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Restricted Selection in Paddy [*Oryza sativa* (L.)] for Yield and Quality Components

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ABSTRACT

Expected genetic advances of eleven different traits in forty diverse genotypes of paddy were estimated using restricted selection by restricting selection to only ten traits at a time without changing the per se of the eleventh trait. The characters considered for the present investigation are days to 50% flowering, days to maturity, plant height, panicle length, productive tillers per plant, grains per panicle, test weight, kernel length, kernel breadth, L/B ratio and grain yield per plant. The genetic advances were estimated by assigning equal economic weights to all characters as well as by using inverse of means as economic weights. In both the cases the kernel breadth recorded higher values of genetic advance in almost all cases of restricted selection. The present study also validated our earlier findings that the results and conclusions follow similar trend in both the ways of assigning economic weights i.e., by taking 'equal' economic weights and using 'inverse of means' of respective characters as economic weights.

Key words: *Restricted selection, Paddy, Economic weights.*

INTRODUCTION

Rice (*Oryza sativa* L.) is the important cereal food crop which is feeding more than half of the world's population. It forms the cheapest source of food energy and protein. In India, rice is grown in an area of 44.1 Mha with a production and productivity of 105.5 Mt and 2391 kg ha^{-1} respectively[3]. In Andhra Pradesh, rice is cultivated in an area of 23.9 Lha with a production of 72.3 Lt and productivity of 3022 kg ha^{-1}[3]. Along with yield, quality of grain is gaining lot of importance among the populations who are consuming it as staple food. In such situations breeder has to breed varieties according to the specific requirements of the people. Keeping the emerging requirements, selection procedures in breeding programmes also should be modified time to time. Certain characters should only be improved keeping some characters unchanged to obtain targeted varieties. To enable this kind of selection, Kempthrone and Nordskog[1] introduced the concept of "restricted selection indices" which enables us to restrict change in only some characters without affecting the *per se* performance of other characters.

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MATERIALS AND METHODS

The present investigation was carried at Agricultural College Farm, Bapatla which is located at an altitude of 5.4 m MSL, 15^0 54' N latitude and $80^0$90' E longitude with forty diverse paddy genotypes obtained from five different rice research stations situated in Andhra Pradesh *viz.,* Ragolu, Maruteru, Nellore, Jangamaheswarapuram and few lines from Bapatla. Restricted selection was carried out for eleven different yield and quality components *viz.,* days to 50% flowering, days to maturity, plant height, panicle length, productive tillers per plant, grains per panicle, test weight, kernel length, kernel breadth, L/B ratio and grain yield per plant. Material was sown in Randomized Complete Block Design and observations were recorded on ten randomly selected plants per treatment per replication and were used for statistical analysis. Certain traits *viz.,* days to 50% flowering, days to maturity, 1000-seed weight kernel length, kernel breadth and L/B ratio were recorded on plot basis.

Restricted selection was imposed with 5% selection intensity, only on ten traits at a time without disturbing the per se of remaining eleventh trait. All the possible eleven cases were worked out according to Singh and Chaudhary[6] and the expected genetic advances of the ten characters subjected to selection in each of the eleven cases were estimated. For taking up this kind of restricted selection, each character is to be assigned with an economic weight. In the present study we have assigned the economic weights in two different ways; first one by assigning equal economic weights *i.e.,* by assuming 'one' as economic weight for all the traits and second way of assigning weights is by using inverse of means of the traits under study as their respective economic weights.

RESULTS AND DISCUSSION

The estimates of expected genetic advances of all the ten traits in each of the eleven cases, when equal economic weights were assigned are presented in the table 1.

In the first case when selection is restricted to ten characters without affecting the performance of days to 50 % flowering, highest estimate of genetic advance was recorded in case of kernel breadth (151.264) followed by L/B ratio (112.075) and 1000 seed weight (2.741) while the least estimate was observed in case of kernal length (-39.653).

In the second case of restricted selection when selection is restricted to ten characters without affecting the duration for maturity, highest estimate of genetic advance was recorded by kernel breadth (157.572) followed by L/B ratio (118.030) and 1000 seed weight (2.701) while the least value was observed for kernal length (-42.538).

In the third case when selection is not applied on productive tillers per plant, the highest estimate of genetic advance was recorded by kernel breadth (168.424) followed by L/B ratio (126.679) and 1000 seed weight (2.685) while the least value was observed for kernal length (-46.892).

In the fourth case where plant height was not subjected to selection the highest estimate of genetic advance among the remaining ten characters was recorded by kernel breadth (162.167) followed by L/B ratio (124.581) and 1000 seed weight (2.627) while kernal length (-49.550) recorded the least value.

In the fifth case where panicle length is not considered for selection, kernel breadth (173.157) recorded the highest estimate of genetic advance followed by L/B ratio (129.941) and 1000 seed weight (3.037) while kernal length (-49.680) recorded the least value.

In the sixth case when selection is restricted to ten characters leaving grains per panicle, kernel breadth (29.453) recorded the highest estimate of genetic advance followed by L/B ratio (23.439) and 1000 seed weight

(1.305) while kernal length (-5.170) recorded the least value.

In the seventh case when selection is restricted to ten characters without 1000 seed weight, highest estimate of genetic advance was recorded by kernel breadth (172.186) followed by L/B ratio (129.858) and panicle length (2.858) while the least value was observed for kernal length (-47.832).

In the eighth case when selection is restricted to the combination of ten characters which does not include kernel length, highest estimate of genetic advance was observed kernel breadth (43.027) followed by L/B ratio (30.712) and 1000 seed weight (2.696) while plant height (0.400) recorded the least value.

In the ninth case when selection is imposed on the combination of ten characters which does not include kernel breadth, highest estimate of genetic advance was recorded by kernel length (12.614) followed by 1000 seed weight (2.682) and seed yield per plant (2.534) while the least value was observed in case of L/B ratio (-0.525).

In the tenth case of restricted selection when selection is restricted to ten characters without affecting the L/B ratio, highest estimate of genetic advance was recorded by kernel length (11.135) followed by kernel breadth (6.624) and 1000 seed weight (2.699) while the least value was observed for plant height (0.448).

In the eleventh case when selection is restricted to the combination of ten characters which does not include seed yield per plant, highest estimate of genetic advance was recorded by kernel breadth (2.534) followed by 1000 seed weight (2.508) and L/B ratio (2.448) while the least value was observed by grains per panicle (0.907).

The trait, kernel breadth recorded highest estimate of expected genetic advance in nine different cases of restricted selection and second highest estimate when L/B ratio was not included in the selection (Table 1.). Same trend *i.e.,* a particular trait recording highest expected genetic advance in majority of the restricted selection cases was also observed in our earlier studies when equal economic weights were used in case of finger millet[8]

The estimates of genetic advances of all the ten traits in each of the eleven cases, when the "inverse of means" used as their respective economic weights are presented in the table 2. In the first case when selection is restricted to ten characters without affecting the performance of days to 50 % flowering, highest estimate of genetic advance was recorded in case of kernel breadth (1.227) followed by L/B ratio (0.822) and 1000 seed weight (0.079) while the least estimate was observed in case of kernal length (-0.110).

In the second case when selection is restricted to ten characters leaving days to maturity, kernel breadth (1.325) recorded the highest estimate of genetic advance followed by L/B ratio (0.906) and 1000 seed weight (0.079) while kernal length (-0.153) recorded the least value.

In the third case where productive tillers per plant was not subjected to selection the highest estimate of genetic advance among the remaining ten characters was recorded by kernel breadth (1.269) followed by L/B ratio (0.899) and 1000 seed weight (0.072) while kernal length (-0.097) recorded the least value.

In the fourth case when selection is not applied on plant height, the highest estimate of genetic advance was recorded by kernel breadth (1.541) followed by L/B ratio (1.054) and 1000 seed weight (0.079) while the least value was observed for kernal length (-0.222).

In the fifth case where panicle length is not considered for selection, kernel breadth (1.439) recorded the highest estimate of genetic advance followed by L/B ratio (0.991) and 1000 seed weight (0.083) while kernal length (-0.223) recorded the least value.

In the sixth case when selection is imposed on the combination of ten characters which does not include grains per panicle, highest estimate of genetic advance was recorded by kernel breadth (0.314) followed by kernel length (0.204) and L/B ratio (0.165) while the least value was observed in case of days to maturity (0.008).

In the seventh case when selection is restricted to ten characters without 1000 seed weight, highest estimate of genetic advance was recorded by kernel breadth (1.614) followed by L/B ratio (1.125) and panicle length (0.071) while the least value was observed for kernal length (-0.247).

In the eighth case when selection is restricted to the combination of ten characters which does not include kernel length, highest estimate of genetic advance was observed kernel breadth (0.550) followed by L/B ratio (0.327) and 1000 seed weight (0.079) while grains per panicle (0.005) recorded the least value.

In the ninth case when selection is imposed on the combination of ten characters which does not include kernel breadth, highest estimate of genetic advance was recorded by L/B ratio (0.187) followed by kernel length (0.155) and 1000 seed weight (0.080) while the least value was observed in case of grains per panicle (0.004) and days to maturity (0.004).

In the tenth case of restricted selection when selection is restricted to ten characters without affecting the L/B ratio, highest estimate of genetic advance was recorded by kernel breadth (0.495) followed by kernel length (0.162) and productive tillers per plant (0.080) while the least value was observed for grains per panicle (0.005).

In the eleventh case when selection is restricted to the combination of ten characters which does not include seed yield per plant, highest estimate of genetic advance was recorded by kernel breadth (0.033) followed by 1000 seed weight (0.032) and days to maturity (0.030) while the least value was recorded by plant height (0.026) and L/B ratio (0.026).

It was evident from the above findings that when "inverse of means" are used as their respective economic weights, the trait kernel breadth recorded highest estimate of expected genetic advance during almost all cases of restricted selection except in the case where the same character (kernel breadth) is not included in set of traits consider for selection. Similar observations *i.e.,* a single character recording highest estimate of expected genetic advance in majority of restricted selection cases when inverse of means were used as economic weights was reported by different researchers in different crops[4] in foxtail millet; Kumar[2], in sugarcane; Srilakshmi and Babu[8], in finger millet). Further the results of this investigation also indicate that along with kernel breadth, L/B ratio and 1000 seed weight recorded higher values of expected genetic advance in almost all cases of restricted selections in both cases when equal economic weights as well as inverse of means are used as economic weights.

The present study also validates our earlier findings that almost similar results and conclusions will be obtained in both cases of assigning economic weights *i.e.,* by using "equal" economic weights and by using "inverse of means" of different traits as their respective economic weights[5,7,8,9].

Table 1: Genetic advance estimates (ΔG_i) in 11 cases of restricted selections of 40 genotypes of paddy when equal economic weights are assigned

Case No.	Character	Days to 50% flowering	Days to maturity	Productive tillers per plant	Plant height	Panicle length	Grains per panicle	1000-seed weight	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Seed yield per plant
1.	Days to 50% flowering	0.000	0.875	1.393	0.307	2.410	0.508	2.741	-39.653	151.264	112.075	2.360
2.	Days to maturity	1.404	0.000	2.213	0.389	2.171	0.509	2.701	-42.538	157.572	118.030	2.032
3.	Productive tillers / plant	1.395	0.598	0.000	0.366	2.431	0.511	2.685	-46.892	168.424	126.679	2.406
4.	Plant height	1.397	0.519	1.957	0.000	1.728	0.538	2.627	-49.550	162.167	124.581	1.857
5.	Panicle length	1.561	0.451	2.454	0.523	0.000	0.533	3.037	-49.680	173.157	129.941	2.131
6.	Grains per panicle	0.792	0.376	0.728	0.668	1.401	0.000	1.305	-5.170	29.453	23.439	0.907
7.	1000-seed weight	1.436	0.606	1.908	0.398	2.858	0.524	0.000	-47.832	172.186	129.858	2.508
8.	Kernel length (mm)	1.427	0.537	1.928	0.400	2.325	0.486	2.696	0.000	43.027	30.712	2.422
9.	Kernel breadth (mm)	1.439	0.521	1.810	0.471	2.290	0.486	2.682	12.614	0.000	-0.525	2.534
10.	L/B ratio	1.441	0.570	1.847	0.448	2.291	0.489	2.699	11.135	6.624	0.000	2.448
11.	Seed yield per plant	2.360	2.032	2.406	1.857	2.131	0.907	2.508	2.422	2.534	2.448	0.000

Table 2: Genetic advance (ΔG_i) values in 11 cases of restricted selections of 40 genotypes of paddy when inverse of means are assigned as economic weights

Case No.	Character	Days to 50% flowering	Days to maturity	Productive tillers per plant	Plant height	Panicle length	Grains per panicle	1000-seed weight	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Seed yield per plant
1.	Days to 50% flowering	0.000	0.009	0.067	0.008	0.061	0.005	0.079	-0.110	1.227	0.822	0.030
2.	Days to maturity	0.016	0.000	0.075	0.009	0.058	0.005	0.079	-0.153	1.325	0.906	0.027
3.	Productive tillers / plant	0.012	0.011	0.000	0.008	0.053	0.004	0.072	-0.097	1.269	0.899	0.029
4.	Plant height	0.015	0.008	0.071	0.000	0.062	0.005	0.079	-0.222	1.541	1.054	0.026
5.	Panicle length	0.017	0.003	0.079	0.012	0.000	0.005	0.083	-0.223	1.439	0.991	0.027
6.	Grains per panicle	0.014	0.008	0.070	0.009	0.062	0.000	0.074	0.204	0.314	0.165	0.028
7.	1000-seed weight	0.016	0.005	0.070	0.009	0.071	0.005	0.000	-0.247	1.614	1.125	0.032
8.	Kernel length (mm)	0.016	0.006	0.077	0.009	0.059	0.005	0.079	0.000	0.550	0.327	0.028
9.	Kernel breadth (mm)	0.018	0.004	0.068	0.009	0.059	0.004	0.080	0.155	0.000	0.187	0.033
10.	L/B ratio	0.014	0.008	0.080	0.010	0.059	0.005	0.079	0.162	0.495	0.000	0.026
11.	Seed yield per plant	0.030	0.027	0.029	0.026	0.027	0.028	0.032	0.028	0.033	0.026	0.000

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