The Bioscan 8(3): 919-924, 2013
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES
www.thebioscan.in

SCREENING FOR SHEATH BLIGHT RESISTANT GENOTYPES AMONG MUTATED POPULATION OF RICE CV. PUSA BASMATI-1

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KEYWORDS
Rhizoctonia solani
Rice, Pusa Basmati-1
Induced mutation
Gamma radiation

Received on :
08.03.2013

Accepted on :
15.04.2013

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ABSTRACT
The present investigation was undertaken to identify the resistant genotypes amongst mutated rice population of the variety Pusa Basmati-1 induced by the gamma radiation (15kr). The variability in disease reaction was observed among mutated rice genotypes. Out of the total 8345 mutant lines, 23 lines belong to same class depicting 0 to 20 AULPC value and 3052 mutant lines come under the class having more than 200 AULPC. Out of 8345 mutated rice population 298 resistant genotypes were identified after screening under field conditions. Significant variation was observed in the disease reaction among the selected mutant population with respect to control (nonmutated). The selected genotypes depicting very low AULPC (Area Under Lesion Progress Curve) value have been advanced to M_2 generation and screened with non-significant deviation for disease score. Non-significant variation in morphological expression and in yield attributes among the selected mutants was also reported. Thus, these genotypes could be considered a potential source for disease resistance against the sheath blight of rice and could be used further in the crossing programme for development of sheath blight resistant rice variety.

INTRODUCTION

Rhizoctonia solani Kuhn [Teleomorph: *Thanatephorus cucumeris* (Frank) Donk] is most widely distributed and destructive pathogen of rice causing sheath blight. It is prevalent in almost all rice growing areas of the world (Dasgupta, 1992) as well as India (Reddy and Reddy, 1986) and has become a major constraint to rice production during the last two decades (Kobayashi, 1997). Due to its wider host range (Roy, 1973; Tsai, 1974; Kozoka, 1975), it is very difficult to manage through other disease management methods, except resistance breeding. But, the complex genetic nature of resistance to sheath blight and genetic variability of the pathogen increases the difficulty in developing resistant host genotypes, as well as in effectively deploying available tolerant cultivars. Unfortunately, at present, there is no known rice variety which is either immune or possesses high degree of resistance to sheath blight disease in the eastern part of India, only moderate or low level of resistance is present (Dwivedi, 2004). Mutation would be better option for creating variability and to develop resistant genotypes against sheath blight disease of rice. Mutation breeding is one of the most effective ways of inducing genetic variability and creating new mutant lines with desirable traits. Induced mutations have played a vital role for the improvement of rice by developing a large number of semi-dwarf and high yielding varieties around the world.

The Pusa Basmati-1 is a popular rice variety in India but it is highly susceptible to sheath blight disease (*R.solani)*. Completely resistant sources to rice sheath blight are yet to be identified from cultivated rice genotypes (Groth and Lee, 2003). Induced mutation breeding may play an important role in identifying individual mutants for rice germplasm improvement (Hu and Rutger, 1992). There are the reports of improvement of different rice genotypes for qualitative (leaf colour, reducing plant height, early maturation period, starch content etc.) and quantitive traits (disease resistance) (Alias *et al.*, 1988; Hadzim *et al.*,1988). Thus, during present investigation we have tried to generate sheath blight resistant genotypes amongst mutated population of rice var. Pusa Basmati-1 that may be effectively used in developing sheath blight resistant rice genotypes in future.

MATERIALS AND METHODS

Plant material

The seeds of Pusa Basmati-1 rice variety (breeder seed) were collected from Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University and were treated with 60 $_{co}$ gamma rays (y) at 15 kr (Kill roentgen) dose for duration of 4 minutes and 30 seconds at the Department of Floriculture, National Bureau of Botanical Research Institute (NBRI), Lucknow. The mutated seeds were grown in nursery and later on healthy seedlings were transplanted in main fields at 21days of growth stage. The genotypes were screened under field conditions in Kharif season for two consecutive years i.e. 2009-10 and 2010-11 for selection of resistant genotypes against *R. solani*. In M_1 generation, individual plant represents one single genotype. Some potent mutant genotypes were selected based on the disease evaluation from 10,000 plant population, consisting both mutant and control lines and their seeds were harvested separately. In M_2 generation, disease resistance of selected mutants was confirmed by growing

progeny to row method. The genotypes depicting very low AULPC (Area Under Lesion Progress Curve) value have been advanced to next generation (i.e. M_3 and M_4). Control lines of PB-1(non-mutated) were grown along with the mutated lines for resistance screening.

Fungal isolate and inoculum preparation

The most aggressive isolate A-1 of *Rhizoctonia solani,* isolated from rice genotype HPR-2172 at Masodha, Faizabad, U.P (Kumar *et al*., 2008), was taken for resistance screening. After placing sclerotia of *R. solani* onto potato dextrose agar (PDA) under aseptic conditions, cultures were grown at 25°C + 2°C under continuous light. Mycelial bits or immature sclerotia taken from 7-day-old culture were cut and used as inoculum.

Plant Inoculation

Under field conditions, the mutated population of rice plants cv. Pusa Basmati-1 was inoculated at growth stage (GS) 2 with mycelial bits (approx. 0.25 mg) or immature sclerotia of *R. solani* (Singh *et al*., 2002).

Disease Scoring

Infected plants were examined for lesion development and disease severity was assessed on the basis of lesion length. Initial data were collected after eight days of inoculation and subsequent data of progressing lesion were recorded on three different dates each at eight days interval i.e. 8, 16 and 24 days after inoculation (DAI) (Kumar *et al*., 2008). The length of individual lesion was measured by using centimeter scale. The lesion development was calculated as Area Under Lesion Progress Curve (AULPC) of a particular lesion (Chattopadhyay *et al*., 2013) by using the following equation of AUDPC suggested by Shaner and Finnay (1977) without considering any severity scale.

$$AULPC = \sum_{i=1}^{n} [\{Y_i + (Y_i + 1)\}/2\{(t_i + 1) - t_i\}]$$

Where, Y_i = disease level at time t_i.

$(t_i + 1)-t_i$ = Time (days) between two lesion scores.

n = no of observations (score).

Morphological observation

Observations on plant height, number of tillers were recorded on individual plants of M_1 and five plants of M_2 generation for screening of potential yielding genotypes.

Statistical Analysis

The data was analysed by using statistical tools of paired t-test with 95% level of significance to see the non-significant difference between the mean AULPC values of two generation (i.e. M_1&M_2).This is great help in screening programme and in selection of genotypes resistant to sheath blight disease depicting low AULPC value.

RESULTS AND DISCUSSION

Induced mutation breeding in rice crop is used as very effective technique in improving major agronomic traits, resistance to pest and diseases, grain physical parameters and eating quality (Md. Nazir *et al*., 1998). There are various reports of induced mutation for improvement of qualitative and quantitative traits of various rice genotypes by gamma rays (ã) and EMS (Zhou *et al*., 2006) and also for non-lodging, high-yielding, long grain rice from three elite Basmati cultivars like Basmati-370, Pusa Basmati-1 and Pakistan Basmati by gamma rays (ã) mutation (Patnaik, 2006). But only few reports are available for disease resistance aspect. In this case, a total of 298 rice mutants were screened with better disease resistance from an M_1 population and were advanced to next M, generation. Significant variation was observed in the disease reaction and phenotypic expression among the mutated population consisting of 8345 plants as compared to the control consisting 1673 plants. 298 mutant plants were screened based on the field data for disease resistance and the average plant height and number of tillers per hills were also recorded (Table-1). The AULPC values of mutated rice population ranged between 0 to >200 whereas in control (untreated) it was calculated between 160-180 in both generations (M_1 & M_2). The whole plant population were categorized into different AULPC classes based on differential disease response and those showing AULPC values ranging between 0-100 were selected for advancement to next generation (M_2). The genotypes showing AULPC values of zero (0) were discarded because it was assumed that it may be due to disease escape. The panicle of the selected plants were harvested individually, threshed and dried to bring optimum moisture for storage. Screening in M_2 generation clearly supports the disease reaction of various mutant lines. These identified mutant genotypes could be considered being a potential source for disease resistance against the sheath blight of rice. Similarly mutantion induced lines of variety Mahsuri were released for blast resistance with improved cooking and eating qualities (Hadzim *et al*., 1988; Hadjim *et al*., 1994; Faruq *et al*., 2003). The screening of mutant line Zhe-101 selected from the mutant progenies of Indica rice cultivar showed the significant improvement in disease resistance to blast and bacterial blight (Wen-chao *et al*., 2004). The elite US rice cultivar "Katy" having "*Pi-ta*" gene for blast (*Magnoporthe grisea*) resistance was mutated by using chemical (EMS) and physical mutagens (Fast neutrons and Gamma rays) to explore the molecular basis of disease resistance (Jia *et al*., 2004). Several researchers have used mutant lines in different crops for disease resistance. Phadvibulya *et. al*., 2009 obtained YVMD (Yellow vein mosaic disease) resistant okra lines advanced up to 7th generation. However, only a small portion of the plants of the mutant lines appeared to be resistant throughout the whole growth duration; others eventually exhibited the yellow vein symptoms. Genetic analysis using 72 molecular markers revealed that 45 resistant accessions were indica type. Three accessions were identified two as aromatic, and one each as temperate japonica and tropical japonica. Breeders could use these findings to choose sheath blight resistant accessions for cultivar improvement (Limeng Jia *et. al*., 2011). Mosaddeque *et. al*., (2008) Conducted that studies on forty-four test entries of parental lines of rice with one susceptible and one resistant check were screened against sheath blight. Ten lines were resistant, 31 were moderately resistant and 3 showed moderately susceptible reaction at maximum tillering stage. 25 sesame

Table 1: Field screening data of selected mutated rice genotypes of Pusa Basmati-1 showing low AULPC value in M_1 and M_2 generation

Genotypes	Mean AULPC value		Plant height(cm)	Tillers/ Hill	Genotypes	Mean AULPC value		Plant height (cm)	Tillers/ Hill
	M_1 generation	M_2 generation				M_1 generation	M_2 generation		
R-01,M-23	16.80	18.15	98	7	R-40,M-52	15.63	30.42	108	8
R-01,M-32	34.81	55.25	108	10	R-43,M-01	46.81	62.85	101	5
R-01,M-34	47.24	52.87	108	7	R-43,M-24	23.90	60.04	101	7
R-01,M-35	32.40	50.49	100	18	R-43,M-32	19.74	43.74	96	4
R-01,M-51	26.00	36.32	106	11	R-44,M-39	31.26	72.55	100	5
R-01,M-42	50.82	45.79	96	7	R-44,M-61	60.62	74.64	92	7
R-01,M-45	43.20	65.07	100	11	R-45,M-15	65.64	66.49	91	11
R-03,M-05	30.00	98.57	88	5	R-45,M-25	72.87	97.42	98	11
R-03,M-15	84.87	77.16	102	10	R-45,M-31	36.84	36.06	40	13
R-03,M-18	39.40	62.58	106	5	R-45,M-45	28.80	39.39	37	7
R-03,M-42	26.92	48.36	108	8	R-45,M-62	30.86	37.44	87	9
R-03,M-61	26.28	36.37	104	11	R-46,M-03	13.68	28.18	104	7
R-03,M-64	31.65	26.26	101	4	R-46,M-06	8.40	24.41	38	13
R-04,M-36	22.40	40.71	111	3	R-46,M-11	30.43	31.21	72	5
R-04,M-51	34.00	33.97	120	7	R-46,M-16	23.21	25.64	105	14
R-04,M-53	16.85	26.38	100	12	R-46,M-19	13.27	30.32	98	6
R-04,M-58	26.80	35.51	107	12	R-46,M-47	26.87	39.60	90	12
R-04,M-59	26.82	34.05	105	13	R-47,M-30	14.53	31.98	96	6
R-07,M-05	22.81	55.93	93	6	R-47,M-31	54.72	36.48	98	12
R-07,M-34	8.90	19.59	114	12	R-42,M-32	67.38	61.20	99	8
R-07,M-60	45.20	51.47	100	7	R-47,M-43	30.89	49.18	101	7
R-07,M-08	31.68	42.63	110	6	R-49,M-20	26.40	39.94	100	10
R-07,M-59	48.00	31.09	118	6	R-49,M-26	27.23	39.56	98	10
R-07,M-52	25.64	18.61	104	4	R-49,M-37	24.00	55.83	88	8
R-07,M-22	19.62	34.87	106	5	R-49,M-42	30.80	44.62	97	6
R-07,M-33	12.85	32.57	108	8	R-50,M-15	20.82	69.54	98	10
R-07,M-35	17.91	39.02	103	13	R-50,M-43	22.81	34.57	100	6
R-08,M-34	54.00	88.22	108	9	R-50,M-26	29.69	31.74	95	6
R-08,M-35	12.43	53.96	101	4	R-50,M-23	38.42	39.99	104	7
R-08, M-44	13.62	37.51	103	4	R-50, M-38	28.56	36.95	87	8
R-08,M-60	35.67	78.52	117	12	R-51,M-44	45.60	55.49	102	5
R-08,M-64	47.6	62.06	101	6	R-51,M-09	25.20	37.22	107	6
R-08,M-65	24.82	35.32	100	5	R-51,M-31	26.00	54.66	98	4
R-09,M-08	33.84	54.2	90	4	R-51,M-40	46.41	51.83	100	7
R-09,M-16	21.61	32.27	83	3	R-51,M-32	29.22	31.75	86	11
R-09,M-20	68.49	49.46	97	8	R-51,M-39	24.40	62.58	100	8
R-09,M-38	95.23	104.37	109	6	R-52,M-10	35.23	36.75	102	11
R-09,M-67	92.40	118.82	123	7	R-52,M-13	38.40	50.83	94	5
R-09,M-47	89.21	101.4	108	5	R-52,M-15	55.62	66.49	97	7
R-09,M-54	98.88	97.88	110	6	R-52,M-21	75.24	48.13	106	8
R-10,M-58	28.00	67.265	107	11	R-55,M-46	28.80	59.02	105	4
R-10,M-59	50.81	78.11	106	1	R-55,M-56	39.64	56.06	100	10
R-10,M-62	22.47	51.85	102	10	R-55,M-34	24.49	28.16	82	10
R-11, M-11	45.29	60.27	98	6	R-55,M-11	76.44	90.35	97	5
R-11,M-01	71.20	68.38	103	10	R-55,M-52	35.69	45.11	96	4
R-11, M-10	37.24	49.34	102	4	R-55, M-53	78.65	90.01	100	7
R-11,M-27	58.36	71.30	81	9	R-53,M-05	64.40	94.15	90	6
R-11,M-37	75.68	66.96	108	6	R-53,M-06	42.40	59.10	95	8
R-11,M-40	42.40	65.89	108	9	R-53,M-19	55.22	62.59	90	4
R-11,M-53	42.80	56.50	111	9	R-53,M-21	74.48	73.95	92	6
R-13,M-01	85.66	96.43	104	7	R-53,M-28	21.64	35.72	91	7
R-13,M-02	78.84	51.07	102	9	R-53,M-25	43.20	68.58	92	10
R-13,M-07	34.40	27.23	100	6	R-53,M-38	24.43	31.87	100	4
R-13,M-45	30.43	22.33	104	10	R-53,M-09	70.40	36.66	111	7
R-13,M-51	55.61	45.3	113	6	R-56,M-10	81.21	97.42	103	7
R-13,M-62	78.80	51.89	102	10	R-56,M-24	36.45	45,17	104	7
R-14,M-02	68.82	54.34	110	9	R-56,M-42	46.80	51.87	92	6
R-14,M-20	85.24	77.125	100	7	R-56,M-52	42.65	50.41	102	5
R-14,M-35	89.60	68.615	113	9	R-58,M-05	48.68	46.20	108	8
R-14,M-36	89.62	70.82	86	6	R-58,M-10	75.60	80.54	77	10
R-14,M-49	31.47	57.59	102	7	R-58,M-34	85.61	105.67	73	5
R-14,M-58	28.70	51.66	107	9	R-58,M-36	45.62	30.46	92	6

Table 1: Cont.....

Genotypes	Mean AULPC value		Plant height(cm)	Tillers/ Hill	Genotypes	Mean AULPC value		Plant height (cm)	Tillers/ Hill
	M_1 generation	M_2 generation				M_1 generation	M_2 generation		
R-14,M-60	89.61	94.46	96	4	R-58,M-38	75.66	88.83	94	11
R-16,M-09	89.28	80.54	97	7	R-58,M-44	91.67	88.58	97	6
R-16,M-14	58.44	63.79	95	5	R-58,M-07	66.88	105.46	104	5
R-16,M-42	84	57.76	92	6	R-58,M-19	32.89	57.04	89	3
R-16,M-62	81.22	84.54	105	11	R-58,M-28	95.62	109.17	96	7
R-16,M-63	70.98	80.08	92	10	R-58,M-39	55.20	49.72	82	7
R-17,M-07	86.42	89.26	103	8	R-58,M-45	70.24	63.40	88	8
R-17,M-16	49.20	37.46	98	11	R-58,M-48	58.45	89.68	103	5
R-17,M-20	89.24	67.48	100	6	R-58,M-49	53.66	60.57	90	6
R-17,M-52	69.22	87.94	105	5	R-57,M-09	64.90	83.75	108	6
R-17,M-54	72.81	89.66	107	7	R-57,M-11	24.72	46.70	105	4
R-19,M-03	54.80	68.05	105	11	R-57,M-17	42.86	49.71	96	6
R-19,M-15	78.00	65.75	105	5	R-57,M-40	72.43	79.46	97	7
R-19,M-30	80.11	98.44	78	8	R-57,M-18	89.25	87.26	103	4
R-19,M-48	72.40	58.04	101	5	R-57,M-57	74.00	92.83	106	7
R-19,M-61	91.63	81.54	103	4	R-59,M-04	54.86	73.94	105	5
R-20,M-28	28.44	55.04	90	8	R-59,M-07	41.68	48.47	109	4
R-20,M-22	32.47	57.76	88	4	R-59,M-10	56.71	53.55	94	4
R-20,M-34	42.48	29.38	90	7	R-59,M-36	56.85	58.06	98	9
R-20,M-36	24.82	72.14	98	5	R-59,M-58	80.48	67.34	96	9
R-20,M-42	49.61	62.52	95	9	R-61,M-01	85.22	81.35	104	6
R-20,M-45	49.27	47.1	100	13	R-61,M-46	37.69	40.15	92	11
R-21,M-07	27.40	61.35	105	12	R-61,M-12	98.43	100.43	96	7
R-21,M-10	73.23	65.58	100	10	R-61,M-31	44.00	57.76	98	5
R-21,M-23	62.24	50.91	104	5	R-63,M-17	65.23	69.77	100	8
R-21,M-33	24.68	68.00	104	9	R-63,M-16	50.44	64.84	86	7
R-21,M-30	88.80	71.35	94	9	R-63,M-45	72.36	67.89	99	10
R-21,M-52	76.86	87.58	94	12	R-69,M-58	80.78	65.71	103	11
R-22,M-11	98.82	83.40	92	4	R-70,M-05	88.12	64.1	103	5
R-22,M-15	59.61	79.02	95	6	R-70,M-17	26.76	80.92	110	7
R-22,M-22	28.00	29.67	90	10	R-70,M-18	52.46	77.46	114	9
R-22,M-42	92.21	97.43	102	12	R-70,M-22	42.80	50.14	100	10
R-22,M-55	95.26	75.9	100	3	R-73,M-02	58.23	56.07	102	5
R-23,M-39	90.49	72.96	100	4	R-73,M-11	68.41	75.62	72	3
R-23,M-46	38.80	44.65	114	7	R-73,M-15	59.23	67.68	94	7
R-23,M-60	68.41	58.33	110	12	R-73,M-29	83.35	95.80	98	9
R-23,M-63	98.89	100.76	92	17	R-73,M-38	54.24	77.33	100	6
R-25,M-03	90.40	107.11	100	5	R-76,M-17	74.36	86.6	92	6
R-25,M-25	75.62	84.38	92	4	R-76,M-38	25.60	44.95	108	9
R-25,M-30	70.73	61.23	98	12	R-76,M-42	74.98	88.50	115	9
R-25,M-32	56.32	51.10	102	12	R-77,M-14	44.40	59.02	105	9
R-25,M-40	47.88	52.22	109	7	R-77,M-23	24.45	33.11	102	6
R-26,M-07	75.60	89.93	98	10	R-77,M-36	14.81	28.89	88	5
R-26,M-10	20.85	45.65	98	10	R-77,M-43	49.63	74.28	96	7
R-26,M-24	40.78	59.56	93	4	R-77,M-49	24.34	75.00	94	7
R-26,M-27	85.20	92.12	76	7	R-77,M-53	62.45	49.08	90	7
R-26,M-54	71.63	79.12	107	12	R-77,M-12	51.62	77.96	105	12
R-29,M-09	66.34	74.84	94	7	R-77,M-26	65.28	80.3	102	6
R-29,M-19	42.40	67.97	96	7	R-71,M-36	74.53	82.85	95	8
R-29,M-37	26.52	38.93	100	7	R-71,M-38	23.28	31.56	90	8
R-29,M-38	70.23	91.37	107	8	R-71,M-18	75.20	90.55	101	9
R-29,M-45	89.63	67.42	112	11	R-79,M-20	74.45	97.16	110	14
R-27,M-10	56.55	62.04	96	14	R-79,M-25	87.62	90.04	106	6
R-27,M-15	22.64	15.99	95	10	R-79,M-34	23.24	23.45	95	6
R-27,M-24	30.37	39.89	103	10	R-79,M-35	82.75	79.37	108	5
R-27,M-27	80.48	98.99	100	10	R-79,M-46	34.80	59.09	96	8
R-27,M-31	26.40	89.21	102	10	R-80,M-26	49.80	58.99	102	4
R-31,M-02	68.81	79.95	108	13	R-80,M-34	22.82	54.61	100	4
R-31,M-21	84.75	92.32	95	8	R-80,M-59	22.41	72.26	105	12
R-31,M-24	84.94	103.03	94	7	R-81,M-22	22.45	64.04	85	11
R-31,M-25	52.74	75.86	100	9	R-82,M-11	28.76	63.44	90	8
R-31,M-40	47.25	52.16	100	4	R-82,M-16	71.63	79.01	100	8

Table 1: Cont.....

Genotypes	Mean AULPC value		Plant height(cm)	Tillers/ Hill	Genotypes	Mean AULPC value		Plant height (cm)	Tillers/ Hill
	M_1 generation	M_2 generation				M_1 generation	M_2 generation		
R-31,M-41	81.22	93.67	96	3	R-83,M-16	29.22	57.99	100	4
R-33,M-15	58.80	72.99	96	6	R-83,M-28	76.80	41.22	102	8
R-33,M-17	50.24	80.43	97	7	R-85,M-02	15.62	25.28	88	7
R-33,M-26	47.24	55.17	103	8	R-104,M-67	70.50	81.58	100	7
R-33,M-30	33.66	31.29	103	5	R-107,M-14	70.31	59.52	102	11
R-33,M-43	56.83	45.72	102	3	R-107,M-52	24.34	24.24	102	7
R-33,M-51	69.66	54.95	105	11	R-109,M-11	32.54	69.15	108	7
R-34,M-34	20.00	23.57	82	7	R-109,M-32	78.11	81.81	102	7
R-34,M-54	23.61	43.06	98	13	R-109,M-33	52.83	62.94	94	7
R-34,M-56	30.44	82.65	92	17	R-109,M-38	33.65	42.91	94	7
R-34,M-60	16.58	22.25	110	13	R-109,M-50	46.81	48.94	108	10
R-34,M-63	35.23	96.88	1.8	13	R-108,M-03	22.87	25.24	103	13
R-35,M-04	72.86	89.76	96	8	R-108,M-12	56.60	36.15	94	7
R-35,M-32	52.49	71.09	98	10	R-108,M-27	48.10	37.76	108	13
R-35,M-40	55.22	49.05	104	12	R-108,M-31	52.73	61.22	110	3
R-35,M-35	81.60	94.47	97	12	R-139,M-47	62.40	75.93	96	9
R-35,M-37	58.34	73.05	85	11	R-140,M-43	24.50	31.32	83	3
R-35,M-43	48.87	31.29	105	11	R-140,M-45	34.92	55.66	100	10
R-37,M-22	84.84	99.97	108	5	R-140,M-48	74.35	55.85	98	10
R-37,M-28	92.49	108.41	96	6	R-140,M-51	74.23	68.24	100	4
R-37,M-37	32.43	54.53	108	9	R-140,M-52	14.85	17.90	104	4
R-40,M-41	29.65	59.18	98	9	R-141,M-02	32.11	54.84	108	9
R-40,M-43	16.42	19.99	100	10	R-141,M-03	48.84	63.21	104	4
R-40,M-45	12.87	13.27	104	9	R-141,M-04	58.80	65.87	104	5
R-40,M-47	14.58	12.04	102	11	R-141,M-09	54.24	79.94	100	3
Control	180.75	170.68	100	10	Control	180.75	170.68	100	10

Statistical Analysis t -calculated = 0.384 t -tabulated = 1.65

As the calculated value of't'-test does not exceed the critical 't'-value (tabulated) with 95% level of significance at 298 degree of freedom, there is no significant difference between the mean values for the two set of data for M_1 and M_2 generation showing the same level of resistant expression of any genotype in field.

Table 2: Class intervals of AULPC values and frequency distribution of mutated (M_1) rice genotypes

Sl.No	Range of AULPC space values	Frequency distribution of genotypes
1	0-20	23
2	21-40	97
3	41-60	73
4	61-80	57
5	81-100	46
6.	101-120	189
7.	121-140	374
8	141-160	539
9	161-180	1790
10	181-200	2145
11	>200	3052
Total mutant line	8345	
Control line	1673	

genotypes were evaluated and found that the genotypes in the resistant category and specifically "Birkan", a recently released cultivar for large seed and high yield, seems to possess also the resistance to the Fusarium wilt disease. This genotype could be used as source of resistance to the wilt in the breeding programmes aiming to develop sesame suitable to intensive management (Soner and Ilhan, 2010). Immanuel Selvaraj *et. al*. (2011) observed twenty one rice genotypes that were screened to identify the rice blast disease reaction. Sixteen genotypes which were already reported to have resistance genes reacted negatively to the blast disease. Four genotypes were found to be susceptible. Twenty five rice (*Oryza sativa* L.) germplasm lines with high levels of resistance to SB (sheath blight) were developed. The lines were developed from 25 yr of recurrent selections of crosses and backcrosses of various SB-resistant sources and U.S. cultivars (Rush *et. al*. 2011). But for resistance to sheath blight of rice, no such previous reports were available. Here we have generated a probable resistance source to combat sheath blight of rice. The resistant mutants have been identified and screened and would be advanced to future generations like M_4 using single progeny descent row method. These advanced resistant mutants can be utilized in breeding programmes for development of sheath blight resistant rice variety for Eastern U.P.

ACKNOWLEDGEMENTS

This research is a part from the first author's M.Sc. (Ag.) work. The authors gratefully acknowledge the support of UGC, Govt. of India for granting financial support during M.Sc. (Ag.) programme.

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