

Sources of Variation in Participatory Varietal Selection Trials with Rainfed Rice: Implications for the Design of Mother-Baby Trial Networks

GARY ATLIN, THELMA PARIS, AND BRIGITTE COURTOIS

Abstract

Little information has been published on the repeatability of participatory varietal selection (PVS) trials. Repeatability estimates, which can be derived from the combined analysis of trials over locations and years, are useful for determining the number of replications and the optimal blocking structure of PVS trials. Variance components were estimated from a series of upland and lowland PVS trials conducted in the states of Jharkand and Bihar in eastern India, and used to estimate the repeatability of means. In both sets of trials the cultivar \times site \times year variance component was larger than the cultivar \times site component, indicating that there was little specific adaptation to sites within the trials series. Participatory varietal trials conducted on-farm under farmer management were quite repeatable; replication over 5 sites was predicted to result in a repeatability of more than 0.5 in both data sets. Simulation indicated that a modest benefit is likely from the use of alpha-lattice designs when among-farm variances are large in experiments conducted using the mother-baby design, which treats farms as incomplete blocks.

Introduction

Breeders of rainfed rice in eastern India recognize the need to introduce participatory methods into their variety testing systems to improve the effectiveness of breeding programs. Performance in farmers' fields and in the breeder's nursery can be thought of as correlated traits expressed by a single genotype in separate environments.

Theory developed by Falconer (1989) and extended to the analysis of plant breeding programs by Pederson and Rathjen (1981) and Atlin and Frey (1989; 1990) permits breeding strategies to be evaluated on the basis of the predicted response in the target environment resulting from selection conducted in a breeding nursery. When selection is among pure lines, this response may be modeled using the formula:

$$CR_T = i_s r_G \sqrt{H_s H_T} \sigma_P \quad (1)$$

where CR_T is the correlated response in the target environment (farmers' fields) to selection in a breeding nursery; i_s is the standardized selection differential applied in the selection nursery; r_G is the genotypic correlation between cultivar yields in the selection and target environments; H_s and H_T are repeatabilities or broad-sense heritabilities in the selection and target environments, respectively; and σ_P is the phenotypic standard deviation in the target environment. When response is being predicted for a particular target environment, H_T and σ_P may be considered constants. Therefore:

$$CR_T \propto i_s r_G \sqrt{H_s} \quad (2)$$

Inspection of this relationship indicates three important considerations for designing breeding programs for stress environments:

1. i_s must be maximized by screening large populations, permitting a high selection intensity to be achieved.
2. r_G (or accuracy) must be maximized by ensuring that performance in the selection environment or screening system is highly predictive of performance in the target stress environments.
3. A high level of H_s (or precision) must be achieved, typically through replicated screening.

One reason for the poor performance characterizing many conventional rainfed rice breeding programs is that the research conditions are not reflective of on-farm conditions; in other words, r_G is low. In participatory varietal selection (PVS) programs, the genetic correlation

between performance in the selection and target environments is very high, since selection is conducted in farmers' fields (Atlin et al. 2001). Therefore, the main factor affecting response to PVS in programs of a particular size is H_s . However, the scale and design of PVS schemes needed to achieve acceptable H_s levels is unknown, because no information has been published on the extent of farm to farm variation in cultivar performance in PVS experiments. Variance component estimates from the analysis of PVS trials over locations and years can be used to estimate H of means for grain yield and other agronomic characteristics resulting from a given number of sites and years of testing. These estimates can be used to determine the scale of testing needed to achieve adequate precision from PVS trials and the best method of analysis for PVS programs using the mother-baby model, which treats individual farms as incomplete blocks.

The International Rice Research Institute (IRRI) has conducted PVS trials in rainfed rice over three years in several villages in eastern India. The original objective of these experiments was to compare varietal rankings within and among groups of farmers and breeders (Courtois et al. 2001), but the trials also provide information on the sources of variation for agronomic traits in PVS trials conducted with rainfed rice. This report presents variance components estimated from the combined analysis of on-farm PVS trials over farms and years in two regions in eastern India and their use in estimating the repeatability of means from rainfed rice PVS trials. The implications of these estimates for the design of mother-baby trial networks are considered.

Mother-baby PVS trial networks are now being planned or implemented by several research groups in India. The mother-baby design has two components: the mother trial, in which a complete set of cultivars is evaluated in replicated researcher-managed trials at several locations; and the baby trials, wherein farmers each evaluate a subset of the cultivars tested in the mother trial. Villages and farms within villages may be considered separate blocking strata within a mother-baby trial. Variation in mean yield among farms within villages is expected to be substantial. This variation contributes to the variance of cultivar means when farms are used as incomplete blocks, and can be controlled to some extent by designs that control within-block variation, such as the alpha-lattice design. In establishing these trials, we have found that the lack of easily accessible software for the analysis of alpha-lattice designs is a serious constraint. Sets of baby trials may be analyzed as randomized-complete-block (RCB) design or completely randomized designs, but if among-farm variance is large, losses of precision resulting from selecting on the basis of unadjusted cultivar means are likely to be great. To test this hypothesis, a simulation exercise was also conducted to examine the impact of yield variation among villages and among farms within villages on the relative effectiveness of alpha-lattice and RCB design analyses.

Methods

Variance component estimation in participatory varietal selection trials in rainfed rice. Participatory variety selection trials were conducted under farmer management in three eastern Indian districts in 1997-2000. Upland cultivar trials were conducted in three villages in southern Bihar (now Jharkand) in collaboration with the Central Upland Rice Research Station (CRURRS), Hazaribag. Lowland PVS trials were conducted in collaboration with Rajendra Agricultural University (RAU), Pusa, Bihar. In each set, several varieties were evaluated in unreplicated trials on three or four farms over at least two years. Details of the trials are presented in Table 1; however, they are more completely described by Courtois et al. (2001). Grain yield data were analyzed using the REML algorithm of SAS PROC VARCOMP with a cross-classified model, with cultivars, farms, and years as random factors. Broad-sense heritability or repeatability (H) was estimated as:

$$H = \sigma_G^2 / \{\sigma_G^2 + (\sigma_{GL}^2/l) + (\sigma_{GY}^2/y) + (\sigma_{GLY}^2/ly)\} \quad (1)$$

where σ_G^2 , σ_{GL}^2 , σ_{GY}^2 , and σ_{GLY}^2 are the genotype, genotype x location, genotype x year, and genotype x location x year variance components, respectively, and l and y are the number of locations and

Table 1. Description of participatory varietal selection trials in eastern India.

Location	Cooperating institution†	Ecosystem	No. of years	No. of locations	No. of genotypes	Mean yield (t/ha)
Hazaribag	CRURRS	Upland	3	3	12	1.96
Pusa	RAU	Lowland	2	3	9	4.21

† CRURRS = Central Upland Rice Research Station; RAU = Rajendra Agricultural University.

the number of years, respectively. It should be noted that when estimated from unreplicated trials, the σ^2_{GLY} component also contains the within-trial plot error or residual variance.

Simulating the predictive power of mother-baby trials analyzed as randomized-complete-block versus alpha-lattice designs

A simulation was conducted using the following model:

$$P_{ijklm} = M + Y_i + V_j + YV_{ij} + F(YV)_{k(ij)} + G_l + GY_{li} + GV_{lj} + GYV_{lij} + e_{ijklm} \quad (1)$$

where:

P_{ijklm} = the measurement on a plot containing genotype l on farm k in village j in year i

M = the overall mean of the trials

Y_i = the effect of year i

V_j = the effect of village j

YV_{ij} = the interaction between year i and village j

$F(YV)_{k(ij)}$ = the interaction between year i and village j and farm k

G_l = the effect of genotype l

GY_{li} = the interaction between genotype l and year i

GV_{lj} = the interaction between genotype l and village j

GYV_{lij} = the interaction between genotype l , year i , and village j

e_{ijklm} = the within-village residual

random in the model. An overall mean (M) of 2.2 t/ha was assumed. Effects were generated with the SAS RANNOR function, using the appropriate variance components as function arguments. Variance components used in the simulation were taken from the literature or from analyses of rice variety trial data available at IRRI.

Three scenarios were identified regarding the relative magnitudes of the GYV and F(GYV) variances. In one scenario, there was little variation among farms within villages in mean yield, but considerable variation across villages. In another scenario, there was little variation among farms within villages, but substantial mean yield differences among villages. In the third, variance among villages and among farms within villages was approximately equal in magnitude. (It should be noted that other estimates might lead to different simulation results.) The variance components used in the simulation (listed below) are based on estimates derived from the combined analysis of the Philippine Upland Rice National Cultivar Trials for 1997-99:

$$\sigma^2_Y = 2700$$

$$\sigma^2_V = 5000$$

$$\sigma^2_{YV} = 800000 \text{ or } 500000 \text{ or } 200000$$

$$\sigma^2_{F(YV)} = 200000 \text{ or } 500000 \text{ or } 200000$$

$$\sigma^2_G = 44600$$

$$\sigma^2_{GY} = 39000$$

$$\sigma^2_{GV} = 5000$$

$$\sigma^2_{GYV} = 300000$$

$$\sigma^2_e = 100000$$

s

The SAS program was used to simulate values for P , assuming all factors

Single-replicate PVS trials testing a set of 16 cultivars in 3, 5, or 10 villages were simulated, with 4 cultivars per block. Alpha-lattice designs generated

by the Alphagen program were used. Cultivar means over villages and farms were calculated in three ways:

1. Raw means were calculated over all villages and farms.
2. Data were standardized within farms and then means were calculated over farms and villages.
3. Means adjusted for lattice incomplete block effects were calculated using the REML option of SAS PROC MIXED, with genotypes considered fixed and all other effects random.

The simulation for each of the 9 conditions (3 experiment sizes x 3 estimators of variety means) was replicated 10 times. For each run, the correlation between simulated genotypic values and simulated cultivar mean yields was calculated. This correlation, equivalent to the square root of the heritability of cultivar means, is an easily understood measure of the repeatability of cultivar trials, and is more directly related to their predictive power than is the variance of cultivar means.

Results and Discussion

Variance component estimation in participatory varietal selection trials in rainfed rice

Variance components are presented in Table 2. The relative magnitude of these components varied greatly from trial to

trial. For the upland target environment (TE), site variance was the largest component, reflecting the large range in soil quality among sites. For the Pusa rainfed lowland TE, year to year variances were large. Cultivar effects were significant in two of the three TEs. Cultivar x year interactions were small for all three TEs. Cultivar x site interactions were also relatively small for all three TEs, indicating that cultivars responded similarly across sites within TEs. The residual error for the combined analysis, which contains both the cultivar x year x site and within-site residuals, was large in all cases, indicating that within-site soil heterogeneity and/or random variation in cultivar ranking among sites and years were the most important sources of noise in the trials.

Using the variance components in Table 2, repeatability estimates were calculated for means estimated from 1, 2, 5, or 10 trials for the 2 trial sets in which genotypic variation for grain yield was significant (Table 3). In both cases, means estimated from a single trial had very low repeatability. Replication over 5 sites increased predicted repeatability to more than 0.5 in both data sets.

In summary, these experiments indicate that specific adaptation to sites within the TEs served by the CRURRS and RAU breeding programs appears to be limited. Site to site and year to year variability among PVS trials was large,

Table 2. Variance component estimates from participatory varietal selection trials in eastern India.

Location	σ^2_Y	σ^2_L	σ^2_{YL}	σ^2_G	σ^2_{GY}	σ^2_{GL}	σ^2_{GLY}
Hazaribag	0.02	1.03	0.00	0.13	0.00	0.04	0.29
Pusa	1.36	0.13	0.08	0.20	0.15	0.01	0.20

but rank changes across sites were limited. Replication of trials over 3-5 sites or farms may be sufficient to achieve useful levels of repeatability in PVS trials.

Simulating the predictive power of mother-baby trials analyzed as randomized-complete-block versus alpha-lattice designs

The results of the simulation are presented in Table 4. For trials comprising 3 village replicates, the correlation between genotype value and cultivar means estimated from lattice-adjusted data ranged from 0.45 to 0.51. The correlation increased to

Table 3. Predicted repeatability (H) of cultivar means estimated from 1, 2, 5, or 10 unreplicated on-farm trials conducted in a single season in eastern India.

Location	H			
	1 site	2 sites	5 sites	10 sites
Hazaribag	0.28	0.44	0.66	0.80
Pusa	0.36	0.44	0.51	0.54

Table 4. The effect of trial number, method of estimating means, and the ratio $\sigma^2_{VY}:\sigma^2_{F(VY)}$ on the correlation between genotypic and phenotypic values in simulated mother-baby trials, eastern India.

No. of trials	$\sigma^2_{VY}:\sigma^2_{F(VY)}$	Estimation method		
		Raw means	Standardized means	Lattice-adjusted means
		r	r	r
3	4:1	0.43	0.39	0.45
	1:1	0.37	0.48	0.48
	1:4	0.38	0.46	0.51
5	4:1	0.57	0.56	0.64
	1:1	0.63	0.69	0.72
	1:4	0.61	0.58	0.63
10	4:1	0.54	0.60	0.64
	1:1	0.59	0.64	0.67
	1:4	0.63	0.62	0.67

approximately 0.6 when the number of village replicates increased from 3 to 5, but no increase was observed from increasing the number of villages from 5 to 10. If the variances used in this simulation are representative of rainfed rice trials in eastern India, mother-baby networks consisting of as few as 3-5 village replicates may be adequate for progress from PVS to be made. For all three ratios of $\sigma^2_{VY}:\sigma^2_{F(VY)}$ and all trial sizes, the correlation between genotypic value and the means estimated from trials was greater for lattice-adjusted means than for raw means. Standardization within farms did not consistently improve the relationship between phenotypic and genotypic value. The increase in selection response resulting from the use of lattice designs is expected to be approximately $r_{\text{lattice}}/r_{\text{raw}}$, where r_{lattice} is the correlation between genotypic value and cultivar means estimated with lattice adjustment, and r_{raw} is the correlation for raw means. This ratio is roughly equal to the selection responses that can be expected from lattice adjustment, relative to the analysis of raw means. $r_{\text{lattice}}/r_{\text{raw}}$ was approximately 1.1-1.3 for all simulations, indicating that lattice adjustment may be advantageous even when the number of village replicates is quite large if there is considerable variation in the mean yields of farms.

Conclusions

Participatory varietal selection trials produce repeatable estimates of rainfed rice cultivar means. In the experience of the authors, the repeatability of grain yield estimates from the farmer managed trials was not markedly lower

than for on-station trials. It was also found that rainfed rice PVS trials conducted using the mother-baby model generate estimates of cultivar mean yields with useful precision from testing as few as five farms per cultivar. Random cultivar \times site \times year interaction was the most important source of genotype \times environment interaction (GEI) in eastern Indian rainfed rice. There was no evidence of village-specific adaptation. This is consistent with on-station research on GEI in rainfed rice, which also indicates that cultivar \times site \times year variances are the largest GEI component. Cultivar \times site interactions appear to be rare across sites at similar levels in the toposequence and within geographic regions of the scale served by the CRURRS and RAU breeding programs. The effect of the large cultivar \times site \times year component of the phenotypic variance can be reduced, and H concomitantly increased, by increasing the number of sites and years of testing. Because small rainfed rice breeding programs often cannot easily increase the number of sites they handle, they should consider replication over years to increase the precision of variety trials.

If variance among farms within villages is large, simulation indicates that the alpha-lattice designs can significantly increase repeatability. Standardization within farms was not effective in increasing precision. Freely available, easy to use software for the generation and analysis of alpha-lattice designs is needed by researchers from national agricultural research programs if the mother-baby design is to be widely and effectively adopted.

References

- Atlin, G.N., M. Cooper, and Å. Bjørnstad. 2001. A comparison of formal and participatory breeding approaches using selection theory. *Euphytica* 122:463-475.
- Atlin, G.N., and K.J. Frey. 1989. Breeding crop varieties for low-input agriculture. *American Journal of Alternative Agriculture* 4:53-57.
- Atlin, G.N., and K.J. Frey. 1990. Selecting oat lines for yield in low-productivity environments. *Crop Science* 30:556-561.
- Courtois, B., B. Bartholome, D. Chaudhary, G. McLaren, C.H. Mishra, N.P. Mandal, S. Pandey, T. Paris, C. Piggan, K. Prasad, A.T. Roy, R.K. Sahu, V.N. Sahu, S. Sarkarung, S.K. Sharma, A. Singh, H.N. Singh, O.N. Singh, N.K. Singh, R.K. Singh, R.K. Singh, S. Singh, P.K. Sinha, B.V.S. Sisodia, and R.Thakur. 2001. Comparing farmers and breeders rankings in varietal selection for low-input environments: a case study of rainfed rice in eastern India. *Euphytica* 122(3): 537-550.
- Falconer, D.S. 1989. *Introduction to quantitative genetics*. 3rd Ed. London: Longman.
- Pederson, D.G., and A.J. Rathjen. 1981. Choosing trial sites to maximize selection response for grain yield in spring wheat. *Australian Journal of Agricultural Research* 32:411-424.

Discussion Summary

The discussion dealt with the analysis of incomplete designs and the feasibility of obtaining data and its accuracy in participatory varietal selection (PVS) trials. It was pointed out that there are several incomplete designs and the alpha-lattice design is not always needed. In response to this, the author said that trials are samples of environments; once sampling is effective and frequent enough, data adjustment becomes less important.

Obtaining yield data from baby trials is not trivial. It is easier to obtain yield data from mother trials; however, baby trials are particularly effective for identifying farmers' perceptions and assessments. Researchers in nongovernmental organizations are capable of obtaining appropriate data, but development workers generally are not. It is valuable to know the farm to farm variability for ranking of cultivars and variance components. In the eastern India case study, it was pointed out that special arrangements had to be made to enable station staff to attend the harvest of the baby trials. These arrangements included a car, a moisture meter, and other items. Additional people were hired as well. The logistical difficulties of obtaining yield data from baby trials may limit the ability of some programs to secure quality data.