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Research Article

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Morphological Traits as Selection Indices in Rice Landraces of Odisha

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ABSTRACT

Direct selection for grain yield per se is often not reliable due to complex nature, controlled by non-additive gene action and is believed to have low heritability. In most of the cases experimental error associated with yield measurements and inter genotypic competition often bias the outcome of selection for higher yield. Therefore, several workers in different crop plants have emphasized the need of indirect selection for yield through the use of component traits governed by genes with additive effect and having strong correlation with grain yield. As no single trait could be taken as an adequate criterion of selection for yield, therefore, selection indices provide a useful method by making use of several correlated traits for greater efficiency of selection in yield. In the present study on selection indices it revealed that the thirteen character index was superior over the direct selection for yield per se. On the basis of twelve character selection index promising genotypes namely FR 13A, Damodarbhoga, Mrunalini, Ganjeijata, Dhulia, Kadalipendi, Upahar, Kanchan, Ganjamgedi and Kanthakamal may be used for future breeding programme. It was interesting to note that the relative rankings of genotypes selected on the basis of per se performance and index score differed signifying the importance of selection index over direct selection on grain yield.

Keywords: *Morphological traits, Per se performance, Rice landraces, Selection indices.*

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the principal staple foods for a major part of world's population (FAO, 2017). India is the second largest producer after China with a production of 166.5 million metric tons during 2017 and 2018. (Statista, 2019). Rice grown area in Odisha was 3963000 hectare with production of 97.94 lakh metric tons during the year 2016-17 (Odisha Economic Survey, 2017-18). Rice is adapted to different agro-ecosystems such as irrigated, rainfed upland, rainfed lowland and flood prone areas. In spite of its wider adaptability, in India, most of the rice varieties are vanishing very fast because of faulty agricultural practices (Mishra & Sinha, 2012). Now a day's farmers have replaced the local varieties with high yielding varieties for cultivation. Generally the high yielding varieties have lower adaptability and susceptible to different stress conditions. But local varieties are of vast importance in agriculture as they are the store house of infinite important genes as they have evolved in particular environment since millions of years (Mishra & Sinha, 2012).

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Landraces anchorage a great genetic potential for rice improvement. Genetic improvement mainly depends on the amount of genetic variability present in the germplasm (Govindaraj et al., 2015). They are endowed with tremendous variability. This highly rich variability of complex quantitative traits still remains unutilized. In Odisha, a large number of local landraces of rice are available with vast genetic variability for different characters. Collection, characterization and evaluation of landraces are crucial aspect of the pre breeding process earlier to rice improvement. Realizing the importance, the present study was undertaken to evaluate fifty five local landraces along with checks to find out useful criteria for selection of yield through construction of selection indices and identify promising cultures for their possible use in future breeding program.

MATERIALS AND METHODS

The trial was conducted involving fifty-five rice landraces of Odisha, four improved varieties and five high yielding varieties suitable for lowland ecology. The trial was laid out at Rice Research Station, Odisha University of Agriculture and Technology, Bhubaneswar during kharif, 2014. The trial materials were evaluated in randomized block design (RBD) with two replications with spacing of 20 cm x 15cm. To raise a normal crop, recommended cultural practices and need based plant protection measures were followed. Observations were recorded for twelve morphological characters *viz.,* plant height (PH), flag leaf area (FLA), effective tillers per plant (EBT), panicle length (PL), fertility percentage (FP), filled grains per panicle (FGP), straw yield per plant (SYP), 100-grain weight (GW), grain yield per plant (GYP), harvest index(HI) and grain Length/Breadth ratio (LB) on five competitive plants from each replication selected randomly from the middle row of each plot, where as character like days to 50% flowering (DF) was recorded on plot basis. The recorded data were subjected to statistical analysis based on the sample mean for different studied characters. The data were analysed by using analysis of variance ANOVA (Panse & Sukhatme, 1961) and different genetic parametes were analysed. Selection indices were constructed using the methods developed by Smith (1936) based on the discriminant function of Fisher (1936). Selection indices and their relative efficiencies in terms of expected genetic advance in yield were calculated according to the method stated by Singh and Chaudhary (1985).

RESULT AND DISCUSSION

Total sixty four lowland rice genotypes including fifty five local landraces collected from different parts of Odisha, four improved and five high yielding genotypes were evaluated in rainfed lowland situation at the Rice Research Station of Department of Plant Breeding and Genetics, OUAT, Bhubaneswar during kharif 2014. Different yield and yield attributing traits were examined and selection indices were constructed with grain yield as the economic criterion along with eleven different characters. From the variance analysis (Table-1) significant amount of genetic variation was displayed for all the studied characters. Characters having higher magnitude of genetic variance such as filled grains per panicle, plant height, fertility percentage and flag leaf area maybe sorted out as important selection criteria for realization of higher productivity in rice.

Grain yield is a complex trait, controlled by non-additive gene action and is believed to have low heritability, hence direct selection for grain yield based on *per se* performance is often not trustworthy and effective. Further, inter genotypic competition and large experimental error related with seed yield measurements often predispoes the selection for higher seed yield. Therefore, several workers have realized the importance of indirect selection for seed yield through the use of component traits governed by genes with additive effect and with strong correlation on grain yield. Smith (1936) suggested that a superior way of utilizing correlation with different traits having high heritability is to construct a selection index, which combines the information on all the characters associated with the dependent variable seed yield. Thus, selection index refers to a linear arrangement of characters associated with seed yield. As no single character could be considered as a sufficient measure of selection for seed yield, therefore, selection indices provide a helpful method by making use of several correlated traits for greater efficiency of selection in seed yield (Das et al., 2000; Mathur, 2011).

In the present investigation, selection indices were constructed with grain yield as the economic criterion and eleven different characters namely days to 50% flowering, plant height, flag leaf area, effective tillers per plant, panicle length, fertile grains per panicle, grain fertility%, 100-grain weight, grain L/B ratio, straw yield per plant, harvest index as the component characters. The twelve character index including all the twelve characters was used for the selection of superior genotypes. Those genotypes which occupied better rankings in the above selection indices were selected for their potential use. The expected genetic advance selection index over direct selection on grain yield have been presented in Table 2. The predicted genetic advance from different indices at 10% selection intensity ranged from 5.176 q/ha in one character index to 5.208 q/ha in twelve character index. Thus, in terms of predicted genetic advance, the outcome of the present investigation brought out superiority of twelve character index over direct selection for yield *per se*. This is in general agreement with those of Purohit and Majumdar (2009), Fazlalipour et al. (2008), Bastia et al. (2008), Sabouri et al. (2010), Singh et al. (2013) and Alam et al. (2014). The promising genotypes with better ranking in the twelve character index with their grain yield and index score have been presented in Table 3. It was interesting to note that the top six entries *i.e.* FR 13A, Damodarbhoga, Mrunalini, Ganjeijata, Dhulia and Kadalipendi had their *per se* yield performance and the index score in the same order. On the basis of twelve character selection index promising genotypes namely FR 13A, Damodarbhoga, Mrunalini, Ganjeijata, Dhulia, Kadalipendi, Upahar, Kanchan, Ganjamgedi and Kanthakamal may be used for future breeding programme.

In the present study relative rankings of genotypes selected on the basis of *per se* performance and index score differed indicating the importance of selection index over direct selection for grain yield. Most of the published works on selection indices based on index scores disclose the genotypic value of a genotype and the relative efficiency has been evaluated in terms of genetic advance. However, the weight of such expectations in selecting genotypes on the basis of different selection indices is often questioned as it changes due to disparity in the composition of genotypes, choosen traits for the construction of selection indices and the experimental errors associated with seed yield measurement. Therefore, it becomes crucial to study the relative efficiency of different selection criteria and to test the validity of expected superiority of selection indices over direct selection by testing the promising genotypes during appropriate field trials.

Table 1: Analysis of variance of twelve characters (mean sum of squares) for 64 lowland rice genotypes

Sl No.	Character	Source of variation(df)		
		Replication(1)	Genotype(63)	Error(63)
1	Days to 50% flowering	18.625	21.605**	2.696
2	Plant height (cm)	42.750	745.071**	135.528
3	Flag leaf area (cm^2)	0.266	130.030**	11.702
4	Effective tillers/plant (no.)	0.321	3.971**	1.067
5	Panicle length (cm)	0.461	13.587**	1.463
6	Filled grains per panicle (no.)	668.000	1625.599**	481.885
7	Fertility percentage (%)	2.438	174.691**	43.641
8	100 -grain weight (g)	0.227	0.500**	0.030
9	Grain L/B ratio	0.016	0.403**	0.015
10	Straw yield/plant (g)	-0.016	40.217**	3.806
11	Harvest index	0.001	0.008**	0.001
12	Grain yield/plant (g)	0.963	19.810**	1.298

Table 2: Expected genetic advance selection index over direct selection on grain yield

Index no and no of characters	Character	Expected GS*
1(One character index)	GYP	5.176
2(Two character index)	GYP+DF	5.178
3(Three character index)	GYP+DF+PH	5.179
4(Four character index)	GYP+DF+PH+FLA	5.180
5(Five character index)	GYP+DF+PH+FLA+EBT	5.181
6(Six character index)	GYP+DF+PH+FLA+EBT+PL	5.182
7(Seven character index)	GYP+DF+PH+FLA+EBT+PL+FGP	5.187
8(Eight character index)	GYP+DF+PH+FLA+EBT+PL+FGP+FP	5.191
9(Nine character index)	GYP+DF+PH+FLA+EBT+PL+FGP+ FP +GW	5.196
10(Ten character index)	GYP+DF+PH+FLA+EBT+PL+FGP+ FP +GW+LB	5.196
11(Eleven character index)	GYP+DF+PH+FLA+EBT+PL+FGP+ FP +GW+LB+SYP	5.201
12(twelve character index)	GYP+DF+PH+FLA+EBT+PL+FGP+ FP +GW+LB+SYP+HI	5.208

*** GS at 10% selection intensity**

Table 3: Selection of genotypes on the basis of 12 character index

Sl No.	Genotype	Index score	Grain yield/ plant (g)
1	FR 13A	21.406(1)	20.32(1)
2	Damodarbhoga	20.462(2)	19.15(2)
3	Mrunalini	18.178(3)	16.97(3)
4	Ganjeijata	17.693(4)	16.93(4)
5	Dhulia	17.558(5)	16.78(5)
6	Kadalipendi	17.377(6)	16.27(6)
7	Upahar	17.262(7)	15.39(9)
8	Kanchan	17.020(8)	15.14(10)
9	Ganjamgedi	16.989(9)	15.48(7)
10	Kanthakamal	16.626(10)	15.44(8)
11	Haladichudi	15.782(11)	14.63(11)
12	Nilarpati	15.675(12)	14.38(13)
13	Madhabi	15.244(13)	14.44(12)
14	Bankoi	15.244(14)	13.60(14)
15	Dhinkiasali	14.643(15)	12.76(21)

Figure in the parantheses indicate relative ranking of genotypes

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