

Assessment of Agro-morphological Characters among Complete Panicle Emergence Mutants of Samba Mahsuri (BPT-5204)

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Authors' contributions

This work was carried out in collaboration among all authors. Author BS carried out experiment in field for three seasons and wrote the protocol. Authors PG, JK, MDE managed the literature searches and performed the statistical analysis. Authors GSL, APP, RMS, VRS, KPH, PS and AKS associated with this research. Author MSM designed the study and give suggestion and ideas on improvisation of the study. All authors read and approved the final manuscript

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ABSTRACT

Aims: The aim of the present work was to generate complete panicle emergence mutants of Samba Mahsuri (BPT-5204), using the chemical mutagen, ethyl methane sulphonate (EMS)

Place and Duration of Study: The field evaluation was carried out repeatedly in two locations at Indian Institute of Rice Research, Rajendranagar and at ICRISAT Patancheru Hyderabad. The duration of the study was three successive seasons in triplicates namely, june-2014, january-2015 and june-2015.

Methodology: Seedlings of 28-30 days old were transplanted in 5 lines (each line containing 20 plants) into the field. The plant spacing was 20 cm by 15 cm with density of one hill. The field was

irrigated throughout the experiment with average of 10 cm water above the soil level. Regular hand weeding was embarked upon to free the plant of inter specific competition. The phenotypic data was recorded for CPE mutants through visual assessment. The characteristics that required measurements were done according to the usual procedure. The Distinctness, Uniformity and stability of the CPE mutant lines have been recorded following (DUS) test guidelines by UPOV guidelines for rice (38) & Yoshida S (44).

Results: The identified stabilized thirteen complete panicle emergence (CPE) mutants showed superior agro morphological characters, compared with wild type (BPT-5204). The mutants CPE-2 and CPE-3 took 100 days to flowering and CPE-4 and CPE-7 mutants showed superiority for panicle length, and CPE-5 exhibited good performance for grain yield. In correlation analysis CPE trait had a significantly positive correlation with PH and TGW and negative correlation with 50%DFF. The CPE mutants used in the present study exhibited variability for most of the studied traits. Significant variation was detected in the identified stabilized CPE mutants for plant height, panicle length, flag leaf length and width, 50% flowering, different grain types and 1000 grain weight.

Conclusion: The present study discovered adequate genetic divergence in the thirteen stabilized CPE mutants for various qualitative and quantitative traits. The promising mutants identified during the current study have the potential to be used in future breeding programs for getting productive and quality results.

Keywords: Samba Mahsuri (BPT-5204); mutation; complete panicle exsertion (CPE); biotic; abiotic.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is an important staple food for more than half of the world's population [1, 2,3,4,5]. In India 70-75% of the people mainly depend on rice. Rice plays an important role in shaping the cultures, diet and economies of millions of people by provide food and nutritional security eradicating poverty [6]. Rice is not only the most important food crop but a model plant that has attracted broad interests in basic and applied research [7,3,5]. Rice act as a main source of income of many peoples in the world and it occupies a major position in many countries because for its importance in traditional diets [8]. In the year 2017 total rice production in the world is 754.6 million tons [9]. Many other problems such as unabated growth of population in India, demand of the rice is gradually increasing. To meet the demand of rice consumer's maximization of yield and achieving acceptable grain quality is top most priority in rice Improvement programs. Rice is a global leading food crop and it is an important item to mutagenesis. Food grain production was exceeds, and there are number of constraints like biotic, abiotic stresses, incomplete panicle emergence, lodging etc hampering the yield production [10]. For genetic and physiological assessments of yield contributing factors in rice, Induced rice mutants are used as important research tools. Since 1960s, to till date several collections of mutant lines from different species have been isolated and successfully used in

many different areas of plant biology and crop breeding [11]. Samba Mahsuri (BPT-5204) is one of India's most popular and highly prized rice varieties, cultivated in 1-2 million hectares of land across India. But unfortunately Samba Mahsuri variety is susceptible to many biotic, abiotic stresses and exhibits incomplete panicle emergence, leads to reduction in the 10-20% total crop yield. Complete panicle emergence is economically important trait which influences the emergence of panicle out of flag leaf, resulting in to the complete grain filling and increase crop yield [12]. Therefore, mining of superior and desired genotypes within the mutant germplasm of elite rice variety Samba Mahsuri is important for the rice breeders. Hence, assessment of Samba Mahsuri mutants is very important in rice breeding from the standpoint of selection and conservation of different Samba Mahsuri mutant lines for further utilization in crop improvement programs. Induced mutagenesis is one of the powerful tools to increase the extent of variation in the gene pool of rice. Mutation breeding approaches are being widely used throughout the world for biotic, abiotic stresses in various crops [13,14]. Chemical mutagen EMS is more effective than physical mutagens [15,16,17] and it mainly causes GC to AT transition in theplant genome [17,18,19]. Chemical mutagenesis has been widely used to create genetic variability for breeding research and genetic studies [20].

The aim of the present work was to generate complete panicle emergence mutants of Samba

Mahsuri (BPT-5204), using the chemical mutagen, ethyl methane sulphonate (EMS).

2. MATERIALS AND METHODS

2.1 Identification of Mutants having Complete Panicle Emergence in Mutagenized Population of Samba Mahsuri (BPT-5204)]

A total of 10,500 individual Samba Mahsuri (BPT-5204) mutant M₂ seeds were sown on nursery beds and the 28-30 days old seedlings were transplanted in 5 lines (each line containing 20 plants) into the field. The plant spacing was 20 cm by 15 cm with density of one hill. The field was irrigated throughout the experiment with average of 10 cm water above the soil level. Regular hand weeding was embarked upon to free the plant of inter specific competition. The M₂ seeds of 10,500 lines were observed carefully for the identification of useful mutants, which have some agronomic value i.e. complete panicle emergence. In M₂ generation, 155 individual potential lines were identified with the desired trait and they were forwarded to M₃ generation. In M₃ generation, 31 plants were selected on the basis of special trait of inheritance and these lines were forwarded to M₄ generation and grown in multiple rows to observe uniformity. In M₄ generation 22 entries were selected based on uniform maturity. The selected 22 individual uniform maturity entries were forwarded to M₅ generation and grown in three replications. Three replications were transplanted in randomized complete block design (RCBD) mode. In M₅ generation, thirteen uniform maturity entries were selected based on the yield parameters and the selected thirteen entries were forwarded to M₆ generation and grown in three replications each along with checks. The selected thirteen entries were advanced to further generations up to M₈. Mohapatra, T., et al. [6] (Table: 1).

Table 1. Generation wise screening of CPE lines (M2-M8)

Generation	CPE Entries
M2	155
M3	31(22 Uniform+9 Non uniform)
M4	22(Uniform)
M5	13 Uniform
M6	13 Uniform
M7	13 uniform
M8	13 Uniform

2.2 Assessment of Samba Mahsuri Mutants for Complete Panicle Emergence

In order to characterize complete panicle emergence mutants of Samba Mahsuri, screening carried out in a randomized complete block design (RCBD) at two different locations namely IIRR, Rajendranagar, Hyderabad, situated at 17.53N latitude and 78.27E longitude, 545 m altitude, with a mean temperature of 31.2°C and mean annual precipitation of 988.3 mm. The pH of soil was recorded as 8.53 and 8.58, before and after planting, respectively and, at ICRISAT Patancheru Hyderabad. Complete panicle emergence in mutants was measured at the time of maturity from the base of panicle to the tip of the last spikelet Zhan, Chengfang et al. [21] and Zhao, C. F. et al. [22]. The mutant lines panicle internodes were emerged completely from the flag leaf. The mutants with panicles emerged completely from the flag leaf were selected as Samba Mahsuri mutants with complete Panicle emergence. To know, the complete panicle emergence mutants of Samba Mahsuri, this Indica variety (BPT-5204) was extensively screened, for the three seasons in triplicates namely, june-2014, january-2015 and june-2015. Samba Mahsuri (BPT-5204) panicles emerge partially and the partially emerged panicles produce chaffy grains/partially-filled grains and affect the unabridged grain recovery during harvesting. This characters makes Samba Mahsuri is an ideal genotype for identifying mutational changes in traits of panicle exsertion.

2.3 Evaluation of Agro-morphological Characters of CPE Promising Mutants

The phenotypic data was recorded for CPE mutants through visual assessment. The characteristics that required measurements were done according to the usual procedure. The Distinctness, Uniformity and stability of the CPE mutant lines have been recorded following (DUS) test guidelines. The phenotypic data was recorded at maturity stage of the rice crop for characters like panicle morphology and data for quantitative characters like plant height, number of tillers/plant, number of reproductive tillers/plant, flag leaf length, flag leaf width, panicle length, grain type, days to 50% flowering, number of spikelet's/panicle, total plant yield, and 1000 seed weight were also recorded as per the guidelines by UPOV guidelines for rice [23] & Yoshida S [12] (Table 2).

The plant height was refers to the longest distance between the plant base and the tip of the highest leaf (or panicle, whichever is longer) as per the guidelines by UPOV guidelines for rice [23] and Yoshida S. [12]. It was measured from the base of the plant to the tip of main panicle (Table 2). Total number of tillers/plant and total number of productive tillers/plant was calculated by physical assessment at the time of maturity stage of the plant (Table 2). Flag leaf length and flag leaf width was measured in centimeters using a ruler, at the time of grain filling stage of the plants [12]. Panicle length was measured in centimeters at the time of maturity stage of the plant [12]. Panicle length was measured from the base of the panicle to the tip of last spikelet prior to harvesting. Complete panicle exertion was measured in centimeters at the maturity stage of the plant. Complete panicle exertion was measured from the flag leaf to the panicle base using a ruler Zhan Chengfang, et al. [21] and Zhao, C. F. et al. [22]. Grain length and breadth of CPE mutants was measured with a vernier caliper Hailiang Mao. et al. [24]. Randomly selected ten fully filled grains from each genotype were lined up length-wise along a vernier caliper to measure grain length and then arranged by breadth to measure grain width. Thirteen CPE promising mutants were observed for days to 50% flowering. The total numbers of days taken from the date of sowing to exertion of the panicle tip above the sheath of the flag leaf [23]. The time when 50 percent of the panicles have at least partially exerted from the boot are considered as 50% heading of a plant [25]. The potential number of filled grains per panicle has been essentially established by the number of fertilized flowers (kernels), and these are calculated at the time of maturity stage of the plants. All, flowers which are fertilized can become filled grains [25]. Single plant yield was calculated after harvesting of the genotypes. Five individual plants were selected randomly from each genotype to calculate the single plant yield [26]. 1000 fully filled grains from each genotype were collected after harvesting to calculate the test weight [26] (Table 2).

2.4 Statistical Analysis

The thirteen genotypes of one and half years RCBD mean data were subjected to analysis of variance (ANOVA), and phenotypic coefficient of variation (PCV), using SPAR 2.0 software [27]. Pearson correlation coefficient was analyzed using R statistical software (3.2.0) [4].

Agro morphological characters were carried out at the 50% flowering stage and full maturity stage of the plants. In this study 13(M8) complete panicle emergence mutant lines of agro-morphological characters data were recorded for following 12traits. Quantitative characters of CPE mutants are given in Table 3.

3. RESULTS AND DISCUSSION

Assessment of CPE mutants through various morphological traits is an important step for assessment of its genetic potential. Improve in grain yield potential is the most important goal of the rice breeders. To enhance the yield and yield contributing traits in rice, mutation breeding is the best available choice. Samba Mahsuri is a popular rice variety with good cooking quality characteristics. It is susceptible to many biotic and abiotic stresses and it exhibits incomplete panicle emergence. To overcome this problem, increase the extent of variation in gene pool of rice by using mutation breeding is the potent way. To develop a rice variety with medium slender grain, good cooking quality, and early duration with high yielding than Samba Mahsuri is the biggest task for plant breeders. So, in this current study Samba Mahsuri was used to create genetic variation through EMS mutagenesis (Mutation breeding).Stabilized thirteen CPE mutants were analyzed separately for different agronomic traits. The analyses of variance of different Samba Mahsuri CPE mutant lines based on genotypes for quantitative traits are shown in Table 3. Analysis of variance indicated that the difference among genotypes for all the traits under study viz., Plant height, number of tillers/plant, number of productive tillers/plant, flag leaf length and width, panicle length, complete panicle exertion, grain type, days to 50% flowering, number of filled grains/panicle, single plant yield and 1000 grain weight were highly significant. Compare with Samba Mahsuri a notable variation was observed among thirteen CPE mutant lines for yield and yield contributing traits (Table 2).

3.1 Plant Height (cm)

Highly significant difference was observed for plant height, among thirteen CPE mutant lines have shown minimum 83 cm (CPE-1) to maximum 120 cm (CPE-7). One mutant CPE-1 showed plant height of 83cm, is equal to wild type plant height (Table 3).Among thirteen CPE mutants, 84.6% genotypes showed short (91-100 cm) plant height (excluding panicle), and 15%

genotypes showed medium (111-130 cm) plant height.

3.2 Number of Tillers/Plant

All thirteen CPE mutants were showed less tillers/plant ranging from minimum 15 (CPE-10) to maximum 24(CPE-1).where as in wild type total tiller number/plant is 27(Table 3). Among thirteen CPE mutants highest number of genotypes 69.2% showed 15-20 tillers/plant and 30.7% showed 21-25 tillers/plant. A notable variation was observed among thirteen CPE mutants for number of tillers/plant.

3.3 Number of Productive Tillers/Plant

Number of productive tillers/plant was ranging from minimum 13 (CPE- 3) to maximum 23 (CPE-1), whereas wild type showed 15

reproductive tillers (Table 3). For the character number of productive tillers/plant a total of ten genotypes (76.9%) showed medium (11-20) productive tiller number/plant and three genotypes (23.07%) showed many (>20) productive tiller number/plant. Highly significant differences were observed among thirteen CPE mutants for number of productive tillers.

3.4 Flag Leaf Length (cm)

In CPE mutant's flag leaf length ranging from minimum 26 cm (CPE-3 & CPE-9) to maximum 33 cm (CPE-11).In case of wild type length of the flag leaf is 35 cm (Table. 3 & Fig. 1A). For the character leaf length, 69.2% accessions exhibited short leaf type (25-30 cm), and 30.7% accessions were of a medium type (31-35 cm). Length of the flag leaf in CPE mutants was less compared with wild type.



Fig. 1A. Measurement of CPE mutant lines flag leaf length

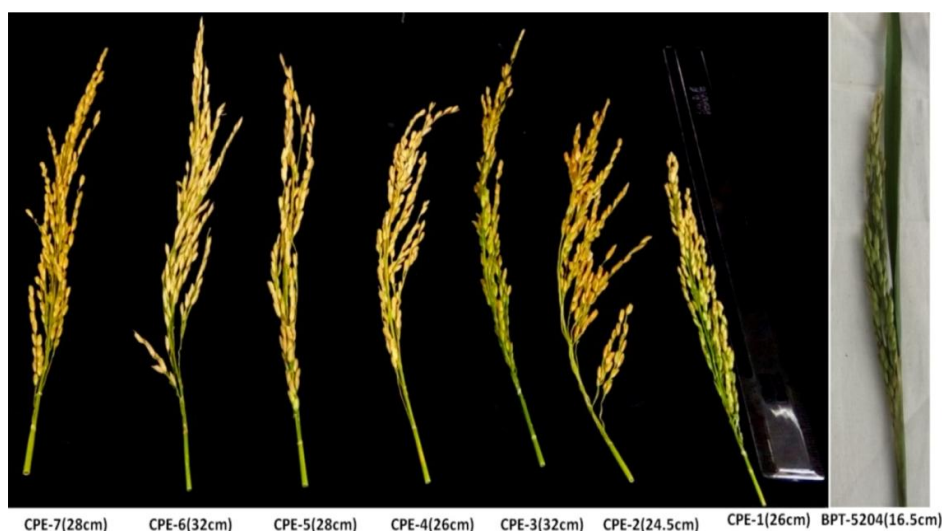


Fig. 1B. CPE mutants showed significant variation in panicle length

3.5 Flag Leaf Width (cm)

In CPE mutant's flag leaf width ranging from minimum 1.2 cm (CPE-1, 9 & 10) to maximum 2.2 cm (CPE-4). In case of wild type width of flag leaf is 1.2 cm (Table 3). For the leaf width, among thirteen CPE accessions, highest number of the accessions 92.30% recorded medium type of leaves and 7.69% accessions recorded broad type of leaves. Highly Significant variation was observed among thirteen CPE mutants for flag leaf width.

3.6 Panicle Length (cm)

Stabilized CPE mutant lines showed significant variation in the panicle length. Length of the mutant line panicle ranging from minimum 22 cm (CPE-3) to maximum 32 cm (CPE-4 & CPE-7). In case of wild type length of the panicle is 16.5 cm (Table 3 & Fig. 1B). Among thirteen CPE mutants highest number of the genotypes (76.9%) fall under the long panicle length (PL) category (26-30 cm), and 23.07% genotypes fall under medium panicle length (PL) category (21-25 cm).

3.7 Complete Panicle Exsertion (CPE)

CPE mutants showed significant difference in panicle exsertion ranging from maximum CPE-7 (6.8 cm) to minimum CPE-1 (2 cm). But in case of wild type 10-20% panicle choking was observed. In Samba Mahsuri 4-5 cm panicle was present within the flag leaf (Table 3 & Fig. 1D & 1E). For the character CPE highest number of genotypes

46.1% exhibits 4-6 cm of complete panicle exsertion, 30.7% genotypes showed 2-4 cm of complete panicle exsertion and, 23.0% genotypes showed 6-8 cm of complete panicle exsertion (Fig. 1F.).

3.8 Grain Type

Four different grain types were identified among thirteen CPE mutant lines. The mutants with different grain types like long slender (L/B>3.0), long bold (L/B<3.0), medium bold (L/B<2.5), and medium slender (L/B 2.5-3.0) were identified. Eight mutant genotypes 61.5% (CPE-1,3,7,9,10,11,12 &13) showed medium slender grain type (MS) like wild type, two mutant genotypes 15.3% (CPE-5 & 6) showed long slender grain (LS), two mutants 15.3% (CPE-2 & 4) showed medium bold (MB) and one mutant genotype 7.69% (CPE-8) showed long bold (LB) grain type (Table 3 & Fig. 1H).

3.9 Days to 50% Flowering

Among thirteen CPE mutants CPE-2 & 3 showed minimum 100 days and CPE-1, CPE-9 & CPE-10 showed maximum 115 days to 50% flowering. Among thirteen genotypes three genotypes showed 115 days to 50% flowering like wild type (Table 3). For the character time of heading (50% of plants with panicles) were observed and noticed that 76.9% genotypes were of medium type (91-110 days), and 23.07% genotypes fall under late type (111-130 days). Significant variation was observed among thirteen mutants for days to 50% flowering.

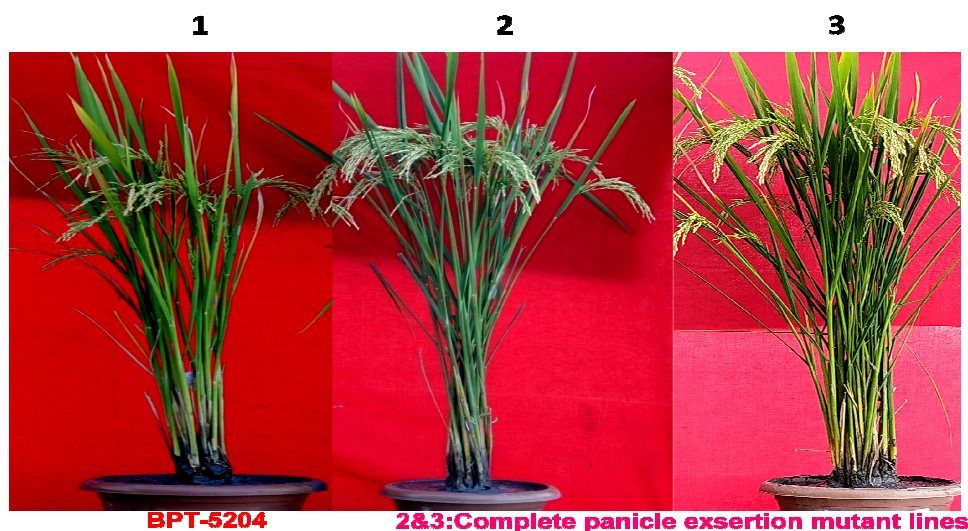


Fig. 1C. Comparison between wild type and CPE mutants

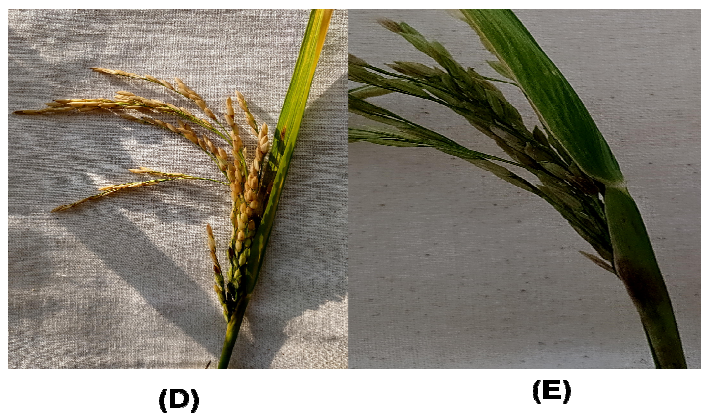


Fig. 1D. Incomplete panicle exertion in Samba Mahsuri (BPT-5204) during grain filling stage
Fig. 1E. Disease caused by incomplete panicle exertion in Samba Mahsuri panicle during grain filling stage



Fig. 1F. Phenotypic variation of complete panicle exertion in Samba Mahsuri CPE mutants

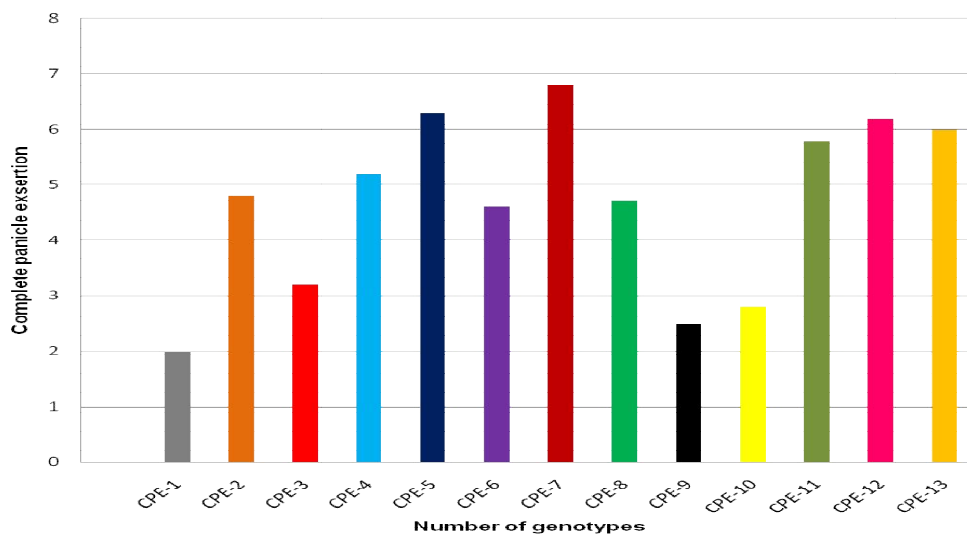


Fig. 1G. CPE mutants showed significant difference in complete panicle exertion

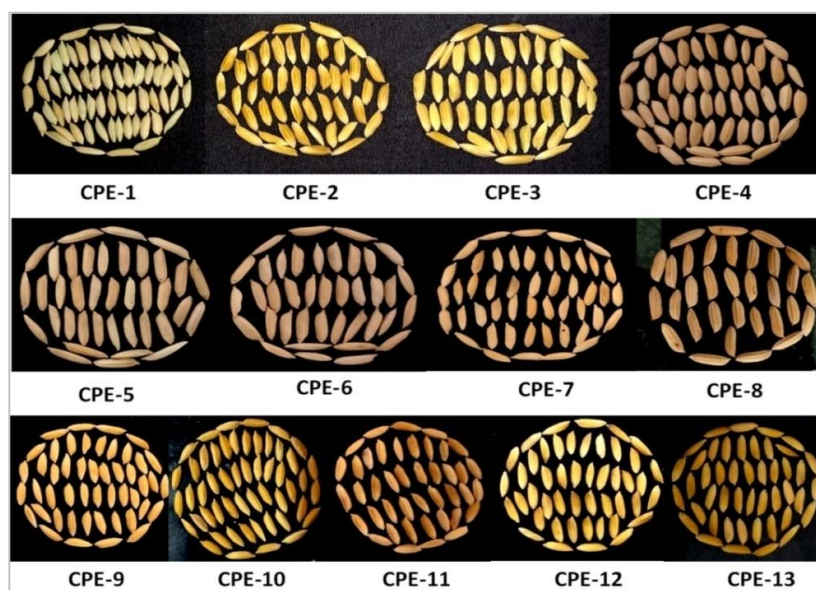


Fig. 1H. CPE mutant lines with different grain types

3.10 Number of Filled Grains/Panicle

Among thirteen CPE mutants CPE-13 had the lowest number of filled grains/panicle (202), and CPE-11 had the highest number of filled grains/panicle (225). In case of wild type number of filled grains per panicle is 200, which is lower than the CPE mutant lines (Table 3). For the character number of filled grains/panicle 38.4% genotypes fall under 201-210 grains/panicle category, 38.4% genotypes fall under 211-220 grains/panicle category and 28.0% genotypes fall under 221-230 grains/panicle category. Significant variation was observed among thirteen mutants for number of grains per panicle.

3.11 Single Plant Yield (gr)

The highest grain yield per plant was observed in the CPE-5 (26.4gr) and lowest was observed in the CPE-3 (20gr), which is higher than the wild type 15.8gr (Table 3). For the character single plant yield highest number of the genotypes 92.3% showed 20-25gr single plant yield and 7.6% showed 25-30gr single plant yield. Highly significant difference was observed among thirteen mutants for plant yield.

3.12 1000 Seed Weight (gr)

1000 seed weight was ranging from maximum 23.99gr (CPE-5) to minimum 14.12gr (CPE-1). Among 13 CPE mutants CPE-1 showed less (14.12 gr) 1000 seed weight, compare with wild

type. Test weight of wild type is 15.2gr (Table 3). For the character grain weight of 1000 fully developed grains, highest number of the genotypes (76.9%) showed low grain weight (15-20 g) and 23.0% genotypes showed medium grain weight (21-25 g). Among thirteen genotypes significant variation was observed for 1000 seed weight.

4. CORRELATION DATA BETWEEN AGRO-MORPHOLOGICAL CHARACTERS OF CPE MUTANTS

The results of correlation analysis reveals that CPE trait showed positive and highly significant correlation with plant height ($r=0.84$), flag leaf length ($r=0.71$), test weight ($r=0.55$), and flag leaf width ($r=0.51$) respectively. However, number of reproductive tillers/plant ($r=0.94$) showed highly positive and significant correlation with number of tillers/plant. Among eleven characters panicle length showed positive correlation with flag leaf length ($r=0.67$), and plant height ($r=0.62$) showed positive correlation with test weight, flag leaf length ($r=0.52$) and panicle length ($r=0.41$). Flag leaf length showed positive significant correlation with flag leaf width ($r=0.50$) (Fig. 11).

However, days to 50% flowering showed highly significant negative correlation with CPE (-0.53), test weight (-0.73), plant height (-0.43), flag leaf length (-0.08), and flag leaf width (-0.24) respectively.

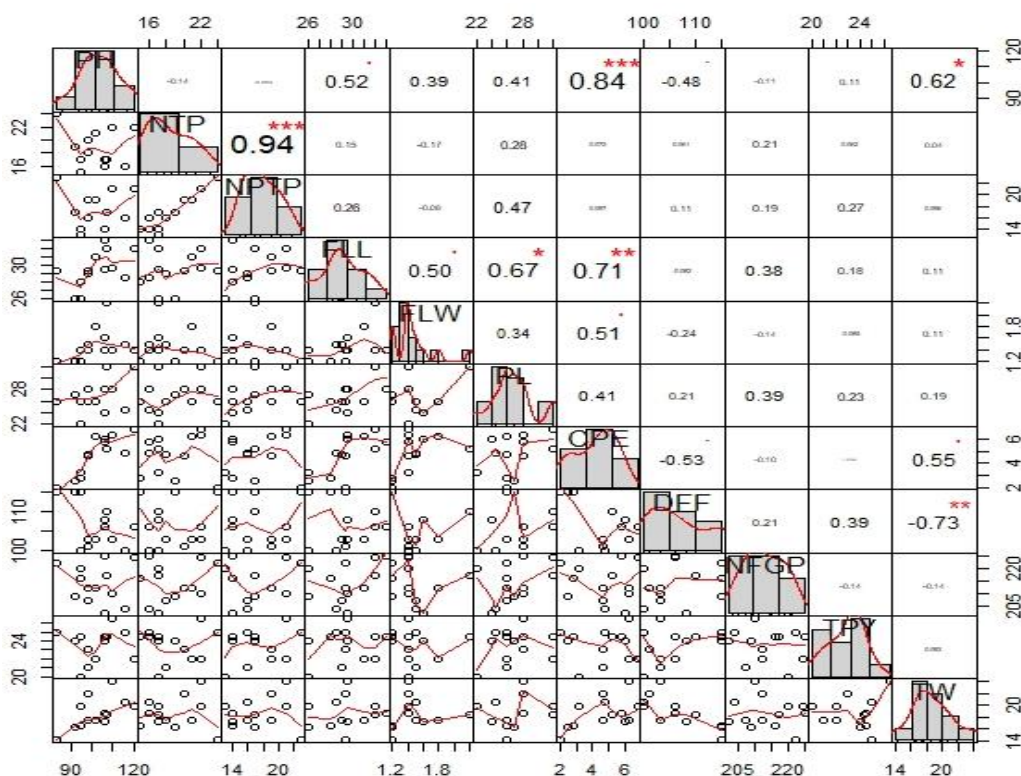


Fig. 11. Pearson's correlation coefficients among thirteen CPE mutants

PH=plant height, PL=panicle length, FLL=flag leaf length, NTP=number of tillers/plant, NRT= number of reproductive tillers/plant, FLW=flag leaf width, SPY= single plant yield, DFF=days to 50% flowering, TW= 1000 test weight, NFGP= number of filled grains/panicle

In this present study, among thirteen CPE mutants, eleven genotypes showed semi dwarf plant height (80-110 cm) and exhibits higher single plant yield. Plant height is a complex trait in rice crop [28,29,30]. Reduction in plant height may reduce yield losses and enhance their resistance to lodging (1). Semi dwarf plant height is a key feature for higher yield production and it has been extensively utilized in the improvement of rice throughout the world [31,32]. The genotypes, which were produced more number of effective tillers/plant that showed higher grain yield in rice [33,34]. Yaqoob et al. [35] and Tiwari et al. [36] were observed significant variations among genotypes for days to maturity, plant height, panicle length, 50% flowering, spikelets/panicle, number of fertile spikelet's and grains yield/plant. Similarly in this current study all the genotypes had significant variation with each other. Joshi et al. [37] described that, test weight (1000 grain weight) have been used by several researchers for characterizing rice varieties. In this current study we found that number of filled grains/panicle (NFGP) has

highest positive direct effect on yield. According to Yolanda and Das [38] and Zahid et al. [39] number of filled grains panicle-1 has highest positive direct effect on yield. It implies that the number of filled grains per panicle could be considered as critical criteria for yield improvement Samonte et al. [40] and Mahto et al. [41]. Correlation studies for a number of agronomic traits with panicle exertion (PE) have been reported by Yang et al. [42] and Hori et al. [31]. Earlier researchers reveal that the panicle exertion was positively correlated with PH, PL, and TGW [39,21,22]. It implies that PE plays a crucial role in the regulation of grain weight. Similarly in this present study we found that CPE had a significantly positive correlation with PH and TGW. It had a significant positive correlation with FLL, and FLW. However, in this present study highest correlation was corresponded to the total tillers and effective tillers. Flag leaf length was positively correlated with plant height, flag leaf width and panicle length. Plant height showed positive correlation with effective tillers and panicle length. It signifying the role of plant

Table 2. CPE promising mutant's quantitative traits methodology

List of quantitative traits		
Growth trait/yield trait	Denotation	Method of evaluation
Plant height(cm)	PH(cm)	The average height from the base to the tip of the main panicle
Number of tillers/plant	NT(number)	Count the number of tillers per plant
Number of productive tillers/plant	NPT(number)	Count the number of productive tillers per plant
Flag leaf length(cm)	FL (cm)	measure the length of the flag leaf
Flag leaf width(cm)	FLW(cm)	Calculate the width of the flag leaf
Panicle length(cm)	PL(cm)	Measure the panicle length from the node below the lowest branch on the panicle to the top of first superior spikelet
Complete panicle exertion	CPE(cm)	Measure from the flag leaf to the panicle base using a ruler
Grain type	GT	Record the different grain types in the all the accessions
Days to 50% flowering	DFF(days)	Count the number of days from seeding to flowering
Number of filled grains/panicle	NFG/P(number)	Count the number of spikelet's per panicle
Yield/Plant(gm)	Y/P(gm)	Weigh total grains produced per plant
1000 grain weight(gm)	1000GW(gm)	Weigh any 1000 filled grains

Table 3. Agro-morphological data of CPE mutants

Trait/ Characters	Wild type		Complete panicle emergence mutants												
	BPT-5204	CPE-1	CPE-2	CPE-3	CPE-4	CPE-5	CPE-6	CPE-7	CPE-8	CPE-9	CPE-10	CPE-11	CPE-12	CPE-13	
PH	83.0	83.0	116.0	95.0	107.0	110.0	98.0	120.0	98.0	92.0	95.0	106.0	102.0	106.0	
NTP	27.0	24.0	16.0	17.0	17.0	22.0	20.0	22.0	18.0	19.0	15.0	16.0	21.0	17.0	
NPTP	15.0	23.0	16.0	13.0	17.0	21.0	19.0	21.0	16.0	17.0	14.0	14.0	19.0	14.0	
FLL	35.0	29.3	28.5	26.0	32.0	29.6	29.3	32.0	29.0	26.0	28.0	33.0	31.0	29.5	
FLW	1.2	1.2	1.5	1.4	2.2	1.4	1.4	1.4	1.5	1.2	1.2	1.4	1.8	1.6	
PL	16.5	26.0	24.5	22.0	32.0	28.0	28.0	32.0	26.0	27.0	26.0	28.0	26.0	24.0	
CPE	0.0	2.0	4.8	3.2	5.2	6.3	4.6	6.8	4.7	2.5	2.8	5.8	6.2	6.0	
GT	MS	MS	MB	MS	MB	LS	LS	MS	LB	MS	MS	MS	MS	MS	
DFF	115.0	115.0	100.0	100.0	110.0	103.0	101.0	106.0	103.0	115.0	115.0	106.0	103.0	108.0	
NFGP	200.0	222.0	204.0	220.0	217.0	210.0	212.0	224.0	207.0	209.0	216.0	225.0	212.0	202.0	
TPY	15.8	25.0	25.0	20.0	24.4	26.5	23.0	22.0	21.0	24.0	24.5	24.5	22.0	24.0	
TW	15.2	14.1	20.6	19.7	18.4	24.0	21.8	19.9	17.5	16.3	16.5	18.5	17.5	17.2	

PH: Plant height; NTP: Number of tillers/plant; NPTP: Number of productive tillers/plant; FLL: Flag leaf length (cm); FLW: Flag leaf width (cm); PL: Panicle length (cm); CPE: Complete Panicle exertion; GT: Grain type; DFF: Days to 50% flowering; NFGP: Number of filled grains/panicle; TPY: Total plant yield (gm); TW: 1000 seed weight (gm)

height in enhancing the panicle length by large stem reserve mobilization [43]. Similar results were also reported by Shishir Sharma et al. [44] and Wattoo et al. [45], Rajeswari and Nadarajan [46], Surek and Beser [47] It is well known that 50% flowering (DFF) is one of the most important agronomic trait in rice [48,49]. Current study reveals that DFF had a highly significantly negative correlation with CPE, which was similar to the results reported by [39,21,22]. However, in this current study we found that DFF had significantly negative correlation with PH, TGW, FLL and FLW. The CPE mutants used in the present study exhibited variability for most of the studied traits. Significant variation was detected in the identified stabilized CPE mutants for plant height, panicle length, flag leaf length and width, 50% flowering, different grain types and 1000 grain weight.

5. CONCLUSION

In the present study the CPE accessions showed ample range of divergence in the various qualitative and quantitative traits. The promising mutants identified during the current study have the potential to be used in future breeding programs for getting productive and quality results. These phenotypic characters were played key role in crop improvement. This material can use as donor material, which provides wide scope for selection of superior and desired genotypes for breeders to transfer into another genetic background for further improvement.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Mather Kristie A, et al. The extent of linkage disequilibrium in rice (*Oryza sativa* L.). *Genetics*. 2007;177(4):2223-2232.
- Rana, Md Masud, et al. Genetic diversity analysis of NERICA lines and parents using SSR markers. *Int. J. Plant Soil Sci*. 2018;23(6):1-10.
- Sasaki A, et al. A mutant gibberellin-synthesis gene in rice. *Nature*. 2002; 416(6882):701-702.
- Suman K et al. Variation of grain quality characters and marker-trait association in rice (*Oryza sativa* L.); 2019.
- Yuan LP, Virmani SS. Status of hybrid rice research and development. *Hybrid rice*. 1988;7-24.
- Mohapatra T, et al. EMS induced mutants of upland rice variety Nagina22: generation and characterization. *Proceedings of the Indian National Science Academy*. 2004; 80(1):163-172.
- Feng et al. 2002; Goff et al., 2002; Sasaki et al., 2002; Yu et al.; 2002.
- DES, DACFW; 2016. Available:<http://agricoop.nic.in>
- FAO (Food and Agriculture Organization) Rome; 2017. Available:<http://faostat.fao.org/>
- Mohanty, Samarendu, et al. Rice and climate change: Significance for food security and vulnerability. *International Rice Research Institute*. 2013;14.
- Fu, Hao-Wei, You-Fa Li, Qing-Yao Shu. "A revisit of mutation induction by gamma rays in rice (*Oryza sativa* L.): implications of microsatellite markers for quality control. *Molecular Breeding*. 2008;22(2):281-288.
- Yoshida, Shouichi. *Fundamentals of rice crop science*. *Int. Rice Res. Inst*; 1981.
- Ashraf M. Inducing drought tolerance in plants: Recent advances. *Biotechnology Advances*. 2010;28(1):169-183.
- Alcantara TP, Bosland PW, Smith DW. Ethyl methanesulfonate-induced seed mutagenesis of *Capsicum annuum*. *Journal of Heredity*. 1996;87(3):239-241.
- Bhat TARIQ A, Khan AH, Parveen SAHBA. Comparative analysis of meiotic abnormalities induced by gamma rays, EMS and MMS in *Vicia faba* L. *J Indian Bot Soc*. 2005;84:45-48.
- Botticella E, Sestili F, Hernandez-Lopez A, Phillips A, Lafiandra D. High resolution melting analysis for the detection of EMS induced mutations in wheat *Sbella* genes. *BMC Plant Biol*. 2011;11:15610. 1186/1471-2229-11-156.6.
- VRK Reddy. Cytogenetic effects of gamma rays and ethyl methane sulphonate in chilli pepper (*Capsicum annuum* L.). *Cytologia*. 2000;65(2):129-133.
- Koornneeff M, Dellaert LWM, Van der Veen JH. EMS-and relation-induced mutation frequencies at individual loci in

- Arabidopsis thaliana (L.) Heynh. Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis. 1982;93(1): 109-123.
19. GM Rao. Efficiency and effectiveness of gamma rays and EMS in rice. *Cytologia*. 1977;42(3-4):443-450.
 20. Potupureddi, Gopi, et al. Identification of agro-morphological characters in sheath blight tolerant lines of Samba mahsuri (BPT-5204) rice variety. *Bull. Environ. Pharmacol. Life Sci*. 2017;6:41-45.
 21. Zhan, Chengfang et al. Genome-wide association analysis of panicle exertion and uppermost internode in rice (*Oryza sativa* L.). *Rice*. 2019;12(1):72.
 22. Zhao CF, et al. Analysis of QTLs for panicle exertion and its relationship with yield and yield-related traits in rice (*Oryza sativa* L.). *Genet Mol Res*. 2016;15(2):gmr-15027423.
 23. UPOV Guidelines for rice (*Oryza sativa* L.), TG 16/4. 1985;2-18.
 24. Mao Hailiang, et al. Linking differential domain functions of the GS3 protein to natural variation of grain size in rice. *Proceedings of the National Academy of Sciences*. 2010;107(45):19579-19584.
 25. Slaton N. Rice production handbook. University of Arkansas, United States Department of Agriculture; 2011.
 26. Shivani D, et al. Character Association Analysis for Yield, Yield Attributes in Swarna X Type 3 Ril Population of Rice; 2018.
 27. Sangeetha A, et al. Statistical package for agricultural research (SPAR 2.0). *J. Indian Soc. Agric. Stat*. 2008;62:65–74.
 28. Aslam Sagar M, Akram M, Ashraf M. Agronomic and quality traits of some elite rice genotypes. *Pakistan Journal of Scientific and Industrial Research*. 1995; 38:348-350.
 29. Ali SS, et al. Heritability of yield and yield components of rice. *Pakistan Journal of Agricultural Research*. 2000;16(2):89-91.
 30. Cheema AA, Awan MA, Iqbal J. Improvement of plant height architecture in basmati rice. *Pakistan Journal of Agricultural Research (Pakistan)*; 1987.
 31. Hori, Kiyosumi, et al. Variation in heading date conceals quantitative trait loci for other traits of importance in breeding selection of rice. *Breeding Science*. 2012; 62(3):223-234.
 32. Madhubabu P, et al. Evaluation of grain yield, quality and nutrients content in four rice (*Oryza sativa* L.) Genotypes. *Current Journal of Applied Science and Technology*. 2017;1-12.
 33. Dutta RK, MA Baset Mia, Sakina Khanam. Plant architecture and growth characteristics of fine grain and aromatic rices and their relation with grain yield. *International Rice Commission Newsletter*. 2002;51:51-55.
 34. Kusutani A., et al. Studies on the varietal differences of harvest index and morphological characteristics of rice. *Japanese J. Crop Sci*. 2000;69:359-364.
 35. Yaqoob M, Hussain N, Rashid A. Assessment of genetic variability in rice (*Oryza sativa* L.) genotypes under rainfed conditions. *Journal of Agricultural Research*. 2012;50:311-319.
 36. Tiwari Dinesh K, et al. Studies on genetic variability for yield components in rice (*Oryza sativa* L.). *Advances in Agriculture & Botany*. 2011;3(1):76-81.
 37. Joshi MA, et al. Varietal characterization of rice (*Oryza sativa* L.) based on morphological descriptors. *Seed Research-New Delhi*. 2007;35(2):188.
 38. Yolanda JL, Vijendra Das LD. Correlation and path analysis in rice (*Oryza sativa*). *Madras Agricultural Journal*. 1995;82:576-577.
 39. Zahid M, Afzal, et al. Correlation and path analysis studies of yield and economic traits in Basmati rice (*Oryza sativa* L.). *Asian J. Plant Sci*. 2006;5(4):643-645.
 40. Samonte PB, SO, Wilson LT, McClung AM. Path analyses of yield and yield-related traits of fifteen diverse rice genotypes. *Crop Science*. 1998;38(5): 1130-1136.
 41. Mahto RN, Yadava MS, KS Mohan. Genetic variation, character association and path analysis in rainfed upland rice. *Indian Journal of Dryland Agriculture Research and Development*. 2003;18(2): 196-198.
 42. Yang YaoLong et al. Genetic analysis of culms traits in rice. *Molecular Plant Breeding*. 2011;9(2):160-168.
 43. Zafar Nabeela, Summaira Aziz, Masood SHAHID. Phenotypic divergence for agro-morphological traits among landrace genotypes of rice (*Oryza sativa* L.) from Pakistan. *International Journal of Agriculture and Biology*. 2004;6(2):335-339.
 44. Shishir Sharma*, Amrit Pokhrel, Anup Dhakal, Ankur Poudel. Agro-morphological

- characterization of rice (*Oryza sativa* L.) landraces of Lamjung and Tanahun District, Nepal. Department of Agronomy, Plant Breeding and Agriculture Statistics, Institute of Agriculture and Animal science, Tribhuvan University, Lamjung Campus, Lamjung, Nepal; 2020.
45. Wattoo Javed Iqbal, et al. Study of correlation among yield related traits and path coefficient analysis in rice (*Oryza sativa* L.). African Journal of Biotechnology. 2010;9(46):7853-7856.
46. Rajeswari S, Nadarajan N. Correlation between yield and yield components in rice *Oryza sativa* L. Agricultural Science Digest. 2004;24(4):280-282.
47. Sürek halil, Necmi beşer. Correlation and path coefficient analysis for some yield-related traits in rice (*Oryza sativa* L.) under thrace conditions. Turkish Journal of Agriculture and Forestry. 2003;7(2):77-83.
48. Matsubara, Kazuki, et al. Ehd3, encoding a plant homeodomain finger-containing protein, is a critical promoter of rice flowering. The Plant Journal. 2011;66(4): 603-612.
49. Takahashi, Yasuyuki, et al. Variations in Hd1 proteins, Hd3a promoters, and Ehd1 expression levels contribute to diversity of flowering time in cultivated rice. Proceedings of the National Academy of Sciences. 2009;106(11):4555-4560.

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