Statistical Applications in Breeding and Genetics

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1. Introduction

The initiation of the work in statistical genetics involving analysis of breeding data on Beetal goats dates back to 1940 when this Institute in its formative stages was working as a statistical section of ICAR. This work under the illustrious leadership of Professor P. V. Sukhatme led, for the first time, to the appreciation of the power of Statistics in drawing inferences on issues in animal sciences and other fields. With the reorganization of research activities under the Indian Council of Agricultural Research during the 70s the stage was set for making the impact of this discipline felt in the research arena of the country. After the recognition of this Institute as a full-fledged Institute of ICAR the work on statistical genetics, which involved research initiatives, both of theoretical and applied nature in plant and animal breeding was carried out in the Division of Animal Sciences. The activity of research in statistical genetics was, further strengthened by carving out a "Statistical Genetics Cell" from the Division of Animal Sciences in 1978. Realizing the importance of this area of research and the amount of work done in the past, the 'Quinquennial Review Team (1971-1981)' as well as the some of the UNDP experts who visited this Institute from time to time recommended that research in the field of statistical genetics and other areas like biometry, bio-assay and bio-statistics must be carried out on a much larger scale rather than by a small cell. Consequent on these recommendations the Division of Bio-statistics and Statistical Genetics came into existence in March 1985. Subsequently, the name of the Division was changed to 'Biometrics', in 1998. New theoretical developments were made from time to time and numerous methodologies for application in plant and animal breeding and related areas were developed. The major research contributions made during last 25 years by the scientists and students in the area of statistical genetics are reviewed. Prior to this period the work has been exhaustively reviewed by Narain *et al.* (1987).

In the next few sections we have given a brief account of the important research and academic accomplishments in the area of statistical applications in genetics and breeding. In the discussion of research achievements, the material has been organized under different heads. At the end a complete list of publications of the scientists, that formed the main basis of the highlights of research achievements, have been provided in this article.

2. Estimation of Genetic Parameters

Most of the economic characters in agricultural crops and dairy animals are quantitative in nature. There is a wide range of variability in these characters which depends on the genetic make up of the individuals and the environment in which they are grown. Breeders use this variability for getting improvement in economic characters through efficient selection strategies. The information on genetic parameters, such as heritability, repeatability and genetic correlation is a pre-requisite for making efficient selection strategies by the geneticists and breeders. Keeping in view the importance of these parameters a number of studies have been conducted at the institute, which are as follows.

2.1 Estimation of heritability

There are two main approaches to the estimation of heritability (h^2) in farm animals, one based on intra-sire regression of offspring on dam and the other based on variance components from full-sib or half-sib analysis. Heritability being a fraction of additive genetic variance to the phenotypic variance should normally lie between 0 and 1. However, when estimated from sample, it frequently turns out to be either negative or takes values exceeding unity due to sampling fluctuations. Such estimates are termed inadmissible estimates. All that has been tried at the Institute is to obtain admissible estimate of heritability and a precise estimate of its variance.

The problem of inadmissible estimates

Extensive investigations on this problem led to the working out of optimum sample sizes and structures (Prabhakaran and Jain, 1987, a, b, c, 1988, Prabhakaran and Sharma, 1994a, 1995). However, as pointed out by Prabhakaran and Jain (1988) all such probabilities can be reduced to F cumulative probabilities through Satterthwaite(1946) approximation and then computed using Hastings (1955) procedure, without losing much in accuracy. Jogendera Singh (1992) extended the study to cover the heritability under the practical definition in which heritability is the fraction of total fixable genetic variance to the total phenotypic variance. He also computed the probabilities for the unbalanced hierarchical model through Monte Carlo simulation. His results were largely in agreement with those of Prabhakaran and Jain(1988). He also observed that the data imbalance did not pose much of a problem when the observations are fairly good in number and are taken in an optimum fashion. Walke (1993) computed the probabilities of inadmissible estimates of intra-sire regression empirically by resorting to the simulation procedure of Ronningen (1974) and found that the probabilities were in close agreement with the theoretical probabilities as reported in Prabhakaran and Jain (1987a). Subsequently Shukla (1993) considered heritability estimation under finite population assumptions, its effect on the probability of inadmissible estimates and the related saving in sample size requirement.

Improved estimators of heritability

Garg *et al.* (1984) estimated the information on genetic parameters such as heritability of economic characters as well as on vital characteristics such as rate of mortality, infertility, abortion, sex-ratio involuntary culling etc. in respect of the Indian herds of cattle and buffaloes. When non-availability of suitable data becomes a major constraint, the only way to obtain meaningful estimates of heritability is to go in for restricted estimators, which can shrink the estimates so as to make them fall within the permissible range. Accordingly, a number of restricted estimators were proposed (Verma and Jain, 1989, Prabhakaran and Jain 1990) and illustrated (Prabhakaran and Seema Jaggi, 1996) for improved estimation of heritability. Kaur and Bhatia (1993) conducted an empirical study of different restricted estimation procedures and found that the estimator with minimum average squared bias is superior to other estimators including the MINQUE and MINIMAX estimators of Verma and Jain (1989).

Variance estimation

Prabhakaran and Jain(1987d) showed that the traditional formula for variance of intra-sire regression heritability is not tenable in view of the random sampling of parents involved and suggested a new expression for the unconditional variance by considering both the offspring and dam observations as random variables. Prabhakaran *et al*. (1990) proposed two new estimators of this variance and compared

for their efficiency. A better approach to the estimation of variance of broad sense heritability was suggested by Prabhakaran and Jain (1986). Prabhakaran *et al*. (1991) based on probabilistic arguments established an identity useful in finding the moments of sample moments of bivariate normal random variables, with applications in many practical situations, established. The variance of intra-sire regression heritability was derived to illustrate its use. The bootstrap procedure was also used (Jugnu *et al.* 1999, Singh and Wahi, 2001) for evaluation of different mating designs, from the point of view of getting precise estimates of heritability. More specifically, the investigation is focused on two aspects, the optimum sample size and structure for half-sib and full-sib mating designs and the design giving least variances under optimum structures, depending upon the level of population heritability. Wahi and Rao (2004, 2005) made an empirical investigation on the estimation of heritability in presence of non-genetic fixed effects under half-sib mating design and it was found that the method of fitting constants commonly used for estimation and adjustment for all fixed effects taken in the model irrespective of their significance, prior to estimation of heritability, has been found comparable in terms of percent bias to that of estimates based on mixed model techniques. Prabhakaran and Rao (2008) developed a new approach for estimation of variance of sample heritability from full-sib analysis and they found that the variance estimates obtained by the new approach are comparable to that of the bootstrap estimates and can be used for estimation of variance of heritability.

Estimation using bootstrap technique

Application of bootstrap technique for the variance estimation of genetic parameters was initiated in 1992 in the form of a research project entitled Application of bootstrap technique for studying the statistical properties of genetic parameters. Subsequently this technique was used for the estimation of variance and confidence intervals of heritability and genetic correlation [Bhatia *et al.* 1994; Bhatia and Jayashankar, 1996 a,b, 1998; Wahi *et al.* 1998]. Rao (1997) and Rao and Prabhakaran (2001) proposed an approach of obtaining robust estimates of heritability using bootstrap technique on components of variances.

No formulae give the exact variance of heritability and genetic correlation estimators; the expressions available are quite complex. Therefore, a number of studies (Bhatia *et al.* 1994; Bhatia and Jayasankar, 1996 a,b,1998) were conducted on the suitability of bootstrap technique for obtaining a reasonably good estimate of standard error and in computing interval estimates for these parameters. Bhatia *et al.* (1994) discussed its use for variance estimation. Bhatia and Jayasankar (1996a) computed confidence intervals as well as bias corrected confidence intervals for half-sib correlation heritability adopting the non-parametric bootstrap procedure and demonstrated the workability of the procedure. The procedure was extended to the unbalanced data situation by Bhatia and Jayasankar (1996b). They compared the non-parametric and parametric bootstrapping procedures for estimation of precision and determination of confidence intervals for the half-sib and offspring-parent regression heritabilities and showed that the adequacy of non-parametric approach for any kind of sample data. Subsequently, Wahi *et al.* (1998) applied the non-parametric bootstrap technique to obtain the standard errors and percentile as well as bias-corrected percentile intervals for heritability and genetic correlation estimated from sib analysis and parent-offspring regression. They found that the bootstrap estimates of variance of heritability were always very much lower than those computed from approximations and nearly 200 and 1500 bootstrap replications were needed for obtaining a reliable estimate of standard error and confidence interval respectively.

Bayesian estimation of heritability

Rao and Kumar (2001) used Bayesian Using GIBSS Sampling (BUGS) to obtain numerical estimates of parameters of posterior distribution and variance components along with heritability under half-sib mating design with small sample data. A comparison of this approach with traditional approaches, *viz.,* ANOVA, Maximum Likelihood (ML) and Restricted Maximum Likelihood (REML) establishes the suitability of the former over later for heritability estimation. Kumar *et al.* (2004) further used BUGS approach to estimate variance components and heritability under two-way nested random effects model. Here too Bayesian technique out performs the other traditional approaches for heritability estimation.

Robust estimation of heritability

Kiran *et al*. (2003) studied the empirical distributions of the estimates of heritability from half-sib and full-sib data using analysis of variance estimates of variance components. They found that under half-sib mating design, the heritability estimates always follow normal distribution irrespective of the population parametric values. However this is not true for all the situations of full-sib mating design, particularly at low parametric values of heritability. Under sire component estimation of full-sib heritability, the form of distribution is gamma. Kiran (2003) developed a multivariate approach to estimate the variance components and thereby heritability. Estimates obtained under multivariate approach are compared with that obtained under traditional procedures like ANOVA, ML and REML through simulation studies. The estimates obtained through multivariate approach have lower bias and also have lower mean square error than ANOVA and REML estimates. Kiran *et al*. (2004) studied the effects of the aberrant values, outliers and non normality on heritability estimation and it has been found that the robust method of estimation of heritability provides precise estimates as compared to all other traditional methods of heritability estimation.

Heritability of herd-life in dairy cattle

For dairy cows length of productive life or herd-life is a trait of major economic importance and is dependent in the culling decision of individual milk producers. Malhotra (1988) studied the retention time and its relationship with production and reproduction traits of dairy cattle and buffaloes. From this study it was concluded that 3/8 breds and 7/8 breds respectively have lowest and highest culling rates among the cross bred animals when the animals have completed their first lactation. Bhatia *et al.* (1992) studied the culling patterns of different categories of dairy animals through a non-parametric approach. Bhatia and Malhotra (1995 a,b) discussed some aspects of estimation and comparison of retention times in dairy cattle as well as the relationships between the retention time and explanatory variables. Using the path analysis (Paul 1997, Paul and Bhatia 2000a) derived formulae for heritability of herd-life from the correlation between half-sib for the traits. The reliability of the formulae has been demonstrated through simulation.

Stayability is a threshold trait in dairy cattle, which needs a special kind of statistical treatment. Herd-life, a measure of stayability depends on a number of traits including milk production. A realistic measure of heritability of stayabilty can be obtained only if the herd-life is adjusted for production and other auxiliary traits. Kaur (1990) developed an index for assessing the worth of a male on the basis of phenotypic values of his male and female progeny for all-or-none traits. It was shown that maximum gain in accuracy was obtained when the auxiliary traits are included in the index and the phenotypic and additive genetic

correlation between main and auxiliary traits are of opposite signs. Magnussen and Kremer (1995) considered the beta-binomial model for estimating heritability of binary traits using the concepts of selection response and realized heritability. Making use of this idea Paul and Bhatia (2000b) first converted the herd-life adjusted for production to a binary trait using threshold probability and then used the resultant trait for the determination of heritability. The performance of beta-binomial method was further compared, empirically, with that of Dempster and Lerner (1950) method and other procedures of computing narrow sense and family-mean heritability. The comparison was done for different family as well as herd sizes in both adjusted and unadjusted herd-life situations using the relative root mean square error as the basis of comparison. From the results, it is concluded that the family size and herd size have an important role in the estimation of heritability of stayability. While the procedures was based on real data, beta-binomial and Dempster-Lerner showed encouraging results and those based on family mean exhibited were quite unreliable estimates of heritability. The work was later extended to cover unbalanced data situations (Paul and Bhatia, 2001,2002a, b). The important message from the studies is that in situations where assigned values of stayability are unavailable the beta-binomial method is preferable to all other procedures. Further, in case of threshold models the adjustment for auxiliary traits is crucial in the estimation of heritability of stayability (Paul and Bhatia 2002b).

Iqbal *et al.* (2004) obtained the estimates of heritability of stayability by different methods and that too for non-normal, unbalanced and more than one auxiliary trait situations. A modified beta-binomial approach has been proposed to estimate the heritability of stayability. Whenever prior information on the relationship between stayability, production and other reproductive traits are available, one should go for adjustment of two characters for arriving at the true estimate of heritability. Behera (2007) studied the heritability of threshold character (mastitis disease) in sahiwal breed of cows by estimating heritability by different methods and found that the estimate based on beta-binomial method is more precise than other methods.

Yield survival relationships and culling patterns

Yield survival relationships in dairy cattle and buffaloes were studied in detail by Bhatia (1984) and Narain and Bhatia (1984b) with the help of survivorship and hazard functions, which again brought out the unsuitability of animals, with higher exotic inheritance level, for Indian conditions. The concept of censoring in dairy cattle was introduced (Bhatia, 1984; Malhotra,1988) for the first time and the culling patterns of different categories of crossbred animals were studied(Bhatia *et al*. 1992a) using the culling and retention functions (Bhatia and Malhotra, 1995a,b). Bhatia *et al*. (1992b) studied the genetic aspects of stayability(a term related to longevity of dairy animals), of animals with different proportions of exotic inheritance, through heritability and genetic correlations. In the identification of factors responsible for culling of a cow, the above studies have also made use of the various statistical properties and the form of the distribution of retention times. In another study Bhatia *et al*. (1987) used Bayes discriminatory analysis in identifying important traits influencing culling in dairy cattle. Bhatia and Muzumdar (1990a, b) conducted an interesting investigation on the association between various traits with their continuous discrete distribution mixture.

Estimation of generalized heritability

Some work on the estimation of generalized heritability was also undertaken (Lal Chand and Narain, 1991, Narain and Lal Chand, 1994). Similar studies, on growth performance of crossbred

goats were undertaken by Lal Chand *et al.* (1997, 1998b). The relationship among the various genetic groups is ascertained by plotting the second dominant root against the first root of the determinantal equation.

2.2 Repeatability estimation in biennial bearing crops

Biennial rhythm or alternate bearing tendency is quite common in perennial crops. The statistical treatment of experimental data is not straightforward when biennial trend is present, because the variance of biennial effect gets confounded with error variance. The estimation of repeatability in perennial crops is one area, which had needed intervention. Two new procedures (Wahi,1994) based on two-year moving averages were proposed and shown to be superior to conventional approaches based on ANOVA and principal components in terms of robustness to biennial disturbances. Wahi and Rao (2001) obtained the expressions for the estimates of variance of these two estimators of repeatability based on two-year moving averages in perennial crops.

2.3 Estimation of genetic correlation

Genetic correlation is one of the important genetic parameters widely used by the breeders and geneticists in the selection and improvement programs. For obtaining admissible estimates of heritability and genetic correlation from half-sib analysis Amemya (1985) proposed a procedure based on partitioning the difference of mean sum of squares and product matrices in respect of 'between sires' and 'within sires' into two components, one of which is positive definite, and using the positive definite component for getting the required estimates. Following this, Lal Chand *et al.* (1998a) determined admissible estimates of heritability and genetic correlation utilizing breeding data of Sindhi Cows on three dairy traits and further demonstrated the workability of the procedure.

Evidence in the literature shows that the estimation of genetic correlation is based on the assumption of normality of the data. Deviation from normality assumption, presence of outliers may have influence on the estimates of genetic correlation. The estimates of genetic correlation under the normal, non-normal distributions, in presence of outliers and probability of inadmissible estimates of genetic correlation have been obtained under half sib mating design [Sarika (2004); Sarika *et al.* (2006a,b)]. The bias in the estimates increases considerably in presence of outliers as compared to normal data. There was considerable decrease in standard errors and mean square errors with increase in sample size. Wahi *et al.* (2006) studied statistical properties of genetic correlation using bootstrap technique and obtained the optimum number of bootstrap replications required for estimating the variance of the genetic correlation.

3. Gene-flow Technique for Optimum Selection Strategies

In a population with overlapping generations, the gene flow approach which involves a series of matrix operations based on a matrix specifying the transfer of genes between different sex-age groups provides an exact description of selection response. This technique has been modified to include certain more realistic situations involving non-random mating and stage-structured populations (Muralidharan, 1990, Muralidharan and Jain 1992a, b, 1993, 1995). For developing the theory a 'transmittable genetic value' for an individual has been defined as the average value of its expected progeny resulting from any system of mating which is analogous to the concept of 'breeding value' defined for a random mating population. Also, the genotypic value is characterized in terms of transmittable and residual genetic values and the corresponding components of variance are derived accordingly. These variances can be

estimated by the conventional procedure based on resemblance between relatives. Sreekumar (1994) studied the genetic gain on deleting and restricting various traits in different selection strategies.

4. Crossbreeding Studies

A number of studies based on military dairy farm data have been undertaken. These studies have helped in working out the optimum level of exotic inheritance for better performance, inferring about the nature of gene action as also in determining the heterosis present. The studies also have helped in suggesting plans for evolving new dairy breeds of cattle.

Gene action and heterosis

Sharma and Narain (1986) who considered the gene action in crossbred cattle found that the poly-genes controlling the milk yield traits and age at first calving have probably significant additive and dominance effects, while dry period and calving interval have significant dominance effect only. They also introduced a simple procedure for obtaining the generation means of various crossbred generations, given the proportion of exotic inheritance for that generation. In another interesting study Narain and Sharma (1986) by defining the heterozygosity as the proportion of individuals heterozygous at one more loci gave a formula to determine heterozygosity for a given proportion of exotic inheritance. By fitting regression of various economic traits on proportion of heterozygosity / exotic inheritance, they concluded that the half-bred, which is strictly heterozygous, is optimum for stabilizing the breed resulting from Friesian x Sahiwal crosses. In a subsequent investigation (Sharma and Narain,1988) gene interaction in dairy cattle was studied. Later, Sharma and Pirchner (1991) considered the heterosis in Friesian x Sahiwal crosses. For this they derived the formulae for genetic parameters in various generation mean models in terms of the proportions of parental exotic inheritance and fitted these models to military dairy farm data.

Sharma *et al.* (2000) studied the gene action and heterosis in seven lifetime traits of Holstein-Friesian x Sahiwal crosses by fitting various genetic models to military dairy farm data. The additive-dominance model was found to be adequate for all the traits considered except 'average milk yield per day of productive life'. The heterosis measured from mid-parent varied from 15% in 'total life' to 108% in 'milk yield from all available lactations'. Heterosis measured from superior parent ranged from 6% in 'total milk yield of first three lactations' to 75% in milk yield from all available lactations'.

Explanation for curvilinear response

Although most of the crossbreeding experiments, in dairy cattle, have revealed a curvilinear relation between production and level of exotic inheritance, very little was known about the reasons behind this curvilinear response. In a couple of investigations (Prabhakaran and Sharma, 1994b; Prabhakaran, 2001) the 'fitness reversal' and Genotype x Environment interaction hypotheses of curvilinearity were tested empirically, using military dairy farm data. It was inferred that the curvilinearity is due to the fitness reversal effect of the production genes and GE interaction has nothing to do with this phenomenon.

5. Genotype by Environment Interaction

Genotype-environment interaction (GEI) and yield stability is an area of current interest. The success of crop improvement activities largely depends on the identification of superior varieties for mass propagation. 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 measurement of yield stability. Narain and Bhatia (1984a) have discussed various statistical methods for the analysis of GEI. They also discussed the usual regression approach for explaining GEI by using a non-additive model and the use of external variables to assess the environment along with the basic concepts of stability.

Inter-relationships among stability parameters

Rao (1993) and Rao and Prabhakaran(2000) established certain theoretical inter-relationships among common stability parameters. Knowledge of these relationships is useful from computational point of view as well as in knowing the theoretical basis of the observed similarity in the behaviour of various stability parameters.

Non-parametric stability measures

There is ample justification for the use of non-parametric measures in the assessment of yield stability of crop varieties. Chief advantages are: (i) No assumptions about the phenotypic observations are needed, (ii) Sensitivity to measurement errors or to outliers is much less 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, seems more relevant, (v) These measures are particularly useful in situations where parametric measures fail due to the presence of large non-linear GEI. For these reasons, non-parametric measures are widely employed in the selection of crop varieties especially when the interest lies in cross over interaction [Thennarasu,1995; Raiger, 1997, Raiger and Prabhakaran, 2000, 2001].

It is a known fact that the non-parametric methods are less powerful than their parametric counterparts. The studies conducted against this background by Raiger (1997) and Raiger and Prabhakaran(2000) have shown that when the number of genotypes in the trial is fairly large, the power efficiency of the non-parametric measures will be quite close to those of the parametric measures. So in situations, which are commonly encountered, i.e. those involving a good number of genotypes being performance-tested in a set of environments whose number is neither too small nor too large, the risk of selecting inferior genotypes from the use of non-parametric measures is minimal.

Simultaneous selection measures

Integration of stability with performance through suitable measures will go a long way in selecting high yielding, stable cultivars. Bajpai and Prabhakaran (2000), therefore, developed three new indices for selection of genotypes simultaneously for yield and stability and showed empirically that these indices were superior to Kang's (1993) rank-sum method, which has an inherent weakness that it is weighing heavily towards better yield performers, apart from the arbitrariness in the scoring procedure. Rao *et al.* (2003) and Rao and Prabhakaran (2005) developed statistical procedures based on AMMI model for selecting genotypes simultaneously for high yield and stability. They found that their indices are superior to Bajpai and Prabhakaran (2000) indices. Rao *et al.* (2004) developed two computer programmes, *viz.*, SISGYS1 and SISGYS2 for selecting genotypes simultaneously for yield and stability under genotype x environment x year and genotype x environment situations.

Stability of several traits

Another important question that has to be answered by a varietal testing programme is regarding the assessment of stability simultaneously for several traits. Since economic value of a variety is dependent on a number of traits, it is necessary that stability analysis be performed simultaneously for all the traits. The multi-trait stability analysis for these traits becomes all the more important because the response pattern of these traits might be quite dissimilar in nature and so the usual single trait analysis will not help to reconcile these contrasting assessments into a unified conclusion. Stability for several traits, inter-relationships among common stability measures and non-parametric measures, has received special attention (Balakrishnan and Jain, 1988 a, 1989b). Bajpai (1998) proposed a MANOVA procedure suitable for carrying out stability analysis for several traits simultaneously and illustrated it on Sugarcane data. The results indicated that the technique would be quite useful whenever the GE interaction is largely linear.

Study of crop yield stability

Detection of GE interaction and analysis of yield stability are essential steps in selecting promising crop varieties for large-scale propagation. Various aspects of GE interaction in vegetable crops were considered by Balakrishnan (1986), Balakrishnan and Jain (1988a,b), Balkrishnan *et al.* (1989a,b) and Rao (1993). Broad sense heritability, useful in the selection of promising parents in vegetatively propagated crops, is estimated as a function of variance components in the analysis of variance of multi-location trial data. Rao and Prabhakaran (2001) proposed a bootstrap procedure for obtaining robust estimates of these variance components and illustrated this by computing heritability for different combinations of variety and location numbers. In an empirical investigation on non-linear genotype x environment interactions (Rao and Prabhakaran 2002), the procedures of two-phase regression, refined two-phase regression and non-linear regression were tried on live data on vegetable crops and the strength and weakness of the procedures were brought out. They also suggested a new procedure to overcome the defects in the two-phase regression approach and the procedure was shown to be comparable with Pooni and Jinks (1980) refined two-phase regression procedure. Based on some simulation studies the need for a revisit to the stability concept of crop varieties was highlighted and in-depth study of the GE analysis for the incomplete and unbalanced data sets conducted (Bhatia, 1991a,b, 1992). Kumar (1997) proposed modified BLUP for studying genotype x environment interaction, where genotypes and g x e interaction were considered as random, under heterogeneous variance structure. It was found that accuracy of modified BLUP is more than the conventional BLUP in predicting yield of genotypes in multi-locational trials.

During the last decade new methods have been developed for studying GEI in economically important crops. The performance of different models like Additive Main effects and Multiplicative Interaction Model (AMMI) and Best Linear Unbiased Prediction Model (BLUP) is evaluated based on the "post-dictive' and predictive assessment criteria and it has been found that BLUP is at par with AMMI [Raju (2002 a,b) and Raju *et al.* (2003, 2006, 2009)]. Further he found that varietal assessment by joint regression analysis is highly unsuitable for the case involving large non-linear interactions as its performance is poor as compared to AMMI or BLUP. The ranking abilities of different stability measures have been found to be better under Expectation-Maximization-AMMI (EM-AMMI) with random environmental effects as compared to EM-AMMI and Modified EM-AMMI with fixed environmental effects. A stability

measure W $_{i(AMMI)}$ using EM-AMMI with random environments methodology is recommended to derive stability conclusions from AMMI model when some cells in two-way GEI table are missing. Also, robust and reliable measures of stability have been identified when the GEI effects are not normal (non-normal and contaminated normal distributions).

Incomplete data are primarily the result of a few genotypes having been not tested in all the environments due to various constraints like, insufficient seed, non-germination and pest and disease attack. To tackle such situations Choudhary (2006) proposed several modified AMMI procedures and compared their performance with the traditional methods for selecting genotypes for high yield and stability under incomplete genotype x environment data. Several new simultaneous selection indices under incomplete GEI data have been developed and tested for their performance in selecting genotypes for high yield and stability. Robustness of simultaneous selection indices against different levels of missing observations has been studied. Few simultaneous selection indices have been identified as robust indices even with the occurrence of 20% missing values.

6. Studies on Spatial Patterns

In field experiments the newer concept of spatial relationship among adjacent observations was also brought to the notice of researchers by using geo-statistical techniques such as variography and kriging. Using the notion of co-kriging, the influence of soil characteristics on performance of plant growth traits was illustrated (Samra *et al*. 1987, 1988a,b and 1989). Bhatia and Prasad (2005) studied data processing techniques for statistical analysis of large field variability in hilly and salt affected soil regions and developed software package *Spatial Variability and Interpolation*, which visualize the spatial variability in graphical form was developed. Programs for kriging in regular grids, with four inbuilt fitting models viz., Spherical, Gaussian, Exponential and Logarithmic were also developed.

7. Modelling of Scientific Phenomena in Plant and Animal Breeding

Discriminant and classificatory analyses

Garg *et al*. (1984) using the linear discriminant function showed that infusing exotic inheritance beyond 75% level may result in to significantly lower lactation yield coupled with an enhanced calving interval. For studying the divergence between genetic groups in crossbred cattle Jaiswal and Jain (1989, 1990) proposed genetic group indices on multiple traits under both homogeneous and heterogeneous covariance structures. Comparing the performance of different genetic groups of dairy animals based on multiple traits is likely to yield better information on the economic value of these animals as well as on the optimum level of exotic inheritance at which the crossbred have to be stabilized. Keeping this view, a number of performance indices based on repeated records of animals and linear discriminant function were developed (Lal Chand ,1988, 1990). On the basis of these indices it was concluded that 50% exotic blood is optimum from the point of overall merit of the animal.

In classificatory analysis, the use of Fisher's linear discriminant function rests on the assumption that the relevant data follow multivariate normal distribution and variance- covariance matrices of different populations are equal. These assumptions are seldom fulfilled in the case of performance data generated from crossbreeding experiments. Accordingly, in the comparison of different grades of sheep, Narain *et al*. (1991) used the linear discriminant function based on minimax procedure for classification and found

that this procedure was superior to the conventional method. This was confirmed, by Wahi and Bhatia (1995), in their study based bootstrap technique. Wahi and Kher (1991) made a comparison of different multivariate methods namely, Principal Components Analysis (PCA), Tocher's method and an iterative method of clustering based on successive reallocation of elements based on Mahalanobis D^2 statistic using multiple trait data of Gerbera and Dahlia flowers. It was observed that the clusters formed by iterative method were uniformly more homogeneous and unique as compared to the cluster obtained by the other two methods.

Dash (2007) classified seventy-seven maize (*Zea mays* L.) genotypes by 6 different clustering methods including Artificial Neural Networks (ANN) and compared them based on probability of misclassification. It was found that the performance of ANN method is the best among the six methods of clustering irrespective of the sample size and dissimilarity measures used. Wahi *et al.* (2009) compared five different classical clustering methods and found that the Ward's method performed best with least average percentage probability of misclassification followed by non-hierarchical k-means method irrespective of the sample size. Among the different distance measures used under hierarchical clustering methods, the squared Euclidian distance showed least average percentage probability of misclassification followed by city block distance.

Modelling in crop-insurance

Crop insurance is a system, which ensures the farmer that his return from the crop will not fall below a certain level in times of partial or complete failure. Although the comprehensive crop insurance scheme was introduced in the country in 1985, there was no sound methodology for working out the insurance premium as well as indemnity payable to the farmer when he suffers a loss due to crop failure. Mittal (1989) studied the statistical aspects of crop insurance on normal and transformed yields of paddy and wheat crops in Uttar Pradesh. The premium rates calculated by kernel method of estimation, which is a non-parametric method and independent of any sort of assumptions, were much lower than the normal curve technique. Further, investigations were taken up (Garg *et al.*, 1991, 1994) which were mainly concerned with density estimation for determination of indemnity and insurance premium based on the observed distribution of crop yields.

Compartmental models

Compartmental models are of immense utility in rumen fermentation studies. Keeping this in mind a few stochastic compartmental models for physiological kinetics in animal nutrition were developed by Rana and Narain (1992).

Growth models

Sarkar (1998) compared different mathematical models, viz., Wood's model, Morant-Ganasakthy model and Mitscherlich exponential model, for describing lactation yield of cross bred cattle and found that Morant-Ganasakthy model was found to be best among the three and explained maximum variation in lactation-yield. Thus, it can be used by the dairy farm manager and animal breeders. Kolluru (2000) studied growth patterns of cross bred cattle using five different non-linear growth models. They found that Richard's and Logistic models are suitable and equally good to explain the growth patterns in cross bred cattle. Lal Chand *et al.* (2002) and Wahi *et al.* (2004) applied non-linear models to study the growth pattern in Indian breeds of goats and it was found that Gompertz model showed best fit among different

non-linear models. Growth studies serve as an aid in assessing the maximum production potential of livestock. Kundu (2005) has estimated heritability and genetic correlation for the body-weight data of pig species and estimated growth curve parameters (logistic) using full sib mixed model and half sib mixed model considering sex as fixed effect. Based on the estimate of inflection parameter the logistic model was found to be best fitted for growth curves.

8. Statistical Genomics and Bioinformatics

Sire evaluation under MOET

In the past the statistical analysis of breeding data was handicapped due to non-availability of sufficient amount of data. This constraint having been removed under Molecular Ovulation and Embryo Transfer (MOET) technology, the current need is of efficient statistical analysis of data generated under these programmes. As a preliminary initiative in this direction, Sethi and Jain (1993a, b, 1994) examined the merits of sire evaluation based on multiple traits and partial records and proposed procedures suitable under MOET technology.

Classification of genotypes using RAPD and DNA finger prints

Random Amplified Polymorphic DNA (RAPD) analyses and Amplified Fragment Length Polymorphic DNA (AFLP) analyses, in particular, has been shown to reveal a significant level of DNA polymorphisms in different plant species. These methods are useful for effective germplasm management with respect to estimating diversity, monitoring genetic erosion and removing duplicates from germplasm collections. Notwithstanding the problem of non-reproducibility, these techniques have greater resolving power than the morphological characteristics. Thomas *et al.* (2006) studied the classification of Indian wheat varieties using RAPD based DNA finger prints as well as morphological characters. Kolluru (2006) and Kolluru *et al.* (2007) developed a method to identify a suitable clustering procedure, which could accurately classify sugarcane cultivars, when the AFLP marker data contain missing observations. Among different clustering methods available, fuzzy based clustering technique was identified as the best method to classify AFLP marker based data. Determination of optimum number of markers and their identification by retaining the maximum variability present in the data is a challenging issue. Nearly 35 STMS markers (optimum number) are required for studying the genetic diversity in rice, while retaining the maximum precision in Genetic Distance. Estimation of the standard error of correlation of molecular diversity (Φ_{ST}) in AMOVA (Analysis of molecular variance) has been dealt by bootstrap technique and percentage significance of Φ_{ST}. The estimation of Φ_{ST} is also done by DNA marker site sampling technique.

Detection of quantitative trait loci

Quantitative traits are the traits controlled by many genes and each of the genes has a small effect on the trait. The loci controlling quantitative traits are referred to as QTLs (Quantitative Trait Loci) and the procedure of finding and locating the QTLs are called QTL mapping. During past two decades, molecular approaches have advanced in the identification, mapping and isolation of genes for various crop species. Jambhulkar (2007) examined the inheritance of traits by using molecular genetics and gene mapping techniques. Further, quantitative traits are influenced by the environment and tend to show varied degree of QTL×Environment Interaction (QEI). The results on QTL detection have been obtained by considering the main-effect markers and interaction between markers in the model. The results reveal that Jackknife

procedure and Bayesian methodology have been performed better over traditional procedures of QTL detection even in the presence of QEI.

Bioinformatics

World agriculture achieved a major boost with the completion of the rice genome sequencing in December 2004. Rice is the most important food source for half the world's population. It is the first crop plant to be sequenced and will, therefore, have a great impact in agriculture. The accurate, map based sequence has already led to the identification of genes responsible for agronomically important traits such as genes that affect growth habit to promote yield and photoperiod genes to extend the range of elite cultivars. This could probably provide the key in improving yield to feed an expanding world population at a time of increasing constraints on agriculture. The entire rice genome sequence is available in public domain. Recently, a project on "Computational analysis of SNPs at functional elements of rice genome" has been taken up at the institute in collaboration with National Research Centre for Plant Biotechnology (NRCPB), New Delhi with the objectives (i) to develop a web based information system on functional elements of rice genome (ii) to design and develop a database on SNPs at functional elements of rice genome (iii) to provide online computational facilities to the users engaged in genomic data analysis and (iv) to annotate SNPs in different features of genome through visual graphic display.

The distribution and function of SNPs is an important area of current research in rice genomics. SNPs are useful for genome wide mapping and study of genes responsible for diseases. As the number of SNPs in public databases continues to grow, identifying functional variants has become an important goal of rice genomics. SNPs can alter the function of DNA, RNA and Proteins, and are generally classed by genome location. Efforts are being made at the institute to locate / predict variations that are likely to have effects on functions of different features of genome. Also, it is being tried to develop a local database and information system on functional elements of rice genome

The sequenced genomes of a wide range of organisms, *viz.*, *C. elegans*, *D. melanogaster*, *A. thaliana*, *M. musculus*, *H. sapiens* allow global, comparative analyses of regulatory sequences. The genomic set of splice-site sequences corresponds to a large-scale splicing experiment performed by nature under evolutionary constraints. Roca *et al.* (2008) focused on 5' splice-site (5_ss) sequences of the U2-type GT-AG class, which comprise over 98% of all splice sites, and use disease-causing mutations, human single nucleotide polymorphisms (SNPs), and variations in natural splice sites in the genome (within and between species) to infer properties inherent to 5_ss, with important implications for human genetics. Recently at the institute level, efforts are being made to study the characteristic features of 5' splice sites of rice genome and compare them with other species.

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