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Genetic analysis for yield attributes in F3 populations involving traditional rice (*Oryza sativa* L.) cultivar Poongar

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Abstract
The study was conducted during Rabi 2019-20 under rainfed rice ecosystem to investigate genetic variation, heritability and interrelationship of yield and related attributes in F3 populations of crosses RMD 1 x Poongar and ASD 16 x Poongar. Maximum standard deviation recorded for number of filled grains per panicle in both crosses. The higher magnitude of PCV and GCV were registered for number of productive tillers per plant in both crosses. High heritability coupled with high genetic advance was recorded for number of filled grains per panicle and straw yield in cross RMD 1 x Poongar and number of filled grains per panicle, straw yield and harvest index in cross ASD 16 x Poongar. The distribution of frequency for spikelet fertility was negatively skewed and platykurtic in the both crosses. Single plant yield exhibited positive and significant association with panicle length and harvest index in cross RMD 1 x Poongar and harvest index only in cross ASD 16 x Poongar. Straw yield and harvest index expressed very high direct effect on single plant yield in RMD 1 x Poongar and harvest index had very high direct effect on single plant yield in ASD 16 x Poongar and hence simultaneous selection for these traits can significantly improve the single plant yield in rainfed rice ecosystem.

Keywords: Variability, heritability, descriptive statistics, correlation, rainfed rice

Introduction
Rice (*Oryza sativa* L.) has been widely consumed and planted around the world as an essential food for human beings. Particularly, 80% of rice production in the world comes from Asian countries (Bhat *et al*., 2016) [4]. More than half of the world's population constantly includes rice in their diet, and about 2808 calories are provided by rice per person per day (Jiang *et al*., 2012) [9]. Rainfed rice has been gaining popularity, because current high-yielding varieties have led to an increase in genetic vulnerability, a scarcity of water for irrigation, and a breakdown of resistance genes against emerging races of pathogens due to intensive cultivation. It is important in cropping systems, because of the lack of irrigation facilities and lower cost of production (Fageria *et al*., 2014) [7]. Landraces provides a vast source of genetic variability for the present day rice improvement programme. Diverse plant types is immediately valuable for shaping new varieties and this forms the basic wealth on which plant breeders can operate for reconstructing the existing genotypes (Savitha and Ushakumari, 2015) [19]. Poongar is one of the landraces growing in southern Tamil Nadu and it is early maturing and drought tolerant cultivar widely used in crossing programme in a view to develop early duration drought tolerant genotypes.

The success of developing genotypes with desirable traits would depend on the exploitation of existing variability and therefore it is desirable to collect, evaluate and utilize the available diversity to suit specific need with regards to specific ecosystem. Yield is a complex character, which is highly influenced by the environment, hence direct selection for yield alone limit the selection efficiency and ultimately results in limited success in yield improvement. Study of variability parameters and Descriptive statistics are expected to provide reliable basis for selecting out desirable elite and diverse parents for hybridization and exploitation of variability. The estimates of heritability would be rewarding and helpful to the plant breeder in determining the characters to be considered for the selection. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. Correlation combined with path analysis would give better picture of the cause and effect relationship between different pairs of characters (Sharma, 2010) [20]. This study was therefore conducted to select potential genotypes and to identify the most important characters for breeding programmes by exploiting the genetic variation, heritability, descriptive statistics and association analysis of yield and related attributes of F3 populations involving landrace Poongar under rainfed rice ecosystem.

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Materials and Methods
Details on experimental site and traits
The experimental material comprised with single plant progenies of twenty families from each cross *viz.*, RMD 1 x Poongar and ASD 16 x Poongar which were evaluated in non-randomized block design with two replications as progeny rows keeping 15 x 10 cm spacing at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi during Rabi 2019-20. The experimental site is located at 9" 21' N latitude, 78" 22' E longitudes and an altitude of 242 m above mean sea level with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. The recommended agronomic practices followed to raise good crop stand. The data were recorded on twenty randomly tagged plants from each replication for various quantitative traits studied were *viz,* days to 50% flowering, plant height (cm), number of productive tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility (%), single plant yield (kg), straw yield (kg) and harvest index.

Statistical analysis
Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme (1967) [14]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton (1952) [5]. PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973) [21]. Heritability in broad sense was estimated as per the formulae suggested by Allard (1960) [2] and was categorized as suggested by Johnson *et al*., (1955) [10]. Genetic advance (GA) was estimated as per formula given by Allard (1960) [2]. Genetic advance over mean (GAM) was calculated and was expressed in percentage as suggested by Johnson *et al*. (1955) [10]. The third order statistics skewness and kurtosis were estimated as per Snedecor and Cochran (1994) [22]. Coefficient of correlation was determined using the technique outlined by Dewey and Lu (1959) [6]. The direct and indirect effects were classified based on the scale given by Lenka and Misra (1973) [12].

Results and Discussion
Variability
The potentiality of a cross is measured not only by mean performance but also on the extent of variability. The estimates of genotypic and phenotypic coefficient of variation for different quantitative characters for two crosses in F3 generation are presented in Table 1. According to the results of this table, maximum standard deviation belonged to filled grain per panicle in both crosses. The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study. The perusal of coefficient of variability indicated that wide range of variability was present at both phenotypic and genotypic levels for all the characters under studied. The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits which may be due to higher degree of interaction of genotypes with the environment (Kavitha and Reddy, 2002) [11]. The difference in the magnitude of PCV and GCV for number of productive tillers per plant was of high order in both crosses. The moderate magnitude of PCV and GCV were recorded in both crosses for most of the traits *viz.*, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility (%), single plant yield (kg), straw yield (kg) and harvest index (Table 1.).

Heritability and Genetic advance
Burton (1952) [5] pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Thus, genetic advance is yet another important selection parameter which although independent, represents the expected genetic advance under selection. It measures the differences between the mean genotypic values of the selected lines and the mean genotypic values of original population from which these were selected. According to Panse (1957) [13] if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provided good scope for further improvement. High heritability coupled with high genetic advance was recorded for number of filled grains per panicle and straw yield in cross RMD 1 x Poongar and number of filled grains per panicle, straw yield and harvest index in cross ASD 16 x Poongar (Table 1.). It indicates that most likely the heritability is due to additive gene effects and selection may be effective. This finding is in close agreement with the findings of Babu *et al*. (2012) [3] and Allam *et al.* (2015) [1].

Descriptive statistics
The study on distribution properties by third order statistics such as coefficients of skewness and kurtosis provides insight about the nature of gene action and number of genes controlling the traits respectively. They are more powerful than first and second degree statistics which reveal interaction genetic effects. The skewness and kurtosis values for quantitative traits for both crosses were presented in Table 1. It indicates that for spikelet fertility, the distribution of frequency was negatively skewed and platykurtic in the both crosses. These results are in accordance with Raghavendra and Hittalmani (2015) [16] and Rani *et al*. (2016) [17]. The kurtosis value is less than three for all traits in both crosses. Reported negatively skewed platykurtic distribution recorded that this trait was governed by large number of genes and majority of them displaying dominant and dominant based duplicate epistasis. Hence, mild selection is expected to result in rapid genetic gain for that trait whereas, positively skewed platykurtic distribution indicated that these traits were governed by large number of genes and majority of them displaying dominant and dominant based complementary epistasis. Hence, intense selection is required for immense genetic gain in these traits (Pooni *et al*., 1977) [15].

Interrelationship among traits
In the present investigation, single plant yield exhibited positive and significant association with panicle length and harvest index in cross RMD 1 x Poongar and harvest index only in cross ASD 16x Poongar (Table 2) indicating an increase in single plant yield with an increase in these characters. Therefore, priority should be given to these traits, while making selection for yield improvement. This was in conformity with the findings of Babu *et al*. (2012) [3], Vanisree *et al.* (2013) [23], Islam *et al*. (2015) [8] and Sameera *et al* (2016) [18]. Knowledge on inter relationship between

yield traits may facilitate breeder to decide upon the intensity and direction of selection pressure to be given on related traits for the simultaneous improvement of these traits. In case of cross RMD 1 x Poongar, days to 50% flowering had positive and significant association with productive tillers per plant; panicle length with harvest index; filled grains per panicle with spikelet fertility and spikelet fertility with straw yield. In case of cross ASD 16 x Poongar, filled grains per panicle had positive and significant association with days to 50% flowering, plant height and spikelet fertility. Similar results were reported by Vanisree *et al.* (2013) [23], Islam *et al.* (2015) [8] and Sameera *et al* (2016) [18].

Path analysis gives an idea about how a trait influences grain yield directly and indirectly through other traits. This is very important in giving due weightage to major yield contributing traits while selection. In case of cross RMD 1 x Poongar, straw yield and harvest index expressed very high direct effect on single plant yield (Table 3). Panicle length had high indirect effect on single plant yield through harvest index. Likewise spikelet fertility had high indirect effect on single plant yield through straw yield. In case of cross ASD 16 x Poongar, harvest index expressed very high direct effect and straw yield had high direct effect on single plant yield (Table 3). Plant height, number of productive tillers per plant, panicle length had high indirect effect on single plant yield through harvest index. This was in conformity with the findings of Babu *et al.* (2012) [3], Vanisree *et al.* (2013) [23], Islam *et al.* (2015) [8] and Sameera *et al.* (2016) [18]. Genotypic residual effect (0.14 in RMD 1 x Poongar and 0.10 in ASD 16 x Poongar) indicates that traits under study contribute less than 85% to the variability in single plant yield. It indicates that few other traits which have not been studied here, need to be included to account fully for the variation in single plant yield in rainfed situation.

Table 1: Estimates of mean, variability, heritability, genetic advance and descriptive statistics in F3 populations of two cross

Traits	RMD 1 x Poongar									ASD 16 x Poongar								
	Mean	SD	PCV	GCV	h^2	GA	GAM	SKW	KRT	Mean	SD	PCV	GCV	h^2	GA	GAM	SKW	KRT
DFF	77.72	6.41	8.02	3.38	17.79	2.29	2.94	-0.03	-0.43	74.17	4.34	6.00	5.23	76.01	6.97	9.39	1.13	0.97
PH	130.68	12.18	9.08	4.33	22.77	5.57	4.26	0.58	-0.78	119.70	3.40	2.91	2.18	55.99	4.02	3.36	0.39	0.37
PTP	9.55	2.16	22.08	14.09	40.71	1.77	18.52	0.16	-0.37	9.35	1.92	19.99	13.16	43.33	1.67	17.84	0.16	-0.17
PL	24.17	2.05	8.71	6.39	53.83	2.34	9.66	0.42	-0.28	25.16	1.73	7.05	3.17	20.22	0.74	2.94	0.02	-0.40
FGP	104.45	21.40	20.97	17.59	70.31	31.73	30.38	0.78	-0.32	115.92	24.31	21.51	19.98	86.23	44.30	38.21	0.37	-1.13
SF	91.22	2.61	2.93	1.49	25.84	1.42	1.56	-0.67	0.12	92.03	2.36	2.58	1.35	27.58	1.35	1.46	-0.85	0.98
SPY	0.98	0.35	13.34	10.58	62.87	0.17	17.28	0.17	-1.28	1.07	0.34	16.72	13.75	67.56	0.25	23.27	-0.01	-1.12
SYP	2.50	0.04	14.57	12.11	69.08	0.52	20.73	0.11	-0.13	2.53	0.04	13.73	8.31	36.65	0.26	10.36	0.54	0.54
HI	0.28	0.13	13.09	10.87	69.03	0.05	18.61	0.26	0.17	0.30	0.17	15.45	12.91	69.75	0.07	22.20	0.97	1.00

DFF= Days to 50% flowering; PH= Plant height; PTP= Productive tillers per plant; PL= Panicle length; FGP= Filled grains per panicle; SF= Spikelet Fertility; SPY= Single plant yield; SYP= Straw yield per plant; HI= Harvest index; SD= Standard Deviation; GCV=Genotypic Co-efficient of Variation; PCV=Phenotypic Co-efficient of Variation; h^2=Heritability (Broad sense); GA= Genetic Advance; GAM=Genetic Advance as % of Mean; SKW= Skewness; KRT= Kurtosis.

Table 2: Genotypic correlation coefficients for yield related traits and single plant yield in F3 populations of two cross

Cross	Characters	Days to 50% flowering	Plant Height	Productive tillers per plant	Panicle length	Filled grains per panicle	Spikelet fertility	Straw yield per plant	Harvest index	Single plant yield
RMD 1 x Poongar	Days to 50% flowering	1.000	0.170	0.485**	0.164	-0.044	-0.252	0.025	-0.011	-0.018
	Plant Height		1.000	0.123	0.133	-0.274	-0.262	-0.356*	0.051	-0.247
	Productive tillers per plant			1.000	0.230	0.198	-0.111	-0.026	0.107	0.129
	Panicle length				1.000	-0.059	-0.183	-0.366*	0.524**	0.339*
	Filled grains per panicle					1.000	0.487**	0.252	-0.193	-0.022
	Spikelet fertility						1.000	0.337*	-0.429**	-0.245
	Straw yield per plant							1.000	-0.705**	0.113
	Harvest index								1.000	0.617**
	Single plant yield									1.000
ASD 16 x Poongar	Days to 50% flowering	1.000	0.078	-0.263	0.035	0.643**	0.224	-0.031	-0.117	-0.186
	Plant Height		1.000	-0.026	-0.041	0.352*	0.116	-0.230	0.309	0.216
	Productive tillers per plant			1.000	0.087	-0.226	-0.129	-0.134	0.299	0.294
	Panicle length				1.000	-0.159	-0.228	-0.327*	0.260	0.076
	Filled grains per panicle					1.000	0.480**	-0.111	-0.020	-0.135
	Spikelet fertility						1.000	-0.110	-0.103	-0.235
	Straw yield per plant							1.000	-0.685**	-0.106
	Harvest index								1.000	0.793**
	Single plant yield									1.000

*Significance at 5% level; ** Significance at 1% level

Table 3: Direct and indirect effects of yield related traits on single plant yield in F3 populations of two cross

Cross	Characters	Days to 50% flowering	Plant Height	Productive tillers per plant	Panicle length	Filled grains per panicle	Spikelet fertility	Straw yield per plant	Harvest index	Single plant yield	Residual effect
RMD 1 x Poongar	Days to 50% flowering	-0.064	0.005	0.019	0.004	0.001	0.005	0.028	-0.015	-0.018	0.14
	Plant Height	-0.011	0.027	0.005	0.003	0.008	0.005	-0.396	0.112	-0.247	
	Productive tillers per plant	-0.031	0.003	0.039	0.005	-0.006	0.002	-0.029	0.146	0.129	
	Panicle length	-0.011	0.004	0.009	0.021	0.002	0.003	-0.407	0.718	0.339*	
	Filled grains per panicle	0.003	-0.008	0.007	-0.001	-0.031	-0.009	0.280	-0.264	-0.022	
	Spikelet fertility	0.016	-0.007	-0.004	-0.003	-0.015	-0.019	0.375	-0.587	-0.245	
	Straw yield per plant	-0.002	-0.010	-0.001	-0.008	-0.008	-0.006	1.112	-0.965	0.113	
	Harvest index	0.001	0.002	0.004	0.011	0.006	0.008	-0.784	1.369	0.617**	
ASD 16 x Poongar	Days to 50% flowering	0.016	-0.001	0.001	-0.001	-0.018	0.001	-0.025	-0.159	-0.186	0.10
	Plant Height	0.001	-0.012	0.001	0.001	-0.010	0.001	-0.187	0.421	0.216	
	Productive tillers per plant	-0.004	0.001	-0.004	-0.002	0.006	-0.001	-0.109	0.407	0.294	
	Panicle length	0.001	0.001	-0.001	-0.017	0.004	-0.001	-0.266	0.354	0.076	
	Filled grains per panicle	0.011	-0.004	0.001	0.003	-0.028	0.001	-0.091	-0.028	-0.135	
	Spikelet fertility	0.004	-0.001	0.001	0.005	-0.013	0.001	-0.090	-0.140	-0.235	
	Straw yield per plant	-0.001	0.002	0.001	0.006	0.003	-0.001	0.815	-0.932	-0.106	
	Harvest index	-0.002	-0.003	-0.001	-0.004	0.001	-0.001	-0.558	1.362	0.793**	

** Significance at 1% level ** Significance at 1% level Diagonal values (in bold) denote the direct effects

Conclusion
It is concluded from the variability studies that high heritability coupled with high genetic advance was recorded for number of filled grains per panicle and straw yield in cross RMD 1 x Poongar and number of filled grains per panicle, straw yield and harvest index in cross ASD 16 x Poongar and the major role of additive gene action involved in the inheritance of these traits. Thus, these traits may serve as effective selection parameters during breeding programme in the rainfed rice ecosystem. Study on descriptive statistics expressed that the traits were quantitatively governed by both additive and non-additive gene actions and were controlled by multiple genes showing gene interaction. A perusal of the results thus emphasized the need for selection based on number of productive tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility, straw yield and harvest index for improvement of grain yield in rainfed rice eco system.

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