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Morphological characteristics of derived mutants of Pinilisa rice cultivar

Dionie S. Barrientos[1,*]

[1]Crop Science Department, College of Agriculture, Central Luzon State University, Nueva Ecija, Philippines
*Corresponding author: dioniebarrientos@clsu.edu.ph

Abstract

The investigation used Augmented Design with 50 M_3 generation mutant lines of rice derived from the traditional variety of Pinilisa was evaluated for morphologically characterized. The traits observed similar to the wild type were intermediate blade pubescence, light green blade color, green basal leaf sheath color, erect blade angle, whitish ligule color, for 2-cleft ligule shape, and green culm color. While the traits observed differently among mutant lines were awnless and light green awn color, erect and semi-erect flag leaf angle, partly exserted panicle, just exserted, moderately well-exserted and well-exserted panicle, awnless and whole length awning were based on 19 morphological traits. Cluster analysis using morphological traits revealed a relationship by forming one big cluster among the mutant lines. The wild type was attacked by stem borers which led to dead hearts. The top recorded three mutant lines in terms of days to 50% flowering and days to maturity, were Crop Science Mutant Plant (CSMP) 204a, CSMP 204b and CSMP 203b, 3 short stature, CSMP 204a, CSMP 174 and CSMP 203b, 1 percent filled spikelet/panicle and number of filled spikelet/panicle, CSMP 92a, 6 good tillering ability, CSMP 17, CSMP 121, CSMP 91, CSMP 39, CSMP 203b and CSMP 6, 1 fine heavy grain weight, CSMP 202, 1 high yielding ability, CSMP 81, 1 longest grain length, CSMP 139 and 1 longest grain width, CSMP 114. The highest computed yield of 2.70 t/ha was from CSMP 81 while CSMP 204a, CSMP 204b and CSMP 114 were the early maturing mutant lines.

Keywords: Augmented design, Morphological traits, Mutant lines, M3 generation, Pinilisa

1. Introduction

Mutation breeding is one of the rational tools for the creation of genetic variation [1] in crops that show higher yield and wider adaptability [2]. This rice improvement technique has shown to be useful in developing a large number of mutants with improved agronomic traits. Mutants are individuals carrying a mutation that may be revealed by molecular or phenotyping tools. Derived mutants are populations that have been generated from exposing them to mutagen for mutation breeding purposes. These may have unique useful characteristics that may have the potential of being released as a new variety or as parents in breeding programs for the traits identified.

One of the best ways of developing a new variety is induced mutation. It plays a crucial role that helps in the creation of genetic variation [1] and accelerates the process of trait selection in a short period [3]. The traits that can be improved through the use of induced mutations are yield resistance to abiotic stress, tolerance to biotic stress, and plant architecture, and maturity [4].

Pinilisa rice is a distinct product of the town of Jones, Isabela, Philippines. It was cultivated by the town's ancestors in at least 500 hectares of rain-fed upland farms. The variety is a low yielder and has a longer maturity period. The panicle is prominent for it has a long peduncle and drooping flag leaf. The Pinilisa rice is continuously gaining popularity and acceptance not only in the province but throughout the region due to its aroma, superior quality, and palatability. However, due to its low productivity with 1.013 t/ha, only few hectares have been devoted to growing Pinilisa which leads to low availability of supply in the market [5].

Low productivity and late-maturing hinder the traditional rice varieties to meet the demand of consumers in terms of their market availability, and to compete with the other varieties. In this existing hindrance, mutation breeding is the best alternative to improve the traditional variety Pinilisa. The Department of Crop Science in Central Luzon State University has performed mutation breeding in rice since 2013 which aims to generate lines of high yielding and early maturing Pinilisa rice cultivar.

In this study, M3 generation was evaluated using morphological and agronomic traits. As induced mutation is used in the development of new plant types, monitoring of improvement can only be identified through characterization. In identifying elite individuals, plant characterization has been successfully used in recent years [6]. Morphological markers are very important as they will help to identify specific parental material for specific traits [7]. Morphological and agronomic characterizations serve as a basic prerequisite in data generation for newly generated mutants. Hence, this study was conducted.

2. Materials and methods

2.1 Plant materials source

In M_1 generation, 1 kg Pinilisa seeds was irradiated using gamma rays at a dose of 50 Gy at the Philippine Nuclear Research Institute. M_2 generation seeds used in this study provided by the Department of Crop Science were generated in 2013 by [8,9]. A total of 50 mutant lines was selected, 25 of which was for early maturing of 112 DAS and below while the other 25 was for having heavy grain weight of 23 g/1000 grain and above (Table 1) was collected and studied. Pinilisa, NSIC Rc23 and PSB Rc5 seeds used as check varieties were taken from Philippine Rice Research Institute (PhilRice) Maligaya, Muñoz, Nueva Ecija, Philippines.

Table 1 Fifty M_2 mutant lines with characters used in planting M_3 generation.

NO	Mutant Lines	M2 Generation Character Flowering (DAS)	NO	Mutant lines	M2 Generation Character 1000 grain weight (g)
1	CSMP 62b	80	26	CSMP 51	28
2	CSMP 15a	80	27	CSMP 55	28
3	CSMP 125	80	28	CSMP 19	27
4	CSMP 185	82	29	CSMP 203b	27
5	CSMP 109	82	30	CSMP 11	27
6	CSMP 68	83	31	CSMP 81	27
7	CSMP 92a	83	32	CSMP 61b	27
8	CSMP 159	84	33	CSMP 204b	27
9	CSMP 142	84	34	CSMP 121	27
10	CSMP 17	84	35	CSMP 56	27
11	CSMP 6	84	36	CSMP 49a	26
12	CSMP 97	85	37	CSMP 91	26
13	CSMP 76	85	38	CSMP 34	26
14	CSMP 107	86	39	CSMP 62b	25
15	CSMP 53	86	40	CSMP 39	25
16	CSMP 174	86	41	CSMP 35	25
17	CSMP 61a	89	42	CSMP 115	25
18	CSMP 114	90	43	CSMP 122	25
19	CSMP 139	92	44	CSMP 92b	25
20	CSMP 200	92	45	CSMP 31	25
21	CSMP 49a	94	46	CSMP 113	25
22	CSMP 203a	96	47	CSMP 50	25
23	CSMP 204a	96	48	CSMP 87	25
24	CSMP 193	97	49	CSMP 88	25

CSMP: Crop Science Mutant Plant.

2.2 Seed dormancy and germination test

Seed dormancy was broken using heat treatment at 50 °C in an oven for 2 days. Seed viability test was done by placing 100 seeds in a dish with moistened tissue paper. Germination test was done at room temperature for 5 days.

2.3 Land preparation

The field was plowed thoroughly twice using a tractor and disc harrow. Harrowing was done two weeks after plowing. The field was leveled thoroughly to facilitate uniform irrigation, then it was furrowed using a fabricated mechanical furrower. Construction of bunds was also done to accumulate water in the area.

2.4 Experimental design and layout

The field was laid out following the augmented lattice design with five blocks. The total area was 318.60 m^2 which was further divided into 5 blocks with an alternate distance of 45 cm and 1 m as border and pathway. Each block had 13 entries with a total number of 65 entries. Every plot had an area of 3.08 m^2 with 6 rows and 10 hills with a total of 60 hills in each entry. The length of each plot was 2.2 m, and the width was 1.4 m. The 50 mutant lines were randomly assigned in blocks including the wild type, NSIC Rc23, and PSB Rc5 as check varieties. The soil type in the area was clay, moderately well drained and with a pH of 5.5. The climate was very pronounced, wet during the months of May to October and dry in November to April.

2.5 Transplanting and Replanting

The seedlings were transplanted 18 days after emergence. With the use of a planting guide, the seedlings were planted at 20 cm x 20 cm distance. Three border rows at the top and bottom of each block were transplanted with seedlings of Pinilisa (wild type) with 20 hills each row. Replanting was done seven days after transplanting to complete the plant population.

2.6 Irrigation and fertilizer application

First irrigation was applied during transplanting through flush-flooding. Subsequent irrigations were applied once a week starting from the seedling stage. At panicle initiation and flowering stage, each plot was irrigated twice a week. Water was also made available at the time of fertilizer application. The recommended rate of 40-20-60 per hectare was based on upland rice recommendation of Soil Test Kit (STK) result. The nitrogen was given in three splits, first at 10 days after emergence (DAE), second at 35 DAE, and third at panicle initiation, 70 DAE A 14-14-14 fertilizer was applied once seven days after transplanting (DAT). The potassium (K) was applied twice, first at 10 DAE and second at panicle initiation, 70 DAE.

2.7 Crop protection and harvesting

Weekly monitoring of pests and disease occurrence was conducted by visual observation. These were counted, data were recorded. Rats were controlled by maintaining cleanliness in the experimental area. Furadan at the rate of 18 grams per entry was applied to control the infestation of stem borer on the vegetative stage and it was repeated on the booting stage. Furadan was used to lessen the infestation of stem borers especially in the wild type. Harvesting was done when 85% of grains in panicle became straw colored.

2.8 Data and statistical analysis

Selected mutant lines and wild type were characterized using the Descriptor's List for Rice based on Standard Evaluation System of Rice [8]. Randomly selected ten sample plants for each entry were used in characterization. Nineteen qualitative and nine quantitative traits were gathered at different growth stages of rice plants starting from late vegetative stage until post-harvest stage and were scored in a manner stated for every trait. A dendrogram for the 52 rice genotypes was drawn using Statistical Tool for Agricultural Research (STAR) Version: 2.0.1 for cluster analysis by Agglomerative Method of International Rice Research Institute (IRRI) based on morphological and grain quality traits.

Yield data gathered for augmented design were analyzed by constructing two-way table of check yields and means. Block effect was computed using the formula: rj = Bj – M; where rj = block effect of jth block, Bj = mean of all checks in the block and M = grand mean of the checks. Observed and adjusted yields for each test entry were obtained by deducting the block effect to which it was allotted from observed yield. In working out standard errors for comparing the means, an Analysis of Variance (ANOVA) table was prepared by using replicated data of check varieties.

3. Results and discussion

Of the nineteen qualitative traits gathered, mutants of Pinilisa in its M$_3$ generation grown under aerobic cultivation did not show deviation on the following traits: blade pubescence (BP), blade color (BC), basal leaf sheath color (BLSC), blade angle (BA), ligule color (LC), ligule shape (LS) and culm color (CC) (Table 2). This similarity of traits among mutants with the wild type is an indication that this trait cannot be easily changed through mutation and even when grown under different methods of cultivation. In the study of mutant lines derived from NSIC Rc144, the same observation on the stability of these traits was observed and revealed [10]. Basal leaf sheath, leaf pubescence, and ligule color and shape were found identical to the wild type. The non-

deviation of mutants in the following traits displayed stability and integrity of genes responsible for leaf pubescence, ligule color, blade pubescence, blade angle, and ligule shape which cannot be easily reshuffled by mutation. BP, BA and LS were used in differentiating the parental lines of rice cultivar and awn length [11]. Leaf blade color, leaf sheath color, node base color, awning, distribution of awns, and stigma color are useful traits for the identification of rice cultivar [12]. The displayed phenotypes by organisms were genetically programmed and inherited over generations [13].

Table 2 Morphological traits of the mutant Pinilisa together with the wild type and two check cultivars.

Checked Variety/ Mutant Lines	BP	BC	BLSC	BA	LC	LS	CC	CmA	IC	AnC	SgC	ApC	FLA	PE	PA	SLC	An	GrS	GSi
Pinilisa (Wild type)	In	LG	G	H	W	F2C	LG	-	-	-	-	-	-	-	-	-	-	-	-
PSB Rc5	In	G	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	WE	SD	Whi	Aw	I	ELo
NSIC Rc23	P	LG	GPL	E	YG	F2C	C	Er	LGo	Aw	Pu	RA	SE	WE	SD	Whi	Aw	I	ELo
CSMP 51	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 62a	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	JEx	SD	Whi	Aw	I	ELo
CSMP 55	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	PWE	SD	Whi	WL	I	ELo
CSMP 15a	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	PWE	SD	Whi	Aw	I	ELo
CSMP 19	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	PWE	SD	Whi	Aw	I	ELo
CSMP 125	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	PWE	SD	Whi	WL	I	ELo
CSMP 203a	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 185	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	PWE	SD	Whi	WL	I	ELo
CSMP 11	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 68	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	PWE	SD	Whi	Aw	I	ELo
CSMP 159	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 81	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 142	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 61a	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 97	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	WE	SD	Whi	Aw	I	ELo
CSMP 49a	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	PWE	SD	Whi	WL	I	ELo
CSMP 17	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	PWE	SD	Whi	Aw	I	ELo
CSMP 204a	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	SE	JEx	SD	Whi	WL	I	ELo
CSMP 76	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 121	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	PWE	SD	Whi	Aw	I	ELo
CSMP 91	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	JEx	SD	Whi	Aw	I	ELo
CSMP 107	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 34	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	SE	MWE	SD	Whi	WL	I	ELo
CSMP 53	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 39	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 174	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 35	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 61b	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 115	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 203b	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 204b	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	SE	JEx	SD	Whi	WL	I	ELo
CSMP 122	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	JEx	SD	Whi	Aw	I	ELo
CSMP 15b	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	PWE	SD	Whi	Aw	I	ELo
CSMP 92a	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 49b	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	PWE	SD	Whi	WL	I	ELo

Table 2 Morphological traits of the mutant Pinilisa together with the wild type and two check cultivars. (Continued)

Checked Variety/ Mutant Lines	BP	BC	BLSC	BA	LC	LS	CC	CmA	IC	AnC	SgC	ApC	FLA	PE	PA	SLC	An	GrS	GSi
CSMP 62b	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	JEx	SD	Whi	Aw	I	ELo
CSMP 202	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 31	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	PWE	SD	Whi	Aw	I	ELo
CSMP 114	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 113	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	PWE	SD	Whi	Aw	I	ELo
CSMP 50	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	JEx	SD	Whi	Aw	I	ELo
CSMP 139	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	PWE	SD	Whi	WL	I	ELo
CSMP 87	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	SE	JEx	SD	Whi	WL	I	ELo
CSMP 193	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	SE	PWE	SD	Whi	WL	I	ELo
CSMP 88	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	JEx	SD	Whi	Aw	I	ELo
CSMP 200	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 56	In	LG	G	E	W	F2C	LG	Er	LGo	LG	Wh	Gr	E	JEx	SD	Whi	WL	I	ELo
CSMP 109	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	E	PWE	SD	Whi	Aw	I	ELo
CSMP 92b	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo
CSMP 6	In	LG	G	E	W	F2C	LG	Er	LGo	Aw	Wh	Gr	SE	MWE	SD	Whi	Aw	I	ELo

|								
BP	Blade Pubescence	SgC	Stigma Color	In	Intermediate	C	Colorless	PWE	Partly well exserted
BC	Blade Color	FLA	Flag Leaf Angle	P	Pubescent	LGo	Light Gold	MWE	Moderately well exserted
BLSC	Basal Leaf Sheath Color	PE	Panicle Exsertion	LG	Light Green	Aw	Awnless	SD	Slightly drooping
BA	Blade Angle	PA	Panicle Angle	Gr	Green	Whi	White	WL	Whole length
LC	Ligule Color	SLC	Sterile Lemma Color	GPL	Green with purple lines	Pu	Purple	I	Intermediate
CC	Culm Color	An	Awning	Er	Erect	SE	Semi-erect	GrS	Grain Shape
CmA	Culm Angle	Wh	Whitish	WE	Well exserted	Wh	Whitish	WE	Well exserted
IC	Internode Color	GrSi	Grain Size	YG	Yellowish Green	JEx	Just Exserted	F2C	for 2-cleft
AnC	Awn Color	ApC	Apiculus color	H	Horizontal	RA	Red Apex	ELo	Extra Long
LS	Ligule Shape								

On the other hand, differences among mutant lines were observed on the following traits: awning (An), awn color (AnC), flag leaf angle (FLA), and panicle exsertion (PE). Although no data on the following traits were recorded from the wild type, the appearance of differences among mutants indicate possibility of rearrangement of genetic integrity as manifested in changes in morphology. Mutations, which alter the activity or expression of transcription factors, were involved in physiological and morphological changes associated with domestication and crop species adaptation [13].

It was also observed that the wild type did not complete the life cycle under aerobic cultivation compared with the mutant lines. The wild type showed susceptibility to pest attack by stem borer, resulting in stunted growth and inability to produce any flower. The capability of the mutants together with the check variety to grow in maturity was a manifestation of genetic enhancement for the Pinilisa mutant to be grown under aerobic cultivation. However, this would need further verification.

All mutants and one check cultivar formed into one big cluster while the other check cultivar NSIC Rc23 was on one independent cluster based on clustering analysis (Table 3 and Figure 1). Results of the cluster analysis indicate that mutants came from a common ancestor, the wild type. Although the inclusion of PSB Rc5 in that cluster seemed very interesting for further study. As observed on the gathered morphological traits, PSB Rc5 had the same morphological characteristics observed with most of the mutants while NSIC Rc23 had seven traits different from the mutants. The PSB Rc5 used in the study clustered to the mutant lines due to the limited number of morphological traits used. Characterization based on morphology has some limitations in the accurate identification of the accessions such as limited number of traits to characterize [14] while trait expression, particularly quantitative traits, are subjected to strong environmental influence [15]. However, morphological traits serve as identity mark of mutant lines and provide useful information in breeding programs.

Table 3 Clustering of lines and varieties based on 19 morphological traits.

CLUSTER	NO. OF Mutants/ Checked Variety	Mutants/Checked Variety
I	51	PSB Rc5, CSMP 51, CSMP 19, CSMP 203a, CSMP 81, CSMP 142, CSMP 61a, CSMP 204a, CSMP 76, CSMP 121, CSMP 107, CSMP 35, CSMP 61b, CSMP 115, CSMP 203b CSMP 92a, CSMP 202, CSMP 31, CSMP 113, CSMP 50, CSMP 200, CSMP 62a, CSMP 68, CSMP 91, CSMP 122, CSMP 109, CSMP 55, CSMP 15a, CSMP 185, CSMP 17, CSMP 15b, CSMP 62b, CSMP 92b, CSMP 125, CSMP 49a, CSMP 34, CSMP 39, CSMP 204b, CSMP 49b, CSMP 139, CSMP 193, CSMP 88, CSMP 56, CSMP 11, CSMP 159, CSMP 97, CSMP 53, CSMP 174, CSMP 114, CSMP 87 and CSMP 6
II	1	NSIC Rc23
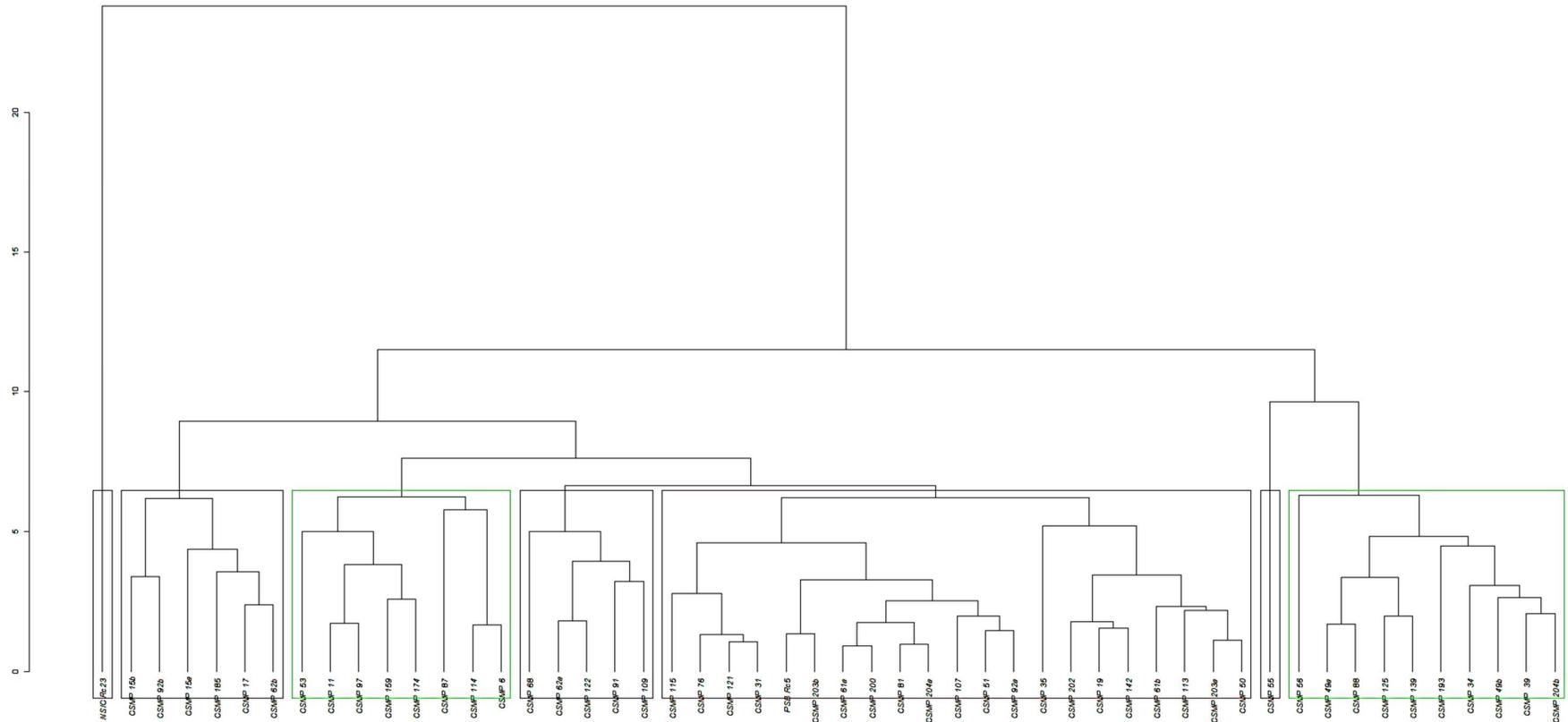
Figure 1 Dendrogram using agglomerative clustering method representing distribution of 52 (50 mutant lines and 2 checked varieties) based on morphological traits.

The days to 50% flowering were from 82 to 101 days after sowing (Table 4). Based on the Standard Evaluation System (SES) for rice [16], among the 50 mutants, 3 were early to flower (82 DAS), 40 (84-99 DAS) were medium, and 7 (100-101 DAS) were late to flower. CSMP 204a, CSMP 204b, and CSMP 114 were the earliest to flower with 82 days after sowing (DAS). Flowering age of rice cultivars is affected by the genetic traits of cultivars [17]. Among the 50 mutant lines, 3 (112 DAS) were early-maturating, 40 (114-129 DAS) were medium, and 7 (130-131 DAS) were late-maturing [16]. CSMP 204a, CSMP 204b, and CSMP 114 were the earliest to mature at 112 days after sowing. Analysis of variance showed significant difference in days to 50% flowering and days to maturity at 5% level. The result is a clear indication of a good trait among the mutant lines that possessed early maturity. Early maturity is considered a desirable trait for rice for it can possibly shorten the period of exposure to the risk of unpredictable environmental factors by early harvesting. Short maturity crop can possibly help maximize the use of land by more cropping per year [10]. The flowering time and maturity of cereals and other crops are controlled by the plants' ability to sense season temperature and day-length signals controlled by vernalization and photoperiodic sensitivity genes [18].

The plant height at maturity was from 76 to 97 centimeters. Based on the Standard Evaluation System (SES) for rice [16], out of 50 mutant lines, 41 were semi-dwarf (<90 cm.) and 9 were intermediate (90-125 cm.). The tallest height of 97 cm. was measured from CSMP 204b while the shortest mutant lines were CSMP 204a, CSMP 174, and CSMP 203b with 76 cm. in height. The result is an indication that these mutant lines carried traits that are semi-dwarf and intermediate in height. Dwarfness plays an important role in lodging and physiological efficiency [19,20]. In addition, short cultivars are usually better adapted to mechanical harvesting [18].

The percent filled spikelet's/panicle ranged from 26.15% to 70.52%. CSMP 92a (70.52%) had the highest percent filled spikelet's/panicle while CSMP 62a (26.15%) had the lowest. Generally, it is the most important quantitative and yield attributing trait. actors such as weather, soil, fertilizer application, and incidence of diseases and insects affect filled spikelet or sterility percentages [21].

The number of productive tillers observed ranged from 6 to 13. CSMP 17, CSMP 121, CSMP 91, CSMP 39, CSMP 203b, and CSMP 6 with an average of 13 number of productive tillers were the highest on M_3 generation. The number of productive tillers determined the number of panicles that eventually affected the yield and total production of the crop [19]. Variation in the number of productive tillers is related to the genetic factors and the environment [22].

The recorded 1000-grain weight ranged from 17.32 grams to 34.55 grams. The heaviest 1000-grain weight was recorded in CSMP 202 while the lightest grain weight was from CSMP 17. Grain weight is an important yield component because it gives information on the size and density of the rice grains. Under most conditions, the 1,000-grain weight of field crops is a very stable varietal character [23].

The observed computed yield of mutant lines was from 1.41 t/ha to 2.70 t/ha (Table 11). CSMP 81 (2.70 t/ha) was the highest among the mutant lines and CSMP 17 (1.41 t/ha) was the lowest computed yield.

The longest grain of 10.76 mm. was obtained from CSMP 139 while the shortest grain of 8.67 mm. was measured from CSMP 107. All the mutants exhibited extra-long grain characteristics. This was based on [16] that greater than 7.5 mm. grain is considered as extra-long. Extra-long grain is a desirable trait for rice as it is preferred by many buyers, and it dictates a higher price. Grain length is one of the important characters in rice grain quality. It is the most adequate character for analyzing the inheritance of grain size because of high heritability of the trait. Grain length may be the best character for analyzing the inheritance of grain size [24]. The longest grain width was obtained by the mutant CSMP 114 (2.60 mm.) with the same grain width to the checked variety NSIC Rc23. The shortest grain length was recorded from the mutant CSMP 204b (2.04 mm.). All the 50 mutants and 2 check cultivars were categorized as intermediate [16]. Grain size and shape are among the first criteria of rice quality that breeders consider in developing new varieties for releasing for commercial production [25].

Table 4 Quantitative traits of mutant lines and check varieties.

Mutant lines and check variety	DF	DM	PHM (cm)	PFS/P	NPT	1000 GW (g)	CY (t/ha)	GL (mm)	GW (mm)
CSMP 51	92	122	87	58.85	12	25.56	2.50	8.92	2.34
CSMP 62a	84	114	91	26.15	8	24.70	1.51	9.71	2.48
CSMP 55	92	122	87	26.54	7	21.74	1.44	10.24	2.16
CSMP 15a	92	122	84	58.82	10	22.83	2.02	10.33	2.05
CSMP 19	92	122	77	41.69	8	26.16	1.82	9.71	2.36
CSMP 125	92	122	90	44.38	6	22.14	1.51	10.52	2.13
CSMP203a	92	122	83	53.25	12	23.52	2.18	9.94	2.45
CSMP 185	92	122	94	31.88	7	19.23	1.52	10.54	2.12
CSMP 11	92	122	83	42.96	11	26.33	1.98	9.35	2.39
CSMP 68	92	122	84	54.06	12	25.40	2.40	9.54	2.46
CSMP 159	92	122	85	53.48	9	24.51	1.75	8.85	2.30
CSMP 81	92	122	87	51.74	9	24.19	2.70	9.52	2.26
CSMP 142	92	122	85	60.90	10	26.76	1.98	9.83	2.45
CSMP 61a	92	122	87	51.54	11	23.61	2.45	9.70	2.33
CSMP 97	92	122	80	56.15	10	22.67	2.21	9.15	2.30
CSMP 49a	92	122	83	50.28	8	24.48	1.54	9.95	2.21
CSMP 17	98	128	80	31.17	13	17.32	1.41	9.86	2.22
CSMP204a	82	112	76	54.53	7	22.57	1.84	9.35	2.25
CSMP 76	98	128	79	27.44	12	23.22	1.54	9.45	2.21
CSMP 121	98	128	84	53.74	13	20.56	1.77	9.75	2.18
CSMP 91	100	130	82	35.00	13	24.08	1.44	9.01	2.20
CSMP 107	84	114	84	42.74	10	24.49	2.02	8.67	2.20
CSMP 34	99	129	95	54.55	12	27.68	2.00	9.97	2.26
CSMP 53	99	129	77	37.68	10	23.54	1.56	9.79	2.30
CSMP 39	99	129	86	32.02	13	22.28	1.90	10.14	2.17
CSMP 174	100	130	76	31.71	10	23.85	1.58	9.48	2.20
CSMP 35	84	114	82	38.88	7	26.98	1.80	9.63	2.55
CSMP 61b	92	122	84	48.67	10	23.61	2.46	9.45	2.25
CSMP 115	92	122	87	41.37	11	25.25	1.98	8.88	2.22
CSMP203b	92	122	76	35.47	13	23.24	1.63	8.84	2.31
CSMP204b	82	112	97	38.37	12	22.57	1.87	9.86	2.04
CSMP 122	98	128	87	60.19	9	23.76	2.37	9.17	2.33
CSMP 15b	84	112	78	44.74	8	22.83	1.78	9.48	2.27
CSMP 92a	92	122	79	70.52	10	24.18	2.66	9.12	2.30
CSMP 49b	84	112	92	47.84	8	22.43	1.64	10.69	2.10
CSMP 62b	84	112	83	27.31	11	24.51	1.58	10.43	2.31
CSMP 202	98	128	82	38.34	11	34.55	1.70	9.49	2.37
CSMP 31	100	130	83	32.32	10	22.41	1.91	9.38	2.24
CSMP 114	82	112	77	61.91	11	34.43	1.88	9.34	2.60
CSMP 113	100	130	82	52.81	12	23.61	1.69	9.75	2.34
CSMP 50	92	122	86	59.07	11	25.82	1.77	9.88	2.52
CSMP 139	99	129	95	38.41	8	19.18	1.52	10.76	2.22
CSMP 87	92	122	92	56.81	7	25.64	1.66	9.50	2.48
CSMP 193	98	128	84	54.84	10	20.94	1.99	10.42	2.06
CSMP 88	92	122	84	30.44	9	23.27	1.60	10.09	2.28
CSMP 200	101	131	83	45.78	12	27.61	2.14	9.31	2.19
CSMP 56	84	112	90	45.30	11	21.13	1.78	10.69	2.38
CSMP 109	101	131	83	31.38	10	25.27	2.02	9.61	2.25
CSMP 92b	92	122	80	59.54	11	22.98	2.59	10.40	2.09
CSMP 6	101	131	81	41.68	13	20.07	1.68	9.41	2.42
NSIC Rc23	64	103	97	62.84	8	26.19	2.76	9.17	2.60
PSB Rc5	86	123	105	46.86	9	20.27	1.97	8.88	2.27
CV	1.82	1.82	4.61	13.88	1.82	1.71	0.30	0.21	0.23

DF = DAYS TO FLOWERING PFS/P = PERCENT FILLED SPIKELETS/PANICLE CY = COMPUTED YIELD
DM = DAYS TO MATURITY NPT = NO. OF PRODUCTIVE TILLERS GL = GRAIN LENGTH
PHM = PLANT HEIGHT AT MATURITY 1000 GW = 1000 GRAIN WEIGHT GW = GRAIN WIDTH

4. Conclusion

Mutants in its M_3 generations remain to have unstable morphological traits which is expected in mutation breeding studies. Their blade pubescence and color, basal leaf sheath color, ligule color, and shape and culm color are traits which can easily deviate from the wild type and the blade angle trait which remain stable despite subjecting them to mutagen. In creating variation, induced mutation is very potent.

Based on the breeding objectives of developing early maturing and higher yielder Pinilisa using this mutation breeding method, the promising mutant lines in the M_3 generation were CSMP 204a, CSMP204b, CSMP 114 with maturity of 112 days after sowing. While CSMP 81 (2.70 t/ha), CSMP 92a (2.66 t/ha), CSMP92b (2.59 t/ha), CSMP51 (2.50 t/ha), CSMP61b (2.46 t/ha), CSMP61a (2.45 t/ha), CSMP68 (2.40 t/ha), CSMP122 (2.37 t/ha), CSMP97 (2.21 t/ha), CSMP203a (2.18 t/ha), CSMP200 (2.14 t/ha), CSMP15a (2.02 t/ha),

CSMP109 (2.02 t/ha), and CSMP107 (2.02 t/ha) were the mutant lines with yield higher than 2 t/ha. Thus, these are good candidate lines that could be evaluated in terms of advance yield trial.

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6. References

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