

Original Research Article

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Selection of Lodging Resistant Lines in Early Generations Using Linked Molecular Markers and Phenotypic Traits in Rice

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ABSTRACT

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Rice crop in cyclone prone coastal areas is most frequently subjected to lodging at reproductive stage causing severe yield loss. Breeding for non-lodging rice varieties is herculean task as it is controlled by structural properties of the culm and weather parameters. Present study aimed to select lodging resistant lines using phenotypic characters and molecular markers in early generations. Co-segregation banding pattern for lodging resistant families with either homozygous donor allele or heterozygous allele for markers RM 20557, RM 5509 among the F₃ families of MTU 7029/II 110-9-1-1-1-1 and for markers RM 6933 and RM 216 in case of F₃ families pertaining to MTU 7029/MTU1121 indicates that these markers can be useful in selection of lodging resistant lines in early generations. Correlation studies revealed that positive correlation of culm diameter with panicle length was observed among the F₃ families of MTU 7029/II 110-9-1-1-1-1 and negative correlation of bending strength with number of ear bearing tillers per plant in case of MTU 7029/MTU 1121 indicates specific contribution of alleles for lodging resistance depends on donors used.

Introduction

Lodging of rice crop is one of the constraints to rice productivity in cyclone prone coastal irrigated ecosystem. Lodging is permanent displacement of vertical stem to leaning horizontally at reproductive phase. It reduces the yield up to 2% for every 1% of lodging (Setter *et al.*, 1997). Besides yield reduction, lodging of rice crop deteriorates quality and impedes manual as well as mechanical harvesting and also increases drying costs. Direct evaluation of lodging resistance requires visual estimates in plots of advanced

breeding lines or cultivars. A true assessment needs simulating conditions favorable to lodging, with a large investment of time, money and resources. But even routine plot scoring cannot be used to evaluate first generations in breeding programs, because their genetic variability is too high to grow plots. Indirect selection for lodging resistance related traits is one of the strategies to develop non lodging rice cultivars. Breaking resistance and lodging index of lower nodes were significantly correlated with visual score of lodging (Islam *et al.*, 2007). Zhang *et al.*, (2009) reported that selection of lodging

resistant cultivars, with thicker culm wall, larger culm wall area, better vascular bundle characters with high cellulose content in their stem would be useful. Wu *et al.*, (2011) reported that the large culm cultivars exhibited greater plant size, culm diameter and flag leaf length and width, as well as lower tiller numbers. Pedigree analysis showed lodging resistance of varieties was closely correlated with that of their parents (Ming-liang *et al.*, 2012). Yang *et al.*, (2012) reported that breaking resistance strengths of three elongation internodes near stem base were significantly correlated with internode wall thickness and panicle length was significantly positively correlated with internode wall thickness. Laza *et al.*, (2014) reported positive correlations of percentage lodging with canopy height, culm length and negative correlation with stem diameter.

Indirect selection through lodging resistant related traits like culm diameter, culm thickness, culm strength, bending strength, basal internodal length, per cent of lodging in early generations is a herculean task as it involves handling of large population. Several workers reported QTLs for culm diameter (Ookawa *et al.*, 2010), culm thickness (Mu *et al.*, 2004), culm strength (Zhu *et al.*, 2008; Yamamoto *et al.*, 2013; Yano *et al.*, 2014), basal internodal length (Mu *et al.*, 2004) will be useful in selection of lodging resistant lines in early generations. Hence present study aimed to screen F₃ families for lodging resistance using molecular markers and phenotypic screening.

Materials and Methods

One hundred eighty F₃ families derived from lodging susceptible parent Swarna and resistant elite lines II 110-9-1-1-1-1 and 160 from Swarna and resistant line MTU 1121 were evaluated in 2 replications along with checks during Rabi 2013-14. Each F₃ family

was planted in 2 rows per replication with row length of 3m with spacing of 20 X15 cm.

Data pertaining to 14 phenotypic characters *viz.*, days to 50 % flowering, plant height, number of ear bearing tillers plant⁻¹, panicle length, number of filled grains panicle⁻¹, spikelet fertility, test weight, grain yield plant⁻¹, culm diameter, culm thickness, culm strength, 4th internodal length, bending strength and per cent of lodging were collected among F₃ families. Lodging resistance traits, culm diameter and culm thickness was measured at 4th internodal length from the top using vernier calipers at 20 days after heading, culm strength and per cent of lodging was measured as per the IRR standard evaluation systems, 2002. Bending strength was measured by pushing hill at 20cm above the ground at 45⁰ angle using Prostrate tester (DIK 7401, Daiki Rika Kogyo Co. Ltd., Tokyo, Japan and it was expressed in g/stem using the following formula as per Bhagat *et al.*, (2011).

Bending strength= [(test reading/40) X (1000/number of tillers)]

F₃ families exhibiting 0 to 25 per cent of lodging was considered as resistant families and families showing per cent of lodging more than 25 per cent were grouped as lodging susceptible.

Genotypic screening with molecular markers

DNA was isolated from the leaf samples of F₃ families collected at 45 days using the method described by Zheng *et al.*, (1995). Microsatellite markers RM 20557, RM 5509 associated with Strong culm 2 (SCM2) (Ookawa *et al.*, 2010) confers for lodging resistance with wider culms on chromosome 6 showing polymorphism between parents were used to screen F₃ families derived from

Swarna and II 110-9-1-1-1-1. Whereas RM 6933 on chromosome 2 and RM 216 on chromosome 10 associated with culm strength (Yano *et al.*, 2014 and Mu *et al.*, 2004) exhibiting polymorphism between parents Swarna and MTU 1121 were used to screen respective F₃ families.

PCR was performed using 10ul reaction mixture comprising of 2.5ul of 20ng of genomic DNA, 1 µl of 10 pmol primer of forward and reverse each, 0.5 µl of 2.5 mM deoxy ribonucleotides (dNTPS), 1 µl of Genei 10 X assay buffer (10 mM TrisHCl (p^H 8.3), 50 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin) and 1 µl of 1 U/µl *Taq DNA polymerase* (Genei ®) and 3 µl of sterile distilled.

Thermo profile of 94°C for 5 minutes for initial, 30 seconds for denaturation, annealing temperature at 58°C for 30 seconds, elongation at 72°C for 1 minute and final extension with same temperature for 1 minute was followed for Eppendorf thermocycler for amplification of the products. The PCR products were subjected to electrophoresis on 3 % high resolution agarose gel unit containing 1 X TAE buffer. The DNA fragments were captured using gel documentation system (SYNGENE Gene flash U.K.).

Data analysis of F₃ families

Clustering of 180 F₃ families derived from MTU 7029/II 110-9-1-1-1-1 cross combination and 160 F₃ families derived from MTU 7029/MTU 1121 was done using 14 characters by Mahalanobis D² Ward's Minimum Variance method. Graphical genotyping of F₃ families was performed using GGT 2.0 version (Van Berloo 1999). Correlation coefficients were estimated for paired character association of 14 characters among the two crosses of F₃ families as per Falconer, 1964.

Results and Discussion

Identification of lodging resistant f₃ families using molecular markers

Marker RM 20557 segregated among 180 F₃ families of MTU 7029/II 110-9-1-1-1-1 as 51.1 % for lodging susceptible parent MTU 7029, 35 % of donor allele of resistant parent II 110-9-1-1-1 and 13.3% heterozygous allelic pattern (Table 1). RM 5509 segregated as 36.7% for lodging susceptible parent MTU 7029, 51.7% donor allele of II 110-9-1-1-1-1 and 8.9% of heterozygote allele. It indicated that both the markers expressed fixation of alleles towards homozygosity of either parents in F₃ generation. These two markers with homozygosity allele of donor and heterozygote allele can be used to select lodging resistant families in early generation of cross MTU 7029/II 110-9-1-1-1-1.

In case of F₃ families derived from MTU 7029/MTU 1121 cross combination, RM 6933 segregated among 160 families as 41.9% towards susceptible parent MTU 7029 and 24.4% for donor allele of MTU 1121 and 21.3 % heterozygous allele. Another marker RM 216 showed segregation pattern of 23.8 % for susceptible parent allele, 42.5% donor parent and 31.9 % heterozygous allele. RM 6933 fixed homozygosity more towards susceptible parent and RM 216 towards resistant parent. Approximately 20-30 % of F₃ families expressed heterozygous allele for both the markers. Selection of lodging resistant loci using these two markers for donor allele and heterozygous allele is useful in early generations.

Identification of lodging resistant lines using phenotypic characters

Analysis of variance revealed significant differences among the F₃ families of both the cross combinations for yield and lodging

related characters. The results of Mahalanobis D^2 revealed that 180 F_3 families of MTU 7029/ II 110-9-1-1-1-1 were grouped into 14 clusters (Table 2). Most of the lodging resistant F_3 families were grouped in first five clusters. Cluster 14 has the highest intra cluster value of 68.25. Inter cluster mean values were higher between clusters 6 and 14 followed by clusters 1 and 14. Cluster 4 had the all lodging resistant lines. Inter cluster values were higher between clusters 6 and 14 (118.73) followed by 1 and 14 clusters (101.55) and the results were depicted in the Table 3. F_3 families with medium duration were grouped in cluster 10 (100.65 days). Clusters 13 has F_3 families with intermediate height (126.88 cm).

More number of ear bearing tillers per plant of 27.92 were observed in cluster 14. Clusters 9, 10, 1 and 4 had the families with long panicles. F_3 lines in clusters 1, 5 and 8 expressed higher spikelet fertility per cent of 88.47, 88.20 and 88.07 respectively. Cluster 4 with more number of filled grains per panicle (237.26) and the cluster 1 consist of F_3 families with highest test weight (21.56 g). Higher grain yield plant⁻¹ was observed in the cluster 14 (33.92 g) followed by cluster 4 (32.12 g).

F_3 families with wider culm (7.45 mm) were grouped in cluster 9. Thicker culms were observed in cluster 12 with mean value of 1.47 mm. F_3 families with strong culm (1.36) and lowest per cent of lodging (0.38) were grouped in cluster 4. Highest bending strength was observed in cluster 2 (51.91 g stem⁻¹). Cluster 12 possessed the genotypes with shortest basal inter nodal length of 6.76 cm (Table 4). Thus, lodging resistant genotypes with high yield, strong and wider culms were grouped in clusters 4 and 14 and these families can be further advanced to next generation for the development of non-lodging high yielding varieties.

One hundred sixty F_3 families derived from MTU 7029/MTU 1121 were grouped into 13 clusters (Table 5). In this cross combination, 150 families were found to be lodging resistant. Lodging susceptible genotypes were fallen under clusters 12, 13 and 9. Highest inter cluster value of 95.26 was observed between clusters 6 and 13 (Table 6).

Lodging resistant lines with shortest duration were grouped in cluster 2 (99.71) and late duration in cluster 12 (111.25) and details are presented in Table 7. Lodging resistant lines with semi dwarf stature were grouped in cluster 5 with mean value of 103.50 cm. More number of ear bearing tillers plant⁻¹ were observed in cluster 4 (16.88).

Lodging resistant lines with long panicles were together formed into cluster 11 (28.23). More number of filled grains panicle⁻¹ was observed in cluster 3 (257.16). Lodging resistant lines with higher spikelet fertility were found in cluster 6 (89.21 %). Lodging resistant lines with bold grains were observed in cluster 7 (22.40 g).

Lodging resistant lines with higher grain yield plant⁻¹ were found in cluster 4 (23.29 g). F_3 families with wider and thicker culms were grouped in cluster 8. Lines with short basal inter nodal length were grouped in cluster 9 (4.78 cm). Higher cluster mean value for bending strength was observed in cluster 6 (99.68 g stem⁻¹) and minimal per cent of lodging was observed in cluster 2 (0.90%). Thus, eight lodging resistant F_3 lines with higher yield were grouped in cluster 4 followed by 14 lodging resistant lines in cluster 8 can be advanced to next generation for development of high yielding non lodging varieties.

But generation of data for large population in early generation in regular plant breeding programmes is herculean task.

Table.1 Performance of lodging resistant loci linked SSR markers over F₃ families in two crosses

Cross	Marker	Chromosome	Position Mb	Missing allele (%)	A (%)	B (%)	H (%)
MTU7029/ II110-9-1-1-1	RM20557	6	27.50	0.60	51.10	35.00	13.30
MTU7029/ II110-9-1-1-1	RM5509	6	27.80	1.10	36.70	51.70	8.90
MTU 7029 / MTU1121	RM6933	2	29.30	12.40	41.90	24.40	21.30
MTU 7029/ MTU1121	RM216	10	5.30	1.80	23.80	42.50	31.90

A: Susceptible parent allele, B: Resistant parent allele H: Heterozygous allele

Table.2 Clustering pattern F₃ families pertaining to cross combination MTU 7029/II 110-9-1-1-1 during *rabi* 2013-14

Cluster number	Number of F ₃ lines in cluster	Number of lodging resistant F ₃ lines	Details of lodging resistant F ₃ lines
1	16	11	LH12-1, LH12-13, LH12-97, LH12-47, LH12-127, LH12-8, LH12-26, LH12-25, LH12-58, LH12-96, LH12-28
2	27	18	LH12-27, LH12-142, LH12-29, LH12-9, LH12-11, LH12-66, LH12-65, LH12-9, LH12-122, LH12-116, LH12-129, LH12-130, LH12-132, LH12-124, LH12-141, LH12-121, LH12-154, LH12-89
3	15	9	LH12-24, LH12-114, LH12-88, LH12-123, LH12-94, LH12-94, LH1-95, LH12-87, LH12-151
4	14	14	LH12-96, LH12-105, LH12-92, LH12-111, LH12-99, LH12-91, LH12-93, LH12-147, LH12-101, LH12-106, LH12-38, LH12-109, LH12-144, LH12-115
5	10	9	LH12-45, LH12-150, LH12-113, LH12-137, LH12-15, LH12-123, LH12-140, LH12-136, LH12-140
6	1	0	LH12-151
7	26	0	0
8	10	0	0
9	10	1	LH12-181
10	10	2	LH12-64, LH12-120
11	10	0	0
12	14	0	0
13	15	0	0
14	2	1	LH12-118
Total	180	65	

Table.3 Intra and inter cluster means of F₃ families pertaining to cross combination MTU 7029/II 110-9-1-1-1-1 during *rabi* 2013-14

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12	Cluster13	Cluster 14
Cluster1	19.52	22.62	23.08	27.11	28.42	85.92	29.19	34.41	34.12	35.76	31.83	34.59	33.41	101.55
Cluster2		13.23	18.37	20.64	20.48	70.11	22.21	31.60	28.02	28.07	28.13	27.56	24.52	96.79
Cluster3			14.71	22.12	20.62	60.72	27.35	32.29	31.46	29.02	26.68	31.54	25.32	85.86
Cluster4				13.75	24.44	83.50	28.19	39.43	33.84	33.00	39.03	38.15	36.84	83.04
Cluster5					13.19	48.29	29.63	35.12	42.37	37.87	38.30	37.04	31.01	82.78
Cluster6						0.00	67.61	55.75	75.05	72.86	63.16	73.71	62.39	118.73
Cluster7							13.28	19.28	19.74	24.83	24.20	20.20	22.02	87.42
Cluster8								17.10	25.40	28.12	25.05	23.48	28.81	86.92
Cluster9									14.96	27.57	26.55	25.88	24.73	99.39
Cluster10										22.63	28.97	29.54	33.80	77.55
Cluster11											16.36	21.90	24.30	100.90
Cluster12												15.93	22.90	88.18
Cluster13													17.75	98.68
Cluster14														68.25

Table.4 Cluster mean values of 14 characters pertaining to F₃ population of MTU 7029/II 110-9-1-1-1-1 during *rabi* 2013-14

Clusters	Days to 50% flowering	Plant height (cm)	No. of ear bearing tillers plant ⁻¹	Panicle length (cm)	No. of filled grains panicle ⁻¹	Spikelet fertility (%)	Test weight (g)	Grain yield plant ⁻¹ (g)	Culm diameter (mm)	Culm thickness (mm)	Culm strength	4 th Inter nodal length (cm)	Bending Strength (g stem ⁻¹)	Lodging (%)
Cluster1	106.47	134.67	10.01	28.47	146.35	88.47	21.56	22.21	7.14	1.01	2.96	7.26	49.30	12.90
Cluster2	107.65	135.58	9.17	26.30	182.67	80.47	15.41	20.21	7.03	1.24	3.17	7.76	51.91	19.02
Cluster3	109.27	133.38	11.04	27.15	135.21	70.20	17.18	22.43	6.41	0.88	2.20	8.14	45.61	16.92
Cluster 4	111.14	133.26	11.60	28.41	237.26	82.37	16.31	32.12	6.60	1.11	1.36	7.62	45.52	0.38
Cluster5	108.15	130.50	10.30	24.25	169.22	88.20	16.53	21.72	5.60	1.06	1.87	10.79	48.83	4.93
Cluster6	111.00	139.17	7.50	25.51	83.50	63.57	13.80	16.67	4.10	0.92	9.00	18.69	20.09	48.03
Cluster7	107.29	139.01	9.97	27.00	220.07	85.99	17.07	20.38	6.66	1.14	7.65	7.56	21.28	78.71
Cluster8	106.60	152.38	10.07	27.74	156.37	88.07	17.89	21.65	6.56	0.90	8.53	9.48	15.69	90.70
Cluster 9	111.50	134.97	10.38	32.12	180.85	80.31	15.69	18.79	7.45	1.21	8.40	7.45	17.63	77.80
Cluster10	100.65	143.65	12.52	29.39	173.09	71.63	14.71	24.62	6.94	1.14	5.93	7.96	23.13	55.76
Cluster11	108.00	140.87	9.15	26.22	113.92	63.99	19.64	24.00	7.29	1.22	7.47	8.22	24.98	87.17
Cluster12	109.36	146.85	11.49	24.40	133.60	83.16	17.23	20.93	7.00	1.47	7.71	6.76	17.22	83.34
Cluster13	111.90	126.88	9.83	25.29	130.33	77.35	15.92	15.11	6.63	1.13	6.88	7.19	27.25	79.52
Cluster14	102.75	137.00	27.92	24.43	187.67	86.03	14.46	33.92	5.75	0.86	5.00	11.58	13.89	49.00

Table.5 Clustering pattern F₃ lines pertaining to cross combination MTU 7029/MTU1121 during *rabi* 2013-14

Cluster number	Number of F ₃ lines in cluster	Number of lodging resistant F ₃ lines	Details of lodging resistant F ₃ lines
Cluster 1	27	27	LH14-1, LH14-306, LH14-71, LH14-167, LH14-179, LH14-308, LH14-23, LH14-314, LH14-170, LH14-189, LH14-315, LH14-11, LH14-93, LH14-118, LH14-188, LH14-28, LH14-35, LH14-80, LH14-12, LH14-310, LH14-166, LH14-56, LH14-108, LH14-121, LH14-311, LH14-183, LH14-195
Cluster 2	14	14	LH14-3, LH14-169, LH14-9, LH14-75, LH14-147, LH14-16, LH14-151, LH14-155, LH14-156, LH14-150, LH14-163, LH14-89, LH14-165, LH14-187
Cluster 3	10	10	LH14-24, LH14-49, LH14-159, LH14-161, LH14-185 LH14-54, LH14-76, LH14-30, LH14-146, LH14-41
Cluster 4	8	8	LH14-160, LH14-301, LH14-317, LH14-176, LH14-199, LH14-309, LH14-313, LH14-198
Cluster 5	20	20	LH14-2, LH14-95, LH14-126, LH14-184, LH14-25 LH14-149, LH14-97, LH14-307, LH14-302, LH14-312, LH14-318, LH14-32, LH14-120, LH14-77, LH14-78, LH14-69, LH14-88, LH14-125, LH14-81, LH14-68
Cluster 6	2	2	LH14-91, LH14-324
Cluster 7	18	18	LH14-4, LH14-37, LH14-39, LH14-26, LH14-27, LH14-102, LH14-113, LH14-137, LH14-18, LH14-130, LH14-131, LH14-31, LH14-79, LH14-86, LH14-104, LH14-174, LH14-175, LH14-124
Cluster 8	14	14	LH14-6, LH14-111, LH14-114, LH14-55, LH14-123 LH14-21, LH14-323, LH14-38, LH14-116, LH14-40 LH14-52, LH14-51, LH14-67, LH14-320
Cluster 9	12	11	LH14-5, LH14-14, LH14-180, LH14-29, LH14-322, LH14-10, LH14-43, LH14-48, LH14-61, LH14-46, LH14-64, LH14-158
Cluster 10	15	15	LH14-42, LH14-148, LH14-63, LH14-164, LH14-100, LH14-98, LH14-128, LH14-87, LH14-70, LH14-129, LH14-90, LH14-96, LH14-105, LH14-110, LH14-319
Cluster 11	7	7	LH14-72, LH14-303, LH14-34, LH14-141, LH14-171, LH14-316, LH14-103
Cluster 12	9	4	L LH14-73, LH14-82, LH14-66, LH14-53
Cluster 13	4	0	0
Total	160	150	

Table.6 Intra and inter cluster means of F₃ families pertaining to cross combination MTU 7029/MTU 1121 during *rabi* 2013-14

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12	Cluster 13
Cluster 1	14.77	18.83	19.84	22.61	21.19	56.47	24.51	21.98	20.42	21.21	37.51	32.42	55.73
Cluster 2		13.90	21.37	34.20	21.22	49.56	26.56	22.51	24.07	23.39	42.21	30.96	62.57
Cluster 3			12.65	25.32	24.48	54.01	27.61	19.24	24.09	26.59	50.46	39.26	52.12
Cluster 4				16.75	37.68	79.55	30.71	27.31	27.20	33.47	45.52	46.73	57.03
Cluster 5					15.06	40.48	25.27	24.92	29.88	23.55	48.28	34.83	69.24
Cluster 6						37.65	46.36	40.75	58.86	43.08	83.46	54.13	95.26
Cluster 7							20.43	20.30	27.67	24.72	45.24	35.39	61.84
Cluster 8								10.63	21.05	20.95	43.01	37.99	56.20
Cluster 9									16.36	21.87	34.21	31.12	43.87
Cluster10										15.79	34.34	28.12	58.52
Cluster11											35.62	43.83	73.73
Cluster12												24.61	45.81
Cluster13													16.66

Table.7 Cluster mean values of 14 characters pertaining to F₃ population of MTU 7029/MTU 1121 during *rabi* 2013-14

Clusters	Days to 50% flowering	Plant height (cm)	No. of ear bearing fillers plant-1	Panicle length (cm)	No. of filled grains panicle ⁻¹	Spikelet fertility (%)	Test weight (g)	Grain yield plant ⁻¹ (g)	Culm diameter (mm)	Culm thickness (mm)	Culm strength	4th Inter nodal length (cm)	Bending Strength (g stem-1)	Per cent of lodging (%)
Cluster1	105.76	106.54	12.23	25.75	159.70	84.48	18.11	20.04	6.42	1.21	2.67	5.85	40.92	1.65
Cluster2	99.71	105.92	9.61	25.77	138.92	83.00	17.94	17.97	6.54	1.17	4.12	5.60	51.44	0.90
Cluster3	104.10	105.99	10.58	26.43	257.16	86.06	18.51	19.81	7.05	1.37	4.30	5.04	44.37	5.90
Cluster4	106.75	107.97	16.88	27.14	193.56	83.53	20.28	23.69	7.12	1.42	3.21	5.99	28.74	1.21
Cluster5	105.70	103.50	8.39	25.30	180.66	84.33	19.69	20.60	6.34	0.90	1.88	6.61	61.95	2.65
Cluster6	107.50	124.17	5.25	24.89	177.75	89.21	20.44	14.50	6.97	1.61	3.33	7.47	99.68	14.07
Cluster7	105.61	117.53	10.37	27.18	158.47	81.13	22.40	18.97	6.98	1.07	2.74	6.56	48.40	1.48
Cluster8	104.93	116.07	9.58	28.13	172.65	83.30	19.83	21.33	7.62	1.62	2.36	5.54	53.83	5.30
Cluster9	108.92	109.27	11.24	27.20	123.88	74.29	18.16	20.49	6.92	1.40	4.75	4.78	42.29	10.30
Cluster10	108.87	107.37	9.80	25.84	129.00	77.01	18.72	13.95	7.22	1.39	2.38	6.34	51.52	2.59
Cluster11	107.79	105.22	13.00	28.23	83.89	51.62	17.52	15.13	6.55	1.43	1.81	6.16	39.62	1.59
Cluster12	106.72	109.42	9.70	25.11	111.07	69.25	18.70	13.76	6.64	1.10	6.33	7.45	46.50	32.44
Cluster13	111.25	111.92	11.33	27.92	170.00	78.72	18.53	18.58	7.07	1.26	8.17	5.18	23.53	97.13

Table.8 Correlation coefficients of F₃ population of MTU 7029/II 110-9-1-1-1-1 during rabi 2013-14

Character	Days to 50% flowering	Plant height (cm)	No. of ear bearing tillers plant-1	Panicle length (cm)	No. of filled grains panicle ⁻¹	Spikelet fertility (%)	Test weight (g)	Grain yield plant ⁻¹ (g)	Culm diameter (mm)	Culm thickness (mm)	Culm strength	4 th Inter nodal length (cm)	Bending Strength (g stem ⁻¹)	Per cent of lodging (%)
Days to 50% flowering	1.0000	-0.0224	-0.1217*	0.0321	0.0115	0.0041	-0.0201	0.0318	-0.0504	0.0560	-0.0603	-0.0534	0.0651	0.0311
Plant height (cm)		1.0000	0.0364	0.1289*	0.0741	0.0122	0.1171*	0.0889	0.0967	0.1004	0.2591**	0.0454	-0.2411**	0.2276**
Number of ear bearing tillers plant-1			1.0000	0.0131	0.0653	0.0067	-0.1180*	0.2727**	-0.0885	-0.0085	-0.0999	0.0691	-0.2905**	-0.0479
Panicle length (cm)				1.0000	0.1859	0.0349	0.0558	0.1226*	0.2565**	-0.0569	0.0208	-0.0820	-0.0329	-0.0189
No. of filled grains panicle ⁻¹					1.0000	0.2660**	-0.1806**	0.2752**	0.0085	-0.1044*	-0.1007	0.0033	0.0336	-0.1317*
Spikelet fertility (%)						1.0000	0.0844	0.0982	-0.0702	-0.0576	-0.0510	-0.0585	0.0551	-0.0666
Test weight (g)							1.0000	-0.0313	0.1709**	-0.0457	0.0249	-0.0550	0.0416	0.0120
Grain yield plant ⁻¹ (g)								1.0000	-0.0052	-0.1086*	-0.2826**	0.0258	0.0757	-0.2763**
Culm diameter (mm)									1.0000	0.3098**	0.0907	-0.2222**	0.0164	0.0739
Culm thickness (mm)										1.0000	0.1442**	-0.1682**	-0.1114*	0.1031
Culm strength											1.0000	-0.0889	-0.7316**	0.8231*
4th Inter nodal length (cm)												1.0000	0.0323	-0.0859
Bending Strength (g stem ⁻¹)													1.0000	-0.7247
Per cent of lodging														1.0000

Table.9 Correlation coefficients of F₃ population of MTU 7029/MTU 1121 during dry season of 2013-14

Character	Days to 50% flowering	Plant height (cm)	No. of ear bearing tillers plant ⁻¹	Panicle length (cm)	No. of filled grains panicle ⁻¹	Spikelet fertility (%)	Test weight (g)	Grain yield plant ⁻¹ (g)	Culm diameter (mm)	Culm thickness (mm)	Culm strength	4th Internodal length (cm)	Bending Strength (g stem ⁻¹)	Lodging (%)
Days to 50% flowering	1.0000	0.0585	0.0551	0.0330	-0.0663	-0.1117*	0.0038	-0.0183	-0.0152	0.0760	-0.0212	-0.0298	-0.0519	0.2263**
Plant height (cm)		1.0000	-0.0171	0.1054	-0.0420	-0.0128	0.0754	-0.0034	0.2747**	0.0384	-0.1146*	0.0898	-0.0377	0.0999
Number of ear bearing tillers plant ⁻¹			1.0000	0.0795	-0.0144	-0.0340	-0.0883	0.0987	-0.0292	0.1524**	0.0468	-0.0785	-0.7905**	-0.0407
Panicle length (cm)				1.0000	-0.0134	-0.1168*	0.0952	0.0766	0.2354**	0.1369*	-0.0275	-0.0900	-0.1097*	0.0559
No. of filled grains panicle ⁻¹					1.0000	0.4928**	0.1188*	0.3116**	0.0797	0.0453	-0.0601	-0.0695	0.0708	-0.0294
Spikelet fertility (%)						1.0000	0.1107*	0.2685**	0.0174	-0.0576	-0.0140	0.0905	0.0524	-0.0961
Test weight (g)							1.0000	0.1460**	0.1051	-0.0394	-0.0602	0.0398	0.1369*	-0.0896
Grain yield plant ⁻¹ (g)								1.0000	0.0208	-0.0095	-0.0820	-0.1735**	-0.0534	-0.1007
Culm diameter (mm)									1.0000	0.4179**	-0.0441	-0.0592	0.0014	0.0303
Culm thickness (mm)										1.0000	-0.0158	-0.1270*	-0.0968	0.0362
Culm strength											1.0000	-0.0897	-0.2232**	0.5315**
4th Internodal length (cm)												1.0000	0.1298*	-0.0463
Bending Strength (g stem ⁻¹)													1.0000	-0.2409**
Per cent of lodging														1.0000

Character association studies of yield and lodging related traits among F₃ families

Grain yield per plant expressed positive significant association with number of ear bearing tillers plant⁻¹, panicle length and number of filled grains per panicle and negatively associated with culm thickness, culm strength and per cent of lodging (Table 8). Per cent of lodging was positively correlated with plant height and culm strength. Per cent of lodging was negatively correlated with grain yield per plant and number of filled grains per panicle. Selection of lodging resistant lines with high yield along with strong culm is desirable in evolving lodging resistant rice varieties from the cross, MTU 7029/II 110-9-1-1-1. Bending strength was negatively correlated with plant height, number of ear bearing tillers per plant, culm thickness and culm strength. Basal inter nodal length was negatively correlated with culm diameter and culm thickness. Culm diameter was positively associated with panicle length and test weight. *SCM2* has pleiotropic effect on APO (Apparent panicle organization) as reported by Ookawa *et al.*, (2010). In the present study also culm diameter had positive association with panicle length and donor II 110-9-1-1-1-1 possessed longer panicles with higher yield. Culm strength positively associated with thicker culms. Favourable alleles for lodging resistant lines might be obtained due to allelic interaction of dwarf and strong culm loci. Therefore indirect selection for lodging resistant genotypes with strong culm, minimal per cent of lodging and higher yield is useful in crop improvement. Laza *et al.*, (2014) and Ming-liang *et al.*, (2012) reported positive correlations between percentage lodging and plant height.

Grain yield per plant exhibited significant positive association with number of filled grains per panicle, spikelet fertility % and test

weight, culm thickness and negatively correlated with basal inter nodal length. Per cent of lodging was positively correlated with days to 50% flowering, culm strength and negatively associated with bending strength among F₃ families of MTU 7029/MTU 1121 (Table 9).

In this case, selection of lodging resistant lines with more number of filled grains panicle⁻¹ having high spikelet fertility %, test weight and thicker culm with minimal basal inter nodal length is rewarding. Bending strength was negatively correlated with number of ear bearing tillers plant⁻¹, panicle length and culm strength and positively associated with test weight and basal inter nodal length. Negative association of *SCM3* and *SCM4* QTLs conferring for bending strength with number of productive tillers per plant was observed by Yano *et al.*, (2014). Lower elongating internodes have negative association with ear bearing tillers per plant. Basal inter nodal length was negatively associated with grain yield plant⁻¹ and culm thickness. Culm strength negatively correlated with plant height. Culm thickness has positive association with number of ear bearing tillers per plant, panicle length and culm diameter. Positive association of culm diameter with plant height and panicle length was observed.

Lodging resistant lines selected though phenotypic characters in both crosses showed co-segregation banding pattern of either homozygous donor allele or heterozygous alleles for the markers used in respective cross indicating usefulness of molecular markers in selection of lodging resistant lines. Selection of lodging resistant lines depends on contribution of resistant alleles from respective donors even though same susceptible parent used. These molecular markers validated in another F₃ population derived from susceptible parent MTU 1061 and resistant parent BPT 2270, markers

RM5509 and RM 20557 were showed co-segregation banding pattern for resistant and susceptible families indicating that these markers can be useful in selection of lodging resistant lines in early generations.

Correlation studies revealed that markers RM 20557, RM 5509 are useful in selection of lodging resistant line as positive correlation of culm diameter with panicle length was observed among the F₃ families of MTU 7029/II 110-9-1-1-1-1 as in case of linked QTL SCM2 showing similar type of association. Bending strength showed negative association with number of ear bearing tillers per plant was observed in case of F₃ families of MTU 7029/MTU 1121 and similar type of association was observed for SCM 3 and SCM4 and marker RM 6933 is in the vicinity of SCM 4 on chromosome 2. Using above markers associated with lodging resistant related traits would help in selection of lodging resistant lines with homozygosity for donor allele and heterozygous alleles in early generations rather on indirect selection using phenotypic characters of lodging related traits

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References

- Bhagat, K.P., Sairam, R.K., Deshmukh, P.S and Kushwaha, S.R. 2011. Biochemical analysis of stem in lodging tolerant and susceptible wheat (*Triticum aestivum* L.) genotypes under normal and late sown conditions. *Indian Journal of Journal of Plant Physiology*. 16(1): 68-74.
- Falconer, D.S. 1964. *Introduction to Quantitative Genetics*. Longmann. London and New York. Pp. 294-300.
- Islam, M.S., Peng, S., Visperas, R.M., Ereful, N., Bhuiya, M.S.U and Julwquar, A.W. 2007. Lodging related morphological traits of hybrid rice in a tropical irrigated ecosystem. *Field Crops Research*. 101: 240-248.
- Laza, M.R., Shrestha, S., Mendez, K.V., Dingkuhn, M and Lopez, M. 2014. Morphological characterization of component traits for lodging resistance in rice. Abstracts of International Rice Congress 2014, October 27 to November1 2014, Bangkok, 1354.
- Ming-liang, D., Zhen-x,i A., Qian, Z., Yumin, C., Wei-hua, L and Lu-yuan, D. 2012. Relationship between lodging resistance and either agronomic traits or parents lodging resistance in plateau japonica rice. *Chinese Journal of Rice Science*. 26(3): 325-330.
- Mu, P., Zi-chao, L., Chun-ping, L., Hong-liang, Z and Xiang-kun, W. 2004. QTL analysis for lodging resistance in rice using a DH Population under lowland and upland cultural Conditions. *Proceedings of the 4th International Crop Science Congress*. 26 September - 1 October 2004, Brisbane, Australia.
- Ookawa, T., Hobo, T., Yano, M., Murate, K., Ando, T., Miure, H., Asno, K., Ochiai, Y., Ikeda M., Nishitani, R., Ebistani, T., Ozaki, I., Angeles, E.R., Hirasana, T and Matsuoka, M 2010. New approach for rice improvement using a pleiotropic QTL gene for lodging resistance and yield. *Nature Communications* <http://nature.com>.
- Setter, T.L., Laureles, E.V and Mazaredo, A.M. 1997. Lodging reduces yield of rice by self-shading and reductions in canopy photosynthesis. *Field Crops Research*. 49: 95-106.
- SES, IRRI 2002. *Standard Evaluation System for Rice*. International Rice Research Institute, Philippines.

- Van Berloo, R. 1999. GGT: Software for the display of graphical genotypes. *Journal of heredity*. 90(2): 328-329.
- Wu, L.L., Liu, Z., Jun-Min, W., Cong-Yi, Z and Kun-Ming, C. 2011. Morphological, anatomical, and physiological characteristics involved in development of the large culm trait in rice. *Australian Journal of Crop Science*. 5(11): 1356-1363.
- Yamamoto, K., Yamamoto, T., Sugiyama, C., Hirasawa, T and Ookawa, T. 2013. Estimation of the locus for strong culm traits, using reciprocal chromosome segment substitution lines derived from the cross between rice varieties, koshihikari and takanari. *Proceedings of 7th International Rice Genetics Symposium*, 5 - 8 November 2013, Manila, Philippines. 435 Pp.
- Yano, K., Ookawa, T., Taiichiro, A., Aya, K., Ochiai, Y., Hirasawa, T., Ebitani, T., Takarada, T., Yano, M., Yamamoto, T., Fukuoka, S., Wu, J., Ando, T., Ordonio, R.L., Hirano, K and Matsuoka, M. 2014. Isolation of a novel lodging resistance QTL gene involved in strigolactone signaling and its pyramiding with a QTL gene involved in another mechanism. *Molecular Plant*. 8(2): 303-315.
- Yang, H., Fang, X., He, H and Xie, Z. 2012. Relationship of characteristics of culm construction to lodging resistance and yield of Fujian-bred super-rice cultivars. *Chinese Journal of Eco Agriculture*. 20: 909-913.
- Zhang, X., Li, H., Li, W., Xu, Z., Chen, W., Zhang, W and Wang, W. 2009. The lodging resistance of erect panicle japonica rice in Northern China. *Scientia Agricultura Sinica*. 42(7): 2305-2313.
- Zheng, K., Subudhi, P.K., Domingo, J., Magantay, G and Huang, N. 1995. Rapid DNA isolation for marker assisted selection in rice breeding. *Rice Genetics News Letter*. 12: 255-258.
- Zhu, L.H., Zhong, D.B., Xu, J.L., Yu, S.B and Li, Z.K. 2008. Differential expression of lodging resistance related QTLs in rice (*Oryza sativa* L.). *Plant Science*. 175: 898-905.

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