Journal of Pharmacognosy and Phytochemistry
Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(3): 2161-2164
Received: 21-03-2018
Accepted: 25-04-2018

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Coefficient of variation (GCV & PCV), heritability and genetic advance analysis for yield contributing characters in rice (*Oryza Sativa* L.)

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Abstract
Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. The estimates of heritability, coefficients of variability and genetic advance computed for 12 yield contributing traits. Genetic parameters for yield and its correspondent characters in rice were estimated from a trial with four CMS lines, fifteen testers, three checks and sixty crosses evaluated for twelve characters related to yield. In general, the magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. High estimates of heritability and genetic advance in broad sense and narrow sense were recorded for all characters *viz.*, spikelet fertility, days to 50% flowering, days to maturity, spikelets per panicle, harvest-index, L/B ratio, 1000-grain weight, plant height, grain yield per plant, biological yield per plant, panicle bearing tillers per plant, panicle length. High heritability coupled with high genetic advance in percent of mean was observed for all the traits.

Keywords: heritability, variability, genetic advance in rice

Introduction
Rice (*Oryza sativa* L.) is the world's most staple food for about 2.5 billion people and which may escalate to 4.6 billion by the year 2050. More than 40 per cent of the world's population depends on rice as the major source of calories. To meet the food demand of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 million tones every year (1), which is possible through heterosis breeding and other innovative breeding approaches.

Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice. Plant breeders commonly select for yield components which indirectly increase yield. Heritability (h^2) of a trait is important in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program. El-Malky *et al*. (2003) observed high broad sense heritability estimate of 98.89% for days to maturity, 75.20% for the number of tillers per plant, 41.74% for the number of panicles per plant, 98.97% for 1000 grain weight and 90.87% for panicle weight. Babar *et al*. (2007) also reported high heritability of 0.74 for panicle length, 0.75 for plant height, 0.63 for the number of panicles per plant, 0.64 for days to heading and 0.81 for grain yield. On the other hand, Kato (1997) [19] estimated low broad sense heritability of 0.16 for the number of panicles per plant and 0.20 to 0.33 for number of spikelet per panicle.

The relationship between rice yield and yield components has been studied extensively at phenotypic level; Sharma and Choubey (1985) [37] and Dhanraj and Jagadish (1987) [11] reported that yield per plant was positively correlated with the number of productive tillers per plant, the number of panicles per plant and spikelets per plant and 1000 grain weight while Prasad *et al*. (1988) [28] observed positive correlations between grain yield per plant and the number of spikelets per panicle, the number of fertile grains per panicle and 1000 grain weight. Bai *et al*. (1992) [5] reported that grain yield is positively correlated with the number of productive tillers per plant, and the number of grains per panicle.

The success of any breeding program depends on understanding the genetic nature of the character of interest, creation and prediction of genetic variability in subsequent generations and their inter relationship with other characters. Yield is a complex character and is influenced by various other characters therefore it is essential to understand the association of other characters with yield in addition to the information on genetic variability. Yield contributing traits are interrelated and highly influenced by the environments (Chandra *et al*. 2007; Nayak *et al*. 2008; Prasad *et al*. 2001; Eswara Reddy *et al*. 2013) [9, 24, 29, 13].

It is essential to estimate the various types of gene action for the selection of appropriate breeding procedure to improve the quantitative and qualitative characters (Banumathy *et al.* 2003) [7]. Keeping in view the genetic studies in parental lines of hybrid rice were undertaken to estimate the genetic component of variance for yield and its components and to compute the heritability and genetic advance for 12 characters.

Materials and Methods

Four CMS lines having the WA cytoplasmic background *viz*., IR 68885A, IR 58025A, IR 68897A, and IR 79156A used as lines and fifteen promising rice varieties *viz*., NDR 1126,NDR 1127, IR 27723, CR 2499, Sugandha 5, NDR 3112-1, NDR 2701, NDR 2702, NDR 2704, NDR 2706, NDR 370131, NDR 370132, NDR 370133, IR 87651 and NDR 2705 were used as testers, three checks (NDR 2064, NDR 2065 and NDR 359) were the experimental materials of this study. The crosses will be made into "line x tester" mating design (Kempthorne, 1957) [20] to produce 60 crosses. All the Eighty two genotypes were sown in Randomized Block Design (RBD) with three replications at the Instructional farm of Genetics and Plant Breeding, NDUAT Kumarganj Faizabad (U.P.) India, during 2013 *kharif* season. A standard spacing of 15cm x 20cm was adopted for planting. Recommended packages of practices were followed during the crop growth period. Observations were recorded for twelve characters *viz.*, days to 50% flowering, plant height (cm), panicle length (cm). effective tillers per plant, total no. of spikelets per panicle, total number of filled spikelets per panicle, total number of chaffy spikelets per panicle, spikelet fertility %, 100-grain weight (g), harvest index (%), length of spikelet (cm), breadth of spikelet (cm), and grain yield per plant (g days to 50% flowering, days to maturity, plant height, Panicle bearing tillers per plant, panicle length, 1000 grain weight, Spikelets per panicle, Spikelet fertility (%), Harvest-index (%), L/B ratio, Grain yield per plant (g) and Biological yield per plant (g). Genotypic and phenotypic, Coefficient of variation**,** heritability and genetic advance were estimated for all twelve characters.

Results and Discussion

The results of coefficient of variation, heritability and genetic advance are presented in table-1. In general, the magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were recorded for panicle bearing tillers per plant (PCV=22.40%, GCV=21.83%), spikelets fertility (PCV=22.96%, GCV=22.91%), 1000-grain weight (PCV=24.88%, GCV=24.67%), biological yield per plant (PCV=28.33%, GCV=27.79%), harvest index (PCV=23.64%, GCV=23.46%), L/B ratio (PCV=24.94%, GCV=24.77%) and grain yield per plant (PCV=28.46%, GCV=28.08%). The moderate estimates (10-20%) of PCV and GCV were recorded for days to 50% flowering (PCV=16.72%, GCV=16.62%) days to maturity (PCV=11.54%, GCV=11.47%), plant height (PCV=12.72%, GCV=12.51%), panicle length (PCV=10.98%, GCV=10.47%) and spikelet per panicle (PCV=18.64%, GCV=18.55%). have expressed low estimates (<10%) of coefficient of variation for both the parameters. The similar results were observed for the above twelve characters are broadly in agreement with earlier reports in rice. These findings were also reported by Chaudhary *et al*. 2004; Babar *et al*. 2009; Anjaneyulu *et al.* 2010; Jayasudha and Sharma, 2010; Karthikeyan *et al.* 2010; Akhtar *et al.* 2011; Garg *et al.* 2011; Pandey, 2012; Seyoum *et al.* 2012; Basavaraja *et al.* 2013; Sathya and Jebaraj 2013; Warkad *et al.* 2013) [10, 4, 3, 16, 18, 1, 14, 25, 36, 6, 35, 44].

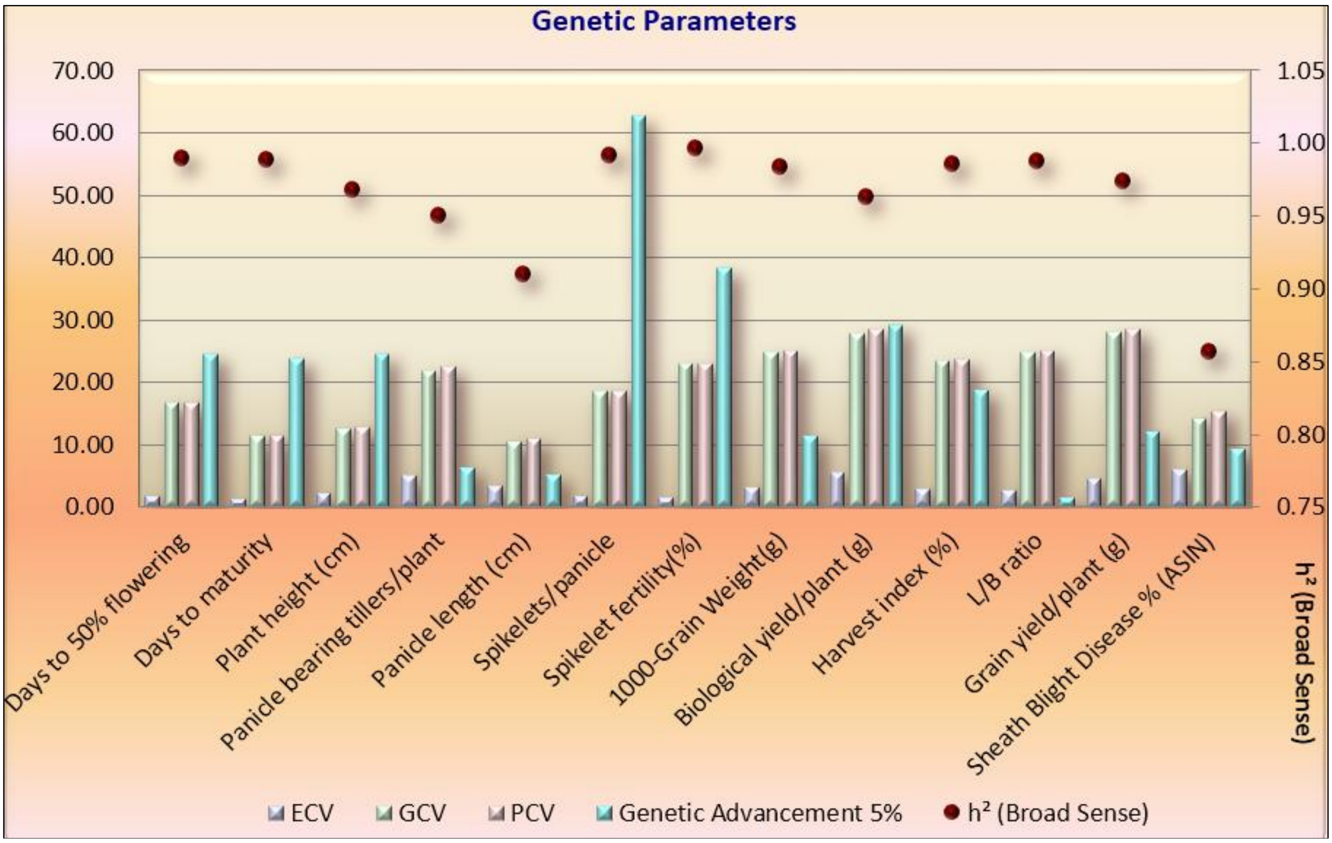

Fig 1: Representing ECV, GCV, PCV, genetic advancement and h^2 (broad sense)

Table 2: Estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability and genetic advance in percent of mean among 12 characters in rice

Character	Coefficient of variation (%)		Heritability (%)		Genetic components		Degree of dominance	Genetic advance	Genetic advance in % of mean
	Genotypic (GCV)	Phenotypic (PCV)	Broad sense	Narrow sense	Additive variance	Dominance variance			
Days to 50% flowering	16.62	16.72	99.00	72.58	38.15	15.07	0.63	24.44	34.05
Days to maturity	11.47	11.54	99.00	91.99	33.53	2.38	0.27	23.74	23.47
Plant height (cm)	12.51	12.72	97.00	65.96	19.61	9.50	0.70	24.55	25.34
Panicle bearing tillers per plant	21.83	22.40	95.00	60.13	1.43	0.90	0.79	6.33	43.82
Panicle length (cm)	10.47	10.98	91.00	61.22	1.88	1.09	0.76	5.27	20.56
Spikelets per panicle	18.55	18.64	99.00	31.65	184.33	724.18	1.98	62.60	38.04
Spikelet fertility (%)	22.91	22.96	100.00	27.90	0.58	2.11	1.90	38.37	47.08
1000- grain weight (g)	24.67	24.88	98.00	35.11	0.89	2.40	1.64	11.42	50.39
Biological yield per plant (g)	27.79	28.33	96.00	50.67	21.04	22.27	1.03	29.04	56.14
Harvest-index (%)	23.46	23.64	99.00	52.83	1.49	1.12	0.87	18.75	47.96
L/B ratio	24.77	24.94	99.00	22.53	0.00	0.07	3.35	1.49	50.71
Grain yield per plant (g)	28.08	28.46	97.00	45.81	3.10	4.45	1.20	12.12	57.07

The estimates of heritability in narrow sense (h^2ns) have been classified by Robinson (1966) into three categories *viz.,* high (> 30%), medium (10-30%) and low (<10%). High estimates of heritability in narrow sense were recorded for almost all characters *viz.,* days to maturity (91.99), days to 50% flowering (72.58), plant height (65.96), panicle length (61.22), panicle bearing tillers per plant (60.13), harvest-index (52.83), biological yield per plant (50.67), grain yield per plant (45.81), 1000-grain weight (35.11) and spikelets per panicle (31.65). Moderate estimates of heritability in narrow sense were also recorded for only spikelet fertility (27.90) and L/B ratio (22.53). The high estimates of heritability and genetic advance observed for the above characters are closed in agreement with the earlier reports in rice. These findings were also reported by Suman *et al*. 2005; Panwar *et al*. 2007; Pradhan *et al.* (2007), Rashid *et al.* (2008), Babar *et al*. 2009; Arvind *et al*. 2011; Saleem *et al.* (2010), Saidaiah *et al.* (2010), Yadavendra *et al.* 2011; Kiani and Nematzadeh, 2012, Singh *et al*. 2012) [42, 26, 27, 30, 4, 33, 32, 21, 25].

The estimates of heritability in broad sense (h^2bs) have been classified by Robinson (1966) into three categories *viz.,* high (> 75%), medium (50-75%) and low (<50%). High estimates of heritability in broad sense were recorded for all characters *viz.,* spikelet fertility (100.00), days to 50% flowering (99.00), days to maturity (99.00), spikelets per panicle (99.00), harvest-index (99.00), L/B ratio (99.00), 1000-grain weight (98.00), plant height (97.00), grain yield per plant (97.00), biological yield per plant (96.00), panicle bearing tillers per plant (95.00), panicle length (91.00). The high estimates of genetic advance in per cent of mean (>20%) using broad sense heritability were recorded for all the characters *viz*., grain yield per plant (57.07), biological yield per plant (56.14), L/B ratio (50.71), 1000-grain weight (50.39), harvest-index (47.96), spikelet fertility (47.08), panicle bearing tillers per plant (43.82), spikelets per panicle (38.04), days to 50% flowering (34.05), plant height (25.34), days to maturity (23.47) and panicle length (20.56). High heritability coupled with high genetic advance in percent of mean was observed for all the traits. The high estimates of heritability and genetic advance observed for the above characters are broadly in agreement with earlier reports in rice. These findings were also reported by Islam *et al*. 2004; Sharma and Sharma 2005; Suman *et al.* 2005; Manna *et al.* 2006; Singh *et al*. 2007; Karad and Pol 2008; Singh *et al.* 2008; Vijayalakshmi *et al.* 2008; Bughio *et al.* 2009; Raut *et al.* 2009; Sarangi *et al.* 2009; Akinwale *et al.* 2011; Garg *et al.* 2011) [15, 38, 42, 23, 9, 17, 41, 43, 8, 31, 34, 2, 14].

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