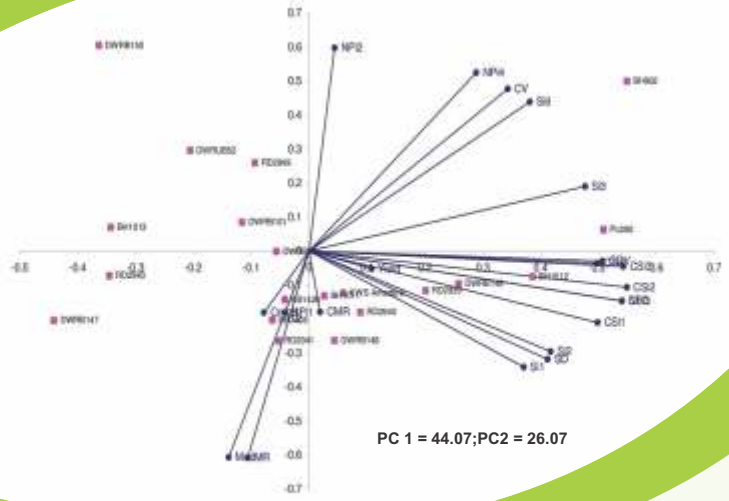
Research Bulletin # 38

GxE interaction study of coordinated barley trials by Non parametric measures



Ajay Verma

Vishnu Kumar

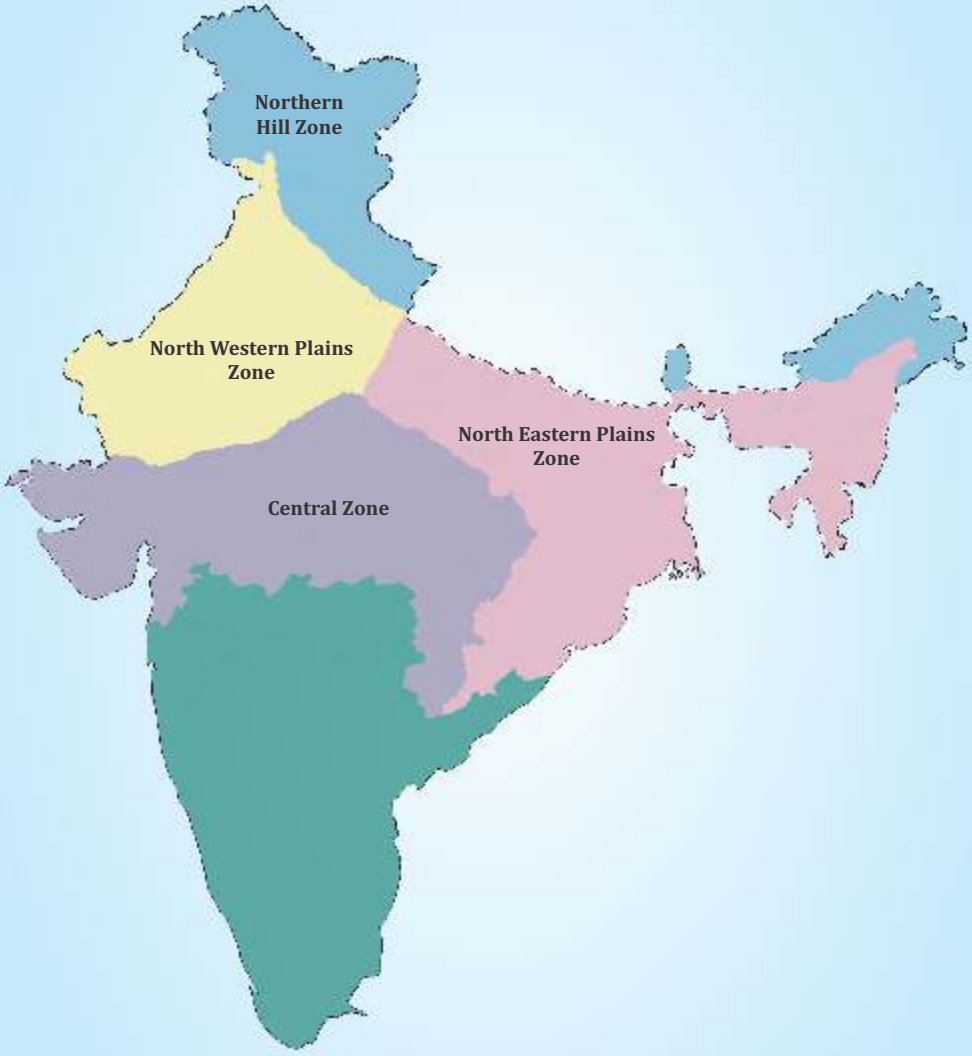
Jogendera Singh

AS Kharab

GP Singh

ICAR- Indian Institute of Wheat and Barley Research

Post Box #158, Agrasain Road, Karnal-132001 (Haryana) India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Hill Zone
North Western Plains
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North Eastern Plains
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Central Zone

GxE interaction analysis of coordinated Barley trials by Non Parametric Measures

"Genotype x environment interaction is of major importance to the plant breeder in developing improved varieties because the relative rankings of varieties grown over a series of environments may differ statistically, causing problems in plant selection." Medina

Ajay Verma
Vishnu Kumar
Jogendera Singh
AS Kharab
GP Singh

ICAR- Indian Institute of Wheat and Barley Research
Post Box #158, Agrasain Road, Karnal-132001 (Haryana) India

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Contents

Preface

The state of change in environmental conditions concerns the scientists, farmers, policy planners of the country. The ability/ inability, of living organisms to adapt to these changes at the necessary speed, determine the continuation, extinction, or evolution of species. Genotype by environment interaction (G x E) defined as the differential response of genotypes under change(s) in the environment. When populations are not confined to one area, individuals must possess desirable genetic make-up to survive in the environment. This may require a slight difference in usual features, or the ability to initiate various defense mechanisms in plants as per environmental determinates. Plant breeders have utilized G x E interaction to put forward the higher yielder products that will fetch the more prices to augment farmer income. The sole purpose of this bulletin is to provide a basic understanding of G x E interactions in terms of its potential causes, models, and practical applications. Variation among species results from either of two phenomena, genotypic or phenotypic variation. Genotypes are assessed by observing differential effects on their expression. This implies that the most popular method of determining G x E interaction is by studying the resulting phenotypes under the influence of the environment. However, most researchers suggest that because variation in a character may result from variation in either genotype or environment, heritable and non-heritable, character variation cannot be determined by only inspecting the phenotypes. It is important to know the environment of an organism and its genetic history.

The major objective of this bulletin is to apply non parametric measures to investigate the crossover and non crossover interaction in multi environment trails METs to identify barley genotypes that posses simultaneous high mean yield and stable yield performance across different locations of the country. The linear association among considered non parametric measures, for evaluating stable yield performance of barley genotypes, were also studied.

What is GxE Interaction?

In a crop improvement program, potential genotypes of promising traits are evaluated in different environments as a prerequisite before selecting desirable ones that show stability across environments. The major challenge before breeders is to develop cultivars or genotypes which are stable or well adapted to a wide range of diverse environments. Genotype x environment interaction (GxE) to understand yield stability is an area of current interest. The success of crop improvement activities largely depends on the identification of suitable varieties for large scale cultivation. A variety can be considered superior if it has potential for high yield under favorable environment and at the same time a great deal of phenotypic stability. A number of statistics, parametric as well as non-parametric have been proposed for the study of yield stability. The improved genotypes are evaluated in multi-environment trials (METs) to judge their performance across different environments. This will help to select the best genotypes for specific environments. The multi-environment trials are planned to identify genotypes suitable for different areas as well as the ability to perform across a range of geographic locations and, possibly, years (seasons). In most cases, significant - genotype × environment cross over interaction (GxE) is observed, complicating selection for improved yield. GxE interaction is a major problem when comparing the performance of genotypes across environments. GxE interaction is evident from not consistent performance of the genotypes from one environment to another. A genotype that has stable trait expression across environments contributes little to GxE interaction and its performance should be more predictable from the main effects of genotypes and environments as compared to the performance of an unstable cultivar. Meaningful interpretation of GxE interaction can be very much facilitated by statistical modeling.

In simple terms genotypic (G), environments (E) and genotypic x environments (GxE) effects for two genotypes evaluated in two environments defined as follows:

Genotype-environment	E_1	E_2	Difference (E effect)
G_1	a	c	$\Delta_1 = c - a$
G_2	b	d	$\Delta_2 = d - b$
Difference (G effect)	$\Delta_3 = b - a$	$\Delta_4 = d - c$	

GxE interaction: $(\Delta_2 - \Delta_1) = (\Delta_4 - \Delta_3)$ or $(d - b) - (c - a) = (d - c) - (b - a)$ or $(\Delta_1 + \Delta_4) = (\Delta_2 + \Delta_3)$ or $(c - a) + (d - c) = (d - b) + (b - a)$.

The genotype effect, Δ_3, represents change (or influence) due to genotypes in environment E_1 and Δ_4 is the change due to genotypes in environment E_2. The environmental effect, Δ_1, represents change due to environments for genotype G_1 and Δ_2 is the change due to environments for genotype G_2.

Total effect (T) = G + E + GE = (d – a) ;

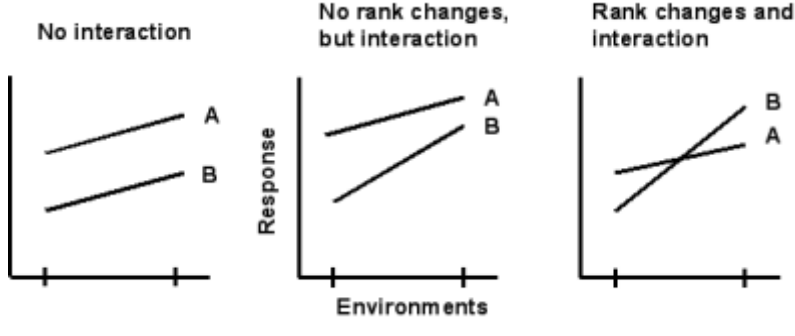
GxE = T – G – E.

A distinction must be made between GxE interaction and genotype-environment correlation. Correlation occurs if genotypic and environmental effects are not independent. There is an interaction if the differences between the average phenotypic values for two genotypes changes in different environments, but there is correlation if particular genotypes tend to be associated with positive and other genotypes with negative, environment effects.

Types of GxE Interactions

Purely environmental effects, reflect the different ecological potential of sites and management conditions, are not of direct concern for the breeding or recommendation of plant varieties. Genotypic main effects (i.e. differences in mean yield between genotypes) provide the only relevant information when genotype × environment (GE) interaction effects are absent or ignored. However, differences between genotypes may vary widely among environments in the presence of GxE interaction effects as large as those reported in literature findings. In general, GxE interactions are considered a hindrance to crop improvement in a target region. Moreover, such effects may contribute, together with purely environmental effects, to the temporal and spatial instability of crop yields. Temporal instability, in particular, has a negative effect on farmers' income and, in the case of staple crops, contributes to food insecurity at national and household level. On the other hand, GxE interactions may offer opportunities, especially in the selection and adoption of genotypes showing positive interaction with the location and its prevailing environmental conditions (exploitation of specific adaptation) or of genotypes with low frequency of poor yield or crop failure (exploitation of yield stability).

Increasing awareness about the importance of GxE interactions has demanded genotypes to be assessed under in multi-environment setup, regional trials for cultivar recommendation or for the final stages of elite breeding material selection. GxE effects should not be ignored, rather analysed using appropriate techniques, as it helps to explore the potential opportunities. The most important GxE effects for targeting cultivars or for selection of material are the crossover type affecting top yielder genotypes. Such effects imply a change of ranks between environments rather than a simple variation in the extent of the difference



$$S_P^2 = S_G^2 + S_E^2 + S_{GE}^2$$

between genotypes. However, all GxE interaction effects arising from lack of genetic correlation among environments (including those relating to low yielder and not necessarily of the crossover type) can be relevant if the results for a given research data set are extrapolated to produce information on the GxE effects that are likely to be met in breeding for a target region.

Genotype–environment interactions can be grouped into three broad categories

1. No GxE interaction,
2. Non crossover interaction
3. Crossover interaction.

As the number of environments and the number of genotypes increase, the number of possible GxE interactions (given by GE!/G!E!) increases tremendously. With only two Gs and two Es, and with only a single criterion, at least four different types of interactions are possible. Thus, with ten Gs and ten Es, 400 types of interactions are possible, which would certainly make their implications and interpretation more difficult to comprehend

No GxE interaction

When there is no GxE interaction, the effects of each of the risk factors are consistent (homogeneous) across the levels of the other risk factors. A 'no' GxE interaction occurs when one genotype (e.g., G1) consistently performs better than the other genotype (G2) by approximately the same amount across both environments. In such a situation, single genotype tested in one environment (E) provides universal results. When there is no noise, experimental results would be exact in identifying the best genotype without error, and there would be no need for replication. Within this context, one replication at one environment would be sufficient to identify the better genotype. Figure illustrates those genotypes G1 and G2 perform similarly in two environments, because their responses are parallel and stable. This type of stability, also referred to as biological stability, is desirable in crop improvement. Figure also illustrates a no GxE interaction. Genotype G1 performs better than genotype G2 in both environments. The norms of reaction (variations in trait expression across a range of environments for a given genotype) for the two genotypes are additive. The inter genotypic variance remains unchanged in the two environments and the direction of environmental modification of genotypes is the same in figure, there is a main effect of genotype, and in Figure there is a main effect of environment.

Non crossover GxE interaction

A non crossover GxE interaction is said to occur when one genotype (G1) consistently outperforms another (G2) across the test environment. However, unlike in figure, the differential performance is not the same across the environments. Figure represents a non cross over type of interaction. Genotypes G1 and G2 respond differently to the two environments but their ranks remain unchanged. The response of the two genotypes under different environments is not additive, the magnitude of inter genotypic variance increases, and the environmental modification of the two genotypes are in the same direction.

Crossover GxE interaction

The differential and non stable response of genotypes to diverse environments is referred to as a crossover interaction when the ranks of genotypes change or switch from one environment to another. Crossover interaction implies that no single genotype is superior in multiple environments. If the yield performance of genotype differs from trial to trial, especially when the effects are positive in some studies and negative in others, no general recommendation can be made. Differences in the response of genotypes to the environments may necessitate the development of geographic-specific breeding strategies. Figure represents a crossover, rank change type of interaction. The direction of environmental modification of genotypes G1 and G2 is opposite: the performance of G1 increases and that of G2 decreases. The genotypic ranks change between the two environments, but the magnitude of inter genotypic variance remains unchanged. Figure also represents a crossover interaction as genotypes switch ranks between the two environments. It also represents a change in magnitude of inter genotypic variance changes. In first environment E1, the difference between genotypes G1 and G2 is smaller than that in second environment E2, and the direction of environmental modification of the two genotypes is the same. Figure illustrates a crossover interaction with the environmental modification in opposite direction; performance of G1 increases but that of G2 decreases

This situation is different from that illustrated in figure in that the magnitude of inter genotypic variance increases between environments.

Genetic structure & GxE interaction

The magnitude of a GxE interaction is influenced by the genetic structure of the

genotype. Genotypes with less heterogeneity or heterozygosity generally interact more with the environment than mixtures of genotypes, because of lower amounts of adaptive genes. The genetic structure of a population differs mainly in two respects: the level of heterozygosity at the population level and the amount of genetic heterogeneity within the individual. In the absence of GxE interactions, the variance between individuals (in cases where the individuals are genetically alike) is expected to be homogeneous. In contrast to the population-based studies where the average effect of an environmental exposure is compared between groups, the identification of susceptible individuals within populations via genotyping allows a better estimation of the true magnitude of the effect of an environmental exposure on the population at risk.

Modeling the interaction

To understand the relationship between genotype performance and the environment, lets begin with the fundamental relationship of G, E, phenotype (P), and GxE interaction model in randomized field trials. If no interaction between G and E is assumed, then phenotypic expression represented as P = G + E. However, observed phenotype is a function of G, E, and their interaction effects.

For GxE interaction to produce an array of phenotypes and be detected via a statistical procedure there must be at least two distinct genotypes evaluated in at least two different environments. The components of GxE interactions can be explained as follows :

$P = G + E + GxE$

This model can be further written as: $P_{ij} = \mu + G_i + E_j + (GE)_{ij}$ it follows from this model that for a given genotype, there can be many phenotypes depending upon the environmental conditions.

This model can be written from a statistical standpoint as:

$P_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ijk}$

where, P_{ij} is phenotype of an individual with G_i and E_j, μ is the overall mean and ε_{ijk} is the random error for the kth genotype in the group with Gi and Ej.

Importance of GxE Interaction in coordinated setup

Genotype x environment interaction has heavy implications on the evolution of species. As under constant or unpredictable environmental conditions, genetic variance reduces population average fitness and increases the risk of extinction for sake of the species. The rate of evolution in the mean phenotype in response to selection is proportional to the product of the additive genetic variance in the trait and the intensity of directional selection. Genetic variability is often less critical than other determinants of population persistence for short-term objectives. But over time, it can play the decisive role in allowing a population to persist and adapt in a changing environment effects. Today, efforts put into conservation have focused on genetic events in small populations. However, long-term preservation of biodiversity requires understanding not only of the demography and genetics of small populations but also the ecology and evolution of abundant species.

The association between the environment and the phenotypic expression of a genotype constitute the GxE interaction. In crop improvement programme a large number of genotypes are tested over a range of environments (locations, years, growing seasons, etc.). The occurrence of the genotype (G) x environment (E) interaction effect complicates the selection of superior genotypes for a target environment. In the absence of G x E interaction, the superior genotype in one environment may be regarded as the superior genotype in all others, whereas the presence of the G x E interaction confirms particular genotypes expresses superior performance in particular environments. The GxE interaction determines if a genotype is widely adapted for an entire range of environmental conditions or separate genotypes must be selected for different sub environments. When GxE interaction occurs, factors present in the environment (temperature, rainfall, etc.), as well as the genetic constitution of an individual (genotype), influence the phenotypic expression of a trait. The impact of an environmental factor on different genotypes may vary implying that the productivity of plant may also vary from one environment to the next. Oftenly breeding plans may focus on the GxE interaction to select/identify the best genotypes for a target set of environments. One of the basic principle indicated by the GxE interaction is that even if all the plants were created equally (same genotypes), they will not necessarily express their genetic potential in the same way when environmental conditions (drought, temperature, disease pressure, stress, etc.) vary. This important concept may require genetic engineering of plants specifically tailored to their environmental conditions. Distinguishing genotypic and phenotypic variation is often difficult. Genotypic variation originates from differences in the genome of different individuals. The phenotypic variation occurs when individuals are exposed to

different environmental conditions. In phenotypic variation, individuals adapt in response to specific environmental condtions. Acclimation, for some organisms, can occur several times without changing the genetic nature of an individual.

Methods to study GxE Interactions

The phenotype has been confidently defined as a linear function of genotype, environment and their interaction. Various scientists had already reflected that variety × season interactions were basic estimates of adaptability. Genotype × environment interactions further subdivided into linear and nonlinear partitions. Initial models were based on the regression techniques for measuring the stability of populations grown from single and thee-way crosses of maize. Depending upon the final goal of the breeder and the character under consideration, two concepts of stability were of great importance in literature as for biological and agronomic concept. The concept of genotype-environment interactions leads to measure the agronomic stability of the genotype. More over the biological concept stable genotype is one, whose phenotype shows little deviation from the expected expressed trait level when tested over a number of environments. Numerous parametric as well as non–parametric measures have been proposed in large number of publications for the measurement of yield stability.

Parametric methods

Large number of statistical methods have been developed over time to describe and interpret G x E under multi environmental trail studies. The variance components have been estimated from the combined analysis of variance in conjunction with pattern analysis (clustering and ordination) to predict the response across the studied environmental conditions, to understand/decipher the relationships if any between genotypes and environments. This will help to describe general as well as specific adaptation of genotypes. This information is particularly useful to breeders because it can be of help determine the relative importance of developing cultivars for all environments of interest vis-a-vis developing specific cultivars for identified mega-environments of the country.

The features of stable genotype are complex due to genotype x environment interactions. Plant breeders under crop improvement programme target this interaction and undertake multi environment trials in appropriate and inappropriate environments. In this way, differential responses of genotypes for changing environmental conditions are used to estimate the average yield and to identify stable genotypes possessing high yield. This may be considered that the GxE are due to predictable and unpredictable effects. In addition, the adaptability of a cultivar results from its stability under different conditions. There are various

methods for describing the effects of GxE along with identifying and recommending stable genotypes in breeding programs. The conventional methods are grouped in parametric (univariate and multivariate) and nonparametric approaches based on different strategies. The univariate parametric strategy includes the methods which are based on variance components and joint regression analysis procedures. The combined variance analysis is the most common method used for the identification of GxE interaction in repeated multi-environment trials. Environmental variance (EV) [Roemer (1917), as reported in Becker and Leon (1988)], Francis and Kanenberg's (1978) coefficient of variability (CV), Wricke's (1962) ecovalence (W^2), Shulka's (1972) stability variance (SH), Plaisted and Peterson's (1959) mean variance component for genotype environment interaction (GEI) (PP59), Plaisted's (1960) variance component for GEI (P60), regression analysis as detailed by Finlay and Wilkinson (1963) , Eberhart and Russell's (1966) deviation from the regression line (S^2_{di}) and regression coefficient (b_i), Perkins and Jink's (1968) (PJ), and Freeman and Perkin's (1971) (FP) methods have been widely used as important measures of stability. Though there are well-recognized statistical and biological limitations in the regression approach (Lin et al. 1986;Westcott 1986; Crossa 1990; Flores 1998). Other univariate measures are Hanson's (1970) Genotypic stability index (Di2), Hernandez's (1993) desirability index (DI), Kataoka's (1963) yield reliability index (I_i), Pinthus's (1973) coefficients of determination (R^2), geometric adaptability index (GAI) (Mohammadi and Amri 2008), Lin and Binn's (1988) superiority index (P_i), and type IV stability concept (Sy(l) 2 a) and (Sy(l) 2 b).

Non-parametric measures

A non parametric test (aliases known as distribution free test) does not make any assumptions about the underlying distribution of research data points (viz. data comes from a normal distribution). As compared to, mostly used, parametric test, which makes certain assumptions about a population/ parameters(for example, the meanor standard deviation). In general, the word “non parametric” doesn't convey that nothing is known about the population. However, it usually means that population data points does not have a normal distribution. For example, an important assumption for the one way analysis of variance (ANOVA) implies that the data comes from a normal distribution. Moreover, if data points are not normally distributed, use of ANOVA would not be appropriate, but as an alternative nonparametric test–Kruskal-Wallis test is available. Parametric tests have greater statistical power i.e. likely to find a true significanteffect. Use nonparametric tests would be more appropriate if assumptions like normality are

being violated. Nonparametric tests even perform well with non-normal continuous data points.

When to use it

Non parametric tests are used when data points are not normal. Therefore the key is to figure out normally of data points. A normal distribution has no skew. Basically, it's a centered and symmetrical in shape. Kurtosis refers to how much of the data is in the tails and the center. The values of skewness and kurtosis for a normal distribution are 0 and 3. Other reasons to use nonparametric tests:

If one or more assumptions of a parametric test have been violated.

- If sample size is too small to run a parametric test.
- Data showed presence of outliers values that cannot be removed.
- Sometimes objective is to test for the median rather than the mean as median is used for very skewed distribution.

Modeling GxE interaction under multi environmental trials (METs) helps to determine phenotypic stability of genotypes, but this concept has been defined in different ways and quite large numbers of stability parameters have been developed. There are two major approaches exploited in literature to study GxE interaction as well as determine specific and general adaptation of genotypes. The first and the most common approach are parametric, which relies on distributional assumptions about genotypic, environmental, and their interaction effects. The second major approach is the nonparametric or analytical clustering approach, which relates environments and phenotypes relative to biotic and abiotic environmental factors without making specific modeling assumptions. For practical applications, however, most breeding programs incorporate some elements of both the approaches. The parametric stability methods have good properties under certain statistical assumptions, like normal distribution of errors and interaction effects; however, the performance may not be of same level if these assumptions are violated. This implies the use of parametric measures for significance of variances and variance-related measures sensitive to the underlying assumptions. Thus, an alternative approach that would be robust to deviations from common assumptions, would be based on nonparametric measures.Validity and accuracy of results from classical statistical analyses depend on several assumptions including normal distribution, independence of observations and variance homogeneity. Nonparametric methods, which do not presuppose these assumptions, used seldom for agronomy and plant breeding trials under coordinated system. Due to the rapid development of nonparametric methods in recent years, however, efficient nonparametric counterpart for

commonly used statistical methods are available for several important experiment designs.

There are ample justifications for the use of non-parametric measures in the studies to assess the yield stability of crop varieties. The chief advantages are: (i) No assumptions about the phenotypic observations are needed, (ii) Sensitivity to measurement errors or to outliers is much less as compared to parametric measures, (iii) Additions or deletions of one or a few genotypes do not cause distortions to non-parametric measures (iv) Most of the time, the breeder, is concerned with crossover interaction, an estimate of stability based on rank-information, therefore, non-parametric seems more relevant, (v) These measures are particularly useful in situations where parametric measures fail due to the presence of large non-linear GxE interaction. For these reasons, non-parametric measures are widely employed in the selection of crop varieties especially when the interest lies in cross over interaction.

Methods of Bredenkamp, Hildebrand and Kubinger considered the usual linear model for interactions i.e. defined as deviations from the additivity of main effects. The method of van der Laan-de Kroon defined interactions according to the crossover interaction model (Baker, 1988). Interactions exist if rank orders of cultivars are different between environments (or if rank orders of environments are different between cultivars). In this concept, interactions are used only insofar as they cause rank changes. This is different from the usual concept of deviations from the additive model, since interaction may not necessarily be rank interaction. In many situations invoking practical applications, however, such as selection in plant breeding, a decision is based on rank orders. For such cases, this concept must be of particular relevance and interest.

Bredenkamp method transformed the observed X_{ijk}-values for all environments as well as for genotypes into ranks R_{ijk} of one single rank order. The test statistic based on these ranks for genotypic, environmental and interaction effects were calculated as :

$$\chi^2_{(G)} = \frac{12l}{N^2(N+1)} \sum_{i=1}^{l} R^2_{i..} - 3(N+1)$$

and distributed as approximately χ^2 (Chi square) , with l-1 degrees of freedom where N= l*m*n.

Test statistic for environmental differences as follows :

$$\chi^2_{(E)} = \frac{12m}{N^2(N+1)} \sum_{j=1}^{m} R^2_{.j.} - 3(N+1)$$

follows c^2-distribution with m-1 degrees of freedom. Statistic for a test of genotypes × environment interaction as :

$$\chi^2_{(G\times E)} = \frac{12lm}{N^2(N+1)} \sum_{i=1}^{l} \sum_{j=1}^{m} (R^2_{ij.} - \frac{1}{m^2} R^2_{i..} - \frac{1}{l^2} R^2_{.j.}) + 3(N+1)$$

c^2-distributed with (l-1)(m-1) degrees of freedom (Bredenkamp, 1974;Lienert, 1978).

Hildebrand Method applied separate set of transformations for genotypes, environments and interaction effects.

For test of genotypes the observed X_{ijk}-values are transformed as ($X^*_{ijk} = X_{ijk} - X_{ij.} + X_{i..}$) and these transformed values ranked into a single rank order as ($X^*_{ijk} \rightarrow R_{ijk}$) then test statistic calculated as :

$$\chi^2_{(G)} = \frac{12}{(N+1)} \sum_{i=I}^{l} (\bar{R}_{i..} - \bar{R}_{...})^2$$

follows approximately c^2-distributed, with l-1 degrees of freedom.

The testing of Environments effects transformed X_{ijk}-values as ($X^*_{ijk} = X_{ijk} - X_{ij.} + X_{.j.}$) subsequently these values ranked into a single rank order with test statistic as :

$$\chi^2_{(E)} = \frac{12}{m(N+1)} \sum_{j=1}^{m} (\bar{R}_{.j.} - \bar{R}_{...})^2$$

follows is approximately c^2-distributed, with m-1 degrees of freedom and N = lmn.

Test of interaction Effects

X_{ijk}-values are transformed as ($X^*_{ijk} = X_{ijk} - X_{i..} + X_{.j.} + 2X_{...}$) and ranked into a single rank order with corresponding test statistic for genotypes × environment interaction as:

$$\chi^2_{(G\times E)} = \frac{12}{lm(N+1)} \sum_{i=1}^{l} \sum_{j=1}^{m} (\bar{R}_{ij.} - \bar{R}_{i.} - \bar{R}_{.j.} + \bar{R}_{..})^2$$

is approximately c^2-distributed, with (l-1)(m-1) degrees of freedom (Hildebrand, 1980; Kubinger, 1986).

Kubinger method

This method also applied different transformations as per test statistic as first X_{ijk}-values are ranked and then these ranks are transformed and ranked again.

Test of Genotypes

X_{ijk}-values are ranked into a single rank order as $X_{ijk} \rightarrow R_{ijk}$. Ranks are transformed as ($R^t_{ijk} = R_{ijk} - R_{ij.} + R_{i..}$). The R^t_{ijk}-values are ranked into R^*_{ijk}. Test statistic for genotypes calculated as:

$$\chi^2_{(G)} = \frac{12}{l(N+1)} \sum_{i=1}^{l} (\bar{R}^*_{i..} - \bar{R}^*_{...})^2$$

is approximately c^2-distributed, with l-1 degrees of freedom.

Test of Environments

X_{ijk}-values are ranked into a single rank order as $X_{ijk} \rightarrow R_{ijk}$. These ranks are transformed as $R^t_{ijk} = R_{ijk} - R_{ij.} + R_{.j.}$. These R^t_{ijk}-values are ranked into R^*_{ijk}.

Test statistic for environment

$$\chi^2_{(E)} = \frac{12}{m(N+1)} \sum_{j=1}^{m} (\bar{R}^*_{.j.} - \bar{R}^*_{...})^2$$

is approximately c^2-distributed, with m-1 degrees of freedom and N = lmn.

Test of Interaction Effects

First X_{ijk}-values are ranked into a single rank order as $X_{ijk} \rightarrow R_{ijk}$. Ranks are transformed as $R^t_{ijk} = R_{ijk} - R_{i..} - R_{.j.}$. Then R^t_{ijk}-values are ranked into R^*_{ijk}. Test statistic for genotypes × environment interaction

$$\chi^2_{(G \times E)} = \frac{12}{lm(N+1)} \sum_{i=1}^{l} \sum_{j=1}^{m} (\bar{R}^*_{ij.} - \bar{R}^*_{i..} - \bar{R}^*_{.j.} + \bar{R}^*_{...})^2$$

is approximately c^2-distributed, with(l-1)(m-1) degrees of freedom and N = l*m*n (Kubinger,1986).

Van der Laan-de Kroon Method

Interactions detected by this method correspond to crossover interactions of parametric methods (Baker, 1986). That means that interactions are used only

insofar as they lead to different rankings of the genotypes and / or environments. Therefore, this method requires rank orders for each environment or for each genotype separately.

Test of genotypes

X_{ijk}-values are ranked for each environment separately into the ranks R_{ijk}. Test statistic for genotypes as

$$\chi^2_{(G)} = \frac{12}{lmn^2(ln+1)} \sum_{i=1}^{l} R^2{}_{i..} - 3m(ln+1)$$

is approximately c^2-distributed, with l-1 degrees of freedom.

Test of Environments

X_{ijk}-values are ranked for each genotype separately into the ranks R_{ijk}. Test statistic for environmental differences

$$\chi^2_{(E)} = \frac{12}{lmn^2(mn+1)} \sum_{j=1}^{m} R^2_{.j.} - 3l(mn+1)$$

is approximately c^2-distributed, with m-1 degrees of freedom.

Test of Interaction Effects (Crossover Interactions)

X_{ijk}-values are ranked for each environment separately into the ranks R_{ijk}. Test statistic for crossover interaction of genotypes x environments interaction as :

$$\chi^2_{(G\times E)} = \frac{12}{ln^2(ln+1)} \left(\sum_{i=1}^{l}\sum_{j=1}^{m} R^2{}_{ij.} - \frac{1}{m^2}\sum_{j=1}^{m} R^2{}_{i..}\right)$$

is approximately χ^2-distributed, with (l-1)(m-1) degrees of freedom.

The hypothesis of no environmentally caused changes in rank orders (within genotypes) can also be tested using this method (de Kroon and van der Laan, 1981; van der Laan, 1987).

Genotype is stable over environments if its ranks are similar over environments. It has maximum stable performance if its ranks are the same over environments. These ranks stability measure define stability in the sense of homeostasis or the ability of a genotype to stabilize itself in different environments. Each statistic that measures the similarity or dissimilarity of the ranks for each genotype can be used as an appropriate stability parameter.Procedure proposed by van der Laan and de Kroon seems to be the most appropriate one particularly for applications in plant breeding. This approach uses a modified concept of interaction (rank-interaction), where the common interaction terms are only utilized in so far as they lead to different rankings of the genotypes in different environment. Such a concept must of course be of particular relevance for the plant breeder who is interested in rankings and selection.

Rank based nonparametric methods for assessing GxE interactions and stability analysis had been developed over the years. For a two-way dataset with *k* genotypes and *n* environments, the phenotypic value of *i*th genotype in *j*th environment denoted as X_{ij}, where *i*=1,2 ..., *k*, *j*=1,2, ...,*n*, ,r_{ij} as the rank of the *i*th genotype in the *j*th environment, and $\bar{r}_{i.}$ as the mean rank across all environments for the *i*th genotype.

Huehn (1990b) proposed nonparametric measures :

$$S_i^{(1)} = \frac{2\sum_{j}^{n-1}\sum_{j'=j+1}^{n}|r_{ij}-r_{ij'}|}{[n(n-1)]} \qquad S_i^{(2)} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{\sum_{j=1}^{n}|r_{ij}-\bar{r}_i|} \qquad S_i^{(3)} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{\bar{r}_{i.}}$$

$$S_i^{(4)} = \sqrt{\frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{n}} \qquad S_i^{(5)} = \frac{\sum_{j=1}^{n}|r_{ij}-\bar{r}_i|}{n} \qquad S_i^{(6)} = \frac{\sum_{j=1}^{n}|r_{ij}-\bar{r}_i|}{\bar{r}_{i.}}$$

$$S_i^{(7)} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_{i'})^2}{(n-1)}$$

The nonparametric stability statistic $S_i^{(4)}$ is similar to that of Yau and Hamblin (1994), which used relative yield not only to give equal weight to each environment, but also to provide a measure of yield stability. The method of Yau and Hamblin (1994) expresses the yield of each genotype, in each environment, in a way relative to the average of the environment in which it was determined, assigning the value 100 to the latter. Huehn (1990) proposed the correction for the trait value of ith genotype in jth environment as (X_{ij}* = X_{ij} - $X_{i.}$ +$X_{..}$) was the corrected phenotypic value ; $X_{i.}$ was the ith genotye in all environments and $X_{..}$ was the grand mean. These seven mentioned nonparametric measures of phenotypic stability were calculated as per the original (uncorrected) and corrected values of genotypes in considered environments.

$S_i^{(1)}$ measure the mean absolute rank difference of a genotype over environments, with $S_i^{(1)}$ = 0 for a genotype with maximum stability, while $S_i^{(2)}$ calculates the variance between the ranks over environments, with zero variance being an indication of maximum stability. The nonparametric $S_i^{(1)}$ and $S_i^{(2)}$ statistics are measures of stability alone and have strong correlation with each other even when using the uncorrected yield data, being nearly perfectly correlated with each other if the uncorrected yield data is adjusted for genotypic effects using the corrected values. However, the values of the $S_i^{(1)}$ and $S_i^{(2)}$ statistics obtained using the uncorrected yield data and the corrected data are often considerably different and show only medium or low correlation . The $S_i^{(1)}$ statistic is preferred for practical applications because it is very easy to calculate and allows a clear and objective interpretation as it represents the average absolute rank difference between the

environments. Furthermore, an efficient test of significance is available for this statistic.

For practical application in crop improvement and agronomy, a combination and simultaneous consideration of the yield and stability in one parameter is of particular interest and importance. Some procedures have been published for this approach (construction of an index, diverse parameters based on the deviations from the maximum yield in each environment etc), however few of these approaches are based on ranks. $S_i^{(6)}$ measures the sum of absolute deviations of the ranks r_{ij} from mean $\tilde{r}_{i.}$, where these deviations are expressed in $\tilde{r}_{i.}$ units. This measures realized a confounding and simultaneous evaluation of yield stability and yield since the numerator measures stability (variability of the ranks r_{ij}), while denominator reflects yield level (mean of ranks r_{ij}). An additional, but only slightly modified rank based measure was also propsed and used $S_i^{(3)}$. Both rank based measures are conceptually quite similar. These measures $S_i^{(6)}$ and $S_i^{(3)}$ express stability in units of yield. In one intends such a simultaneous consideration and confounding of yield and stability by application of $S_i^{(6)}$ and $S_i^{(3)}$ the transformation of original data points X_{ij} of course cannot be applied in the calculation of denominator of $\tilde{r}_{i.}$, since hereby the effect of genotype i would be eliminated from the data. But denominator must reflect the yield level of genotype i. For the application of these measures, two computational procedures are available :

1. Numerator and denominator are both calculated with the original data X_{ij}
2. Numerator is calculated with transformed data X^*_{ij} while denominator is based on the original data $X_{ij.}$

Approximate tests of significance based on the normal distribution have developed for $S_i^{(1)}$ and $S_i^{(2)}$. It can be shown on that one of the most crucial points in developing new stability parameters must be the availability of efficient tests of significance 1) for testing the stability of a single genotype and 2) for testing stability comparisons between certain genotypes. With this global test based on A with k degree of freedoms an efficient statistitcal test is available to decide whether or not there are significant differences in stability between the genotypes. To test the stability of single genotypes B can be applied in the form of chi square test with one degree of freedom. If the global chi square test is significant one may look for stability difference among genotypes using standard procedure for multiple comparisons among the observed $S_i^{(1)}$ values.

$Z_i^{(1)} = \left[S_i^{(1)} - E(S_i^{(1)})\right]^2 / V_{ar} S_i^{(1)}$ $Z_i^{(2)} = \left[S_i^{(2)} - E(S_i^{(2)})\right]^2 / V_{ar} S_i^{(2)}$

$s^v = \sum_{i=1}^{k} Z_i^{(v)}$ c^2_{kdf} $i = 1,2$ would have C^2_{1df} $E\left[(S_i^{(1)})\right] = \frac{K^2 - 1}{3K}$

under the null hypothesis that all genotypes are equally stable the means and variances may be computed from the discrete uniform distribution as

$E\left[(S_i^{(2)})\right] = \frac{K^2-1}{12}$ $V_{ar}(S_i^{(1)}) = \frac{(K^2-1)\left[(K^2-4)(N+3)+30\right]}{45K^2N(N-1)}$

$V_{ar}(S_i^{(2)}) = \frac{(K^2-1)\left[2(K^2-4)(N-1)+5(K^2-1)\right]}{360N(N-1)}$

An other very simple method based on ranks for combining yield and stability has been purposed by Kang (1988) ranks were assigned for mean yield, i.e. genotype with the highest yield receiving the rank of 1, and ranks for the stability variance of Shukla (1972)/Ecovalence , such as lowest estimated value receiving the rank of 1. The sum of these two ranks provides a final index, in which the genotype with lowest rank-sum is regarded as the most desirable. But no statistical tests of significance of these procedures have been provided. Kang and Pham (1991) have compared several methods of simultaneous selection of yield and stability. Further more for each procedure dealing with simultaneous evaluation of yield and stability, the approximate weighting of both measures is unsolved problem. Various indices have been discussed derived from equal weights for variance and yield and from 2,3,4 and 5 times more weight for yield as compared to variance.

Thennarasu (1995) proposed as stability measures the nonparametric statistics $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, and $NP_i^{(4)}$ based on ranks of adjusted means of the genotypes in each environment, and defined stable genotypes as those whose position in relation to the others remained unaltered in the set of environments assessed.

In these measures r^*_{ij} was the rank of X^*_{ij}, $\bar{r}_{i.}$ and M_{di} were the mean and median ranks for original, where $\bar{r}^*_{i.}$ and M^*_{di} were the same parameters computed from the corrected yield values.

The adjusted rank, r^*_{ij}, is determined on the basis of the adjusted phenotype values (X^*_{ij}), where $\bar{X}^*_{i.}$ is the mean performance of the ith genotype. The ranks, obtained from these adjusted values (X^*_{ij}), depend only on G x E interaction and error effects. Using the adjusted rank values defined above, following nonparametric measures were proposed as:

$$NP_i^{(1)} = \frac{1}{m}\sum_{j=1}^{m} \mid r_{ij}^* - M_{di}^* \mid$$

$$NP_i^{(2)} = \frac{1}{m}\left(\frac{\sum_{j=1}^{m} \mid r_{ij}^* - M_{di}^* \mid}{M_{di}}\right)$$

$$NP_i^{(3)} = \frac{\sqrt{\Sigma(r_{ij}^* - \bar{r}_{i.}^*)^2/m}}{\bar{r}_{i.}}$$

$$NP_i^{(4)} = \frac{2}{m(m-1)}\left[\sum_{j=1}^{m-1}\sum_{j'=j+1}^{m}\frac{\left|r_{ij}^* - r_{ij'}^*\right|}{\bar{r}_{i.}}\right]$$

Inter Quartile & Inter Decile based measures

For an estimation of yield stability of genotypes in various environments two new nonparametric stability statistics ($NS_i^{(1)}$ and $NS_i^{(2)}$ have been used which are based upon the ranks of the genotypes in each environment. These statistics use median as a non parametric central tendency, and two nonparametric index of statistical dispersion as inter-quartile range and inter-decile range. The $NS_i^{(1)}$ and $NS_i^{(2)}$ nonparametric stability statistics are similar to the nature and concept of environmental coefficient of variation. It has been observed form literature indicated that the stable genotype based on the lowest values of these two nonparametric statistics, had the highest mean yield among studied genotypes. These nonparametric statistics would be useful for simultaneous selection for avrage yield and stability. Further these measures would be very helpful in selection for yield stability and determination of favorable genotypes in plant breeding programs.

If X_{ij} is denoted as observed mean value of the i th genotype in the j th environment (i = 1, 2, .. ., M; j = 1, 2, . . ., N). Then, r_{ij} is considered as the rank of genotype i in environment j with the lowest value of rank 1 and the highest value is rank of K. The concept of yield stability is practicable; a genotype is the most stable over test environments if its ranks are similar over environments, and so maximum stability = equal ranks over all test environments. The two nonparametric stability statistics are proposed as

$$NS_i^{(1)} = (Q_3 - Q_1)/M_{di}$$

$$NS_i^{(2)} = (D_9 - D_1)/M_{di}$$

In the above nonparametric statistics, $Q_3 - Q_1$ is the inter-quartile range, also called the mid- spread or middle fifty, is a nonparametric index of statistical dispersion, being equal to the difference between the upper and lower quartiles. M_{di} is the median of the genotypes' ranks in the test environments. Also, $D_9 - D_1$ is the inter-decile range is the difference between the first and the ninth deciles. The inter-decile range is another nonparametric index of statistical dispersion of the values in a set of data, similar to the inter-quartile range. Normally central tendency of ranks is the median and its related measures of dispersion are inter-quartile or inter-decile range. It would be interesting that compare these nonparametric stability statistics with the environmental coefficient of variation (CV). The CV was designed primarily to exploration in investigation on the physiological basis for yield stability, and was found more practical to characterize genotypes on a group basis rather than individually. However, this procedure and its related concept could be used in the coordinated set up trails as it represents a

most simple and descriptive tool for GxE interaction of genotypes' stability. Considering these benefits of CV concept, using new nonparametric stability statistics ($NS_i^{(1)}$ and $NS_i^{(2)}$) could be useful in GE interaction interpreting and identification of the most stable genotypes especially in nonparametric strategy.

Ranking method of Ketata et al (1989) ranked genotypes in all environments based on yield separately. Then the mean and standard deviation of the ranks of each genotype considering its yield are calculated. In this method a genotype with maximum performance gains rank 1 and if a genotype exhibited mean rank closer to 1 and less standard deviation of the rank was known as the most stable variety. Graphs of mean grain yield vs. nonparametric measures σ_{gy} values and at the same time graphs of kr versus σ_r values could enhance visual efficiency of genotype selection based on genotype by environment interaction. A genotype is considered stable if its kr or gy value is relatively consistent in all the environments. i.e. , showing low kr or high gy and having a low σ_r (Flores et al. , 1998). The σ_r, calculated from the yield rank of genotypes in each environment (r_{ij}) based on the uncorrected mean yield values (X_{ij}), is expressed as

$$\sigma_r = \sqrt{\sum_{j=1}^{q} \frac{(r_{ij} - \bar{r}_{i.})^2}{q-1}}$$

The σ_{gy}, calculated from the grain yield of genotypes in each environment (gy_{ij}) based on the uncorrected mean yield values (X_{ij}), is expressed as

$$\sigma_{gy} = \{ \sum_{j=1}^{q} \frac{(gy_{ij} - \bar{g}_{i.})^2}{q-1} \}^{1/2}$$

Rank Correlation

Rank correlation is an important and useful tool for studying the statistical relations among stability parameters, finding the best method to use as an alternative for other methods, and eliminating similar parameters. An attractive statistical tool for the comparison and groping of environments (or genotypes) can be easily carried out: two environments are considered more similar if they produce more similar rankings of the tested genotypes.

Spearman correlation

Of all the statistics based on ranks, the Spearman rank-order correlation coefficients r was the earliest to be developed and is perhaps the best known today. It is a measure of association between two variables which requires that both variables be measured in at least an ordinal scale so the objects under study may be ranked in two ordered series. The similarity between two environments that means the "distance" between these two environments can be quantitatively expressed by Spearman's rank correlation coefficient between the rankings of the genotypes in these two environments, numerous techniques of cluster analysis can be applied to group the environments with respect to this measure of similarity. Suppose N genotypes are ranked on each of two non parametric measures. For example, N genotypes were ranked in the order of their yields as per two non parametric measures as X_1, X_2, X_3, ... X_N and Y_1, Y_2, Y_3, ... Y_N. The rank order correlation may be used to determine the relation between the X's and the Y's. The correlation between these ranks would be perfect if and only if $X_i = Y_i$ for all the genotypes. Therefore it would seem logical to use the various differences $d_i = X_i - Y_i$ as an indication of the disparity between the two sets of rankings. The magnitude of these various d_i's gives an idea of how close is the relation between ranks. If the relation between the two sets of ranks were perfect, every d_i would be zero. The larger d_i's, the less perfect is the association between the two variables. In computing a correlation coefficient it would be awkward or inconvenient to use the d_i's directly. One difficulty is that the negative d_i's would cancel out the positive ones when we tried to determine the total magnitude of the discrepancy between the rankings, even though it is the magnitude rather than the sign of the discrepancy which is an index of the disparity of the rankings. However, if d_i^2 is employed rather than d_i, this difficulty is circumvented,. It is clear that the larger the various d_i's, the larger will be the value of $\sum d_i^2$, which is the sum of the squared difference for N pairs of data. The derivation of the computing formula for r is fairly simple. It is done by simplifying the formula for the Pearson product moment

correlation coefficient r when the data are comprised of ranks.

Spearman's rank correlation analysis estimates the correlation among ranks as follows :

$$\bar{r}_s = 1 - \frac{6\sum_{i=1}^{n} d_i^2}{n(n^2-1)}$$

where d_i difference between two ranks for ith genotype and considered for n number of correlated pairs. An appropriate generalization from two up to arbitrary number of environments can be easily carried out by applying Kendall's coefficient of concordance. This quite simple quantitative measure for similarity of rankings of the tested genotypes in several environments has received little attention in the literature.

Kendall's coefficient of concordance

An appropriate generalization from two to large number of environments can be easily carried out by applying Kendall's coefficient of concordance. This quite simple quantitative measure for similarity of rankings of the tested genotypes in several environments has received little attention in the literature.

Association among k sets of rankings can be observed by using the Kendall coefficient of concordance (W). Spearman's r_s and Kendall's W expresses the degree of association between two variables measured in or transformed, to ranks, W expresses the degree of association among k such variables, that is the association between k sets of rankings. Such a measure may be particularly useful in studies of reliability and also has applications in studies of clustering of non parametric measures.

Rationale

As a solution to the problem of ascertaining the overall agreement among k sets of rankings it might seem reasonable to find the Spearman rank-order correlations (the r_s's) between all possible pairs of the rankings and then compute the average of these coefficients to determine the overall association. This procedure, require to compute $\binom{K}{2}$ rank-order correlation coefficients. Unless k were very small, such a procedure would be extremely tedious.

The computation of W is much simpler; moreover, it bears a linear relation to the average r_s taken over all groups. Average values of the Spearman rank-order correlation coefficients among the $\binom{K}{2}$ possible pairs of rankings as

$$\text{Ave}(r_s) = \frac{kW-1}{k-1}$$

Another approach would be visualize the data structure for no agreement among the several sets of ranking and then to imagine how it would look if there were prefect agreements among the several sets of rankings. The coefficient of concordance would then be an index of the divergence of the actual agreement shown in the data from the maximum possible or perfect agreement.

To compute W, the data are first arranged into a k×N table with each row representing the ranks assigned by a particular non parametric measure to the N genotypes. Next, find the sum of ranks $\bar{R}_i$ in each column of the table and divide each by k to find the average rank $\bar{R}_i$ Then sum these $\bar{R}_i$ and divide that total by k to obtain the mean value of the $\bar{R}_i$'s. Each of the $\bar{R}_i$ may then be expressed as a deviation from the grand mean the greater will be degree of association among the k sets of ranks. W may be computed as:

$W = \frac{\sum_{i=1}^{N}(\overline{R_i}-\bar{R})^2}{N(N^2-1)/12}$ where k = number of sets of rankings; N = number of non parametric measures being ranked

$\overline{R}_i$ =average of the ranks assigned to the *i*th measure; $\overline{R}_i$ =average of the ranks assigned across all non parametric measures.

$N(N^2 -1)/12$ = maximum possible sum of the squared deviations, i.e., the numerator which would occur if there were perfect agreement among the k rankings and the average rankings were 1,2,..., N.

Kendall's W is an estimate of the variance of the row sums of ranks Ri divided by the maximum possible value the variance can take; this occurs when all variables are in total agreement. Hence, values vary between $0 \leq W \leq 1$, more over 1 represent perfect concordance.

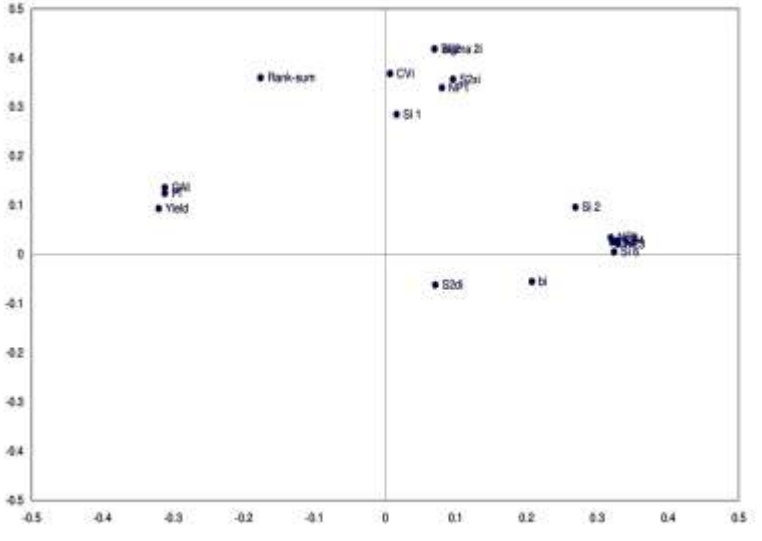
Testing of the significance of W values carried out as $c^2 = m(n-1)*W$. This quantity is asymptotically distributed like chi-square with c^2 with v = n-1 degrees of freedom. This approach is satisfactory only for moderately large values of m and n. Critical table values for W for $n \leq 7$ and $m \leq 20$ are available; otherwise, as an alternative F statistic may be computed as F = (m-1)*W/(1-W) distributed like F with $v_1 = n-1-2/m$ and $v_2 = v_1(m-1)$ degrees of freedom.

Biplot Analysis

Graphical presentations of a data set form an integral part of any statistical analysis - graphical displays not only present the information contained in the data but can also be used to extract information that is difficult or even impossible to extract by means of traditional parametric multivariate analyses. In order to represent the observed data set as accurately as possible, the lower dimensional display space should be chosen such that the loss of information resulting from the dimension reduction is as small as possible. If the dissimilarity between two measurement vectors is measured by some distance metric, then in order to minimise the loss of information, the lower dimensional display space should be chosen such that it represents the set of distances between the measurement vectors as accurately as possible according to some criterion. Biplot is a joint map of the samples and variables of a data set. Applying biplot methodology enhances the informativeness of the lower-dimensional graphical display by adding information regarding the measured variables. The 'bi' in 'biplot' refers to the fact that two modes, namely genotypes and environments, are represented simultaneously and not to the dimension of the display space. In the biplot each row (sample) and column (variable) of the data matrix under consideration is represented by a vector emanating from the origin. These vectors are such that the inner product of a vector representing a row and a vector representing a column approximates the corresponding element of the data matrix. Rows of the data matrix are represented only by the endpoints of the corresponding vectors so that samples and variables can be easily differentiated in the biplot. The PCA biplot is, as its name indicates, closely related to PCA itself. Principal component analysis (PCA) is a multivariate linear dimension reduction technique and probably the most popular of the techniques that fall into that category. Three reasons why PCA is such a popular dimension reduction technique are that (1) PCA provides a nested solution i.e. if $k > r$, then the r-dimensional PCA solution is contained within the k-dimensional PCA solution, (2) it is easy to understand and (3) much research has been done on the topic. The magnitude of a variable's coefficient in a particular principal component measures the contribution of the variable to that principal component in the presence of the other measured variables, that is, it measures the variable's multivariate contribution to the principal component. It is evident that when PCA is performed on the standardised measurements, the variable with the greatest absolute coefficient for a particular principal component, is also the variable most strongly correlated with that principal component. Since “there are many patterns and relationships that are easier to discern in graphical displays than by any other data analysis method” (Everitt, 1994), it is always desirable to graphically represent a data set to be investigated and to do so as accurately as

possible. Given that humans can only visualise objects which are at most three-dimensional, it is the graphical representation of a data matrix in one, two or three-dimensional space which is usually of interest.

PCA biplot is a special case of the biplot. In the r-dimensional PCA biplot a sample is represented by a point with coordinate vector given by the first r principal component scores associated with that sample while a variable is represented by a vector stretching from the origin up to the point with coordinate vector given by the coefficients of this variable in the first r principal components. The conclusions drawn from a PCA biplot are however meaningless if the biplot poorly represents the observed data set. Measures of the quality of the various individual aspects of the PCA biplot are required in order to evaluate to what extent the relationships and predictions suggested by a PCA biplot are representative of reality. PCA biplot is not designed to represent the group structure underlying a data set consisting of samples that are structured into a number of predefined groups. By using different plotting characters and/or colours to represent samples belonging to different groups as well as imposing convex hull for each of the groups, certain differences between the groups may be suggested by the PCA biplot.

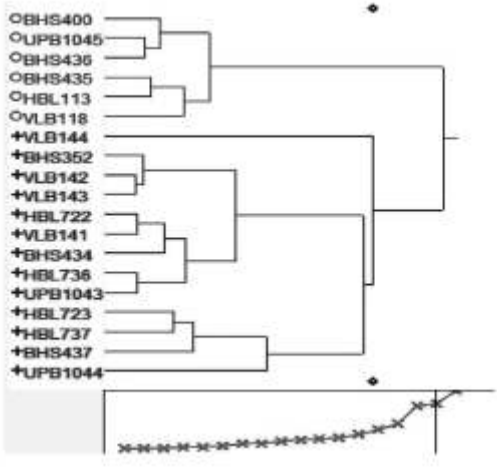


Cluster Analysis : Ward's Method

With increases in the breeding materials used in crop improvement programs, methods to correctly classify the variability are assuming considerable significance. Multivariate analytical techniques are widely used in analysis of genetic diversity, which simultaneously analyze multiple measurements on each individual under study by allowing simultaneous, use of morphological, biochemical, or molecular marker data. Among multivariate analytic tools, cluster analysis, principal component analysis (PCA), principal coordinate analysis (PCoA), and multidimensional scaling (MDS) are commonly appeared useful.

"Cluster analysis" refers to "a group of multivariate techniques whose primary purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptions are mathematically gathered into the same cluster". The resulting clusters of individuals should then exhibit high internal (within cluster) homogeneity and high external (between cluster) heterogeneity. Thus, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart. There are broadly two types of clustering methods: (i) distance based methods, in which a pair-wise distance matrix is used as an input for analysis by a specific clustering algorithm, leading to a graphical representation (such a tree or dendrogram) in which clusters may be visually identified; and (ii) model-based methods, in which observations from each cluster are assumed to be random draws from some parametric model, and inferences about parameters corresponding to each cluster and cluster membership of each individual are performed jointly using standard statistical methods such as maximum-likelihood or Bayesian methods. At present, distance-based methods are most frequently applied. Distance-based clustering methods can be categorized into two groups: hierarchical and nonhierarchical. Hierarchical clustering methods are more commonly employed in analysis of genetic diversity in crop species. These methods proceed either by a series of successive mergers or by a series of successive divisions of group of individuals. The former, known as "agglomerative hierarchical" methods, start with a single individual. Thus, there are initially as many clusters as individuals. The most similar individuals are first grouped and these initial groups are merged according to their similarities. Among various agglomerative hierarchical methods, the UPGMA (Unweighted Paired Group Method using Arithmetic averages) is the most commonly adopted clustering algorithm, followed by the Ward's minimum variance method. The nonhierarchical clustering procedures do not involve construction of dendrograms or trees. These procedures, also frequently referred to as "K-means clustering," are based on "sequential threshold," "parallel threshold," or

"optimizing" approaches for assigning individuals to specific clusters, once the number of clusters to be formed is specified . Nonhierarchical clustering methods are rarely used for analysis of intra specific genetic diversity in crop plants. The primary reason could be the lack of prior information about the optimal number of clusters that are required for accurate assignment of individuals. UPGMA dendrograms have tended to predominate past literature. Although some studies indicated the relative advantages of UPGMA clustering algorithm in terms of consistency in grouping biological materials with relationships computed from different types of data), a single clustering method might not be always optimal or effective in revealing genetic associations. Despite some favorable attributes in UPGMA, the underlying assumptions are rarely met. Several clustering methods were compared in grouping maize accessions on the basis of agronomic and morphological characters; UPGMA method was generally consistent with regard to the allocation of clusters, when different types and number of characters were used. UPGMA also revealed higher cophenetic correlation coefficient in comparison to UPGMC, Single Linkage, and Ward's method. Genetic relationships in rapeseed (*Brassica* spp.) cultivars were analyzed on the basis of amplified fragment length polymorphisms (AFLP) by means of UPGMA and Ward's method in combination with Jaccard, Simple Matching, and Modified Simple Matching coefficients. Despite very high correlations between distance matrices obtained through use of different coefficients, and derivation of the same patterns with both clustering methods, Ward's method was found more suitable as it avoided the chaining effects that are often observed with UPGMA. Similar observations were made in analysis of genetic diversity among maize in bred lines based on RFLP data.



Feed Barley

Barley cereal crop has been cultivated for food, feed, forage and brewing purpose. Cereal is grown under varying agro climatic situations of the country. Interpretation of genotype x environment interactions facilitated by the use of statistical methods as interaction complicates the identification of superior genotypes. Twenty seven feed barley genotypes evaluated at fifteen major barley growing locations across the country.

Table 1: Parentage details of feed barley genotypes along with environmental conditions

Code	Genotype	Parentage
IVTIRFB-1	KB1436	LAKHAN/JB137
IVTIRFB-2	BH959	BH393/BH331
IVTIRFB-3	RD2922	RD2809/RD2743
IVTIRFB-4	HUB250	RD2618/RD2660
IVTIRFB-5	BH1004	33rd IBON200/BH902
IVTIRFB-6	UPB1054	IBYT-LRA-M-12(Sr.No.27 of EIBGN 2013-14)
IVTIRFB-7	PL890	DWRUB52/DWRUB62
IVTIRFB-8	JB325	RD2615/DL88
IVTIRFB-9	BH1006	15th HBSN-4/BH902
IVTIRFB-10	HUB113	KARAN280/C138
IVTIRFB-11	KB1434	GLORIA-BAR/COPAL//PM5/BEN/3/SEN/4/PETUNIA1/5/BBSC/CONGONA// BLLU/3/CIRU
IVTIRFB-12	RD2786	RD2634/NDB1020//K425
IVTIRFB-13	BH902	BH495/RD2552
IVTIRFB-14	JB322	JB101/BH331
IVTIRFB-15	UPB1053	IBYT-MRA-12(Sr.No.35 of EIBGN 2013-14)
IVTIRFB-16	PB891	IBON 343/12th HSBN-176
IVTIRFB-17	BH1005	BHMS24A/WG127
IVTIRFB-18	HUB249	RD2618/RD2660
IVTIRFB-19	NDB1634	IBON-HI-40 (2009-10
IVTIRFB-20	BH946	BHMS22A/BH549//RD2552
IVTIRFB-21	RD2923	RD2552/RD2786
IVTIRFB-22	KB1425	K508/NDB1295
IVTIRFB-23	DWRB157	ALANDA02/4/ARIZONA5908/ATHS//ASSE/3/F208.74/5/ALANDA/3/CI08887/CI05761//LIGNEE640-34
IVTIRFB-24	RD2921	RD2508/RD2743
IVTIRFB-25	JB319	LAKHAN/BH353
IVTIRFB-26	RD2552	RD2035/DL472
IVTIRFB-27	DWRB156	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/M9846//CCXX14.ARZ3/PA

Locations	Latitude	Longitude	Altitude (m)
Durgapura	26°51 'N	75° 47 ' E	390
Hisar	29°10 'N	75° 46 ' E	215.2
Ludhiana	30°54 ' N	75° 52' E	247
Tabiji	26°35'N	74°61' E	456.1
Pant Nagar	29 °02 ' N	79° 48' E	237
Karnal	29 °43 ' N	76° 58 ' E	252
Varanasi	25° 20 ' N	83° 03 ' E	75.5
Rewa	24° 31 ' N	81° 15 ' E	365.7
Faizabad	26° 47 'N	82° 12 ' E	113
Kanpur	26° 29 ' N	80° 18 ' E	125.9
Sabour	25° 24 ' N	87° 04 ' E	41
SK Nagar	24°19 ' N	72 °19 ' E	154.5
Sagar	23° 83 ' N	78° 73 ' E	523
Morena	26° 56 ' N	78° 80 ' E	152
Udaipur	24° 34 ' N	70° 42 ' E	582

Table 2: Descriptive statistics and non parametric measures based on original values

Code	Genotype	Yield (q/ha)	MR	SD	CV	Med	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7
IVTIRFB-1	KB1436	32.52	20.87	6.13	0.29	23.00	6.82	7.26	25.19	5.84	4.83	3.47	37.55
IVTIRFB-2	BH959	36.74	16.67	6.43	0.39	18.00	7.52	7.24	34.76	6.06	5.33	4.80	41.38
IVTIRFB-3	RD2922	39.68	11.00	6.60	0.60	10.00	7.64	7.63	55.45	6.29	5.33	7.27	43.57
IVTIRFB-4	HUB250	41.30	10.53	8.35	0.79	9.00	9.71	9.16	92.63	6.85	7.10	10.11	69.70
IVTIRFB-5	BH1004	35.55	16.87	7.14	0.42	19.00	8.29	8.07	42.32	6.83	5.89	5.24	50.98
IVTIRFB-6	UPB1054	39.91	11.53	5.30	0.46	13.00	6.17	5.93	34.14	4.84	4.43	5.76	28.12
IVTIRFB-7	PL890	41.45	10.07	6.80	0.68	7.00	7.41	8.38	64.26	5.93	5.15	7.67	46.21
IVTIRFB-8	JB325	40.76	9.87	6.28	0.64	10.00	7.33	7.44	55.92	6.06	4.94	7.51	39.41
IVTIRFB-9	BH1006	35.52	18.40	6.66	0.36	20.00	7.77	7.44	33.78	6.44	5.57	4.54	44.40
IVTIRFB-10	HUB113	39.51	11.60	6.56	0.57	11.00	7.54	7.75	51.86	6.30	5.17	6.69	42.97
IVTIRFB-11	KB1434	33.79	19.40	6.32	0.33	20.00	7.20	7.48	28.85	6.11	4.99	3.86	39.97
IVTIRFB-12	RD2786	40.52	11.93	7.89	0.66	13.00	9.22	8.96	72.98	7.26	6.48	8.15	62.21
IVTIRFB-13	BH902	40.99	10.13	6.59	0.65	8.00	7.45	7.35	59.97	6.01	5.51	8.16	43.41
IVTIRFB-14	JB322	41.85	8.87	4.79	0.54	9.00	5.66	5.53	36.29	4.60	3.88	6.56	22.98
IVTIRFB-15	UPB1053	38.97	13.00	7.73	0.59	13.00	8.99	9.50	64.31	6.90	5.87	6.77	59.71
IVTIRFB-16	PB891	33.77	19.60	8.19	0.42	24.00	9.07	9.10	47.94	7.74	6.88	5.27	67.11
IVTIRFB-17	BH1005	37.35	15.67	6.07	0.39	15.00	7.16	6.72	32.89	5.52	5.11	4.89	36.81
IVTIRFB-18	HUB249	34.93	18.00	7.65	0.43	18.00	8.91	8.72	45.56	7.23	6.27	5.22	58.57
IVTIRFB-19	NDB1634	37.52	14.27	7.56	0.53	13.00	8.95	8.15	56.14	6.76	6.55	6.89	57.21
IVTIRFB-20	BH946	41.24	11.80	8.82	0.75	9.00	10.25	9.35	92.24	8.39	7.76	9.86	77.74
IVTIRFB-21	RD2923	39.59	12.73	6.86	0.54	14.00	8.11	7.82	51.75	5.89	5.62	6.62	47.07
IVTIRFB-22	KB1425	36.77	15.73	7.52	0.48	18.00	8.67	8.30	50.27	6.60	6.36	6.06	56.50
IVTIRFB-23	DWRB157	39.57	13.93	8.17	0.59	15.00	9.56	8.89	67.10	7.89	7.01	7.55	66.78
IVTIRFB-24	RD2921	38.33	14.73	8.28	0.56	14.00	9.79	8.90	65.09	7.99	7.18	7.31	68.50
IVTIRFB-25	JB319	38.72	13.53	7.42	0.55	15.00	8.78	8.08	57.02	6.74	6.36	7.05	55.12
IVTIRFB-26	RD2552	39.01	13.27	9.71	0.73	11.00	11.33	10.12	99.42	9.34	8.68	9.82	94.21
IVTIRFB-27	DWRB156	40.54	13.00	9.51	0.73	14.00	11.18	10.38	97.38	9.06	8.13	9.38	90.43

According to mean yield, genotype JB322 was the highest yielder followed by PL890 & HUB250, although remarkable differences were evident among the studied feed barley genotypes (Table 2).

The following three descriptive statistics; mean of ranks (MR), standard deviation of ranks (SD) and coefficient of variation of ranks (CV) were calculated for original ranks. According to these statistics, genotypes KB1436 and KB1434 were of stable performance , while genotypes JB322, JB325 and PL890 based on MR, genotypes DWRB156 and RD2552 based on SD and genotypes HUB250 and BH946 based on CV, were identified as of unstable nature. Simple descriptive statistics based on ranks discriminated among genotype performance.

Seven nonparametric measures (S_i^1 ,S_i^2 ,S_i^3 ,S_i^4 ,S_i^5 S_i^6 and S_i^7) based on original yield values indicated genotypes JB322, UPB1054 and KB1434 were the most stable, however, most of studied measures pointed towards RD2552G5 & DWRB156 as the unstable genotypes. Stable genotypes according to Huehn's nonparametric measures from uncorrected values demonstrated high mean yield. In other words, with maintenance of genotype effect in each cell of two-way data, mean yield confounds GEI and affects stability analysis .

Table 3: Descriptive statistics and non parametric measures based on corrected values

Code	Genotype	CMR	CSD	CCV	CMed	CSi^1	CSi^2	CSi^3	CSi^4
IVTIRFB-1	KB1436	13.33	8.99	0.67	11.00	10.53	13.93	148.70	10.53
IVTIRFB-2	BH959	14.07	7.19	0.51	13.00	8.44	8.44	58.60	7.33
IVTIRFB-3	RD2922	13.13	6.75	0.51	11.00	7.85	8.83	53.76	6.86
IVTIRFB-4	HUB250	14.60	8.87	0.61	13.00	10.44	11.03	92.44	8.48
IVTIRFB-5	BH1004	13.60	8.61	0.63	14.00	10.21	10.45	88.06	8.48
IVTIRFB-6	UPB1054	14.33	5.77	0.40	16.00	6.80	7.17	40.67	6.20
IVTIRFB-7	PL890	14.00	6.81	0.49	13.00	7.89	9.84	63.00	6.47
IVTIRFB-8	JB325	13.87	6.65	0.48	14.00	7.71	9.22	62.00	7.50
IVTIRFB-9	BH1006	14.80	8.64	0.58	17.00	9.96	10.83	83.70	9.05
IVTIRFB-10	HUB113	12.40	6.54	0.53	12.00	7.56	7.97	49.13	6.22
IVTIRFB-11	KB1434	13.40	7.94	0.59	14.00	9.28	12.85	106.24	9.55
IVTIRFB-12	RD2786	14.13	8.58	0.61	14.00	10.15	10.18	78.00	8.48
IVTIRFB-13	BH902	13.87	6.61	0.48	12.00	7.43	10.54	59.19	7.38
IVTIRFB-14	JB322	14.80	5.99	0.40	17.00	6.78	9.33	69.63	7.95
IVTIRFB-15	UPB1053	13.33	8.16	0.61	15.00	9.64	9.42	69.98	7.25
IVTIRFB-16	PB891	14.87	7.90	0.53	16.00	9.24	11.48	81.38	8.98
IVTIRFB-17	BH1005	13.53	6.53	0.48	15.00	7.62	8.12	49.21	6.07
IVTIRFB-18	HUB249	13.67	8.98	0.66	13.00	10.57	10.94	103.24	9.00
IVTIRFB-19	NDB1634	13.07	8.18	0.63	12.00	9.66	9.02	73.36	7.74
IVTIRFB-20	BH946	15.00	9.58	0.64	13.00	11.22	11.32	95.97	9.79
IVTIRFB-21	RD2923	14.33	7.02	0.49	15.00	8.25	8.24	50.77	6.27
IVTIRFB-22	KB1425	13.33	8.70	0.65	14.00	10.21	10.25	85.93	7.99
IVTIRFB-23	DWRB157	15.87	8.81	0.56	19.00	10.15	9.36	72.09	8.59
IVTIRFB-24	RD2921	13.73	8.72	0.64	14.00	10.34	9.58	78.64	8.48
IVTIRFB-25	JB319	14.00	7.76	0.55	14.00	9.20	8.76	60.38	7.00
IVTIRFB-26	RD2552	13.80	10.29	0.75	11.00	12.00	10.75	107.73	9.94
IVTIRFB-27	DWRB156	15.13	9.74	0.64	16.00	11.39	10.58	92.25	9.30

Code	Genotype	CSi^5	CSi^6	CSi^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
IVTIRFB-1	KB1436	9.49	10.68	141.61	7.667	0.333	0.551	0.505
IVTIRFB-2	BH959	6.51	6.94	58.88	6.267	0.348	0.445	0.506
IVTIRFB-3	RD2922	5.33	6.09	50.43	5.333	0.533	0.624	0.713
IVTIRFB-4	HUB250	8.16	8.38	96.40	7.333	0.815	0.901	0.991
IVTIRFB-5	BH1004	7.64	8.43	85.55	7.333	0.386	0.530	0.605
IVTIRFB-6	UPB1054	5.42	5.67	41.64	4.733	0.364	0.541	0.590
IVTIRFB-7	PL890	5.98	6.40	63.00	5.267	0.752	0.762	0.783
IVTIRFB-8	JB325	6.21	6.72	61.41	4.933	0.493	0.767	0.782
IVTIRFB-9	BH1006	7.63	7.73	88.49	7.533	0.377	0.494	0.541
IVTIRFB-10	HUB113	5.09	6.16	43.51	5.067	0.461	0.549	0.652
IVTIRFB-11	KB1434	7.39	8.27	101.69	6.467	0.323	0.502	0.478
IVTIRFB-12	RD2786	7.22	7.67	78.74	6.933	0.533	0.718	0.851
IVTIRFB-13	BH902	5.19	5.62	58.63	5.067	0.633	0.730	0.733
IVTIRFB-14	JB322	7.36	7.46	73.60	4.600	0.511	0.935	0.765
IVTIRFB-15	UPB1053	6.60	7.43	66.64	6.467	0.497	0.607	0.741
IVTIRFB-16	PB891	7.03	7.09	86.41	6.467	0.269	0.458	0.471
IVTIRFB-17	BH1005	5.47	6.06	47.57	5.333	0.356	0.425	0.486
IVTIRFB-18	HUB249	8.60	9.44	100.79	7.733	0.430	0.539	0.587
IVTIRFB-19	NDB1634	7.08	8.13	68.47	6.933	0.533	0.560	0.677
IVTIRFB-20	BH946	8.48	8.48	102.83	8.400	0.933	0.830	0.951
IVTIRFB-21	RD2923	5.88	6.16	51.98	5.733	0.410	0.547	0.648
IVTIRFB-22	KB1425	7.45	8.38	81.84	7.333	0.407	0.555	0.649
IVTIRFB-23	DWRB157	8.15	7.70	81.70	7.400	0.493	0.627	0.729
IVTIRFB-24	RD2921	7.52	8.21	77.14	7.467	0.533	0.576	0.702
IVTIRFB-25	JB319	6.43	6.89	60.38	6.400	0.427	0.555	0.680
IVTIRFB-26	RD2552	9.22	10.02	106.19	9.067	0.824	0.750	0.905
IVTIRFB-27	DWRB156	8.80	8.72	99.71	8.200	0.586	0.742	0.876

According to table 3, genotype JB322 followed by UPB1054 were the most stable as well as RD2552 & DWRB156 were of unstable performance based on a corrected dataset that produced a mean of corrected ranks (CMR), standard deviation of corrected ranks (CSD), coefficient of variation of corrected ranks (CCV) and all Huehn's nonparametric measures (CS_i^1 ,CS_i^2 ,CS_i^3 ,CS_i^4 ,CS_i^5 CS_i^6 and CS_i^7). Also genotypes UPB1054 and HUB113 were identified as the most stable and KB1436 and RD2552 were unstable based on the above mentioned nonparametric measures of phenotypic stability. In the mentioned strategy, the following concept of stability was applied; it determines the stability of genotype over environment if its rank is similar over other environments (biological concept).

Nonparametric indices of Thennarasu's evaluated the genotypes performance differently i.e. $NP_i^{(1)}$ pointed towards JB322 and UPB1054 as stable in comparison to others and RD2552 along BH946 unstable (table 3) while , genotype PB891 showed lowest value $NP_i^{(2)}$ followed by KB1434 and because of high value stabilities of BH946 & RD2552 were low, $NP_i^{(3)}$ unlike $NP_i^{(2)}$ identified BH1005 as the most stable followed by BH949. The unstable genotypes based on $NPi^{(3)}$ were JB322 & HUB250. Stability parameters $NPi^{(4)}$ like $NP_i^{(2)}$ identified

PB891 & KB1434 and BH946 but like $NP_i^{(3)}$ pointed towards unstable performance of HUB250. The results of first two NP^s were very similar for unstable performance of RD2552 and last two NP^s towards HUB250 as unstable genotypes.

Clustering of genotypes as per non parametric measures

Ward's method of hierarchical cluster analysis exploited to group genotypes according to yield and different nonparametric measures of phenotypic stability. The clustering considered squared Euclidean distance as dissimilarity measure among genotypes in Ward's method (Figure 1). In Ward's procedure, the dissimilarity between two clusters is shown by the "loss of information" from joining the two clusters with this loss of information measured by the increase in error sum of squares. The cluster analysis revealed four distinct clusters among twenty seven genotypes: cluster of high to moderate yielders consisted of genotypes JB890, PL890, BH902, RD2922 as UPB1054 as the most favorable and next cluster of four genotypes consisted of unstable genotypes RD2552, DWRB156, BH946 and HUB250. Third cluster of six genotypes comprised of moderately yielder genotypes. Finally fourth cluster grouped highly unstable genotypes as per non parametric measures. It seems that according to corrected statistics, genotypes UPB1054, HUB113 and JB322 were the most stable, but when based on uncorrected statistics, genotypes UPB1054 and KB1434 were the most stable. Regarding mean yield regardless of stability, the most favorable genotypes were JB322 and PL890.

Relationship among nonparametric statistics

Spearman's rank correlations among rank of genotypes as per various non parametric measures were then calculated (Table 5). According to results of rank correlations there was a highly significant (p<0.01) positive rank correlation between mean yield with S_i^3 ,S_i^6 $NP_i^{(2)}$ $NP_i^{(3)}$, $NP_i^{(4)}$ and highly significant negative association with MR & CV. Yield expressed low correlation of inverse relation with CS_i^1 ,CS_i^2 ,CS_i^3 ,CS_i^4 ,CS_i^5 CS_i^6 and CS_i^7 . MR had significant negative rank correlation with CV, S_i^6 $NP_i^{(2)}$ $NP_i^{(3)}$ $NP_i^{(4)}$ whereas significant positive with CS_i^1 ,CS_i^2 ,CS_i^3 ,CS_i^4 ,CS_i^5 ,CS_i^6 and CS_i^7 . SD had a highly significant positive with most of the measures either based on original or corrected values. S_i^1 showed highly significant positive rank correlation with S_i^2 ,S_i^3 ,S_i^4 S_i^5 ,S_i^6 ,S_i^7 CS_i^1 ,CS_i^5 CS_i^6 , $NP_i^{(1)}$ and significant positive CS_i^3 ,CS_i^6 , $NP_i^{(2)}$ & $NP_i^{(4)}$. Significant positive association among S_i^s .S_i^3 showed significant correlation with $NP_i^{(s)}$.

S_i^4 and S_i^3 maintained same type of relationship with other measures. Similar behavior expressed by S_i^7 to show positive relationship. CSD showed significant

positive correlation with CS_i^s , and with very low positive interaction with $NP_i^{(s)}$. CS_i^1 had positive significant relationship and very low with $NP_i^{(s)}$. More over CS_i^s were positively associated among themselves. $NP_i^{(2)}$ expressed significant positive rank correlation with $NP_i^{(3)}$ and $NP_i^{(4)}$.

Biplot analysis of non parametric measures

Principal component (PC) analysis based on the rank correlation matrix generated by nonparametric measures was performed understand relationships if any among these measures. Table 4 shows the loading of the first two PCA of ranks of non parametric measures as two first PCs (PC1 and PC2) explained 80.6% (49.36 and 31.23 % by PC1 and PC2, respectively) of the total variance. Better visualization of relationships among the different measures and yield (Y) displayed graphically by biplot . In this plot, the PC1 axis mainly distinguished mean yield besides the measures of CV, MR and S_i^6 from the other measures. Thus, the first principal component separated the measures into two groups according to the two stability concepts (biological and agronomic concept of stability). The second PC separated the nonparametric measures of phenotypic stability into two groups according to the yield and stability (Fig. 2).

The original data-based nonparametric measures showed close correlation with CV, S_i^3 S_i^6 and no relation with CMR, S_i^4 , S_i^7 as vectors corresponding to these measures expressed right angle with vector of yield. Genotypes HUB250, RD2786, DWRB156, UPB1053 and DWRB157 clustered with measures based on original yield values.Corrected data-based nonparametric measures were closely related among themselves and clustered together. Yield showed nearly straight line angle with vectors of MR and Median. These measures favored HUB249, KB1425, BH1004 and PL891.

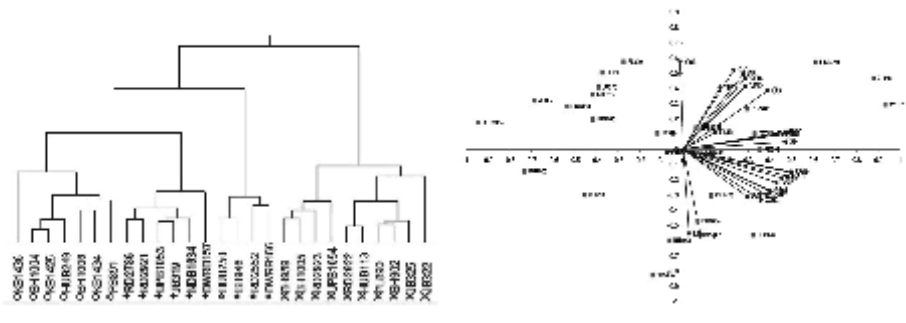


Table 5: Speraman's rank correlation of yield with non parametric measures calculated from original and corrected values

	Yield	MR	SD	CV	Med	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	CMR	CSD	CCV	CMed	CSi1	CSi2	CSi3	CSi4	CSi5	CSi6	CSi7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$
MR	-0.950																									
SD	0.070	0.105																								
CV	0.817	-0.729	0.553																							
Med	-0.889	0.931	-0.027	-0.775																						
S_i^1	0.051	0.113	0.984	0.535	-0.003																					
S_i^2	0.115	0.042	0.957	0.599	-0.078	0.922																				
S_i^3	0.587	-0.464	0.786	0.921	-0.552	0.781	0.793																			
S_i^4	-0.072	0.226	0.933	0.438	0.102	0.951	0.894	0.690																		
S_i^5	0.015	0.163	0.967	0.481	0.038	0.978	0.866	0.739	0.915																	
S_i^6	0.773	-0.671	0.603	0.975	-0.737	0.590	0.605	0.946	0.484	0.567																
S_i^7	0.070	0.105	1.000	0.553	-0.027	0.984	0.957	0.786	0.933	0.967	0.603															
CMR	0.392	-0.172	0.281	0.283	-0.045	0.260	0.200	0.267	0.200	0.276	0.305	0.281														
CSD	-0.239	0.433	0.756	0.193	0.278	0.741	0.701	0.422	0.760	0.734	0.237	0.756	0.155													
CCV	-0.353	0.496	0.672	0.097	0.319	0.665	0.653	0.331	0.710	0.654	0.128	0.672	-0.172	0.916												
CMed	0.002	0.111	-0.017	-0.182	0.358	-0.005	-0.009	-0.141	0.013	-0.015	-0.187	-0.017	0.572	-0.126	-0.246											
cSi1	-0.270	0.447	0.757	0.171	0.295	0.742	0.710	0.402	0.765	0.736	0.211	0.757	0.097	0.988	0.939	-0.131										
cSi2	-0.248	0.392	0.416	0.013	0.232	0.328	0.418	0.096	0.425	0.337	0.034	0.416	0.179	0.687	0.609	-0.111	0.659									
cSi3	-0.319	0.474	0.514	0.000	0.310	0.458	0.506	0.153	0.553	0.460	0.030	0.514	0.070	0.860	0.824	-0.118	0.855	0.898								
cSi4	-0.299	0.455	0.495	-0.003	0.325	0.469	0.440	0.157	0.587	0.470	0.047	0.495	0.244	0.832	0.730	-0.035	0.800	0.870	0.934							
cSi5	-0.237	0.436	0.543	0.033	0.324	0.522	0.491	0.207	0.581	0.521	0.066	0.543	0.251	0.910	0.805	0.028	0.896	0.722	0.912	0.897						
cSi6	-0.308	0.469	0.535	0.004	0.329	0.514	0.509	0.182	0.585	0.511	0.026	0.535	0.038	0.904	0.894	-0.107	0.910	0.716	0.938	0.869	0.959					
cSi7	-0.287	0.464	0.515	0.009	0.318	0.462	0.501	0.153	0.555	0.460	0.034	0.515	0.202	0.857	0.772	-0.045	0.838	0.901	0.985	0.960	0.929	0.922				
$NP_i^{(1)}$	-0.357	0.552	0.729	0.074	0.388	0.724	0.655	0.322	0.758	0.729	0.125	0.729	0.117	0.975	0.917	-0.077	0.972	0.671	0.838	0.819	0.882	0.878	0.835			
$NP_i^{(2)}$	0.733	-0.692	0.518	0.900	-0.831	0.503	0.518	0.855	0.405	0.469	0.906	0.518	0.106	0.247	0.203	-0.357	0.224	0.044	0.083	0.060	0.110	0.105	0.063	0.154		
$NP_i^{(3)}$	0.824	-0.745	0.323	0.853	-0.781	0.290	0.374	0.730	0.221	0.247	0.837	0.323	0.263	0.178	0.086	-0.163	0.132	0.126	0.143	0.133	0.181	0.143	0.153	0.023	0.849	
$NP_i^{(4)}$	0.827	-0.730	0.488	0.949	-0.776	0.477	0.531	0.869	0.389	0.419	0.924	0.488	0.286	0.247	0.153	-0.145	0.223	0.052	0.103	0.089	0.170	0.136	0.109	0.115	0.915	0.936

Critical values of Spearman correlation at 5% and 1% level of significance (df 25) are 0.398 & 0.510 respectively

Dual Purpose Barley

Barley can provide nutrition to the animals through green fodder at vegetative stage and grains, after harvest from the regenerated plants, to human diet. Green vegetative portion of the barley is valuable source of pasture, cut green forage and straw. The crop gives satisfactory grain yield from the regenerated crop. Farm economics favour cultivation of dual purpose crop instead of only grain type particularly for northern plains of country to ensure availability of fodder during lean crop period. Seventeen dual purpose barley genotypes were evaluated at 10 locations by randomized block designs with three replications.

Table 1: Parentage details of dual purpose genotypes along with environmental conditions

Code	Genotype	Parentage
IVTIRTSDP-2	RD2715	RD387/BH602//RD2035
IVTIRTSDP-3	UPB1054	IBYT-LRA-M-12
IVTIRTSDP-4	KB1420	EIBGN(13)-7
IVTIRTSDP-5	BH1008	EIBGN-9/BH902(2009)
IVTIRTSDP-6	RD2927	RD2624/RD2696
IVTIRTSDP-7	RD2035	RD103/PL101
IVTIRTSDP-8	BH1010	BHMS22A/WG81
IVTIRTSDP-9	JB325	RD2615/DL88
IVTIRTSDP-10	RD2925	RD2606/RD2719//RD2660
IVTIRTSDP-11	AZAD	K12/K19
IVTIRTSDP-12	RD2552	RD2035/DL472
IVTIRTSDP-13	KB1401	IBYT-HI (13)-14
IVTIRTSDP-14	UPB1053	IBYT-MRA-12
IVTIRTSDP-15	JB319	LAKHAN/BH353
IVTIRTSDP-16	RD2928	RD2552/BH902
IVTIRTSDP-17	JB322	JB101/BH331
IVTIRTSDP-18	NDB1650	38th IBON-9030 (2006- 07)/NB3

Code	Environments	Latitude	Longitude	Altitude (m)
E1	Durgapura	26°51 'N	75 °47 ' E	390
E2	Bikaner	28° 02' N	73° 31' E	225.3
E3	Ludhiana	30°54’ N	75°52’ E	247
E4	Hisar	29°10'N	75 °46 ' E	215.2
E5	Varanasi	25 °20 ' N	83° 03 ' E	75.5
E6	Kanpur	26°29 ' N	80°18 ' E	125.9
E7	Faizabad	26°47’N	82°12 ‘E	113
E8	Rewa	24 °31 ' N	81°15 ' E	365.7
E9	Kota	25° 21' N	75° 86' E	259.7
E10	Udaipur	24°34 ' N	70 °42 ' E	582
E11	Jabalpur	23°90’ N	79 ° 58’ E	394

Table 2 : Descriptive statistics and non parametric stability statistics based on original values for grain yield of dual purpose barley genotypes

Original	Genotype	Yield	MR	SD	CV	Med	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7
IVTIRTSDP-2	RD2715	23.64	11.18	5.40	0.48	13.00	5.58	5.90	26.08	5.15	4.50	4.42	29.16
IVTIRTSDP-3	UPB1054	30.32	6.91	3.48	0.50	6.00	3.20	4.18	17.50	3.32	2.63	4.18	12.09
IVTIRTSDP-4	KB1420	28.05	10.09	4.83	0.48	10.00	4.89	5.96	23.08	4.60	3.55	3.87	23.29
IVTIRTSDP-5	BH1008	24.57	11.27	5.10	0.45	12.00	5.00	5.82	23.08	4.86	4.07	3.97	26.02
IVTIRTSDP-6	RD2927	26.59	8.82	5.29	0.60	9.00	5.33	5.57	31.71	5.04	4.56	5.69	27.96
IVTIRTSDP-7	RD2035	32.76	6.55	5.16	0.79	6.00	5.25	5.99	40.75	4.92	4.05	6.81	26.67
IVTIRTSDP-8	BH1010	28.06	10.55	4.08	0.39	9.00	4.11	4.11	15.81	3.89	3.69	3.85	16.67
IVTIRTSDP-9	JB325	27.37	9.09	3.91	0.43	10.00	4.15	4.65	16.82	3.73	2.99	3.62	15.29
IVTIRTSDP-10	RD2925	23.34	12.64	4.54	0.36	14.00	4.31	5.68	16.35	4.33	3.31	2.88	20.65
IVTIRTSDP-11	AZAD	31.96	5.64	4.72	0.84	3.00	4.76	5.10	39.48	4.50	3.97	7.74	22.25
IVTIRTSDP-12	RD2552	32.88	5.82	4.00	0.69	5.00	3.76	5.42	27.44	3.81	2.68	5.06	15.96
IVTIRTSDP-13	KB1401	29.06	9.73	4.47	0.46	9.00	4.82	5.17	20.58	4.27	3.52	3.98	20.02
IVTIRTSDP-14	UPB1053	29.43	8.36	6.04	0.72	6.00	6.40	6.39	43.59	5.76	5.19	6.82	36.45
IVTIRTSDP-15	JB319	27.29	9.18	4.49	0.49	11.00	4.78	4.82	21.96	4.28	3.80	4.55	20.16
IVTIRTSDP-16	RD2928	24.55	10.36	5.14	0.50	11.00	5.35	5.99	25.53	4.90	4.02	4.26	26.45
IVTIRTSDP-17	JB322	26.14	10.64	3.53	0.33	11.00	3.73	4.39	11.71	3.36	2.58	2.67	12.45
IVTIRTSDP-18	NDB1650	32.64	5.45	2.70	0.49	6.00	2.76	3.08	13.33	2.57	2.15	4.34	7.27

Table 3: Descriptive statistics and non parametric stability statistics based on corrected values for grain yield of dual purpose barley genotypes

Corrected	Genotype	CMR	CSD	CCV	CMed	CS_i^1	CS_i^2	CS_i^3	CS_i^4	CS_i^5	CS_i^6	CS_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
IVTIRTSDP-2	RD2715	7.55	6.31	0.84	6.00	6.44	6.59	52.84	6.02	5.50	8.02	39.87	2.050	0.158	0.538	0.576
IVTIRTSDP-3	UPB1054	9.73	4.27	0.44	11.00	3.91	4.64	18.73	4.07	3.57	4.04	18.22	7.430	1.238	0.589	0.566
IVTIRTSDP-4	KB1420	10.09	5.24	0.52	11.00	5.11	5.88	27.24	5.00	4.25	4.63	27.49	6.752	0.675	0.495	0.506
IVTIRTSDP-5	BH1008	8.55	5.05	0.59	8.00	5.22	5.99	29.81	4.81	3.87	4.98	25.47	4.214	0.351	0.427	0.463
IVTIRTSDP-6	RD2927	7.73	5.82	0.75	5.00	5.58	5.96	43.76	5.54	5.16	7.34	33.82	1.577	0.175	0.629	0.633
IVTIRTSDP-7	RD2035	9.45	5.99	0.63	8.00	6.40	6.24	37.94	5.71	5.22	6.08	35.87	2.859	0.477	0.872	0.978
IVTIRTSDP-8	BH1010	10.36	4.86	0.47	10.00	4.98	5.10	22.82	4.64	4.21	4.47	23.65	5.785	0.643	0.440	0.472
IVTIRTSDP-9	JB325	7.82	4.26	0.55	8.00	4.53	5.02	23.23	4.06	3.29	4.63	18.16	4.711	0.471	0.447	0.498
IVTIRTSDP-10	RD2925	7.64	5.32	0.70	6.00	5.22	5.55	37.00	5.07	4.63	6.67	28.25	1.865	0.133	0.401	0.413
IVTIRTSDP-11	AZAD	9.09	4.95	0.54	10.00	5.36	5.71	26.94	4.72	3.90	4.72	24.49	6.099	2.033	0.837	0.952
IVTIRTSDP-12	RD2552	9.45	3.62	0.38	9.00	3.84	4.16	13.83	3.45	2.86	3.33	13.07	6.141	1.228	0.593	0.659
IVTIRTSDP-13	KB1401	10.64	5.10	0.48	13.00	5.20	5.53	24.50	4.87	4.28	4.43	26.05	8.720	0.969	0.500	0.535
IVTIRTSDP-14	UPB1053	9.36	6.17	0.66	8.00	6.76	6.30	40.64	5.88	5.49	6.45	38.05	2.578	0.430	0.703	0.809
IVTIRTSDP-15	JB319	8.64	4.15	0.48	9.00	4.36	4.75	19.98	3.96	3.31	4.21	17.25	5.695	0.518	0.431	0.475
IVTIRTSDP-16	RD2928	8.18	5.69	0.70	6.00	5.75	5.76	39.56	5.42	5.11	6.87	32.36	1.736	0.158	0.523	0.554
IVTIRTSDP-17	JB322	9.00	3.74	0.42	7.00	4.07	4.12	15.56	3.57	3.09	3.78	14.00	3.909	0.355	0.335	0.383
IVTIRTSDP-18	NDB1650	9.73	3.98	0.41	10.00	4.11	5.40	16.26	3.79	2.66	3.01	15.82	7.339	1.223	0.695	0.753

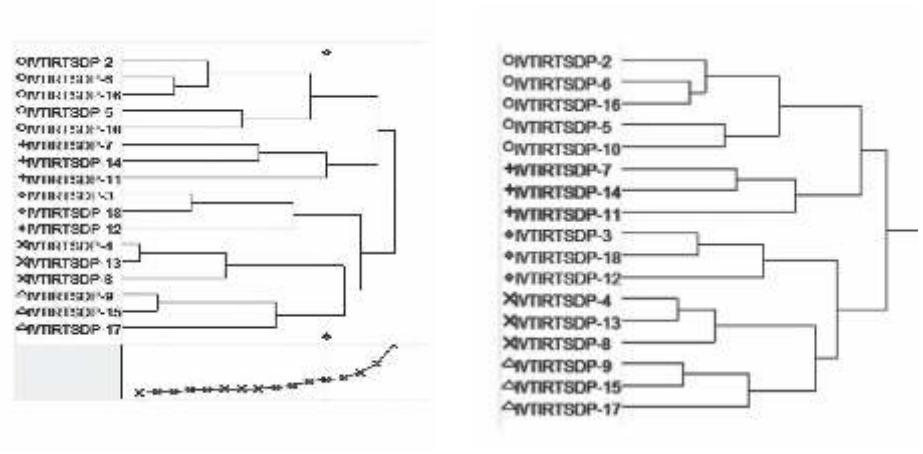


Figure 1: Hierarchical cluster analysis of dual purpose barley genotypes based on non parametric measures by Ward's method

As per average grain yield of dual purpose barley genotypes, RD2552 was the highest yielding with 32.9q/ha followed by NDB1650 and RD2035, although remarkable differences were evident among the studied genotypes (Table 2). The following three descriptive statistics; mean of ranks (MR), standard deviation of ranks (SD) and coefficient of variation of ranks (CV) were calculated for original ranks. MR pointed towards RD2925, BH1008 and SD for KB1401, UPB1054 whereas CV for JB322, RD2925 as stable genotypes, while AZAD, NDB1650 based on MR, UPB1053, RD2715 based on SD and AZAD, RD2035 based on CV, were most unstable. These descriptive statistics based on ranks can be used for genotype comparative evaluation.

Seven nonparametric measures based on original grain yield of genotypes (S_i^1 ,S_i^2 ,S_i^3 ,S_i^4 ,S_i^5 ,S_i^6 and S_i^7) indicated that NDB1650 and JB322 and UPB1054 were the stable genotypes, however UPB1053, RD2715, RD2927, RD2035 were unstable genotypes. According to corrected grain yield (table 3), BH1010 & KB1401 by mean of corrected ranks (CMR), RD2552 & JB322 by standard deviation of corrected ranks (CSD) and RD2552 & NDB1650 were the stable as per coefficient of variation of corrected ranks (CCV). Nonparametric measures of stability based on corrected yield (CS_i^1 ,CS_i^2 ,CS_i^3 ,CS_i^4 ,CS_i^5 ,CS_i^6 and CS_i^7) identified stable genotypes JB322, RD2552, RD2925 and NDB1650 were as per these nonparametric measures.

The cluster analysis based on mean yield and different nonparametric measures by Ward's method revealed two distinct clusters among seventeen genotypes: cluster A consisted of genotypes RD2715, RD2927, RD2928, BH1008, RD2925,

Table 4: Correlation values of yield with non parametric stability statistics for grain yield of dual purpose barley genotypes

	Yield	MR	SD	CV	Med	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	C MR	C SD	C CV	C Med	CS_i^1	CS_i^2	CS_i^3	CS_i^4	CS_i^5	CS_i^6	CS_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$
MR	0.275																									
SD	0.674	-0.174																								
CV	0.254	-0.749	0.702																							
Med	0.266	0.942	-0.200	-0.686																						
S_i^1	0.652	-0.169	0.973	0.695	-0.170																					
S_i^2	0.588	-0.145	0.971	0.643	-0.156	0.934																				
S_i^3	0.426	-0.605	0.848	0.955	-0.567	0.838	0.797																			
S_i^4	0.674	-0.174	1.000	0.702	-0.200	0.973	0.971	0.848																		
S_i^5	0.675	-0.146	0.972	0.696	-0.172	0.977	0.915	0.832	0.972																	
S_i^6	0.326	-0.716	0.760	0.989	-0.668	0.750	0.696	0.978	0.760	0.756																
S_i^7	0.674	-0.174	1.000	0.702	-0.200	0.973	0.971	0.848	1.000	0.972	0.760															
C MR	-0.616	-0.734	-0.278	0.400	-0.652	-0.229	-0.327	0.156	-0.278	-0.248	0.308	-0.278														
C SD	0.895	0.042	0.684	0.455	0.099	0.640	0.600	0.564	0.684	0.680	0.517	0.684	-0.337													
C CV	0.949	0.262	0.735	0.278	0.259	0.711	0.701	0.453	0.735	0.737	0.348	0.735	-0.656	0.850												
C Med	-0.602	-0.665	-0.180	0.417	-0.600	-0.126	-0.183	0.205	-0.180	-0.115	0.352	-0.180	0.887	-0.317	-0.565											
CS_i^1	0.890	0.032	0.652	0.450	0.097	0.603	0.574	0.544	0.652	0.653	0.500	0.652	-0.357	0.983	0.863	-0.347										
CS_i^2	0.705	0.063	0.688	0.419	0.123	0.638	0.688	0.533	0.688	0.676	0.494	0.688	-0.319	0.879	0.778	-0.169	0.854									
CS_i^3	0.971	0.213	0.694	0.320	0.237	0.657	0.627	0.480	0.694	0.695	0.392	0.694	-0.548	0.944	0.949	-0.506	0.946	0.808								
CS_i^4	0.901	0.028	0.697	0.466	0.081	0.648	0.614	0.577	0.697	0.691	0.528	0.697	-0.350	0.999	0.857	-0.328	0.984	0.870	0.950							
CS_i^5	0.900	0.051	0.623	0.420	0.124	0.578	0.537	0.525	0.623	0.619	0.473	0.623	-0.352	0.978	0.846	-0.357	0.980	0.805	0.949	0.979						
CS_i^6	1.000	0.275	0.674	0.254	0.266	0.652	0.588	0.426	0.674	0.675	0.326	0.674	-0.616	0.895	0.949	-0.602	0.890	0.705	0.971	0.901	0.900					
CS_i^7	0.895	0.042	0.684	0.455	0.099	0.640	0.600	0.564	0.684	0.680	0.517	0.684	-0.337	1.000	0.850	-0.317	0.983	0.879	0.944	0.999	0.978	0.895				
$NP_i^{(1)}$	0.282	0.672	0.054	-0.428	0.646	0.076	0.020	-0.279	0.054	0.026	-0.400	0.054	-0.580	0.100	0.154	-0.688	0.027	0.004	0.159	0.089	0.049	0.282	0.100			
$NP_i^{(2)}$	0.195	0.518	0.026	-0.316	0.542	0.045	-0.013	-0.210	0.026	-0.012	-0.300	0.026	-0.343	0.055	0.023	-0.483	-0.021	-0.074	0.107	0.051	0.009	0.195	0.055	0.891		
$NP_i^{(3)}$	-0.010	-0.221	-0.042	0.112	-0.129	-0.061	-0.074	0.056	-0.042	-0.138	0.059	-0.042	0.141	-0.061	-0.181	-0.060	-0.049	-0.298	-0.044	-0.045	0.002	-0.010	-0.061	0.061	0.406	
$NP_i^{(4)}$	-0.017	-0.245	-0.025	0.131	-0.158	-0.037	-0.059	0.071	-0.025	-0.124	0.076	-0.025	0.170	-0.074	-0.181	-0.048	-0.061	-0.308	-0.054	-0.058	-0.012	-0.017	-0.074	0.059	0.398	0.993

Critical values of Spearman correlation at 5% and 1% level of significance (df 15) are 0.521 & 0.604 respectively

RD2035, UPB1053 and AZAD and cluster B consisted of UPB1054, NDB1650, RD2552, KB1420, KB1401, JB319, JB322 genotypes as the favorable. Corrected statistics identified genotypes JB322, NDB1650 and RD2552 were the stable ones, while based on uncorrected statistics, genotypes NDB1650 JB322 and UPB1054 were the preferable. Regarding mean yield regardless of stability, the most favorable genotype would be NDB1650.

Relationship among nonparametric statistics

According to Spearman's rank correlation analysis among all possible pairs there was a highly significant ($p< 0.01$) positive rank correlation between mean yield with SD, S_i^1, S_i^2, S_i^5, S_i^7 and negative correlation observed for CMR, CMed. More over no significant correlation with stability measures $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$. Mean rank (MR) expressed positive correlation with $NP_i^{(1)}$, $NP_i^{(2)}$ and negative with CV, Si^3 ,Si^6, CMR and CMed. SD maintained ($p< 0.01$) significant positive with S_i^1 ,S_i^2 , S_i^3,S_i^5 S_i^7 , CSD, CCV as well as with CS_i^1 ,CS_i^2 ,CS_i^3 ,CS_i^4 ,CS_i^5 ,CS_i^6 and CS_i^7. Also S_i^1 had a highly significant positive rank correlation with S_i^2 , S_i^3 , S_i^4 , S_i^5 , S_i^6,S_i^7 as well as with CS_i^1 ,CS_i^2 ,CS_i^3 ,CS_i^4 ,CS_i^5 ,CS_i^6 and CS_i^7. Subsequently positive correlations seen among Si^s and with CS_i^s. However, $NP_i^{(1)}$ showed negative association with CV, S_i^3, CMR & CMed. While $NP_i^{(2)}$expressed negative rank correlation with CV, S_i^6, CMR and CMed. $NP_i^{(3)}$ maintained negative correlation with most of the measures though the magnitude was of low magnitude. Similar behavior observed for $NP_i^{(3)}$ with other nonparametric measures. Good potential of S_i^3 and S_i^6 for the selection of stable high yielder genotypes. The effect of correction and removing the genotype effect is clear on the negative association between mean yield and CMR. Mean rank (MR) had a significant negative rank correlation with CV and S_i^3 while it had a significant negative rank correlation with CMR, CMed and had low rank correlation with the other CS_i^s nonparametric statistics.

Seven nonparametric measures based on corrected datasets (CS_i^1, CS_i^2, CS_i^3 ,CS_i^4 ,CS_i^5 ,CS_i^6 ,CS_i^7) were correlated with each other. The most prominent relation was no positive or negative association of $NP_i^{(s)}$ with CS_i^s.

Barley crop is cultivated since ancient time for food, feed, medicinal purposes and malt of alcoholic beverages. Today, barley has recognized as a crop of industrial importance as cater the increased demand of malt for brewing, distillation, baby foods and medicinal syrups in domestic as well as international market. Nearly 20-25% of the total barley production of the country is utilized by the malting industries. The demand for malt barley is directly associated with the expansion of the brewery industry .Twenty malt barley genotypes, including checks of six row feed & two row malt, were evaluated at eight major experimental locations of North Western plains zone under irrigated conditions. The randomized block designs with three replications adopted for field trials and recommended cultural practices were followed to harvest the good yield. The grain yield of genotypes were further analysed statistically to calculate non parametric measures.

Nonparametric statistical analysis was presented in Table 2. Genotype KB1426 (27.5 q/ha) was the highest yielder followed by BH1012 and BH1013 as remarkable differences (16.7 to 27.5) were observed. Three descriptive statistics; mean of ranks (MR), standard deviation of ranks (SD) and coefficient of variation of ranks (CV) based on original yield were calculated. These statistics pointed towards DWRB147, DWRB150 and RD2943 were the stable genotypes, while DWRB150 & DWRUB53 based on MR, PL890 & BH1012 based on SD and BH902 & RD2849 based on CV, were unstable ones. These simple descriptive statistics based on ranks able to discriminate genotypes. Nonparametric measures based on original yield suggested DWRUB52 and DWRB147 as genotypes of stable performance, however most of the measures isolated PL890 as the most unstable genotype.

Genotypes evaluation as per descriptive statistics based on corrected yield presented in Table 3. Mean of ranks of (CMR) pointed towards RD2940 followed by RD2939 genotype. CSD and CCV measures identified DWRB150 along with DWRB147 as the stable genotypes. More over BH902 and PL890 were identified as the genotypes with unstable performance. Nonparametric measures based on corrected values identified DWRB147 & DWRB150 as the stable genotypes at the same times BH902 & PL890 unstable genotypes.

For significant tests for S_i^1 and S_i^2 For each genotype Z_i^1 and Z_i^2 values were calculated based on the ranks of adjusted data and summed over genotypes to obtain Z values. As sum of Z_i^1 = 59.77 was greater than critical value of ^{2} =31.41, therefore significant differences were found in rank stability among the twenty genotypes grown in the eight environments and sum of Z_i^2 = 18.75 less than the critical value of ^{2} thus indicating no significant differences in rank stability among

the twenty genotypes grown in the eight environments. Few genotypes were significantly unstable as compared to the other genotypes as observed large *Z* values compared with the critical χ^2 at 5% level of significance for one degree of freedom i.e. 3.84.

The S_i^1 and S_i^2 statistics are based on ranks of genotypes across environments and assign equal weight to all environments. Genotypes with fewer changes in ranking are considered to be more stable. Accordingly RD2849, RD2943 DWRB150 and DWRB147 had the smallest changes in rank and regarded as the stable genotypes unlike to BH902 and PL890. Two other non-parametric statistics S_i^3 and S_i^6 combining yield and stability based on yield ranks of genotypes in each environment. These parameters measure stability in units of the mean rank of each genotype. As for S_i^1 and S_i^2, DWRB150 followed by DWRB147 were the most stable according to the S_i^3 and S_i^6 measures.

Results of Thennarasu's (1995) non-parametric stability statistics, calculated from the ranks of adjusted yield, depicted in Table 3. According to the NP_i^1, DWRB101 and RD2849 were considered stable as compared to other genotypes. RD2943 and DWRB148 had the lowest value of NP_i^2 and were stable genotypes followed by DWR147 and KWS Amadora. Measure, like NP_i^2 identified DWRB150 as the stable genotype, though with lower yield. Most unstable genotype based on NP_i^3 was BH902 followed by PL890 and BH1012, which had the higher mean yield. The NP_i^3 showed a negative relationship with yield. Stability parameter NP_i^4 selected DWRB147 as a stable genotype, followed by RD2943, RD2941, and DWRB148. The results of the three parameters (NP_i^2, NP_i^3 and NP_i^4) were similar as identified BH902, DWRB150 and DWRB147 as unstable, although had lowest minimum yield performances .

Biplot analysis

To better understand the relationships among non-parametric measures and to assess their relationships with the concepts of stability, principal component (PC) analysis based on the rank correlation matrix was performed. Table 4 showed the loadings of the first two PCA of ranks of various measures accounting for 70.08% of the variance of original variables. The relationships among the different stability statistics are graphically displayed in a biplot of PCA1 and PCA2 (Fig. 1) allowing three groups to be distinguished: Group I included CMR, SD, S_i^1, S_i^2,CV, CCV, CS_i^1, CS_i^2 and mean yield. Mean yield was included in the group I suggesting that the genotypes BH1012, DWRB149, BH1011 and RD2940 comprised those methods where yield mean had the main influence on the ranking across environments. Figure 1 shows that these measures are strongly related to grain yield. Based on

these parameters, selection based on grain yield is favored, and is related to the dynamic concept of stability. Group II included measures S_i^3, S_i^6, NP_i^2, NP_i^4 and CV . These provide a measure of stability in the static sense. All these parameters were significantly correlated with mean yield. Therefore, these parameters allow the identification of genotypes adapted to environments with unfavorable growing conditions. Group III consists of parameters that were influenced simultaneously by both grain yield and stability. It was noted that genotypes identified according to these methods showed an average stability, however, these genotypes may not be as good as the responsive ones under favorable conditions. This group included the measures of NP_i^1, MR, Median and CMedian which were negatively associated with the mean grain yield.

Vector view of the biplot showed the degree of the relationships among the indicators. The lines that connect the stability estimates to the biplot origin are called stability vectors. The cosine of the angle between the vectors of two stability indices approximates the correlation between them. For example, measures of G2 expressed positive correlation (an acute angle), the same conclusion was obtained for the G3 stability estimates, while G1 was negatively correlated with G3 indices (an obtuse angle) and independence or very weak correlation (almost right angle) between G1 and G2 stability measures.

Cluster Analysis

Hierarchical cluster analysis of malt barley genotypes by Ward's method based on descriptive and non parametric stability measures along with average yield, was used to classify the genotypes into major groups (Figure 2) . Four major clusters were observed by using the squared Euclidean distance as dissimilarity measure. Group III included the high yielding genotypes BH1012 with BH902 and PL890. These genotypes were identified as unstable genotypes by mean rank measures. Most of the genotypes with moderate to low yields clustered in Group I included genotypes RD2941, BH1011, DWRB148 and KWS Amadora. The other genotypes, which had higher yields clustered in Group II included DWRB149, RD2939 and RD2940 genotypes. Largest group IV consisted of stable genotypes as per measures based on original and corrected grain yield.

Table 1: Environmental conditions and parentage details of barley genotypes

Code	Genotype	Parentage	Code	Environments	Latitude	Longitude	Altitude (m)
IVT-MB-TS-1	KB1426	IBYT-HI(11)-12	E1	Bawal	28 °10 ' N	76° 59 ' E	263
IVT-MB-TS-2	DWRB101	DWR28/BH581	E2	Durgapura	26°51 'N	75° 47 ' E	390
IVT-MB-TS-3	KB1405	IBYT-HI (13-14)-16	E3	Hisar	29°10 'N	75° 46 ' E	215.2
IVT-MB-TS-4	RD2943	DWRUB52/RD2618	E4	Ludhiana	30°54 ' N	75° 52' E	247
IVT-MB-TS-5	DWRB148	DWRB78/DWRB77	E5	Bathinda	30 °21 ' N	74° 95' E	208
IVT-MB-TS-6	RD2849	ISEBON-128 (08-09)/PL705	E6	Karnal	29 °43 ' N	76° 58 ' E	252
IVT-MB-TS-7	BH902	BH495/RD2552	E7	Modipuram	29 °07 ' N	77° 71' E	232
IVT-MB-TS-8	BH1011	EIBGN-17/BH919(2007)	E8	Pantnagar	29 °02 ' N	79° 48' E	237
IVT-MB-TS-9	DWRB149	DWRB78/DWRB77					
IVT-MB-TS-10	PL890	DWRUB52/DWRUB62					
IVT-MB-TS-11	BH1013	28th IBYT-23/DWRUB52					
IVT-MB-TS-12	DWRB150	DWRB54/XANADU					
IVT-MB-TS-13	RD2941	DWRUB49/RD2615					
IVT-MB-TS-14	RD2939	RD2668/IBON-HI 2010-11					
IVT-MB-TS-15	DWRB92	DWR28/DWR45					
IVT-MB-TS-16	DWRUB52	DWR17/K551					
IVT-MB-TS-17	BH1012	33rd IBON71/DWRUB52					
IVT-MB-TS-18	DWRB147	DWRB78/DWRB73					
IVT-MB-TS-19	RD2940	RD2668/PL426					
IVT-MB-TS-20	KWS Amadora	Conchita/ Quench//KWS Bambina					

Table 2: Descriptive statistics and non parametric measures for grain yield (Original)

		Yield	MR	SD	CV	Med	Si^1	Si^2	Si^3	Si^6
IVT-MB-TS-1	KB1426	27.52	12.63	6.00	0.48	12.0	8.09	35.98	19.95	3.03
IVT-MB-TS-2	DWRB101	23.07	9.38	4.47	0.48	8.5	5.96	19.98	14.92	2.75
IVT-MB-TS-3	KB1405	21.98	13.38	5.76	0.43	15.0	6.22	33.13	17.34	2.50
IVT-MB-TS-4	RD2943	17.95	13.00	4.28	0.33	13.5	5.39	18.29	9.85	2.15
IVT-MB-TS-5	DWRB148	24.91	14.38	5.63	0.39	16.0	6.96	31.70	15.43	2.38
IVT-MB-TS-6	RD2849	21.60	7.38	5.58	0.76	6.0	6.70	31.13	29.54	3.86
IVT-MB-TS-7	BH902	22.26	5.00	4.87	0.97	3.5	5.04	23.71	33.20	6.00
IVT-MB-TS-8	BH1011	26.51	11.50	5.37	0.47	13.0	6.39	28.86	17.57	2.87
IVT-MB-TS-9	DWRB149	26.35	10.25	6.25	0.61	11.0	8.17	39.07	26.68	3.90
IVT-MB-TS-10	PL890	19.41	8.88	6.62	0.75	7.5	8.61	43.84	34.58	5.07
IVT-MB-TS-11	BH1013	27.02	9.50	3.55	0.37	10.5	4.70	12.57	9.26	2.42
IVT-MB-TS-12	DWRB150	24.39	4.38	3.34	0.76	3.0	4.22	11.13	17.80	4.69
IVT-MB-TS-13	RD2941	19.46	15.13	5.25	0.35	18.0	6.83	27.55	12.75	2.43
IVT-MB-TS-14	RD2939	20.39	10.38	6.39	0.62	12.0	7.78	40.84	27.55	4.07
IVT-MB-TS-15	DWRB92	16.70	9.25	4.98	0.54	11.0	6.39	24.79	18.76	3.62
IVT-MB-TS-16	DWRUB52	18.56	6.00	3.12	0.52	6.5	3.87	9.71	11.33	3.33
IVT-MB-TS-17	BH1012	27.35	10.63	6.41	0.60	9.5	8.35	41.13	27.09	4.05
IVT-MB-TS-18	DWRB147	18.71	15.25	4.23	0.28	17.5	4.83	17.93	8.23	1.77
IVT-MB-TS-19	RD2940	25.44	10.63	5.58	0.53	12.5	7.70	31.13	20.51	3.36
IVT-MB-TS-20	KWS Amadora	24.05	12.25	4.71	0.38	13.0	6.17	22.21	12.69	2.24

Table 3: Descriptive statistics and non parametric measures for grain yield (corrected)

	CMR	CSD	CCV	Cmed	CSi^1	Zi^1	CSi^3	CSi^6	CSi^2	Zi^2	NPi^1	NPi^2	NPi^3	NPi^4
IVT-MB-TS-1	11.0	5.63	0.51	9.5	7.61	1.062	20.18	3.27	31.71	0.016	8.313	0.693	5.268	0.603
IVT-MB-TS-2	9.8	5.52	0.57	8.5	7.57	0.968	21.90	3.69	30.50	0.051	7.625	0.897	5.166	0.807
IVT-MB-TS-3	10.5	5.90	0.56	12.0	7.65	1.161	23.24	3.71	34.86	0.017	10.500	0.700	5.523	0.572
IVT-MB-TS-4	9.6	4.93	0.51	10.0	5.87	0.704	17.65	3.43	24.27	0.541	8.750	0.648	4.608	0.452
IVT-MB-TS-5	10.3	6.50	0.63	10.5	8.17	2.684	28.83	3.90	42.21	0.539	9.188	0.574	6.078	0.569
IVT-MB-TS-6	9.1	4.97	0.54	8.0	5.70	1.053	18.95	2.79	24.70	0.490	7.719	1.286	4.649	0.772
IVT-MB-TS-7	9.8	7.67	0.79	10.0	9.39	8.685	42.21	5.54	58.79	4.370	8.813	2.518	7.172	1.878
IVT-MB-TS-8	10.6	6.35	0.60	12.0	7.83	1.599	26.53	3.93	40.27	0.330	10.500	0.808	5.936	0.681
IVT-MB-TS-9	11.1	6.85	0.62	11.5	9.13	7.110	29.56	3.87	46.98	1.264	10.063	0.915	6.412	0.891
IVT-MB-TS-10	10.1	7.40	0.73	7.5	9.22	7.618	37.81	5.06	54.70	3.083	7.750	1.033	6.918	1.039
IVT-MB-TS-11	10.0	5.01	0.50	10.0	6.39	0.077	17.60	2.80	25.14	0.440	8.750	0.833	4.690	0.673
IVT-MB-TS-12	10.8	4.06	0.38	10.5	5.48	1.587	10.74	2.42	16.50	1.880	9.188	3.063	3.800	1.252
IVT-MB-TS-13	10.0	6.05	0.60	10.0	8.35	3.331	25.60	4.00	36.57	0.074	8.750	0.486	5.657	0.552
IVT-MB-TS-14	12.0	6.82	0.57	12.5	8.17	2.684	27.17	3.83	46.57	1.189	10.938	0.911	6.384	0.788
IVT-MB-TS-15	11.4	6.00	0.53	13.5	7.74	1.371	22.14	3.36	35.98	0.050	11.813	1.074	5.611	0.837
IVT-MB-TS-16	10.4	5.58	0.54	11.0	6.78	0.020	21.00	3.57	31.13	0.030	9.625	1.481	5.219	1.130
IVT-MB-TS-17	10.1	7.18	0.71	9.0	9.04	6.621	35.64	4.84	51.55	2.245	8.094	0.852	6.716	0.851
IVT-MB-TS-18	11.1	4.79	0.43	12.0	6.43	0.054	14.46	2.79	22.98	0.707	10.500	0.600	4.484	0.422
IVT-MB-TS-19	12.9	6.71	0.52	16.0	8.87	5.693	24.46	3.51	44.98	0.922	14.000	1.120	6.274	0.835
IVT-MB-TS-20	9.5	6.48	0.68	8.5	8.87	5.693	30.95	4.63	42.00	0.513	7.938	0.611	6.062	0.724
$E(S_i^1)$ =6.65	$Var(S_i^1)$=	0.8659	$E(S_i^2)$	=33.25		59.77	$Var(S_i^2)$	=149.21		18.75	c^2 =	3.84	c^2=	31.14

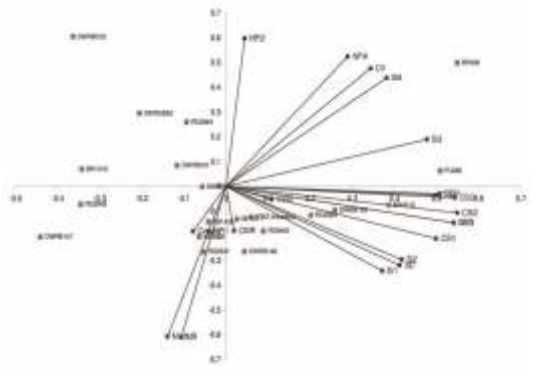


Table 4. Loadings of rank derived from non parametric measures

Measure	Component PC1	Component PC2
Yield	0.062	-0.034
MR	-0.061	-0.398
SD	0.236	-0.208
CV	0.197	0.312
Med	-0.080	-0.397
Si1	0.213	-0.223
Si3	0.273	0.124
Si6	0.219	0.287
Si2	0.239	-0.194
CMR	0.011	-0.118
CSD	0.310	-0.096
CCV	0.290	-0.019
Cmed	-0.045	-0.118
CSi1	0.286	-0.138
CSi3	0.311	-0.030
CSi6	0.286	-0.024
CSi2	0.315	-0.070
NPi1	-0.024	-0.118
NPi2	0.025	0.391
NPi3	0.310	-0.096
NPi4	0.166	0.344
Variance explained %	44.07	26.01

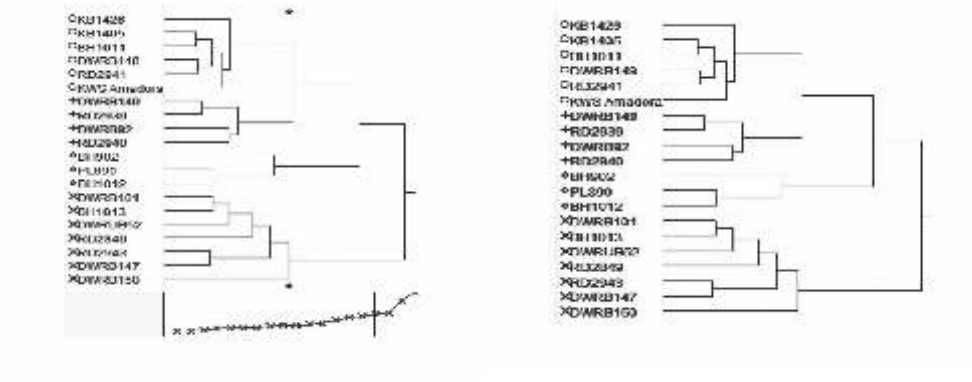


Figure 2: Hierarchical clustering of barley genotypes based on non parametric measures

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ICAR- Indian Institute of Wheat and Barley Research

Post Box #158, Agrasain Road, Karnal-132001 (Haryana) India