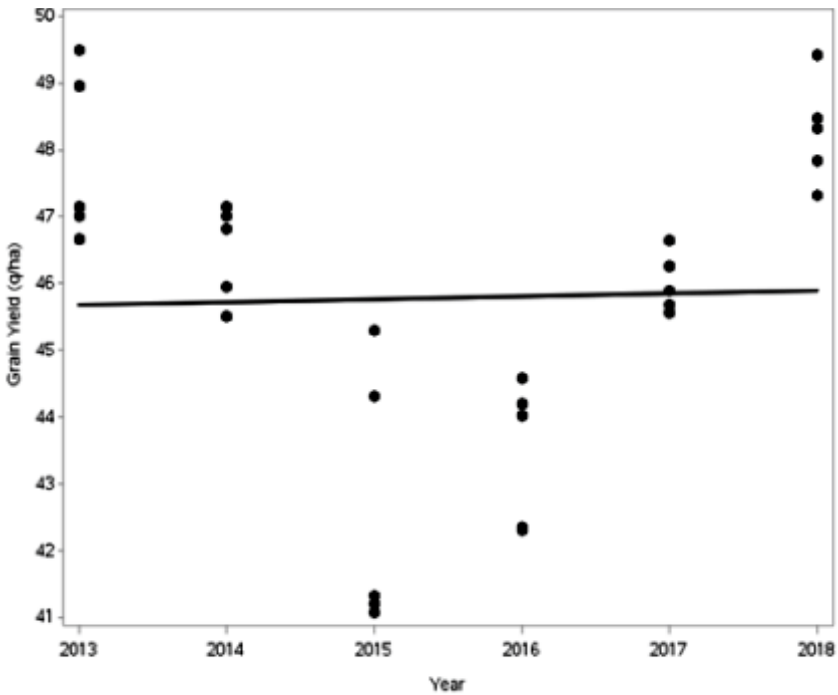| Source	SS	MSS	F value	Pr > F	Root MSE	R-Square	CV	Std Error	t Value	Pr > |t|
Model	0.17	0.17	0.03	0.8668	2.4130	0.0010	5.2694			
Error	163.03	5.82								
Total	163.19									
Parameter	Estimates									
Intercept								1.0046	45.43	< .0001
Year								0.2579	0.17	0.8668

Figure 5: Best Linear Unbiased Predictors for promising genotypes for restricted irrigated timely sown conditions

Regression Equation:
qy= 45.63987 + 0.043657*Year

Figure 6: Regression analysis of BLUP's for promising genotypes for restricted irrigated timely sown

Highly significant change in wheat production had been observed during the studied period for irrigated timely, late sown and restricted irrigated timely sown trials in a major wheat producing zone of the country as reflected in ANOVA tables (1, 2 and 3). Large values of F-test statistic observed for irrigated timely and late sown conditions though corresponding small value seen for restricted irrigation timely sown trials. Significant values of intercept at 0.01 % for first two conditions along with significant value for third condition. More over significant values (at $P < 0.005$) of slope for linear trend exhibited by irrigated timely and late sown trials with significant change at large values of probability for remaining condition. Desirable small value of CV had been portrayed by irrigated timely and late sown trials as compared to large value for restricted irrigated condition. Similar observations were recorded for root mean square error values. More or less same trend were seen for standard error for year as dependent factor.

Scatter plots of BLUP's of promising genotypes over the years were plotted to examine the coefficient of determination (R^2) and linear trend to assess progress in wheat production for irrigated timely, late & restricted irrigated timely sown conditions. Regression analysis for production revealed that under irrigated timely as well as late sown condition, R^2 values were highly significant ($P<0.01$). Under the restricted irrigated timely-sown conditions, small value of R^2 had seen.

Linear trend in the year-wise wheat production in different conditions revealed an increase in average production of promising genotypes in zone by the end of 2017-18. Production figures elevated to the level of 57q/ha (Fig. 2) for irrigated timely, of 50q/ha (Fig. 4) for irrigated late sown and 49q/ha (Fig. 6) for restricted irrigated timely sown trials. However, in 2012-13, average production was 51.6q/ha 42.3q/ha 45.6q/ha and by the end of period 0.62, 0.91 and 0.04 quintal yield could be added in subsequent trials respectively. Although highest yield levels of 58 q/ha (2016-17), 51 q/ha (2016-17) and lowest level nearly 40 q/ha (2014-15) were obtained in irrigated timely, late and restricted irrigated timely sown trials. Low values of CV for irrigated timely and late sown conditions suggested consistent improvement in production levels. More over erratic ups and down observed in restricted irrigated timely sown trials.

Study revealed that during studied period wheat production had progressed nicely in this bigger zone. Fitted straight-line trends by SAS software displayed in corresponding figures indicate that the linear growth was observed under all sown conditions of the zone. During the year 2008-09, the base yield level was 5160, 4233 and 4564 kg/ha respectively (as reflected by intercept of the equation). Restricted irrigated conditions of the zone expressed least yield increase over years with small values of R^2. BLUP analyses of wheat trials showed continuous increase in the grain yield of the genotypes developed by Indian coordinated Wheat Program.

North Eastern Plains Zone

This zone of India comprises eastern Uttar Pradesh, Bihar, Jharkhand, Assam and plains of West Bengal. Wheat is cultivated under highly diverse situations in around 8 million ha area. Among different wheat growing zones, this zone occupies 27% of total wheat area and accounts for 22% of the total wheat production in the country. The average productivity in the NEPZ hovers around 20-21q//ha which is far lower than the national productivity of 30 q/ha regis
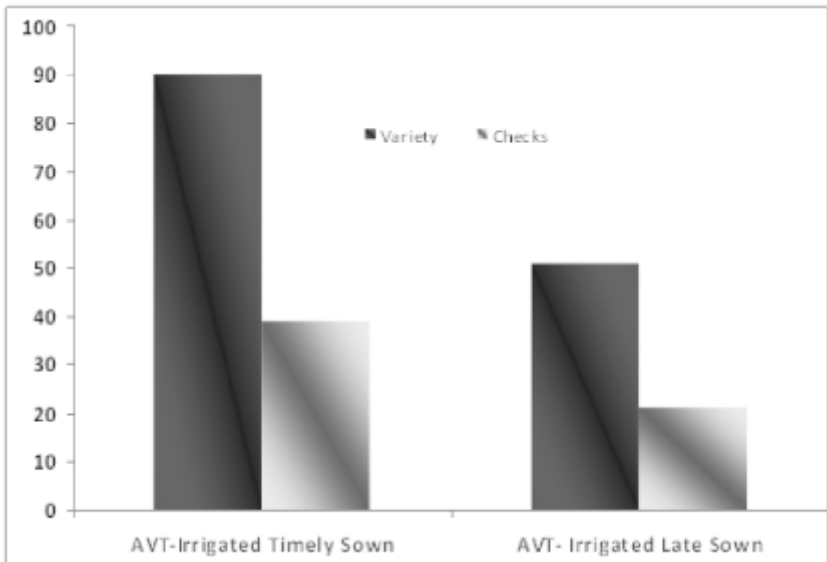
Total wheat genotypes and checks evaluated under NEPZ

Table 1: ANOVA for irrigated timely sown conditions

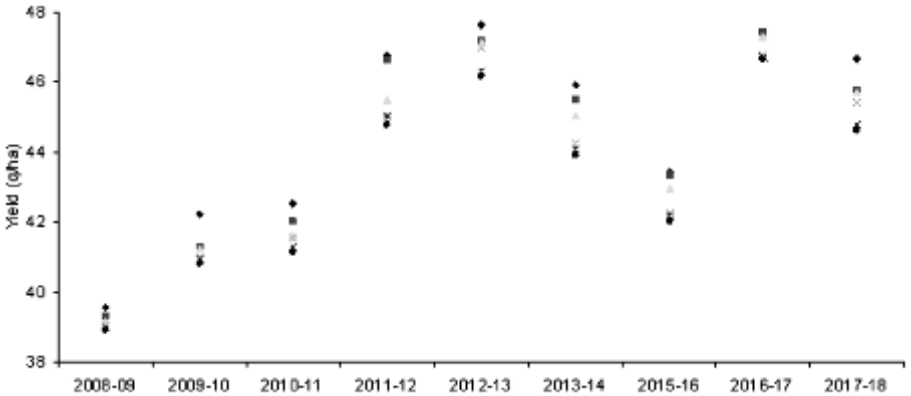| Source	Sum of Squares	Mean Square	F Value	Pr > F	R-Square MSE	Root	CV Error	Stand	t Value	Pr > |t|
Model	150.36848	150.36848	35.38	< .0001	0.4514	2.06149	4.68676			
Error	182.73828	4.24973								
Total	333.10676									
Parameter	Estimates									
Intercept								0.62979	64.65	< .0001
Year								0.10307	5.95	< .0001

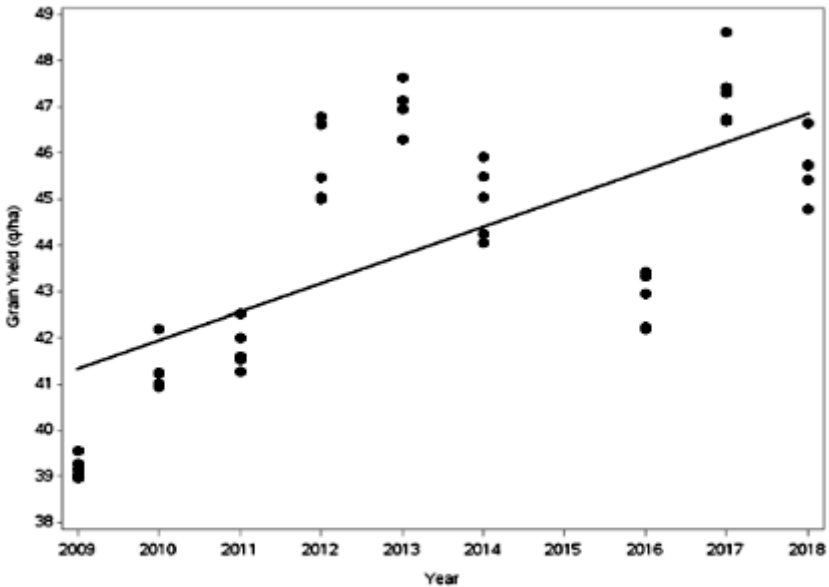
Figure 2: Best Linear Unbiased Predictors for promising genotypes for timely sown conditions

Regression Equation:
qy= 40.71535 + 0.613124*Year

Figure 3. Regression analysis of BLUP's of promising genotypes for irrigated timely sown conditions

Table 2: ANOVA for irrigated late sown conditions

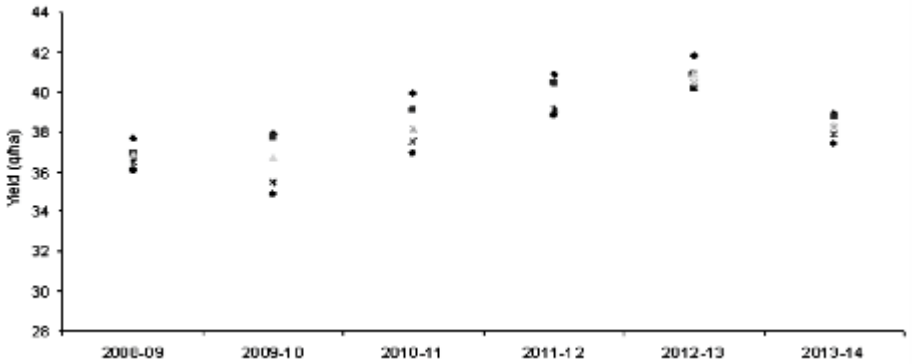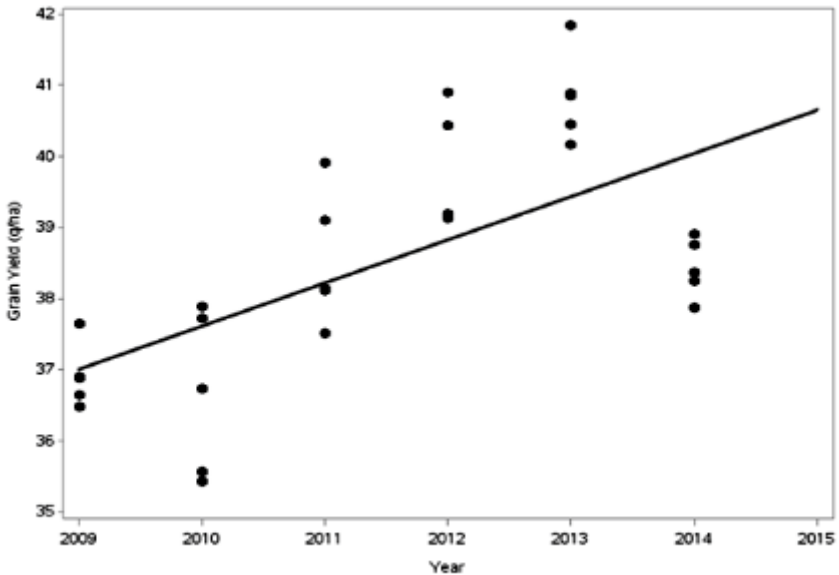| Source	Sum of Squares	Mean Square	F Value	Pr > F	R-Square	Root MSE	CV	Stand Error	t Value	Pr > |t|
Model	32.46775	32.46775	19.29	0.0001	0.4079	1.29747	3.36736			
Error	47.13620	1.68344								
Total	79.60395									
Parameter	Estimates									
Intercept								0.54018	67.38	< .0001
Year								0.13871	4.39	0.0001

Figure 4: Best Linear Unbiased Predictors for promising genotypes for late sown conditions

Regression Equation:
qy = 36.39883 + 0.609147*Year

Figure 5. Regression analysis of BLUP's of promising genotypes for irrigated late sown conditions

Highly significant change in wheat production had been observed for irrigated timely sown and late sown conditions trials in north eastern plains zone of country as reflected in ANOVA tables 1 and 2. Significance of intercept and slope had been reflected in tables for both the conditions.

Year wise BLUP's of wheat production was plotted against the years to examine the coefficient of determination (R^2) as well as linear trend to assess progress in wheat production for irrigated timely and late sown conditions. Regression analysis was applied to same data to test significance level of the R^2 value which was same as recorded in the linear trend line. Regression analysis for production revealed that under irrigated timely and late sown conditions, highly significant values of the R^2 expressed by data sets. More over due to decrease in area under cultivation for late-sown conditions in this zone, trials were discontinued for recent years though yield improvement was highly significant.

Linear trend in the wheat production under both conditions revealed an increase in average production of promising genotypes in this important zone comprising of fertile indo-gangetic plains. The production figures elevated to the level of 46q/ha (Fig. 2) and of 39q/ha (Fig. 4). However, in 2008-09, average production was 38q/ha and 36q/ha. By the end of period, 0.61, and 0.60 quintal yield respectively could be added in subsequent trials. Although highest yield levels of 48 q/ha (2012-13), and 42 q/ha (2012-13) were obtained in irrigated timely, late sown trials but low of values CV justified variable nature of production.

Findings of study confirmed an increase in wheat production of zone in nice manner. Fitted straight-line equations by SAS software indicate that the linear growth was observed under both conditions of zone. During the year 2008-09, the base yield level was 4071 and 3639 Kg/ha respectively (intercept of the equation). The straight line equation depicted the linear trend in yield growth over years and the equations also fitted very well as significant values of R^2=0.45** & 0.41** with corresponding low values of CV i.e. 4.68 and 3.36.

Central Zone

Madhya Pradesh, Chhattisgarh, Gujarat, Rajasthan (Kota and Udaipur divisions) and Jhansi division of Uttar Pradesh are major constituents of Central Zone. This zone is known for premium quality wheat having typically hard lustrous grains with high gluten strength. The advanced varietal trials under irrigated timely sown, late sown, restricted irrigated trials were conducted during the period 2008-09 to 2017-18 at the major locations of this zone.
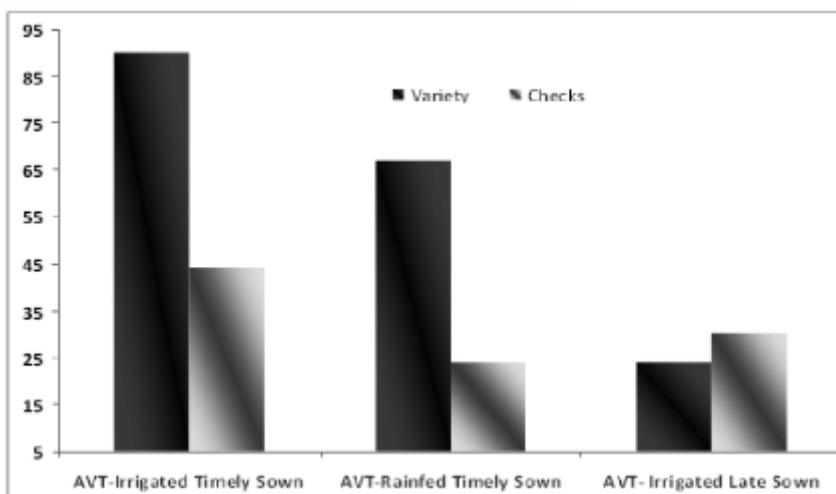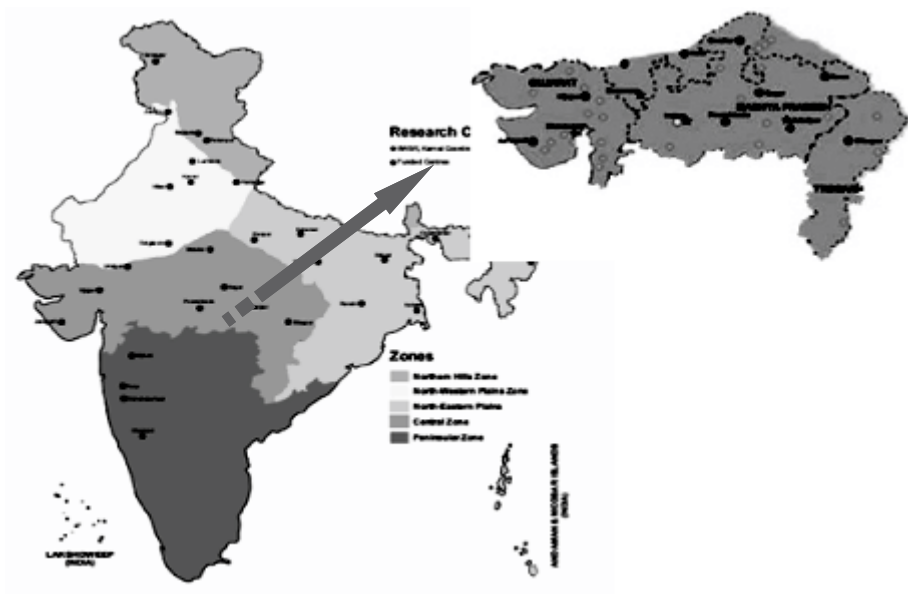
Total wheat genotypes and checks evaluated under CZ

Table 1: ANOVA for irrigated timely sown conditions

Source	Sum of Squares	Mean Square	F Value	Pr > F	R-Square	Root MSE	CV	Stand Error	t Value	Pr > |t|
Model	78.78223	78.78223	13.28	0.0007	0.2359	2.43577	4.73322			
Error	255.11761	5.93297								
Total	333.89984									
Parameter	Estimates									
Intercept								0.76277	64.26	<.0001
Year								0.13124	3.64	0.0007

Figure 2. Best linear unbiased predictors of promising genotypes for irrigated timely sown condition

Regression Equation:
qv = 49.01679 + 0.47825*Year

Figure 3. Regression analysis of BLUP's of promising genotypes for irrigated timely sown conditions

Table 2: ANOVA for irrigated late sown conditions

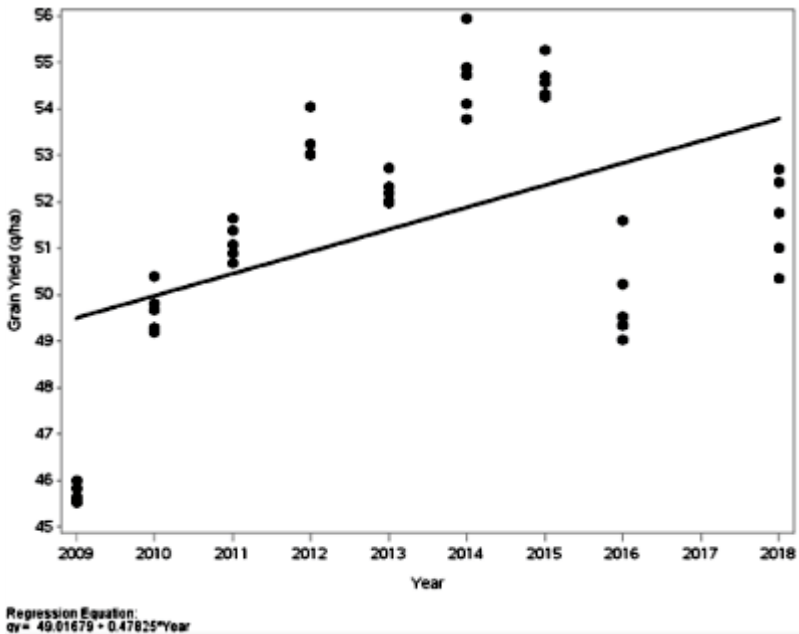| Source	Sum of Squares	Mean Square	F Value	Pr > F	R-Square	Root MSE	CV	Stand Error	t Value	Pr > |t|
Model	59.24885	59.24885	9.10	0.0049	0.2162	2.55143	5.83520			
Error	214.82367	6.50981								
Total	274.07252									
Parameter	Estimates									
Intercept								0.96435	42.64	< .0001
Year								0.21564	3.02	0.0049

Figure 4. Best linear unbiased predictors of promising genotypes for irrigated late sown condition

Regression Equation:
qv= 41.12285 + 0.650543*Year

Figure 5. Regression analysis of BLUP's of promising genotypes for irrigated late sown conditions

Table 3: ANOVA for restricted irrigated timely sown conditions

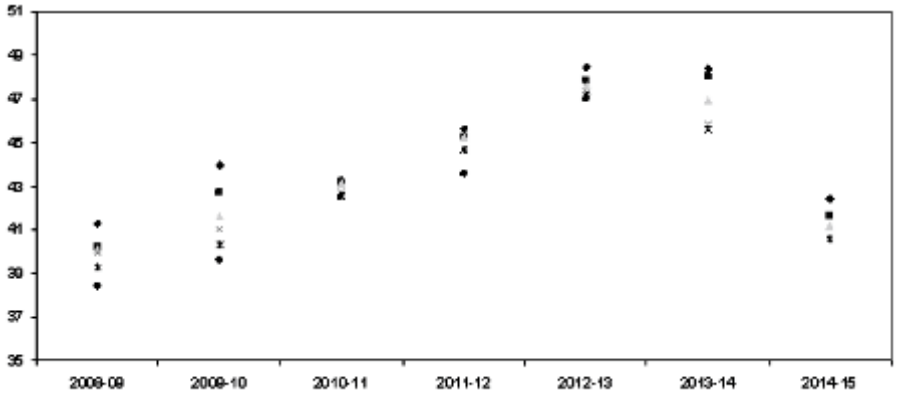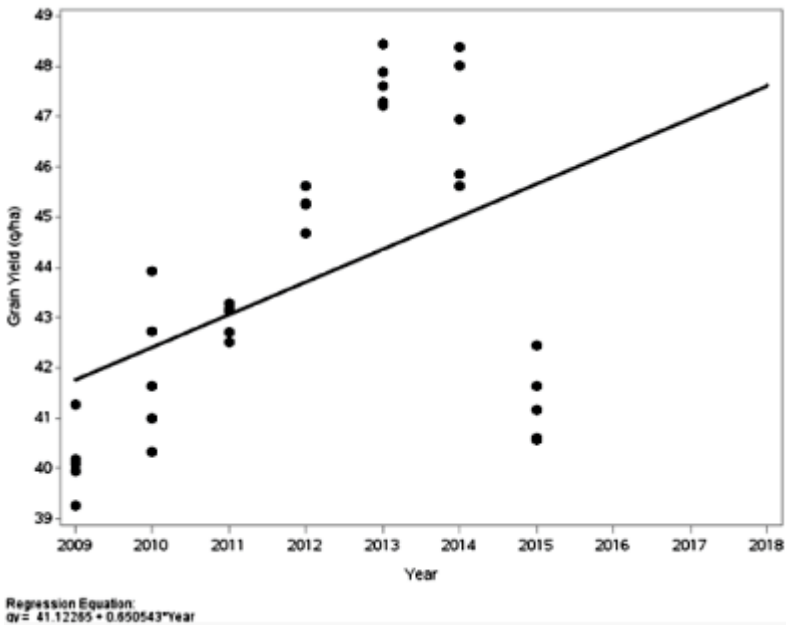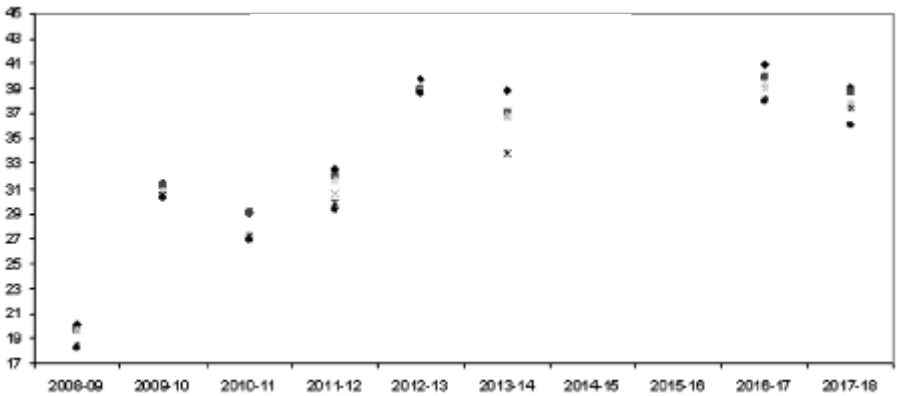| Source	Sum of Squares	Mean Square	F Value	Pr > F	R-Square	Root MSE	CV	Stand Error	t Value	Pr > |t|
Model	1124.75865	1124.75865	75.41	<.0001	0.6649	3.86196	11.74239			
Error	566.75984	14.91473								
Total	1691.51849									
Parameter	Estimates									
Intercept								1.18685	20.26	<.0001
Year								0.20354	8.68	<.0001

Figure 6. Best linear unbiased predictors of promising genotypes for restricted irrigated timely sown condition
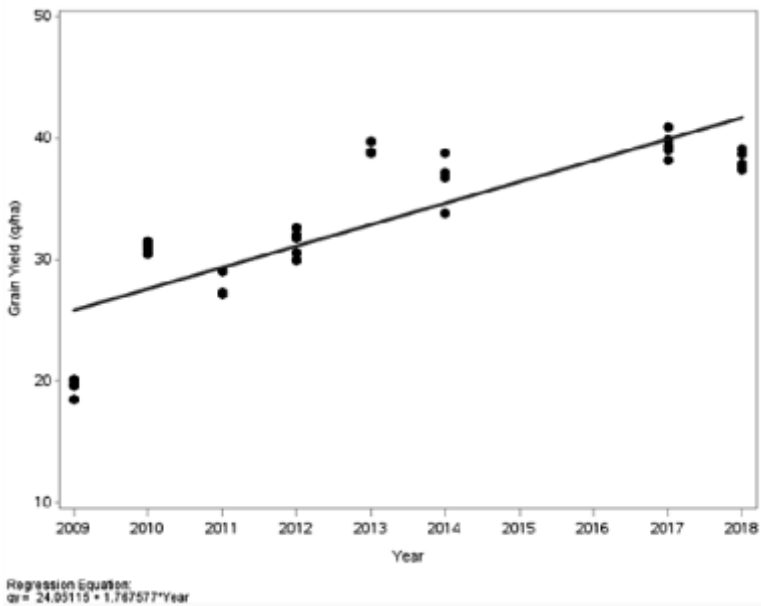

Figure 7. Regression analysis of BLUP's of promising genotypes for restricted irrigated timely sown conditions

Highly significant change in wheat production had been observed during the last ten years span for irrigated timely sown, late sown and restricted irrigated timely sown trials in Central Zone of country as reflected in ANOVA tables (1, 2 and 3). Significance of intercept and slope of linear model had been reflected in tables for three conditions.

Year wise BLUP's of wheat production was plotted against the years to examine the coefficient of determination (R^2) and linear trend for assessing progress in wheat production for irrigated timely, irrigated late & restricted irrigated timely sown conditions. Regression analysis was applied to same data to test significance level of the R^2 value which was same as recorded in the linear trend line. Regression analysis for production revealed that under restricted irrigated timely-sown condition, the R^2 value was highly significant (P<0.01) and significant for irrigated late sown trials (Table 3). Under the late-sown conditions, area under cultivations had decreased in zone so trials were discontinued for further years though yield improvement was highly significant. Significant improvement was also visible in restricted timely-sown conditions of the zone.

Linear trend in the year-wise wheat production in different conditions revealed an increase in average production of promising genotypes in zone and by the end of 2018. The production figures elevated to the level of 52q/ha (Fig. 2) in irrigated timely sown, of 48q/ha (Fig. 4) under irrigated late sown and of 39q/ha (Fig. 6) for restricted irrigation under timely sown. However, in 2008-09, average production was 46, 41 and 20q/ha respectively and by the end of 2018, 0.48, 0.65 and 1.77 quintal yield respectively could be added in subsequent trials. Although highest yield levels of 56 q/ha (2013-14), 48 q/ha (2012-13) and 41 q/ha (2016-17) were obtained in irrigated timely, late and restricted irrigation trials. More over low value of R^2 value justified highly variable nature of production.

Fitted straight-line equations by SAS software displayed in corresponding figures indicate that the linear growth was observed under irrigated timely and late sown as well as restricted irrigated timely sown conditions. During the year 2008-09, the base yield levels were 4901, 112 and 2405 Kg/ha (intercept of the equation). The straight line equations depicted the linear trends in yield growth over years and the equation also fitted well (maximum R^2=0.6649*** for restricted irrigation timely sown) with the yield data. More over yield increase in the zone progressed in linear fashion with annual increment of 47.83, 65.05 and 176.76 kg/ha/yr in irrigated timely, late and restricted irrigated timely sown. Comparatively large value of CV confirmed more production had achieved under restricted irrigation conditions as CV varies from 4.7, 5.8 to 11.7.

Under restricted irrigated timely sown conditions of the zone, highly significant yield increase over years was registered and the linear trend was noticed from the base yield with annual increment of 1.76 q/ha along with highest growth rate per year. Study revealed that last 10 years of wheat production in the zone had witnessed remarkable progress in situation of hue and cry for climate change, hot & dry zone, and wheat yield improved in three production conditions.

Peninsular Zone

This zone comprises mainly of Maharashtra and Karnataka states of India. Three species of wheat viz aestivum, durum, & dicoccum are cultivated in this zone. Bread wheat cultivation is concentrated under irrigated environments, whereas, the cultivation of durum and dicoccum wheat is generally confined to rainfed/restricted irrigation situation. Optimum ambient cool temperature for cultivation of wheat in this zone exists for a very short period causing the wheat to mature in around 90-100 days. Sorghum-wheat is one of the most prevalent cropping systems in western Marathwada and Vidarbha regions of Maharashtra and northern parts of Karnataka. Maize-wheat and sunflower-wheat cropping sequence are being practiced in some parts of Karnataka. Sugarcane-wheat cropping system is also gaining importance in Ahmedanagar and Kolhapur districts of Maharashtra and Belgaum district of Karnataka. High temperature all through the crop cycle, light soils, imbalanced use of organic and inorganic fertilizers, lack of sufficient irrigation are the major reasons for low productivity (15-16q/ha).
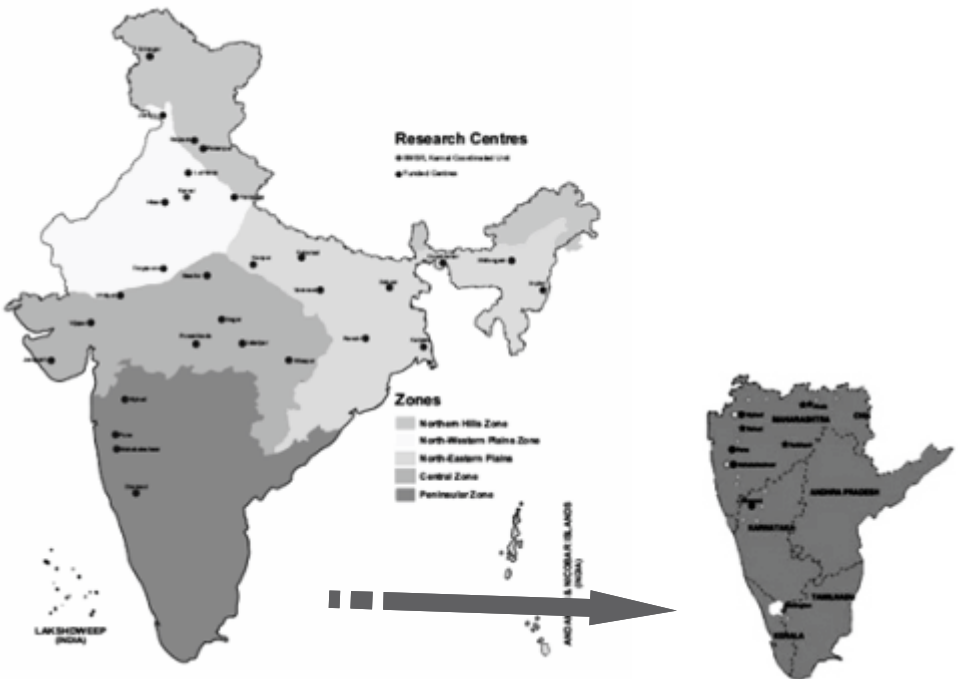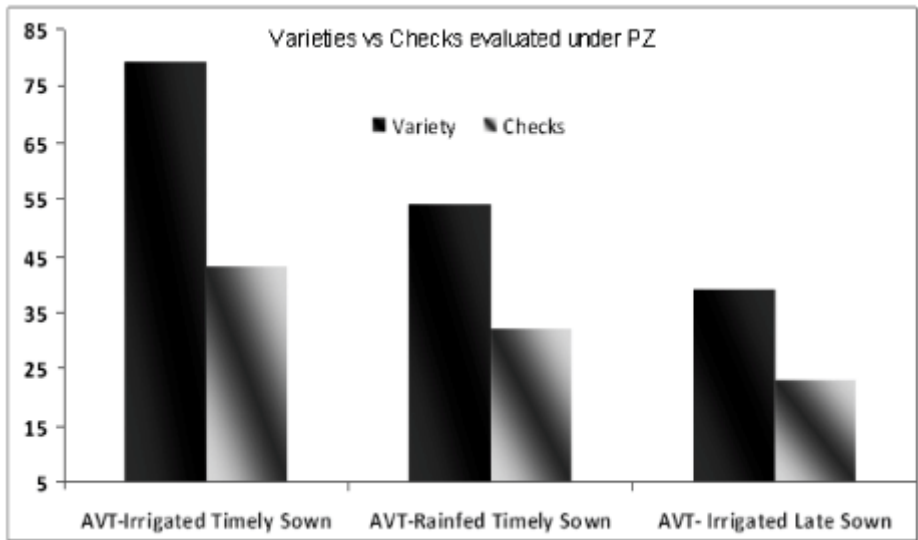
Total wheat genotypes and checks evaluated under PZ

Table 1: ANOVA for irrigated timely sown conditions

Source	SS	MSS	F value	Pr > F	Root MSE	R2	CV	Std Error	t value	Pr > |t|
Model	91.77588	91.77588	16.06	0.0002	2.39082	0.2719	5.26439			
Error	245.78824	5.71601								
Total	337.56412									
Parameter	Estimates									
Intercept								0.77676	54.91	< .0001
Year								0.13803	4.01	0.0002

Figure 2: Best Linear Unbiased Predictors for promising genotypes for irrigated timely sown conditions

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Figure 3: Regression analysis of BLUP's for promising genotypes for irrigated timely sown

Table 2: ANOVA for irrigated late sown conditions

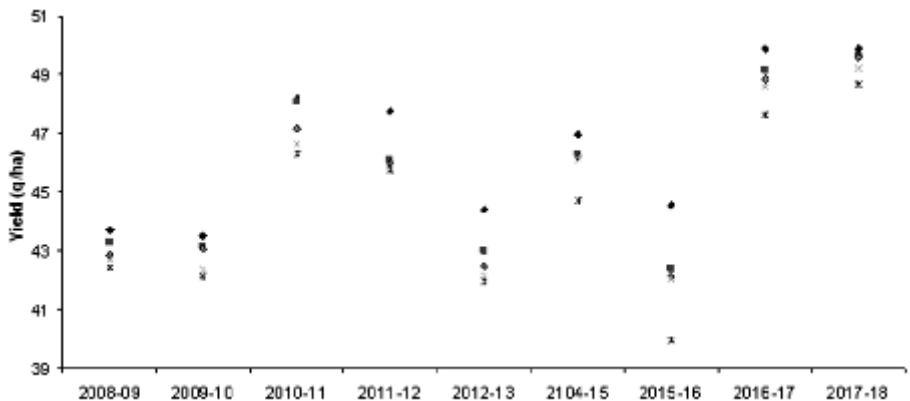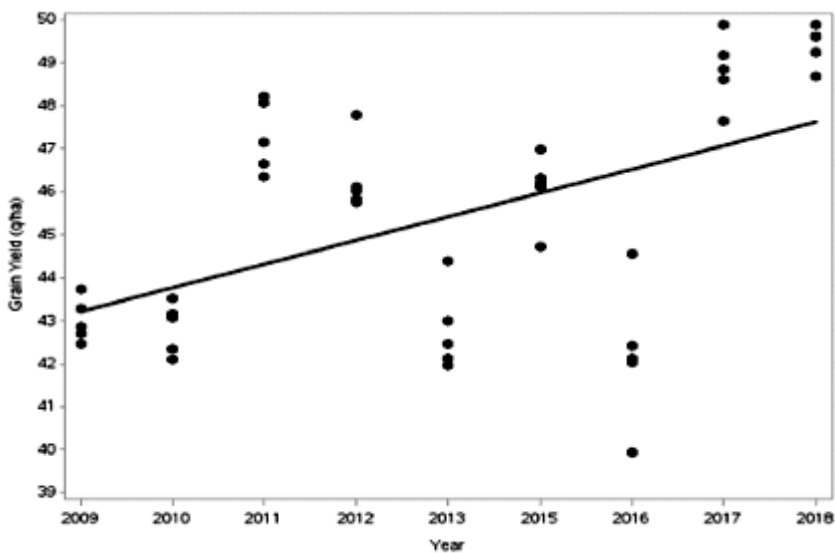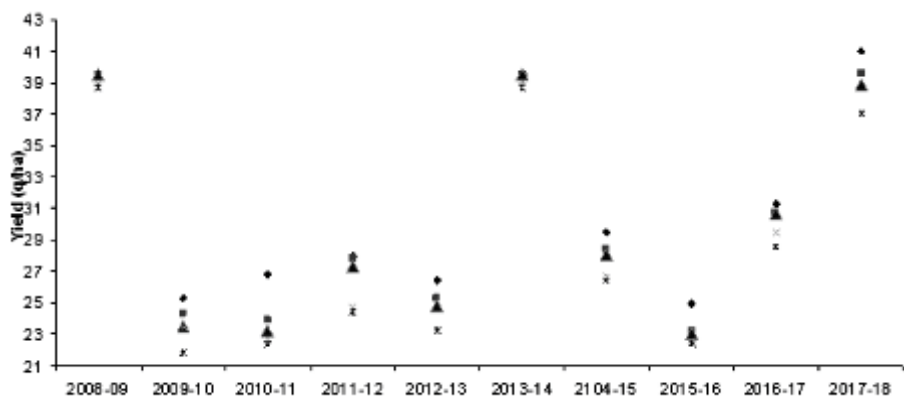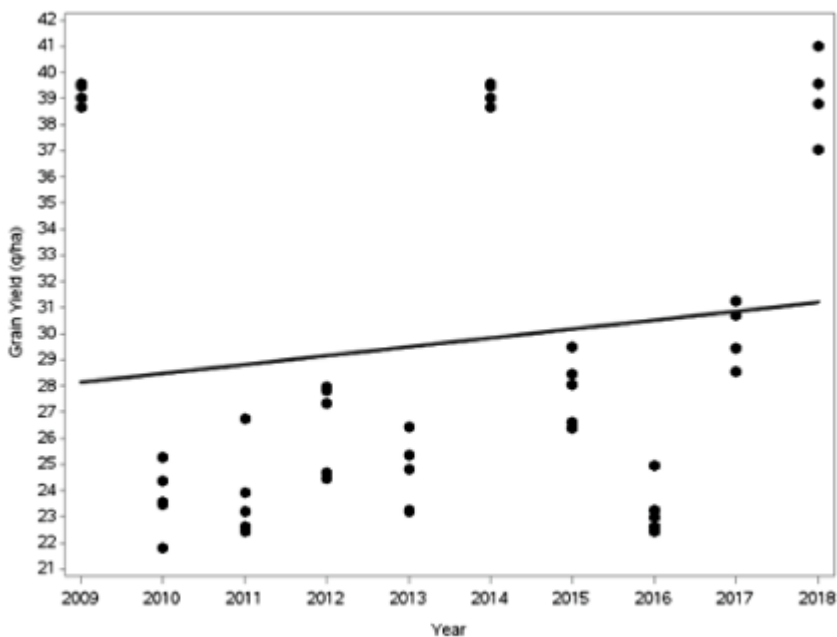| Source	SS	MSS	F Value	Pr > F	Root MSE	R2	CV	Std Error	t Value	Pr > |t|
Model	47.95398	47.95398	1.10	0.3003	6.61315	0.0223	22.27415			
Error	2099.22052	43.73376								
Total	2147.17450									
Parameter	Estimates									
Intercept								2.02035	13.77	< .0001
Year								0.32561	1.05	0.3003

Figure 4: Best Linear Unbiased Predictors for promising genotypes for irrigated late sown conditions

Regression Equation:
gy = 27.81453 + 0.340958*Year

Figure 5: Regression analysis of BLUP's for promising genotypes for irrigated late sown conditions

Table 3: ANOVA for restricted irrigated timely sown conditions

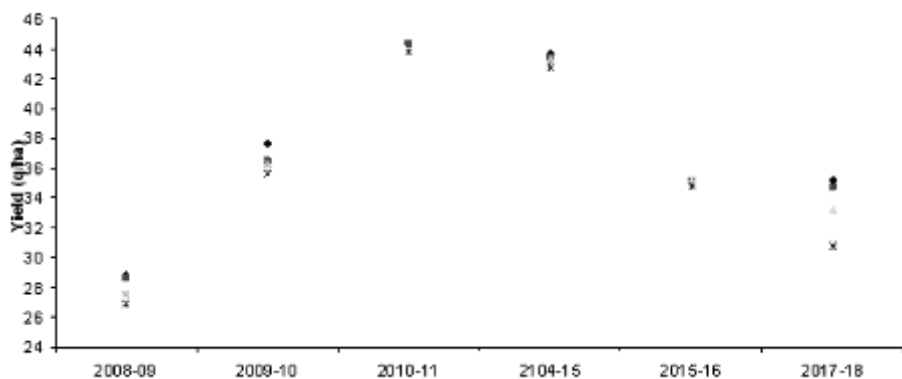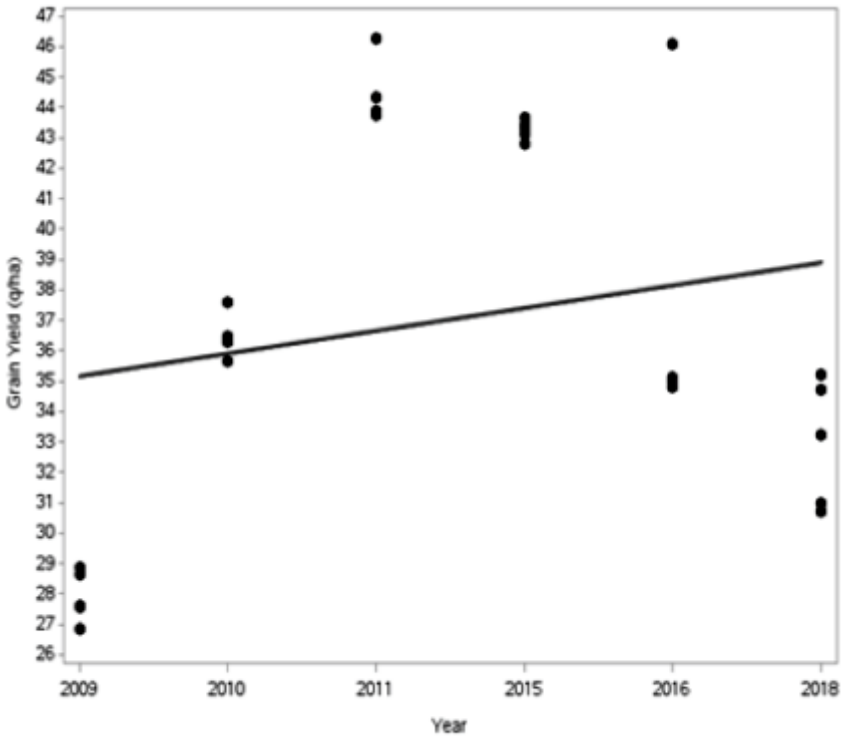| Source	SS	MSS	F value	Pr > F	Root MSE	R2	CV	Std Error	t Value	Pr > |t|
Model	49.66978	49.66978	1.34	0.2577	6.09955	0.0455	16.46732			
Error	1041.72692	37.20453								
Total	1091.39670									
Parameter	Estimates									
Intercept								2.53945	13.55	<.0001
Year								0.65207	1.16	0.2577

Figure 6: Best Linear Unbiased Predictors for promising genotypes for restricted irrigated timely sown conditions

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Figure 7: Regression analysis of BLUP's for promising genotypes for restricted irrigated timely sown

Highly significant changes in wheat production had been observed during the studied time period span for irrigated timely sown, late sown and restricted irrigated timely sown trials in Peninsular Zone of country as observed in ANOVA tables (1, 2 and 3). Highly significant values of intercept reflected for three conditions along with highly significant slope for irrigated timely sown condition. Significant values of slopes were also seen for irrigated late as well as restricted irrigated timely sown conditions.

Scatter plots of BLUP's of yields versus years were plotted to examine the coefficient of determination (R^2) and linear trend to assess progress in wheat production for irrigated timely, late & restricted irrigated timely sown conditions. Regression analysis for production figures revealed that under irrigated timely sown condition, the R^2 value was highly significant (P<0.01).

Linear trend in the year-wise wheat production in different conditions revealed an increase in average production of promising genotypes in zone by the end of 2017-18. The production figures elevated to the level of 50q/ha (Fig. 2) for irrigated timely, of 41q/ha (Fig. 4) for irrigated late sown and 35q/ha (Fig. 6) for

restricted irrigated timely sown trials. However, in 2008-09, average production was 43q/ha, 28q/ha, 27q/ha and by the end of period 0.55, 0.34 and 0.75 quintal yield could be added in subsequent trials respectively. Although highest yield levels of 50 q/ha (2017-18), 40 q/ha (2013-14) and 41 q/ha (2017-18) were obtained in irrigated timely, late and restricted irrigated timely sown trials but low values of R^2 for irrigated late and restricted irrigated timely sown conditions suggested high variability in production values. More over consistent improvement observed in irrigated timely sown trials as justified by highly significant value of R^2.

Study revealed that during a recent decade the wheat production had progressed nicely in this zone. Fitted straight-line equations by SAS software displayed in corresponding figures indicate that the linear growth was observed under all sown conditions of the zone. During the year 2008-09, the base yield level was 4265, 2781 and 2700 kg/ha respectively (as reflected by intercept of the equation). Irrigated timely sown conditions expressed significant yield increase over years (R^2=0.27**) was registered and the linear trend was noticed from the base yield level of 4265 kg/ha with annual increment of 55.31 kg/ha. Comparatively large values of CV for irrigated late sown(22.27) and restricted irrigated timely sown(16.46) trials increased production figures in reflected erratic manner as compared to irrigated timely sown(5.26) situations of the zone.

In End

One of the underlying decisions to be made before choosing among methods or models is how to handle variations in environments and genotypes. It has been known that co-efficient of variation during analysis of coordinated wheat trials vary widely among experiments and/or environments. In classical likelihood approaches, generalized least squares estimators provide best linear unbiased estimators (BLUE) of fixed treatment means and mixed models produce yield best linear unbiased predictors (BLUP) of random effects. The statistical meaning of the word "best" in BLUE and BLUP implies that these estimators are with the minimum variance estimators among all linear, unbiased estimators, i.e. expected to be the most repeatable estimators across repetitions of similar experiments. The challenging underlying assumption for BLUE and BLUP estimators obtained by the common likelihood approaches is that variances are known. The standard practice in likelihood-based estimation approaches is to substitute estimated variances into generalized least squares or in mixed model analysis inspite of known variances. The errors of estimating variances are transferred to the estimators of the genotype means, but the exact inflation of standard errors and confidence intervals of estimators of means are not known. The theoretical difficulties encountered in obtaining the best estimators of means was dealt a series of recommendations on when to pool and when not to pool error variances. Large MET data analysis demonstrated improved estimators when proper accounting for heterogeneity was considered.

Best linear unbiased prediction is an important tool for wheat breeders that may be employed at several stages of the selection in crop improvement process. BLUP of genetic effects may substitute genotype means in early selection stages of wheat improvement trials. In early selection stages, the random nature of genotypes supports the use of mixed models. As large number of evaluated genotypes facilitate estimation of number of variance components and random effects. By assuming environments and genotype-environment terms as random, variances and covariances may be modeled and more information can be integrated into broad as well as for narrow genotype inferences. BLUP prediction is not a new technique. What is relatively new for plant breeders, since software for handling general mixed model has become available, is the possibility of easily defining BLUPs of random effects that contemplate the model complexity and the size of databases in most improvement programs. There are a large number of different combinations of fixed and random effects that can be predicted by the BLUP. For each value to be predicted, there are many alternative models differing with regard to the variance-covariance structure of the random effects. Even for the fixed effects estimation, parsimonious models of the covariance structure increase the prediction accuracy of genotype performance. Mixed model approaches can integrate genotype-by-environment covariances into the

comparison of the genotype means. Mixed models in yield trials conducted at several environments unifies under one general procedure the estimation of stability parameters and average yield performances.

Assumptions of balanced data are not made, but normality is required for maximum likelihood estimation procedures to be performed. There, however, exists an important amount of phenotypic information where these procedures can be applied. Other limitations to the use of mixed model analysis are related to computer time and the possible lack of convergence of likelihood based algorithms employed to estimate variance components. Both problems may be tackled by adjusting the number of model parameters to be simultaneously estimated. Usually there exists more than one strategy to fit the same model. BLUP-based cross predictions consistently improved, the accuracy of predicted performance of genotypes that have been never tested. Different versions of BLUP could be obtained depending on the procedure selected to connect tested and untested cross effects and the model for random genetic effects. BLUPs of genotype-environment combinations in yield trials also performed better than the mean to predict genotype performance in a particular environment. In addition, BLUP accuracy was not dependent on check values, thus they can still be effectively used when check varieties fail. Better performance predictions increased the probability of selecting the best genotypes at crossing, early and late selection stages of the wheat breeding programs. The improved prediction methodology may enable the breeders to increase the selection intensity at earlier stages and possibly shorten selection cycles.

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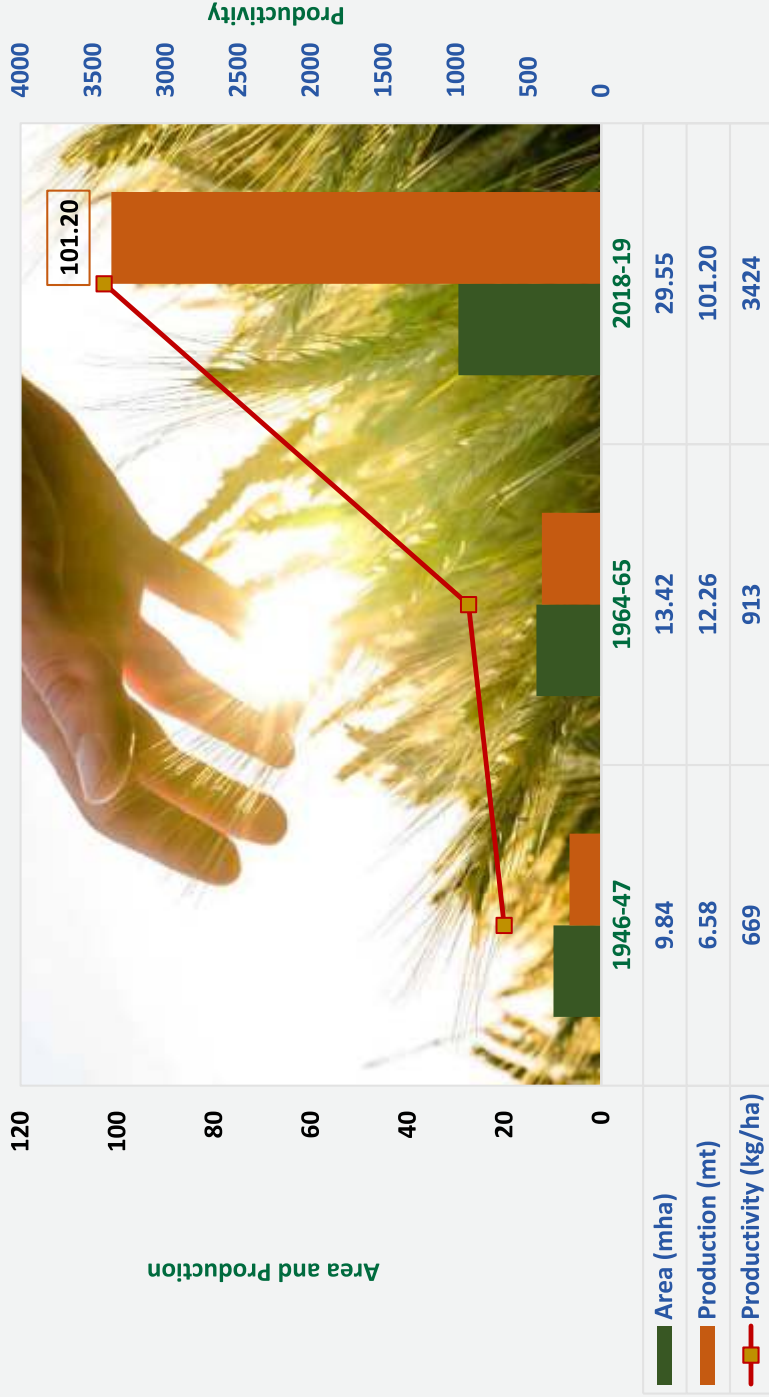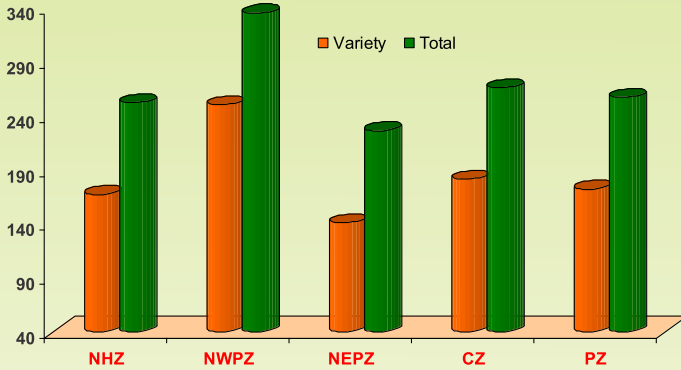
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	1946-47	1964-65	2018-19
Area (mha)	9.84	13.42	29.55
Production (mt)	6.58	12.26	101.20
Productivity (kg/ha)	669	913	3424

Productivity

Area and Production

101.20

Area (mha)
Production (mt)
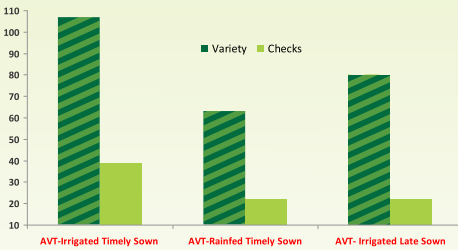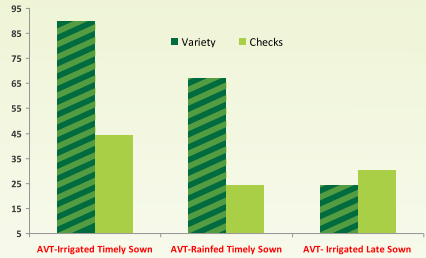Productivity (kg/ha)

Total wheat genotypes evaluated under coordinated system across zones

Varieties vs Checks evaluated under NWPZ

Varieties vs Checks evaluated under CZ

ICAR-Indian Institute of Wheat and Barley Research
Karnal-132001, Haryana