A simple quantitative method to judge the need of participatory plant breeding programme

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Abstract

Participatory plant breeding (PPB) in field crops like rice is gaining rapid attention and importance in modern crop improvement programme to minimize the gap between potential and realized yield in farmers' field. However, as the process is location specific and resource intensive, utility of this method should be tested before investing in such a venture. A group of rice farmers from Terai region of West Bengal were involved in developing a method for justification of initiating a participatory plant breeding programme. Weighted response matrices were constructed according to farmers' and breeders' choices of traits and were further partitioned into more and less important traits. Distance relationship of the matrices revealed that the attribute preferences differ considerably between farmers and breeders, which justify the need of location specific test for PPB. Results indicated moderate deviation between farmers' and breeders selection preferences. Based on the findings, a method is proposed to judge the need of PPB in a specific location.

Key words : PPB, matrix ranking method, rice, group distance

Introduction

Rice is grown in 122 countries as a major food crop providing nourishment to more than half of the world population. India ranks 2nd in rice production being next to China with an annual production of 91 million tons. To feed the ever-increasing population, requirement of rice in India would be 128 million tones by 2012 [1].

Apart from diverse ecological system and poor livelihood of rice farmers, yield gap between farmers' field and potential yield is a major bottleneck in realization of high productivity. Average national productivity of rice in India is around two tons per hectare, although production potential of several national check varieties are over six tons per hectare. Participatory plant breeding (PPB) involving breeders and farmers that aims to develop improved genotypes exploiting farmers' rich heritage of agricultural expertise is a new effective approach in bridging yield gap [2]. The method helps to identify genotypes suited to farmers' need as well as accelerates adoption of new improved genotypes in the farming community.

It has been recently observed that varietal selection involving PPB has become integral component of many national and international plant breeding programmes. While the benefit of PPB is well established from different field trials and on-farm experiments, few approaches have considered the scientific reasoning, basis and methodologies of such experiments [3, 4]. As PPB is a region specific operation suited to the need of local farming community and agro-climatic conditions, the approaches and methodologies have differed in various reports [5, 6, 7]. Although PPB provides reliable output, involving farmers for selection in several segregating populations each comprising of large population is a time consuming and input intensive process. Before attempting such venture it is worthwhile to quantify the difference between farmers' preferences and breeders' criteria for selecting genotypes. If this difference is significantly large, PPB should be aimed to improve productivity at farmers' field. However, if there is little difference between these two criteria, PPB would result in little improvement in performance. In the present discussion we have tried to provide a simpler method to understand quantitatively the difference between breeders' and farmers' objectives which, in course will dictate the need and utility of PPB.

Materials and methods

Twentyfive respondent farmers representing diverse socio-economic status, age, literacy and adaptiveness were selected through random sampling from a list of rice growers from three different regions of the state of West Bengal of India to evaluate twelve rice genotypes in kharif (rainy season) 2005. The rice varieties comprised of early maturing genotypes with advanced breeding lines, released standard varieties and locally preferred medium duration genotypes. A guestionnaire consisting eighteen attributes related to plant characters were provided to the farmers for evaluation (Table 1). Each attribute consisted of three options, each of which was assigned a score 1, 2 or 3 (bad, medium or good, respectively) according to the preference of the farmer. Direct matrix ranking method was followed to construct respective matrices. Farmers were also asked to rank the characters according to their preference in a continuous 0-10 scale. Each weight was averaged over farmers, converted to 0-1 scale and multiplied to average value in the farmers' preference matrix (12 genotypes x 18 questions). Similarly a group of qualified plant breeders were also requested to assign weights on a 0-1 scale to these questionnaires according to their importance following similar procedures. It was observed from farmers' response that out of eighteen attributes only eight obtained > 0.5 weights. These were considered as more important and the rest ten were marked as less important attributes.

Construction of response matrix

Let us consider response of each farmer as a matrix \mathbf{M}_{ij} (i = 1, ..., n,; j = 1, ..., m, n = number of genotypes, m = number of attributes). After construction of twenty five such matrices a final matrix \mathbf{Z}_{ik} (i = 1, ..., n,; k = 1, ..., p, p = number of farmers) was developed by adding individual components of these matrices. Four modified matrices were constructed from \mathbf{Z}_{ik} based on breeders' weight for all attributes, farmers' weight for all attributes, farmers' weight for all attributes, farmers' weight for eight attributes of higher importance and farmers' weight for ten attributes of lower importance by taking average score over number of questions. These matrices were defined as $X_1 = (X_{ik}^{(1)}), X_2 = (X_{ik}^{(2)}), n \times p$

$$X_3 = (X_{ik}^{(3)})$$
, and $X_4 = (X_{ik}^{(4)})$, respectively.
nxp n x p

We define x_{ik} , the element of *ith* row and *kth* column for each matrix as the mean score of attributes of *ith* genotype for *kth* farmer by

$$i = 1, ..., n$$

$$x_{ik} = (\Sigma) W_{j}U_{ij} / m \qquad j = 1, ..., m$$

$$k = 1, ..., p$$
where, W_{j} = weight of the U_{ij} = 1
jth attribute and = 2
= 3 attribute.

Squared distances (Mahalanobis's D^2) between each matrix were worked out to quantify the differences among the matrices. Significance of D^2 was tested using F-test.

Two vectors \mathbf{Y}_1 and \mathbf{Y}_2 were constructed by summing the row-wise elements of matrix \mathbf{X}_1 and \mathbf{X}_2 , respectively that represented the total genotypic scores using breeders' weight and farmers' weight. To find out the mathematical measure of the average relationship between these two vectors, which is indicative of breeder-farmer preference relationships, different statistical models were fitted. The coefficient of determination (\mathbf{R}^2) values were calculated for each fit to find out the best fitted model. Significance of R values was tested by t-test.

Result and discussion

Farmers' preference matrix has been used previously to screen acceptability of rice varieties using participatory approach [8]. In this work, twelve genotypes were studied and response matrices were developed using both farmers' and breeders' ranking as weight (Tables 2 and 3). An overall mean of 371.38 was observed in farmers' response matrix, while the value was 435.71 in breeders' matrix. Significant differences were observed between the total scores obtained for each genotype under both the rankings (t = 14.82, p < 0.01). Genotype Rewa 606 ranked first under both the matrices with scores 422.06 and 481.80 in farmers' and breeders' matrices, respectively. On the other hand, RR 363-152 stood last in both systems with values 311.27 and 396.40, respectively (Tables 2 and 3). However, ranking of other genotypes varied considerably between both the systems (Table 4). Locally cultivated standard genotype Heera was marked second by farmers and fourth by the breeders' weight.

Distances calculated among the four matrices were found to be significantly different from each other. The group distance of X_1 from X_2 , X_3 and X_4 were 20.89, 47.95 and 212.96, respectively indicating breeders' and farmers' matrix were more closely related than the other groups (Table 5). \mathbf{X}_{2} differed from \mathbf{X}_{2} and \mathbf{X}_{4} by 113.47 and 138.67, respectively while distance between X₂ and X_4 was 348.62. Higher D² value between X_1 and X_3 than that of X, and X, indicated that the farmers do not share the same view as breeders towards importance of selection attributes. Some of the characters considered important by the farmers are given least preference by breeder while selecting genotypes. For example, attribute 4 indicating flag leaf angle was given little importance by farmers (weight 0.065), while in breeders' consideration the attribute got higher importance (0.5) due to scientific perception. On the other hand attribute 13 (grain size) was considered highly important by the farmers (weight 0.8) but received moderate weight from the breeders (weight 0.5). It thus revealed that the attribute preferences differed considerably between farmers and breeders in this particular agro-climatic situation, which justified the need of PPB for rice in this region. The comparison of weights also brings out that while involving farmers in PPB, their selection criteria should be critically examined to filter out some unimportant attributes (Table 1). It is expected that a mixed selection criteria involving both breeders' and farmers' preference will intermingle scientific reasoning and age-old experience and would be more helpful in breeding crop varieties to reduce yield gap. Atlin *et al.* [2] suggested that PPB is advantageous over formal plant breeding under marginal low input environments, as correlation between selection and target environments is maximized in this system, but provided no comparable measures to visualize the differences of formal plant breeding and PPB and also suggested that a synthesis of these two systems are necessary to maximize gain from plant breeding.

Fitting different models between breeders' weight and farmers' weight over all characters, six best fit regression models were obtained with high coefficient of determination (Table 6). Of these, the cubic model was most efficient to explain their relationships as observed from its highest R² value. Developing such model has unique advantage that farmers' selection criteria in further plant breeding programme can be realized even without involving farmers and rigorous and resource intensive exercise in each segregating generation may be avoided. Further research would

Table 1. Information requested from selected group of farmers during evaluation of genotypes

Question no.	Characters screened/ related to	Farmers' weight	Breeders weight
1	Plant height (by visual inspection)	0.28	0.32
2	Number of tillers per plant (by counting)	0.65	0.60
3	Number of bearing tillers per plant (by counting)	0.80	0.71
4	Angle of flag leaf (visual inspection)	0.06	0.50
5	Tolerance to pests (Gall midge, Leaf folder)	0.45	0.63
6	Tolerance to diseases (Blast, Bacterial blight)	0.35	0.62
7	Length of panicle (visual inspection)	0.65	0.70
8	Adaptability to region under irrigated ecosystem (Farmers' experience	e) 0.28	0.20
9	Comparison with locally popular genotype	0.65	0.32
10	Tendency to lodge (by visual and feel)	0.05	0.51
11	Number of grains per panicle (visual inspection)	0.60	0.30
12	Per cent filled grains (visual inspection)	0.65	0.70
13	Grain size (visual inspection)	0.80	0.50
14	Grain colour (light yellow, golden yellow, brown)	0.18	0.14
15	Yield (visual estimation)	1.00	0.90
16	Shattering habit (by thrashing individual panicle)	0.24	0.50
17	Palatability of straw as animal feed (by feeling straw)	0.14	0.42
18	Chance of viviparous germination (visual observation)	0.06	0.30

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Table 2.	

Genotype						Fa	rmers						
	-	0	в	4	5	9	7	8	6	10	11	12	13
RBU 9616	14.76	13.70	14.45	12.05	18.62	12.41	13.73	14.50	17.92	14.55	14.72	17.12	13.35
Rewa 422-2	15.19	15.78	17.97	11.87	17.83	13.16	13.74	15.66	12.88	16.58	14.80	16.88	16.37
Rewa 606	16.64	15.71	14.19	16.91	12.70	17.73	17.16	17.42	18.78	16.88	14.01	16.57	19.45
PNR 555-30-15-1	14.31	16.72	14.08	15.10	15.24	14.53	15.46	15.19	15.44	14.16	13.74	14.27	16.23
PNR 570-15-10	15.45	13.36	14.47	12.42	13.32	12.22	13.51	13.03	13.27	14.27	13.98	17.25	19.17
RR 347-2	17.00	15.06	15.64	14.93	16.57	15.06	16.85	15.11	15.46	21.79	15.02	17.04	19.10
Aditya	15.85	14.19	15.78	12.38	17.96	14.37	16.06	14.73	14.31	17.70	14.09	16.29	13.79
RR 363-152	14.27	12.01	10.52	11.90	12.34	13.15	12.70	14.43	14.07	14.01	12.23	13.76	10.39
OR 2058-3	17.22	15.02	12.82	10.95	14.39	12.97	15.11	16.56	14.39	13.92	15.35	17.49	15.28
OR 2085-12	16.80	16.85	16.75	12.59	18.98	16.02	16.12	15.64	16.64	14.71	16.38	17.25	16.78
Heera	16.79	13.71	16.77	14.88	18.55	12.59	15.62	15.86	16.92	20.83	15.51	16.14	18.32
CN 915-20-2-3	17.10	12.74	13.86	11.84	18.28	11.16	10.80	14.48	12.40	13.51	13.36	16.62	19.34
Genotype						Fa	rmers						
	14	15	16	17	18	19	20	21	22	23	24	25	Total
RBU 9616	12.55	14.71	14.32	12.86	13.80	12.84	13.49	14.16	15.14	13.50	18.13	17.48	364.85
Rewa 422-2	13.95	12.70	12.70	13.31	13.24	13.13	13.13	14.02	14.26	18.00	14.66	14.66	366.39
Rewa 606	15.91	19.05	20.51	17.20	15.97	18.35	18.35	13.80	16.40	14.2	18.85	19.41	422.06
PNR 555-30-15-1	12.94	17.72	16.45	15.84	11.66	13.70	13.70	12.40	14.02	13.00	11.88	12.48	360.18
PNR 570-15-10	15.51	16.69	14.51	17.68	14.65	14.82	14.82	15.62	10.96	11.10	12.75	12.75	357.57
RR 347-2	16.32	18.55	18.55	14.04	16.41	14.33	15.38	12.61	13.55	15.30	16.05	15.22	400.90
Aditya	14.21	12.72	13.12	14.30	13.64	12.97	12.37	12.66	14.35	14.90	14.13	14.36	361.21
RR 363-152	12.53	12.14	12.14	11.69	10.35	11.50	11.40	14.52	11.69	9.38	13.78	14.43	311.27
OR 2058-3	14.39	13.79	12.99	12.20	14.85	14.17	14.62	14.54	14.53	12.20	13.07	12.23	354.93
OR 2085-12	15.26	18.09	15.17	16.34	15.74	15.55	16.55	16.15	16.51	17.00	15.30	15.12	404.26
Heera	14.39	15.87	16.73	15.27	14.13	17.08	17.08	15.71	16.35	16.40	17.62	16.22	405.30
CN 915-20-2-3	13.31	16.11	11.28	14.00	13.20	14.51	13.51	16.53	14.47	13.30	10.61	11.32	347.63
											- - -	Mean t-value	371.38 41.43**

Genotype						щ	rmers						
	-	N	ю	4	5	9	7	8	6	10	11	12	13
RBU 9616	16.00	15.80	16.60	13.00	18.90	13.60	15.70	16.50	19.90	17.10	16.90	19.50	15.50
Rewa 422-2	16.90	17.80	19.40	14.50	19.30	14.80	16.60	18.00	16.30	20.10	17.10	19.20	18.20
Rewa 606	18.40	17.60	17.30	19.30	16.00	19.30	18.90	19.30	20.50	19.80	16.30	19.00	22.50
PNR 555-30-15-1	16.40	19.60	17.00	16.80	18.40	17.20	18.20	17.90	18.40	17.50	16.80	17.20	17.30
PNR 570-15-10	18.50	16.60	17.50	15.80	16.60	15.30	17.30	17.10	16.80	17.70	16.70	20.50	21.70
RR 347-2	20.10	18.30	18.70	17.60	19.70	16.40	20.30	16.80	18.40	24.30	18.80	18.80	20.50
Aditya	17.40	16.00	17.20	13.60	19.00	15.80	17.70	16.10	16.70	17.60	15.80	18.20	15.20
RR 363-152	17.40	16.00	14.10	15.60	15.80	16.10	16.20	17.90	18.10	16.90	15.10	17.10	14.00
OR 2058-3	19.60	18.20	16.70	14.80	17.50	16.60	18.40	19.80	18.40	17.40	18.00	20.90	18.10
OR 2085-12	19.40	19.90	19.10	14.70	20.70	19.00	19.60	18.90	19.80	18.60	19.30	20.50	19.90
Heera	18.40	17.20	19.30	17.70	20.00	14.60	18.60	17.30	19.40	22.80	18.30	18.70	19.80
CN 915-20-2-3	19.50	15.80	16.10	14.70	20.30	13.30	14.00	16.50	15.80	16.90	17.30	19.40	21.20
Genotype						L LL	Irmers						
	14	15	16	17	18	19	20	21	22	23	24	25	Total
RBU 9616	13.90	15.90	15.80	14.50	15.90	15.30	15.90	15.90	17.50	14.90	18.70	18.00	407.20
Rewa 422-2	16.80	15.90	15.90	14.70	14.70	15.90	15.90	15.40	16.50	19.40	16.80	16.80	422.90
Rewa 606	18.50	21.40	23.00	19.40	17.90	21.10	21.10	15.60	19.10	17.30	21.50	21.70	481.80
PNR 555-30-15-1	15.70	19.60	18.20	18.20	14.00	16.80	16.80	14.20	17.40	16.10	13.60	13.90	423.20
PNR 570-15-10	18.50	20.40	18.00	20.60	17.30	18.20	18.20	19.00	15.40	14.50	15.60	15.60	439.40
RR 347-2	19.20	21.90	21.90	15.80	18.70	17.40	18.80	14.60	17.60	17.50	18.80	18.00	468.90
Aditya	15.80	15.30	14.20	15.50	15.20	15.10	15.30	13.50	16.40	15.40	15.60	16.00	399.60
RR 363-152	15.30	15.70	15.70	15.80	12.80	15.10	14.10	18.20	15.60	12.70	17.20	17.90	396.40
OR 2058-3	17.60	17.30	16.60	16.00	17.30	17.90	18.50	18.70	17.70	14.90	16.60	15.90	439.40
OR 2085-12	17.50	20.80	17.40	19.20	18.00	18.90	19.80	18.80	18.80	19.30	18.20	17.80	473.90
Heera	17.60	17.90	18.40	15.80	16.60	19.70	19.70	17.50	19.30	18.30	20.10	18.80	461.80
CN 915-20-2-3	16.60	19.10	14.00	16.40	15.80	16.40	15.50	19.40	J6.70	15.70	13.30	14.30	414.00
		:			9			1	:			Mean t-value	435.71 50.45**

** Significant at p < 0.01

November, 2007]

Genotype		· · · · · ·	Rank of genoty	pes based on
	Breeders' weight	Farmers' weight for all characters	Farmers' weight for characters considered relatively more important by farmers (Q. 2, 3, 7, 9, 11, 12, 13, 15)	Farmers' weight for characters considered relatively less important by farmers (Q. 1, 4, 5, 6, 8, 10, 14, 16, 17, 18)
RBU 9616	9 th	6 th	8 th	6 th
Rewa 422-2	7 th	5 th	7 th	8 th
Rewa 606	1 st	1 st	1 st	4 th
PNR 555-30-15-1	6 th	8 th	6 th	10 th
PNR 570-15-10	5 th	9 rd	10 th	7 th
RR 347-2	3 rd	4 th	4 th	1 st
Aditya	10 th	7 th	5 th	11 th
RR 363-152	11 th	12 th	12 th	9 th
OR 2058-3	5 th	10 th	11 th	5 th
OR 2085-12	2 nd	3 rd	3 rd	2 nd
Heera	4 th	2 nd	2 nd	3 rd
CN 915-20-2-3	8 th	11 th	9 th	12 th

Table 4. Ran	s of	genotypes	obtained	from	different	matrices
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Table 5. Pairwise squared distance among four groups

Matrix	X ₂	X ₃	X ₄
X,	20.89 (16.87**)	47.95 (38.50**)	212.96 (170.99**)
X ₂	-	113.47 (91.108**)	138.67 (111.35**)
X ₃	-	-	348.62 (279.93**)

 X_1 = Response Matrix constructed with Breeder's weight

X₂ = Response Matrix constructed with Farmers' weight

X₃ = Response Matrix constructed with Farmers' weight for more important characters

X₄ = Response Matrix constructed with Farmers' weight for less important characters

F-values indicated in parentheses

** Significant at p < 0.01

confirm whether correction of selection made by breeder using such regression relationship can provide as good result as obtained in formal PPB programme. While attempting an input intensive process like PPB, few basic questions need to be addressed satisfactorily. First, is there any difference between breeder's selection criteria and farmers' choice of traits? If both are same, then there is no reason for attempting a PPB programme. Secondly, whether all the characters considered by breeder during varietal improvement are also important to farmers and vice-versa. Most important of all, what kind of relationship do exist between breeder's preference and farmer's preference for these traits.

In this paper we have discussed a method to justify farmer's participation and employing the resultant relationship in plant breeding programme. The method of evaluation consists of following steps:

- Identification of criteria preferred by farmers of the specific region and subdivision of these into more or less important ones.
- Involving farmers to evaluate a set of diverse genotypes based on the criteria.
- 3) Development of matrices of the genotypes using

Type of regression equation	Model		R value
Cubic	$Y = -895281.78 + 8139.91(x) -27.69(x)^{2} + 0.04(x)^{3}$		0.936
Quadratic	$Y= 1093.16-4.21(x) + 0.006(x)^{2}$		0.887
Modified power	Y=127.09 x 1.002 ^(X)		0.881
Exponential	$Y = 127.09 \times e^{0.002}(x)$		0.881
Power	$Y = 0.54 \times (x)^{1.074}$		0.879
Linear	Y = -26.03 + 0.91(x)		0.878
		Mean	0.8903
		t-value	96.55**

 Table 6.
 Best-fit regressions of ranking based on Breeders' weight on that of Farmers' weight (Calculated from total score of every genotype in each matrix)

** Significant at p < 0.01

farmer's preference for all characters, more important characters and less important characters as weight.

- Development of a matrix of these evaluated genotypes using breeder's preferences as weight.
- 5) Calculation of group distance among matrices to understand the difference between breeder and farmer.
- 6) Construction of a best-fit model for interpreting breeder-farmer preference. A participatory plant breeding programme may employ this method of evaluation in several locations and identify the locations where high variation is existing between farmers' and breeders' preferences and initiate PPB in those particular locations only. This would help in better resource allocation and management of the programme.

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