

Morphological Characters of Panicle and Seed Mutants of Rice

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ABSTRACT : Phenotypes of panicle, hull and seed of mutant rice (*Oryza sativa* L.) were characterized. Panicle mutants were classified in 4 groups with their internode length of main rachis, primary rachis, secondary rachis and pedicel. Hull and seed mutants were grouped into 12 based on their mutant characters in shape, size and color of seeds. These natural and spontaneous mutant collections showed distinct phenotypes to wild type rice. This might be useful for the identification of the functions of genetic factors in the Mendelian inheritance.

Keywords: mutants, rachis, spikelet, *Oryza sativa* L.

Mutant plants show abnormality in shape, size, color, texture and even in chemical and nutritional constituents. Especially in rice, these mutants were used as marker lines for genetic mapping based on linkage analysis on the basis of Mendelian inheritance. Currently, with developing molecular genetics, these mutants expressing phenotypic and physiological variations provide an indispensable source for the functional analysis of genes (Hirochika *et al.*, 2004). Recently, genes of important economic traits of rice have been identified using respective phenotypes of mutants. These include *dwarf* caused by defect of gibberellin signaling pathway (Sasaki *et al.*, 2002, 2003), *slender* caused by malfunctioning of a soluble receptor for gibberellin (Ueguchi-Tanaka *et al.*, 2005), *less tiller* caused by malfunctioning of MOC1 protein which is a putative GRAS family nuclear protein (Li *et al.*, 2003; Zou *et al.*, 2005), cytoplasmic male sterility (CMS) restorer caused by given function of Rf-1 gene that encodes a mitochondrial targeted protein with pentatricopeptide repeat motif (Komori *et al.*, 2004). Therefore, to accelerate for accomplishing utilization of the functional genomics in rice, natural and spontaneous mutants have been attended to clone the DNA sequences based on the distinct Mendelian genetics. For cloning DNA sequences as gene causing appropriate heritable phenotypes, identification and characterization of the phenotypes of mutants are necessary. Therefore, here we examined phenotypes of 164 germplasms of natural rice mutant collections in the field.

Increasing yield of rice is strongly demanded in decade for solving the predicted famine resulted by increasing up to seventy billions of earth population. It is urgently demanded to develop both the conventional and molecular breeding for increasing yields. Therefore, finding genes of high yield is urgently required by using phenotypic mutants related to yield. Panicle and tiller development have positive correlation with the yield of rice. Grain yield is generally related with number of tillers and panicle per plant, length and breadth of panicle, number of spikelets per panicle, grain weight, density of spikelets, and fertility of each spikelet (Zou *et al.*, 2005). Grain yield is dependent on length and number of main rachis, primary rachis and secondary rachis of panicle (Komatsu *et al.*, 2001). Spikelet number per panicle is also important parameter because this together with the number of panicle per square meter and mean grain weight determines the grain yield potential of rice (Mishra and Janoria, 2003). Therefore, to find phenotypic mutant of yield parameters is important for both breeding and molecular breeding with gene cloning. Here, we report phenotypic characters of four different panicle mutants and twelve different hull and seed mutants of rice.

MATERIALS AND METHODS

Plant material

Rice mutants from 164 germplasms were grown in summer 2005 in rice research field of Yeungnam University, Gyeongsan, Korea. For identification, YUM number was given for the collection of those mutants. Those mutant collections were originated from spontaneous, chemically induced or ionized radiations. All mutant phenotypes were documented from seedling stage to maturation stage. Among all mutant varieties, 4 panicle mutants and 12 hull and seed mutants were selected and studied for their mutant characteristics.

Three panicles from each five plants of every mutant rice were collected after maturation. Mean values of panicle per plant, length of panicle, number of spikelets per panicle, 100 grain weight, and spikelet fertility were calculated.

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<Received July 3, 2006>

Spikelet fertility

Spikelets of three panicles from each three plant of every phenotype were taken separately. Total fertile, sterile and total spikelets were counted. Fertile seeds were heavy and settled at the bottom of a beaker full of water. However, sterile seeds were light and floated on water. Mean values of spikelet fertility percent was calculated from every mutant type.

Starch test

Seeds were cut and stained with 1% I-KI solution to visualize starch content on the endosperm. I-KI was prepared by dissolving 1g of iodine and 2g of potassium iodide in 100 ml water. Endosperm color of the mutant type was compared

with that of wild type rice.

RESULTS AND DISCUSSION

Among 164 mutant germplasm studied, 4 germplasm of panicle mutants and 12 germplasm of hull and seed mutants were observed with their distinct phenotypes. Panicle, hull and seed mutants were analyzed differently and were documented as follows.

Panicle mutants

Dense panicle (*Dn*)

Gene for dense panicle (*Dn*) is located on chromosome 9 (Kinoshita, 1993; Nagato and Yoshimura, 1998). Two germplasm (YUM1516 and YUM1517) showed dense panicle



Fig. 1. Panicle mutants of rice. (A) Panicle of wild type rice of Japonica cv. Dongjin. Spikelets are arising from primary rachis (r1) and secondary rachis (r2). Flag leaf (fl), Uppermost internode (ui), Pedicel (p) and Spikelets (sp) are well developed. (B) Dense panicle (*Dn*) (YUM1516). Primary rachis, secondary rachis and pedicel are short. Spikelets are compactly arranged. (C) Lax panicle (*lax*) (YUM1505). Long inter node of primary rachis. Secondary rachis is not formed. Spikelets are sparsely distributed. (D) Clustered spikelets (*Cl*) (YUM1406). Short secondary rachis and pedicel are developed from primary rachis. Two to six spikelets are arising from each node of primary rachis, with a magnified part of dense panicle. (E) Neck leaf panicle (*nl*) (YUM1426). Flag leaf sheath (fs) is enclosing basal part of panicle. Bar = 4cm.

phenotype. Panicles were compact with large number of spikelets (Fig. 1B). Most of the spikelets in this mutant were sterile with abnormal and depressed glumes, lemma and palea. Comparing with spikelets of wild type rice (Fig. 1A), the number of secondary branches per primary branch and the number of spikelets per panicle were higher, whereas the lengths of panicle, primary branch and secondary branch were shorter. Phenotype of dense panicle may be due to the short internodes of main rachis, primary rachis, secondary rachis and even the pedicel. Therefore, we suggest that *Dn* gene may cause poor development of internodes of main rachis, primary rachis and secondary rachis. Spikelets were so compact that their normal development was affected and most of the floral organs remained immature and malformed causing most of the spikelets sterile (Fig. 1B). The mean value of yield parameters such as spikelet fertility, number of spikelet per panicle, number of panicle per plant and panicle length was lower than those of wild type rice (Table 1). Overall, because of these characteristics of dense panicle, the yield of *Dn* mutant plants was relatively lower. (Table 1)

Lax panicle (*lax*)

Two germplasms (YUM1521 and YUM1531) showed *lax* phenotype in their panicles. In these mutants, spikelets were sparsely distributed with very few numbers of spikelets on panicle (Fig. 1C). Panicle architecture of the *lax* mutant rice showed less number of nodes with long internodes of main rachis, primary rachis and secondary rachis (Fig. 1C). Excessive elongation of internodes might be the main character of *lax* gene. Mean values of number of panicle, panicle length, number of spikelet per panicle and grain weight were lower than those of wild type rice (Table 1). Even though, number of spikelets per panicle was less, spikelet fertility was normal as that of wild type rice (Fig. 1A). Because of this distinct phenotype in panicle mutant, *lax* gene was relatively focused to elucidate the gene causing this phenotype. Lax panicle (*lax*) is a recessive mutant, located on chromosome 1 and linked with *spl6* (Kinoshita, 1993; Nagato and Yoshimura, 1998). The *LAX1* gene is involved in the determination of architecture by controlling rachis-branch and

spikelet development (Komatsu *et al.*, 2001). Other researches revealed that the *LAX* encodes a basic helix-loop-helix transcription factor, functions to regulate development of meristem, in between the shoot apical meristem and the region of new meristem formation (Komatsu *et al.*, 2003). These indicate that normal *lax* gene is necessary for the development of panicles.

Clustered spikelets (*Cl*)

Seven germplasms (YUM1406, YUM1440, YUM1441, YUM1442, YUM1449, YUM1466 and YUM1478) showed clustered spikelets phenotype (Fig.1D). Spicklets of this mutant rice were arranged on primary or secondary rachis of the panicle with 2-6 spikelets per cluster. The main cause of clustered spikelet might be due to the shortening of secondary rachis and pedicel. In *Cl*, primary rachis was developed as it dose in wild type rice. However, secondary rachis was not elongated, so nodes of the rachis were compact clumping 2-6 nodes on the node of primary rachis from where spikelets were developed in clusters (Fig. 1D). The mean values of spikelet fertility and grain weight are higher than those of wild type rice (Table 1). However, other yield parameters of these mutant germplasms showed negative relation with grain yield comparing with those of wild type rice. Little is known except that the gene for clustered spikelets (*Cl*) is located on chromosome 6 (Kinoshita, 1993; Nagato and Yoshimura, 1998).

Neck leaf (*nl*)

Ten germplasms (YUM1426, YUM1427, YUM1448, YUM1467, YUM1475, YUM1501, YUM1526, YUM1527, YUM1542 and YUM1566) showed neck leaf mutant phenotype (Fig. 1E). Lower part of panicle is enclosed by flag leaf sheath due to the shortening of upper most internode of the panicle. Flag leaf sheath arose at the base of the panicle enclosing basal part of the panicle so that panicles were not well exerted (Fig. 1E). The gene for neck leaf (*nl*) is located on chromosome 5 (Kinoshita, 1993; Nagato and Yoshimura, 1998). The mean values of number of panicle per plant (NP) and number of spikelets per panicle (NSP) showed negative

Table 1. Mean values of different grain yield parameters of Panicle mutant rice.

Panicle Phenotypes	Gene symbol	No.of panicle	Panicle length (cm)	No.of spikelets per panicle	100 grain weight (g)	Spikelet fertility (%)
Wild type rice		31	23	191	2.1	96.51
Neck leaf	<i>nl</i>	20	21	70	3.4	97
Clustered spikelets	<i>Cl</i>	19	20	107	2.7	99.5
Dense panicle	<i>Dn</i>	14	12	111	2	19
Lax panicle	<i>lax</i>	17	16	31	2	96

correlation but other parameters were positively correlated (Table 1) with those of wild type rice. Therefore, total grain yield of neck leaf mutants was lower than that of wild type rice. There is no report for the genes causing *nl* functions.

Hull and Seed mutants

Long sterile lemma (*g*)

Among 164 germplasms, nine germ plasms (YUM1416, YUM1417, YUM1418, YUM1419, YUM1444, YUM1445, YUM1459, YUM1464 and YUM1479) had two long sterile glumes (Fig. 2B). These mutants showed elongated two glumes as the same sizes as those of the lemma and palea. They appeared from the heading stage and remained in all developmental stages (Fig. 2B). The gene responsible for long sterile lemma (*g*) is located on chromosome 1 (Kinoshita, 1993; Nagato and Yoshimura, 1998). Mean values of number of panicle per plant, panicle length and 100 grains weight of this mutant were similar with those of wild type rice. However, mean values of number of spikelet per panicle and spikelet fertility were less than those of wild type rice (Table 2). Even though, most of the parameters were normal spikelet formation and spikelet fertility were low (Table 2).

Black hull (*Bh*)

Two germplasms (YUM1424 and YUM1462) showed black hull phenotype (Fig. 2C). Hull color of matured grains of black hull mutant was black due to pigment deposition in hypodermal cells and trichomes. Hull color of this mutant was developmentally changed. During anthesis stage, color of hulls was purple but changed to black after dough stage. However, the hulls turned to dark black at the maturation stage (Fig. 2C). To date, no gene has been identified causing black hull mutant. Mean value of number of panicle per plant was lower than that of wild type rice but the values of rest of all yield parameters studied were same as those of wild type rice (Table 2).

Beaded grain arrangement (*Bga2*)

Round grains as the shape of bead were found in two germplasms (YUM1423 and YUM1485) (Fig. 2D). Shape of grains was completely round with beaded appearance. Spikelets were compactly arranged (Fig. 2D). *Bga2* germplasms showed high yield characteristics. Except number of spikelets per panicle, other parameters were found to be similar with those of wild type rice. Grain weight were slightly massive than that of wild type rice (Table 2). Therefore, mean value of 100 grains weight was higher than that of wild type rice (Table 2). Genetic information for the beaded grain arrangement mutant has not been found.

Gold hull (*gh*)

Golden hull color was found in 24 germplasms (YUM1416, YUM1421, YUM1424, YUM1425, YUM1432, YUM1437, YUM1438, YUM1444, YUM1446, YUM1448, YUM1458, YUM1459, YUM1460, YUM1461, YUM1463, YUM1468, YUM1469, YUM1476, YUM1480, YUM141485, YUM 1507, YUM1522, YUM1539 and YUM1564). Hull color of these mutants was found to be golden (Fig. 2E). Lemma and palea were purple green during anthesis and they gradually turned to golden at the maturation stage. Glumes of these mutants turned from light green during flowering to yellow, then golden yellow, and finally to golden brown during the maturation stage (Fig. 2E). The gene responsible for gold hull (*gh*) is located on chromosome 2 (Kinoshita, 1993; Nagato and Yoshimura, 1998). Gold hull was common especially in Indica type of rice. It was reported that the white-hull gene, *Wh*, prevents the formation of golden ground pigment and gives a normal straw color. However, there is no gene identified for gold hull phenotypes. Gold hull mutant showed less mean value of number of panicle per plant and spikelet number per panicle (Table 2). However, mean values of panicle length, 100 grains weight and spikelet fertility were normal (*Rh*) (Table 2).

Red hull (*Rh*)

Hull color was found to be red in a rice germplasm (YUM1468) (Fig. 2F). Lemma and palea were purple in color during anthesis. The color turned to red during maturation stage. All yield characters showed their normal value as compared with those of wild type rice except mean value of number of spikelet per panicle, which was lower than that of wild type rice (Table 2). To date, little is known for red hull mutant.

Triangular hull (*tri*)

Triangular hull was found in a rice germplasm (YUM1448). The gene responsible for triangular hull (*tri*) is located on chromosome 2 (Kinoshita, 1993; Nagato and Yoshimura, 1998). The apex of the spikelet was pointed due to pointed structure of lemma and palea while the base was broad making a triangular arrangement (Fig. 2G). Tip of lemma curved over palea, causing the spikelet to appear triangular. Little is known for genetics of triangular hull mutant. Interestingly, mean value of 100 grains weight of this mutant was found to be higher than that of wild type rice (Table 2). However, mean values of rest of all grain yield parameters showed lower than those of wild type rice, resulting low grain yield of triangular hull mutant (Table 2).

Purple hull (*Pr*)

Hull color was found to be purple in six germplasms

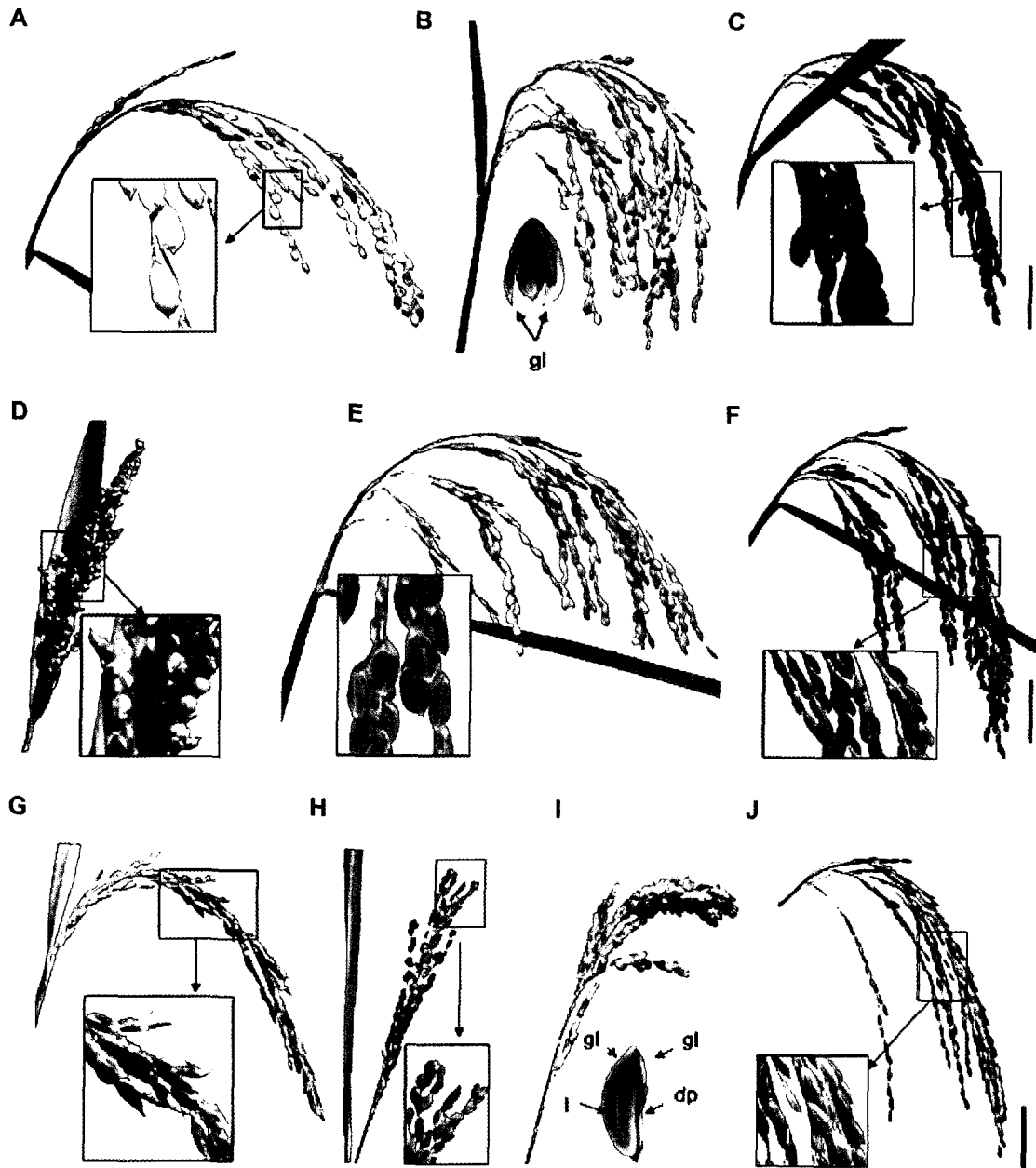


Fig. 2. Hull and seed mutant of rice. (A) Panicle of wild type rice has normal hull shape size and color. Magnified part of panicle is shown in box. (B) Long sterile lemma (YUM1418) with a spikelet having two long glumes (gl) as long as the lemma and palea. Two long sterile glumes same length as the lemma are developed. (C) Black hull mutant (YUM1424) with magnified part of panicle showing black hull color. (D) Panicle of beaded grain rice (YUM1485) with magnified part of panicle. Grains are round, compactly arranged and heavy. (E) Panicle of gold hull (YUM1416). The magnified part of panicle in the box is from the same panicle at dough stage. In milk stage and dough stage golden color development is more than matured stage. (F) Panicle of red hull mutant (YUM1468) with magnified part of panicle showing red hull. (G) Panicle of triangular hull mutant rice (YUM1489) with magnified part of panicle. Tip of the hull is pointed where as base is broad. (H) Panicle of purple hull (YUM1506) with magnified part. (I) Panicle of depressed palea (dp) mutant rice (YUM1500) with a spikelet. In this mutant rice palea development is defective, so it is constricted and is enclosed by lemma. (J) Panicle of brown furrows on hull (YUM1473) with magnified part of panicle. Bar = 4cm.

(YUM1457, YUM 1466, YUM1471, YUM1474, YUM1477 and YUM1506) (Fig. 2H). The gene for purple hull (*Pr*) is located on chromosome 4 (Kinoshita, 1993; Nagato and

Yoshimura, 1998). Spikelets were red, round, small and spikelet fertility was low (Fig. 2H). *Pr* is responsible for distribution of purple color over the entire surface of floral

Table 2. Mean values of different grain yield parameters of hull and seed mutant rice.

Seed and hull Phenotypes	Gene symbol	No. of panicle per plant	Panicle length	No. of spikelets per panicle	100 grain weight (g)	Spikelet fertility (%)
Wild type rice.		31	23	191	2.1	96.51
Triangular hull	<i>tri</i>	28	17	132	2.5	67
Long sterile lemma	<i>g</i>	31	23	85	2.2	88
Golden hull	<i>gh</i>	23	24	141	2.6	96
Black hull	<i>Bh</i>	21	25	189	2.4	98
Brown furrow on hull	<i>Bf</i>	15	16	327	2.5	91
Depressed palea	<i>dp</i>	9	18	107	2	82
purple hull	<i>Pr</i>	25	24	90	2.4	88
Beaded grain	<i>Bga2</i>	30	25	140	3	95
Red hull	<i>Rh</i>	29	22	102	2.5	94
Brown pericarp	<i>Rc</i>	17	20	77	2	88
Red pericarp	<i>RdRc</i>	29	24	151	2.6	90
Purple pericarp	<i>Prp</i>	17	24	253	3	81

glumes, viz. lemma and palea. Gene for purple hull has not been cloned but it has been reported that *pr* deposits high amount of anthocyanin pigments (unpublished data). Mean values of panicle length and 100 grains weight of this mutant rice were higher than those of wild type rice (Table 2). However, mean values of rest of all parameters studied showed lower value than those of wild type rice.

Depressed palea (*dp*)

Development of palea was defective in four rice germplasms (YUM1490, YUM1500, YUM1503 and YUM1517). The gene for depressed palea (*dp*) is located on chromosome 6 (Kinoshita, 1993; Nagato and Yoshimura, 1998). Palea of this mutant was not developed properly and enclosed inside the lemma (Fig. 2I). Palea was smaller and constricted causing abnormal shape of spikelets and kernels. Little is known for the genetics of depressed palea mutant. Except mean value of 100 grains weight, all grain yield parameters studied showed lower value than those of wild type rice (Table 2).

Brown furrows on hull (*Bf*)

Brown longitudinal stripes on the surface of lemma and palea were found on two rice germplasms (YUM1435 and YUM1473). The gene responsible for brown furrow on hull (*Bf*) is located on chromosome 9 (Kinoshita, 1993; Nagato and Yoshimura, 1998). In this mutant rice, mutant phenotype was seen in the floral glumes (Fig. 2J). Brown longitudinal furrows were distinctly developed on the hull (Fig. 2J). Co-existence of *Bf* and its inhibitor *IBf* or deficiency of *Bf* gives normal straw color. The gene of this mutant has not

been identified yet. Mean value of number of spikelets per panicle of this mutant rice was the highest among the examined mutants in this study (Table 2). Mean value of 100 grains weight was slightly higher than that of wild type rice. Since number of spikelets and grain weight are important parameters of grain yield, the germplasm YUM1435 of *Bf* mutant rice can be used for quantitative improvement by breeding and molecular breeding (Table 2).

Pericarp color mutants

Brown pericarp and seed coat (*Rc*)

Brown pericarp and seed coat was observed in three rice germplasms (YUM1437, YUM1438 and YUM1469). The gene responsible for brown pericarp and seed coat (*Rc*) is located on chromosome 7 (Kinoshita, 1993; Nagato and Yoshimura, 1998). The outer layer of rice was brown. *Rc* is responsible for the production of pigment in the so-called brown pericarp rice, which had dark-brown irregular speckles on a reddish brown background (Fig. 3IB). Color development over the entire surface might be due to the co-existence of *Rc* with *Rd*, giving dark red color to the pericarp and seed coat (Fig. 3II). *Rc* might be regarded to have an effect of accumulating pigment in the outer layer. Transverse section of grain showed that endosperm contains starch as in wild type rice (Fig. 3II). When sliced grains were stained with Iodine, color of endosperm changed from white to dark conforming to have same level of starch as in wild type rice (Fig 3II). Mean values of the entire grain yield components of *Rc* germplasm showed lower value than those of wild type rice (Table 2).

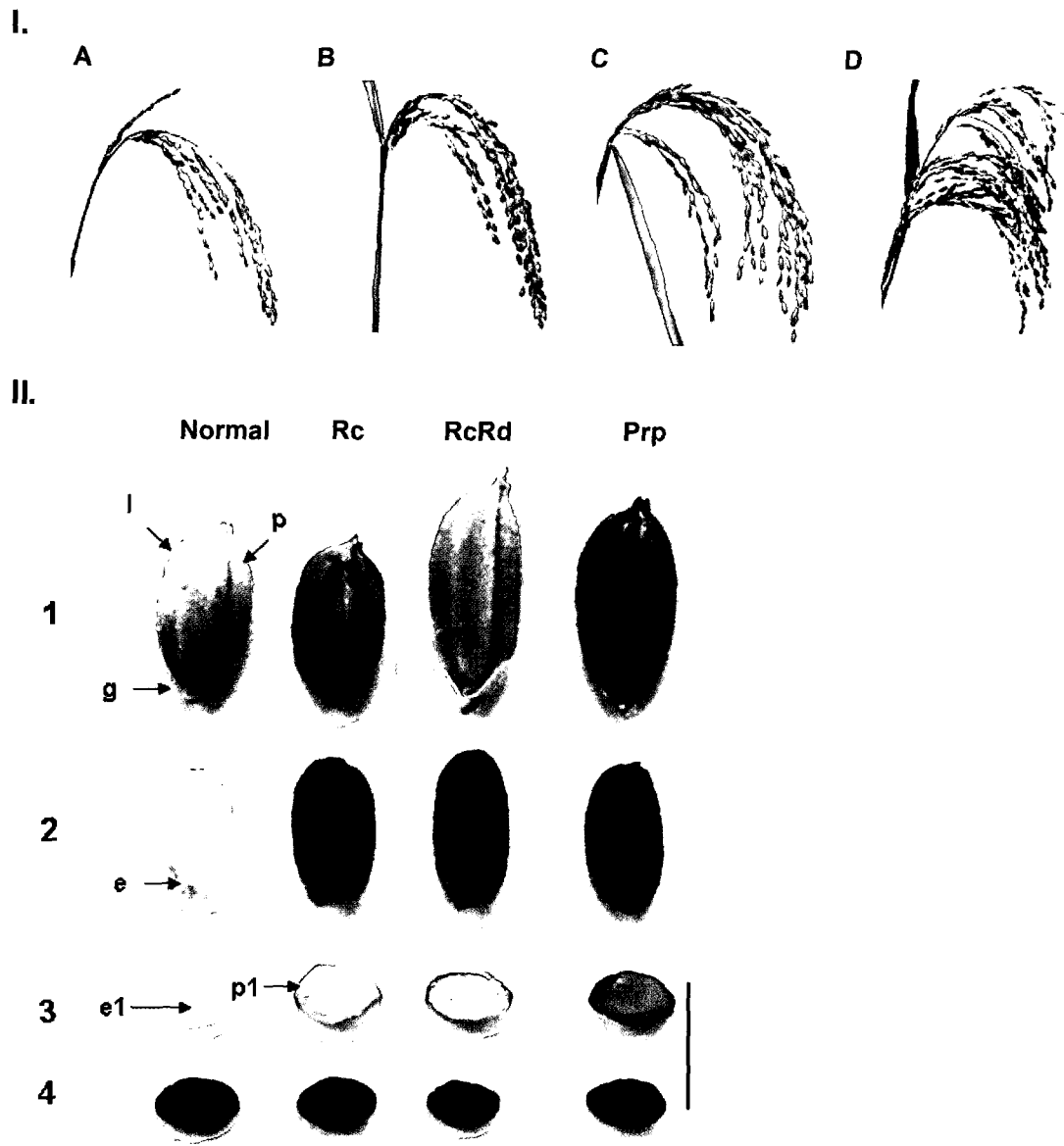


Fig. 3. Seed color mutants. I. (A) Panicle of wild type rice. (B) Panicle of brown rice (*Rc*) (YUM1438). (C) Panicle of red rice (*RcRd*) (YC1420). (D) Panicle of purple pericarp (*Prp*) (YUM1443) mutant rice. Bar = 4cm. II. Dehulled grains of wild type rice, brown rice (*Rc*), red rice (*RcRd*), and purple rice (*Prp*). (1) Spikelets of normal and mutant rice. In the figure; lemma (l), palea (p), and glume (g) are indicated. (2) Dehulled seeds. Embryo (e) is indicated. (3) Transverse section of seeds. Endosperm color is completely white in normal and *RcRd*, yellowish in *Rc* and dark in *Prp*. Endosperm (e1) and pericarp (p1) indicated. (4) Transverse section of all mutant seed types stained with 1% I-KI (Iodine Potassium Iodide) solution. Endosperms of wild type rice, *Rc*, and *Prp* are stained completely dark. Endosperm of *RcRd* is stained reddish black. Bar = 2.5cm.

Red pericarp and seed coat (*RcRd*)

Red pericarp and seed coat was observed in three germplasms (YUM1420, YUM1421 and YUM1474) (Fig. 3IC). Red color in the pericarp and seed coat of *RcRd* mutant rice might be due to the complementary action of *Rc* and *Rd*. Except the color of pericarp, color of endosperm was white as in that of wild type rice (Fig. 3II). To date little is known about the genes causing *RcRd* phenotype. Transverse sec-

tion of grain showed white endosperm indicating normal starch content as in wild type rice. However, transverse section of grain stained with 1% I-KI showed black endosperm with red background (Fig. 3II). This may be due to red color development in some extent in the endosperm. Mean values of number of spikelets per panicle, number of panicles per plant and spikelet fertility were found to be comparatively lower than those of wild type rice. However, rest of the

parameters of these mutants showed positive correlation with yield components.

Purple pericarp (*Prp*)

Outer layer of dehulled grain was found to be purple in one rice germplasm (YUM1443). *Prp* is located on chromosome 4 (Kinoshita, 1993; Nagato and Yoshimura, 1998). Hull color of this mutant turned to faint purple at maturation stage (Fig. 3ID). Outer layer of seed coat of dehulled rice (pericarp) was purple to dark red (Fig. 3II). Purple color of pericarp was started to develop from milk stage and was distinctly observed at dough stage. Transverse section of grain showed blackish endosperm indicating low amount of starch in the endosperm. Stained section of grain was black due to black color of endosperm and also the reaction of starch with iodine (Fig. 3II). The gene for purple pericarp has not been identified yet. Mean values of number of panicle per plant and spikelet fertility were found to be lower than those of wild type rice. However, mean values of rest of the components were higher than those of wild type rice (Table 2).

In this study we described phenotypic characters of four panicle mutants and 12 hull and seed mutants of rice. These abnormal characters affect quality and quantity of rice. However, some of the grain yield characters are superior to those of wild type rice. These mutant resources may be useful for agronomical applications. For examples, distinct genes in these mutants might be used for qualitative and quantitative improvement of rice in conventional breeding and molecular breeding. In addition, since we observed that *RcRd* and *Prp* mutants deposit high amount of secondary metabolites such as anthocyanin family in seed coats, new rice having anthocyanin rich endosperm might be engineered for antioxidant foods and industrial products by using molecular breeding or/and biotechnology. Moreover, in genetics of rice, these mutant genetic stocks are useful for the construction of more accurate linkage map and the physical and genetic maps by molecular cloning technology. Our further challenges are to define the functions of genes in genetic and physiological mechanisms using these mutant phenotypic characters.

ACKNOWLEDGEMENT

We thank Md. Nurul Matin and Hyunmi Ryu, Yeungnam University, for technical assistance. This research was supported by a grant (CG2113) from Crop Functional Genomics Center of the 21st Century Frontier Research Program funded by the Ministry of Science and Technology of Republic of Korea.

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