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## Heritability and genetic advance in rice magic population for yield and its components

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### Abstracts

The present study consists of 395 *indica* MAGIC lines of rice that were evaluated at RARS, Maruteru to study heritability and genetic advance. The highest heritability and high genetic advance were recorded by number of panicles per plant, number of grains per panicle, 1000-grain weight and grain yield per plant. High heritability and moderate genetic advance were observed in plant height at maturity and panicle length. Low heritability and low genetic advance were recorded by days to 50% flowering.

**Keywords:** Heritability, rice magic population, components

### Introduction

Heritability is an index for transmission of a character from one generation to next generation. The selection ability of rice population mainly depends on the extent of heritable difference. Inherited variation revealed primary role for rice breeder to evaluate rice in term of variability. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection. High heritability along with high genetic advance is an indexing point for suitable selection.

### Materials and Method

The present investigation "Heritability and genetic advance in rice MAGIC population for yield and its components" was carried out during *khariif*, 2017 at Regional Agricultural Research Station, Maruteru, West Godavari District of Andhra Pradesh state located at 81.44°E longitude, 26.30 latitude and 5m above mean sea level. The soils are characterized by black alluvial clayey soils, neutral to slightly alkaline in reaction, medium levels of phosphorus and potassium receiving an annual rainfall of 1100 mm. A subset of 395 *indica* MAGIC lines and its genotypic data received from International Rice Research Institute (IRRI), Philippines was used as an experimental material for evaluation of *indica* MAGIC lines for heritability and genetic advance. Seeds were sown in seedling nursery on 21<sup>st</sup> of June, 2017. Seedlings were transplanted in 2 rows of 3.3 m length in a plot with 44 plants in each plot at 25 days after sowing. The spacing was 20 cm between rows and 15 cm between plants. For the subset of *indica* MAGIC populations, the augmented randomized complete block design was adopted to layout the trail. To adjust the row size in augmented randomized complete block design, MTU 1010 named as dummy was added. Six popular varieties were used as check varieties *viz.*, Sahabhazi Dhan, Rasi, IR64, MTU 1010, CSR36 and MTU 1075 replicated six times. Phenotypic data was collected on phenological traits *viz.*, days to 50% flowering, plant height at maturity (cm), number of panicles per plant, number of grains per panicle, panicle length (cm), 1000-grain weight and grain yield per plant (g). The details of observations recorded and methods followed are presented here under character wise.

**Statistical Analysis:** The collected data was statistically analyzed by using Windostat version 9.3.

**Heritability in broad sense [ $h^2$  (b)]:** Heritability in broad sense was estimated as per Allard (1960).

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

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**Genetic advance as per cent of mean (GAM):** Genetic advance was estimated as per the formula proposed by Lush (1940) [9] and Johnson *et al.* (1955) [6].

Genetic Advance (GA) =  $K \times \sigma_p \times h^2$  (b)

Where, K = Selection differential at 5% selection intensity (2.06).

$h^2$  (b) = heritability in broad sense.

$\sigma_p$  = phenotypic standard deviation.

$$\text{GAM} = \frac{\text{GA}}{\text{Grand mean } (\bar{X})} \times 100$$

## Results and Discussion

**Analysis of variance:** The results revealed existence of significant differences among the genotypes studied for all characters except days to 50 per cent flowering.

### Days to 50% flowering

In case of days to 50% flowering, the longest duration was recorded by MIB-5236 (117 days) and MIB-5306 (117 days) followed by MIB-5786 (116 days) and MIB-4923 (114 days). MIB-5400 recorded a lowest number of days to 50% flowering *i.e.* 77 days. The range for days to 50% flowering in the population was between 77- 117 days with an average of

91 days (Table 2). This trait exhibited low heritability (13.64) coupled with low genetic advance as per cent of mean (1.98). Out of 395 genotypes, MIB-5400 (77 days), MIB-5128 (78 days) and MIB-5129 (79 days) flowered within 80 days duration whereas MIB-5236 (117 days), MIB-5306 (117 days), MIB-5786 (116 days), MIB-4923 (114 days), MIB-5503 (113 days), MIB-5072 (113 days), MIB-5516 (113 days), MIB-4964 (113 days), MIB-4932 (142 days) and MIB-5065 (112 days) flowered with > 110 days. 206 genotypes recorded flowering in 80-90 days and 176 genotypes recorded flowering in 91- 110 days. Similar results were reported by Anis *et al.* (2016) [2].

**Table 1:** Distribution of genotypes based on Days to 50% flowering

Range	Number of genotypes
70-80	3
81-90	206
91-100	154
101-110	22
111-120	10

Low heritability (13.64) coupled with low genetic advance as per cent of mean was observed for this trait indicating that the character was highly influenced by environmental effects and selection would be inefficient. Similar results were reported by Khare *et al.* (2014) [7].

**Table 2:** Descriptive statistics of yield and its component traits in a subset of *indica* MAGIC populations during *khari*, 2017

S. No.	Characters	Mean	Range		Standard Deviation		Standard Error Mean
			Maximum	Minimum			
1	Days to 50% flowering	91.00	117.00	77.00	6.46	0.32	
2	Plant height (cm)	125.02	158.00	80.20	63.27	3.18	
3	Number of panicles per plant	10.00	20.60	3.20	3.00	0.15	
4	Number of grains per panicle	128.00	251.70	45.40	31.62	1.59	
5	Panicle length (cm)	26.05	33.41	18.37	2.38	0.12	
6	Test weight (g)	23.20	36.45	16.27	2.98	0.15	
7	Grain yield per plant (g)	14.18	43.17	5.50	6.18	0.31	

### Plant height at maturity (cm)

Plant height showed a wide variation from 80.20cm to 158.00cm with a mean value of 125.02cm (Table 2). The tallest genotype was MIB-5692 (158.00cm) followed by MIB-5289 (157.60cm) and MIB-5587 (157.00cm) while MIB-5269 was shortest with 80.20cm. High heritability (91.51) and moderate genetic advance as per cent of mean (18.92) was observed for this trait.

The genotypes that recorded a plant height of <100cm are MIB-5159 (98.60cm), MIB-5963(98.40cm), MIB-5823 (98.00cm), MIB-4736 (98.00cm), MIB-5128 (97.60cm), MIB-5295 (95.60cm), MIB-5457 (95.40cm), MIB-4964 (95.00cm), MIB-5964 (94.40cm), MIB-5810 (94.00cm) and MIB-5295 (80.20cm). On the other hand, the genotypes that recorded >155cm of plant height are MIB-5853 (156.80cm), MIB-5587 (157.00cm), MIB-5289 (157.60cm) and MIB-5692 (158.00cm).

Plant height is an important trait because it is associated with plant lodging. Old rice cultivars were having higher plant height compared to modern rice cultivars and were also more susceptible to lodging with high rates of nitrogen application. Among the 395 lines evaluated, 206 lines have recorded >120cm indicating semi-tall to tall nature. Modern dwarf varieties are designed in such a way that they are less susceptible to lodging even though they are heavily fertilized with nitrogen (Fageria, 2007) [4]. The genotypes fall under

short stature (<120cm) are 189 in number which offer some resistance to lodging. But some of the genotypes *viz.*, MIB-5650 (119.60cm), MIB-5596 (106.00cm) and MIB-5866 (109.20cm) which were <120cm were prone to lodging. This might be due to weak culm of the plant. While the above shown tallest genotypes which recorded >150cm were not prone to lodging. The reason behind this contradictory situation should be the presence of strong culm.

**Table 3:** Distribution of genotypes based on Plant height at maturity (cm)

Range (cm)	Number of genotypes
<91	1
91-110	73
111-130	236
131-150	74
>151	11

High heritability and moderate genetic advance as per cent of mean was observed for this trait indicating the operation of both additive and non-additive gene action in the inheritance of this trait. Hence, simple selection of this trait is rewarding for further improvement. Similar results were reported by Srihima *et al.* (2015) [15], Nisanth *et al.* (2017) [11] and Divya *et al.* (2018) [3].

### Number of panicles per plant

The number of panicle per plant ranged between 3.20- 20.60 with an average of 9.76 (Table 2). The highest number of panicles per plant was recorded in MIB-4815 (20.60) followed by MIB-5550 (20.40) and MIB-5143 (20.20) whereas the minimum number of panicles per plant was recorded in MIB-5128 (3.20). This trait exhibited high heritability (97.70) and high genetic advance as per cent of mean (59.48).

The genotypes that recorded >16 number per panicles per plant are MIB-5070 (16.20), MIB-5928 (16.20), MIB-5927 (16.40), MIB-5828 (16.60), MIB-5759 (16.80), MIB-5097 (16.80), MIB-5035 (17.80), MIB-5803 (18.00), MIB-4931 (18.20), MIB-4926 (18.6), MIB-5225 (18.60), MIB-4973 (19.60), MIB-5143 (20.20), MIB-5550 (20.40) and MIB-4815 (20.60).

The more the number of panicles per plant more will be the grain yield because this character has direct effect on yield per plant. This is true up to certain number of panicles per plant because most of the high yielding genotypes in this study were having less than or equal to 10 number of panicles per plant. The genotype that shown highest grain yield per plant had only 9 number of panicles per plant. In the present study, MIB-4815 had the highest number of panicles per plant (20.60) but the grain yield per plant in MIB-4815 was only 8.14g/plant. Similarly the next highest genotypes viz., MIB-5550 and MIB-5143 also recorded less grain yield per plant i.e. 13.59g and 13.23g respectively. This is due to large number of panicles per unit area, where there will be source as a limiting factor to fill large sink size which was reported by Fageria (2007)<sup>[4]</sup>.

**Table 4:** Classification of genotypes based on number of panicles per plant according to DUS characterization (Rani *et al.*, 2006)

Category	Range	Number of genotypes
Few	<11	296
Medium	11-20	96
Many	>20	3

High heritability and high genetic advance as per cent of mean was observed for this trait indicating the operation of additive gene action in the inheritance of this trait. Hence, simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Sumanth *et al.* (2017)<sup>[16]</sup>, Nishant *et al.* (2017)<sup>[11]</sup> and Divya *et al.* (2018)<sup>[3]</sup>.

### Number of grains per panicle

The number of grains per panicle ranged between 45.40- 251.70 with an average of 127.94 (Table 2). The maximum number of grains per panicle was recorded in MIB-5617 (251.70) followed by MIB-5669 (220.56) and MIB-4901 (220.00) whereas the minimum number of grains per panicle was recorded in MIB-4736 (45.40). This trait exhibited high heritability (97.11) and high genetic advance as per cent of mean (47.60).

The genotypes that recorded >200 number of grains per plant were MIB-5627 (201.30), MIB-5555 (203.40), MIB-5143 (208.70), MIB-5387 (214.20), MIB-6000 (214.50), MIB-4901 (220.00), MIB-5669 (220.56) and MIB-5617 (251.70). But these genotypes were not recorded highest grain yield per plant even though they were having highest number of grains per plant. This might be because of the presence of more number of chaffy grains than filled grains in the panicle but

only filled grains account directly for grain yield. On the other hand, the highest grain yielders viz., MIB-5867, MIB-5164 and MIB-5964 have recorded 142.00, 135.00 and 126.00 number of grains per plant which might be due to the presence of filled grains in more number than the chaffy grains in the panicle. Similar results were reported by Ranawake *et al.* (2013)<sup>[13]</sup>; Anis *et al.* (2016)<sup>[2]</sup>.

**Table 5:** Classification of genotypes based on number of grains per panicle when compared with Local check

Range	Number of genotypes
<181.23	376
>181.23	19

High heritability and high genetic advance as per cent of mean was observed for this trait indicating the operation of additive gene action in the inheritance of this trait. Hence, simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Sumanth *et al.* (2017)<sup>[16]</sup>, Divya *et al.* (2018)<sup>[3]</sup> and Iqbal *et al.* (2018)<sup>[5]</sup>.

### Panicle length (cm)

In case of panicle length, the longest panicle was recorded in MIB-6003 (33.41cm) followed by MIB-4832 (32.58cm) and MIB-6037 (31.79cm). MIB-4736 recorded a minimum panicle length of 18.37cm. The range for panicle length in the population was between 18.37- 33.41cm with an average of 26.05cm (Table 2). This trait exhibited high heritability (70.35) and moderate genetic advance as per cent of mean (12.87).

There is large variation in panicle lengths of the population. 22 genotypes were recorded panicle lengths of >30cm whereas 192 genotypes recorded panicle length of <26cm and the remaining fall in between 26- 30 cm. MIB-5691, MIB-4831, MIB-5495, MIB-5681, MIB-5692, MIB-5709, MIB-5507, MIB-5174, MIB-4747, MIB-5502, MIB-6039, MIB-5496, MIB-5995, MIB-5323, MIB-5982, MIB-5236, MIB-5143, MIB-5669, MIB-5828, MIB-6037, MIB-4832 and MIB-6003 are the genotypes that were recorded with highest values of panicle lengths. Similar results were reported by Liu *et al.* (2016) while studying 540 rice accessions where he observed panicle lengths ranged from 11.91cm to 39.98cm.

The longest panicle possessing genotypes viz., MIB-6003, MIB-4832 and MIB-6037 recorded 7.14g, 16.77g and 18.55g of grain yield per plant respectively. While the highest grain yielding genotypes viz., MIB-5867, MIB-5164 and MIB-5964 have recorded 25.60cm, 26.50cm and 25.20cm of panicle lengths respectively. This may be due to the disproportion of filled and chaffy grains in the panicle. Similar results were reported by Ranawake *et al.* (2013)<sup>[13]</sup>.

**Table 6:** Classification of genotypes based on panicle length (cm) according to DUS characterization (Rani *et al.*, 2006)

Category	Range (cm)	Number of genotypes
Short	16-20	12
Medium	21-25	180
Long	26-30	181
Very long	>30	22

High heritability and moderate genetic advance as per cent of mean was observed for this trait indicating the operation of both additive and non-additive gene action in the inheritance of this trait. Progeny selection or any modified selection may

be useful in improving this trait. These findings are in agreement with the results reported by Sumanth *et al.* (2017)<sup>[16]</sup>, Nishanth *et al.* (2017)<sup>[11]</sup>, Divya *et al.* (2018)<sup>[3]</sup>.

### 1000 Grain weight (g)

Highest value of 1000 grain weight was observed in MIB-5521 (36.45g) which is followed by MIB-5627 (34.1g) and MIB-5647 (32.6g) whereas the lowest value was recorded in MIB-4802 (16.27g). The mean value of 1000-grain weight was 23.20 and ranged between 16.27- 36.45g (Table 2). Similar results were reported by Meng *et al.* (2016)<sup>[10]</sup>. This trait exhibited high heritability (91.92) and high genetic advance as per cent of mean (23.46).

1000 grain weight also depends upon grain type. According to Ramaiah (1969)<sup>[12]</sup> classification of rice, the genotype MIB-5521 which has got highest value of 1000 grain weight (36.45g) is having medium slender grain type whereas, the genotype MIB-4802 with lowest 1000 grain weight (16.27g) is having short slender grain type. There are 15 genotypes *viz.*, MIB-5521, MIB-5627, MIB-5647, MIB-5592, MIB-5495, MIB-6039, MIB-5654, MIB-4932, MIB-5624, MIB-4931, MIB-5716, MIB-5323, MIB-5502, MIB-5853 and MIB-5375 which are having 1000 grain weight >30g. Most of the genotypes were long bolded type in the population because of which they weighted >25g.

**Table 7:** Classification of genotypes based on 1000-grain weight (g) according to DUS characterization (Rani *et al.*, 2006)

Category	Range (g)	Number of genotypes
Low	15-20	85
Medium	21-25	252
High	26-30	43
Very high	>30	15

High heritability and high genetic advance as per cent of mean was observed for this trait indicating the operation of additive gene action in the inheritance of this trait. Hence,

simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Nishanth *et al.* (2017)<sup>[11]</sup>, Divya *et al.* (2018)<sup>[3]</sup> and Iqbal *et al.* (2018)<sup>[5]</sup>.

### Grain yield per plant (g)

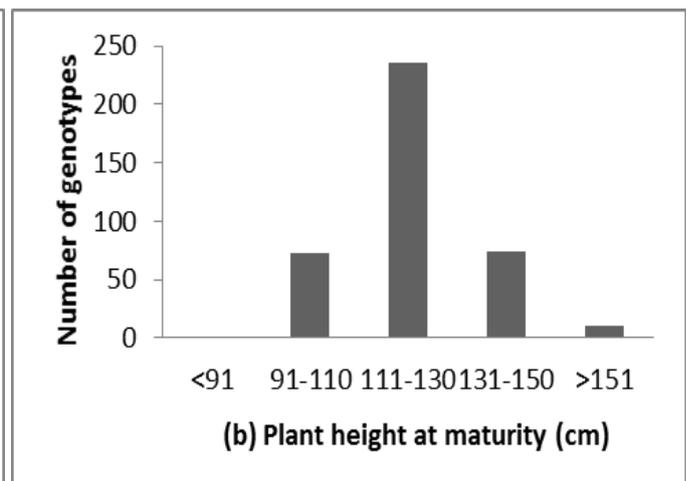
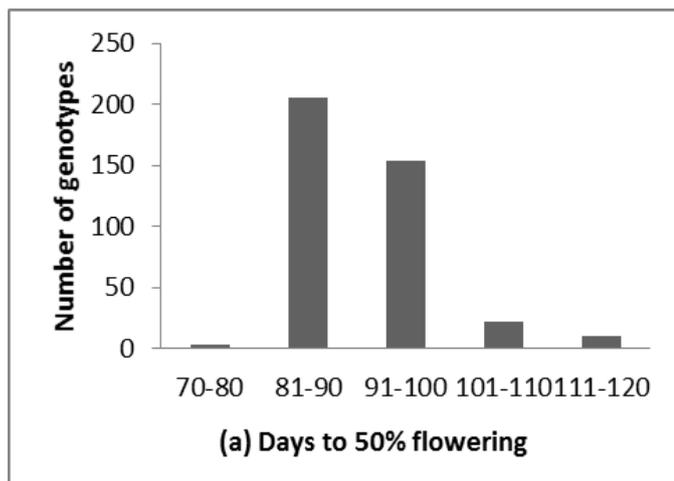
Maximum grain yield was recorded in MIB-5867 (43.17g) followed by MIB-5164 (42.91g) and MIB-5964 (39.84g) whereas a minimum yield of 5.5g was recorded in MIB-5705. The average grain yield per plant was recorded as 14.18g with the range varying from 5.5- 43.17g (Table 2). Similar results were reported by Meng *et al.* (2016)<sup>[10]</sup>. This trait exhibited high heritability (99.37) and high genetic advance as per cent of mean (86.37).

Grain yield is the topmost priority of any rice breeder in developing a variety. Among the 395 *indica* MAGIC lines studied, eight lines *viz.*, MIB-5589, MIB-5964, MIB-5164, MIB-4996, MIB-5867, MIB-5766, MIB-5293 and MIB-5877 had shown superior performance over the local check variety MTU 1075. So they are considered well adapted to the environment and good performers in terms of yield provided with nutrients and water non-limiting and with pests, diseases, weeds and other stresses effectively controlled.

**Table 8:** Classification of genotypes based on grain yield per plant (g) when compared to Local check

Range (g)	Number of genotypes
<36.58	387
>36.58	8

High heritability and high genetic advance as per cent of mean was observed for this trait indicating the operation of additive gene action in the inheritance of this trait. Hence, simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Sumanth *et al.* (2017)<sup>[16]</sup>, Nishanth *et al.* (2017)<sup>[11]</sup>, Divya *et al.* (2018)<sup>[3]</sup>.



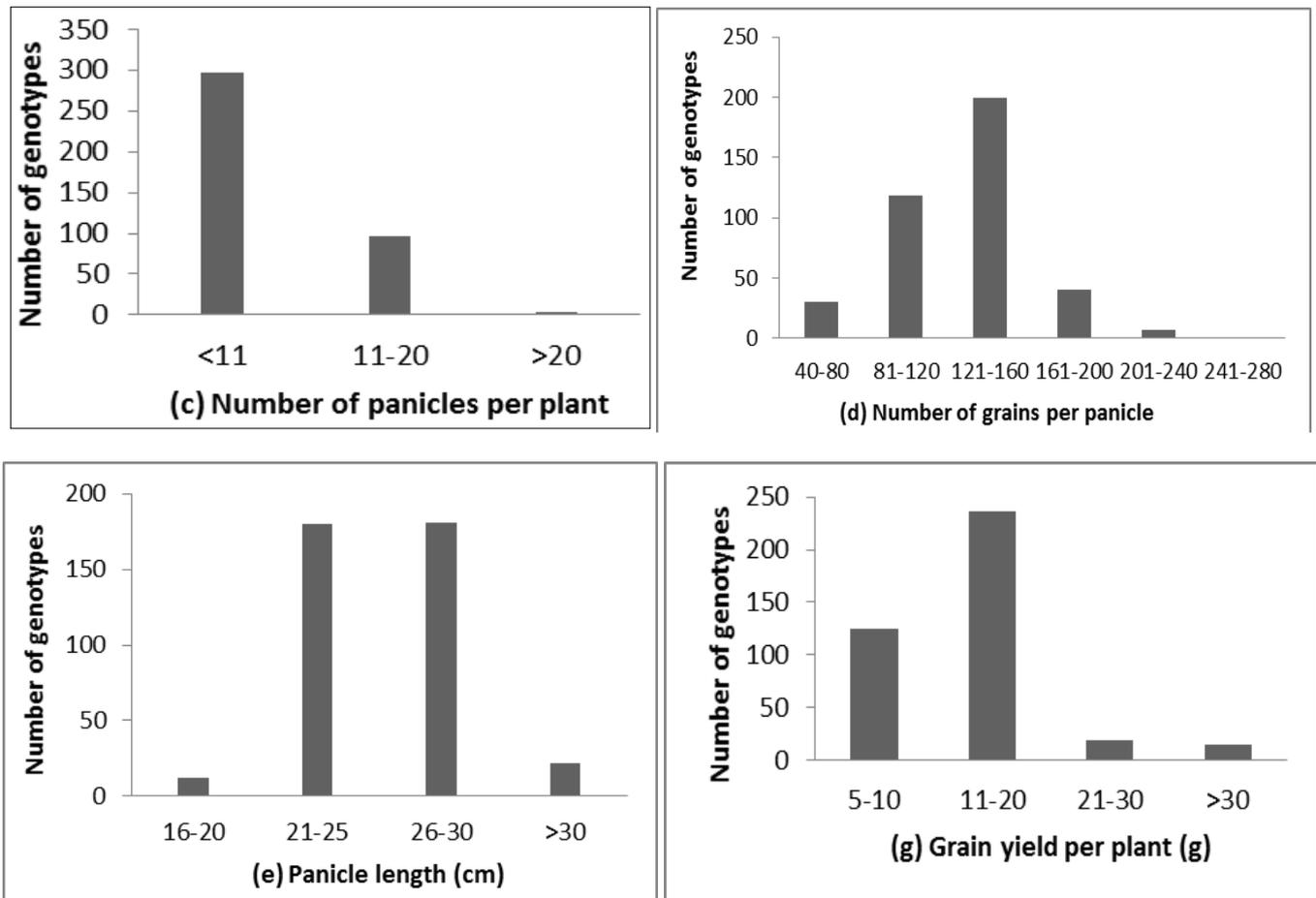


Fig 1: Distribution of a subset of 395 *indica* MAGIC populations of rice

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