Evaluation of Wild *Oryza* Species for Stem Rot (*Sclerotium oryzae*) Resistance

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ABSTRACT

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Initial screening of 55 genotypes in 17 *Oryza* species and subsequent reevaluation of the 24 most resistant entries revealed that several species were significantly more resistant to stem rot than cultivated rice, *O. sativa*. Averaged over both experiments, 15 genotypes representing nine species were more stem rot-resistant than Colusa, the most resistant cultivar in California. In a test conducted on eight of the more resistant entries, the presence or absence of flowering had no overall effect on stem rot development. The best stem rot resistance was found in species with genomes different from cultivated rice; however, stem rot-resistant entries of three species, *O. rufipogon, O. nivara*, and *O. spontanea*, which carry the same genome as cultivated rice, were identified. These entries are expected to be useful donor parents for the interspecific transfer of stem rot resistance to cultivated rice.

Additional key words: disease resistance

Stem rot of rice (*Oryza sativa* L.) caused by *Sclerotium oryzae* Catt. has caused substantial yield reductions in California and other rice-growing areas of the world (3,5,8,11). Yield reductions are caused by unfilled panicles, death of young tillers, chalky grain, and lodging (8). Sclerotia from infected residue overwinter in the soil and serve as primary inoculum in the spring, floating to the water surface when the rice field is flooded and infecting young plants near the water line (10). The most common control measure in California is burning the rice stubble after harvest, which decreases inoculum levels and halts further inoculum buildup (1). Jackson et al (5) reported effective chemical control of stem rot with a single application of triphenyltin hydroxide, but use of this fungicide is restricted to the southern United States.

In California, there are no rice cultivars with a high level of resistance to stem rot (8). The nature of stem rot resistance is reported to be quantitative and of the horizontal type (4), but no consistently stable source of resistance has been found (6).

Wild relatives have often served as sources of disease resistance in crop plants. In cultivated rice, however, only in one case has alien germ plasm been a source of disease resistance, namely the monogenic resistance to the grassy stunt virus found in *O. nivara*, which was transferred to *O. sativa* (7). In our research, rice genotypes representing most of the wild *Oryza* species were screened in a search for greater stem rot resistance than that found in Colusa, the most stem rot-resistant cultivar in California (8).

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MATERIALS AND METHODS

Plants were grown in 18-cm plastic pots and placed in flooded benches for greenhouse studies. Inoculations were made by sprinkling sclerotia of *S. oryzae* onto the water surface near each pot. The D-30 strain of *S. oryzae* was used because it had proved to be the most virulent strain in earlier studies (4). Greenhouse tests, rather than field tests, were used because disease development is usually more severe in field tests.

The rating system developed by Krause and Webster (8), which measures disease severity, was used. Individual tillers were evaluated on a scale of 1–5 when the plants reached maturity, where 1 = no infection, 2 = fungus attacked outer leaf sheaths only, 3 = fungus penetrated all leaf sheaths, 4 = fungus infected the culm, and 5 = culm severely infected. A disease index (DI) was assigned to each plant according to the formula:

$$\mathrm{DI} = \frac{1(n_1) + 2(n_2) + 3(n_3) + 4(n_4) + 5(n_5)}{\text{number of tillers examined}},$$

where n_1 = number of tillers with a rating of 1 and n_2 = number of tillers with a rating of 2, etc. In the greenhouse, plants usually produced 10–30 tillers each, all of which were scored for each plant.

In an initial screening experiment, a split-plot design using the same planting date but two different disease scoring dates was used to screen 55 genotypes representing 17 *Oryza* species for resistance to *S. oryzae*. In January 1978, six replicates of three plants per pot were seeded in greenhouse benches that were flooded when the plants were about 10 cm tall. Inoculation was in April at midtillering. Plants were scored for disease reaction in one group of three replicates at 9 wk and in the other group at 12 wk after inoculation.

In a reevaluation screening experiment, a randomized complete block design was used to retest the 24 most resistant genotypes to stem rot in addition to four controls from the initial screening. Three replicates of three plants per pot were seeded in August 1978 and placed in greenhouse benches as before. Inoculation was in October at midtillering. Plants were scored for disease reaction 9 wk after inoculation.

An experiment to determine the influence of flowering on the disease index, using eight entries of the more resistant *Oryza* A genome species plus two *O. sativa* controls, was planted in the greenhouse in February 1980. A split-plot design with two photoperiod treatments as main plots and genotype as subplots and three replicates of three plants per pot was used. The photoperiod treatments were exposure to 8-hr days for 1 mo at tillering to induce flowering versus the normal longer day length (13–14 hr) prevalent in the spring months. All plants were inoculated at tillering and scored 9 wk later.

RESULTS AND DISCUSSION

In the initial screening experiment, neither the scoring date nor the scoring date × genotype interaction were significant so data were pooled for presentation of average scores (Table 1). Although immunity to *S. oryzae* was not found, several genotypes were significantly ($P \leq 0.05$) more resistant than the standard cultivar Colusa. Many genotypes were photosensitive and did not flower in this experiment, which was conducted under naturally occurring long-day conditions. A higher frequency of nonflowering was evident in the stem rot-resistant genotypes compared to the susceptible lines (Table 1). *O. officinalis* A101399 was the most stem rot-resistant genotype, although it was not significantly different from several others.

Unfortunately, many stem rot-resistant genotypes possess a genome other than

the A genome of *O. sativa*; however, selected entries for three A genome species (2), *O. rufipogon, O. spontanea*, and *O. nivara*, had good resistance. Within the A genome species for which there were multiple entries, ie, *O. rufipogon* and *O. nivara*, there was a wide range of stem rot reactions. For example, an *O. nivara* entry, A360790, was the most susceptible genotype in the test, whereas two other *O. nivara* entries, A101524 and A101512, were among the more resistant genotypes to stem rot. Such ranges of variability indicate that even better sources of stem rot resistance could be found by more extensive sampling of these species.

The California *O. sativa* cultivars, including M-101 and Earlirose as well as the Basmati entry, which was reported stem rot-resistant in Pakistan (J. N. Rutger, *unpublished*), were quite susceptible. Another *O. sativa* cultivar, Tanginbozu, was not significantly different from Colusa (Table 1).

In the reevaluation screening, highly significant differences among genotypes to stem rot were again observed (Table 1). Highly significant genotype differences were also observed when the 28 genotypes common to the two scoring dates for the initial screening plus the one scoring date from the reevaluation screening were combined in a three-scoring date analysis. Comparisons of means showed that 15 genotypes representing nine species were significantly more stem rot-resistant than Colusa. A significant difference between scoring dates ($P \leq 0.05$) in the combined analysis was due to a higher disease index score of 3.3 in the reevaluation test, compared to a score of 3.1 for the same 28 genotypes in the initial screening test.

All genotypes flowered in the reevaluation experiment, which was conducted under naturally occurring short-day conditions. A significant scoring date × genotype interaction was found in the combined analysis because of differential shifts in disease index of some entries in the two experiments. For example, *O. paraguayensis* entry PI 245708 showed a lower disease index in the reevaluation experiment than in the initial screening, whereas *O. rufipogon* entry A100912 showed the reverse (Table 1).

Because stem rot development often accelerates after flowering as plants mature and enter senescence, the influence of flowering was studied on seven resistant A genome species entries that failed to flower in the initial screening experiment plus one resistant entry that flowered (Table 2). Highly significant genotype differences and genotype × flowering interactions were found. The first four entries (Table 2) were again more resistant than the Colusa control under both flowering treatments. Two of the last four entries showed differential response to the flowering treatment. Thus, *O. rufipogon* A100946 showed significantly more disease when

Table 1. Average stem rot disease indices for initial screening and reevaluation experiments and the resulting mean for various genotypes of wild *Oryza* species plus five *O. sativa* controls[a]

Oryza species[b]	Genome	Initial screening[c]	Reevaluation[d]	Mean[e]
O. officinalis A101399	CC	2.1[f]	1.9	2.0
O. officinalis A 101121	CC	2.4	2.5	2.4
O. punctata PI 254570	BBCC	2.5	2.4	2.4
O. eichingeri PI 233491	BBCC	2.5[f]	2.5	2.5
O. paraguayensis PI 245708	CCDD	2.6	2.2	2.4
O. officinalis A101112	CC	2.7[f]	2.3	2.6
O. stapfii PI 237987	A′A′	2.7[f]	2.4	2.6
O. stapfee PI 237987	A′A′	2.8	2.4	2.7
O. rufipogon Al00912	AA	2.8[f]	3.4	3.0
O. rufipogon A100923	AA	2.8	3.6	3.1
O. latifolia PI 269727	CCDD	2.9	2.2	2.7
O. rufipogon A100945	AA	3.0[f]	4.0	3.4
O. nivara A101524	AA	3.1[f]	3.4	3.2
O. nivara A101512	AA	3.1[f]	3.2	3.1
O. australiensis PI 239667	EE	3.1	4.1	3.4
O. officinalis A101116	CC	3.1[f]	2.3	2.9
O. spontanea A100943	AA	3.1[f]	3.4	3.2
O. minuta PI 125257	BBCC	3.2	...	...
O. rufipogon A100946	AA	3.2[f]	4.0	3.5
O. barthii af. 61-1	AA	3.3[f]	...	...
O. glaberrima PI 231194-3	AA	3.3[f]	4.4	3.7
O. glaberrima PI 231194-1	AA	3.4[f]	4.5	3.8
O. breviligulata af. 27-3	AA	3.4	3.5	3.4
O. fatua PI 239671	AA	3.4[f]	3.3	3.4
O. stapfii PI 236393	A′A′	3.4[f]	5.0	3.9
O. alta PI 158813	AA	3.4	...	...
O. glaberrima PI 246351	AA	3.4	...	...
O. minuta A101083	BBCC	3.5[f]	...	...
O. minuta A100134	BBCC	3.5	...	...
O. glaberrima PI 232855	AA	3.5[f]	...	...
O. glaberrima PI 231195	AA	3.5[f]	...	...
O. sativa cv. Tanginbozu	AA	3.5	3.4	3.5
O. sativa cv. Colusa	AA	3.6	3.9	3.7
O. minuta A101089	BBCC	3.6[f]	...	...
O. minuta A101085	BBCC	3.6	...	...
O. minuta A100887	BBCC	3.6[f]	...	...
O. glaberrima PI 231194	AA	3.6[f]	...	...
O. minuta A101097	BBCC	3.6	...	...
O. spontanea A100907	AA	3.6	...	...
O. nivara A101510	AA	3.7	...	...
O. glaberrima PI 231194-2	AA	3.7[f]	...	...
O. spontanea A100900	AA	3.7	...	...
O. rufipogon A100917	AA	3.8	...	...
O. officinalis A101073	CC	3.8	3.6	3.7
O. minuta A101125	BBCC	3.9	...	...
O. glaberrima PI 232853	AA	3.9	...	...
O. glaberrima PI 269630	AA	3.9	...	...
O. sativa cv. M-101	AA	4.0	4.0	4.0
O. sativa cv. Basmati PI 385817	AA	4.0	...	...
O. sativa cv. Earlirose	AA	4.1	4.0	4.0
O. nivara A360789	AA	4.1	...	...
O. glaberrima PI 254568	AA	4.1	...	...
O. glaberrima PI 232854	AA	4.1	...	...
O. nivara A360791	AA	4.1	...	...
O. nivara A360790	AA	4.5	...	...

[a] Disease severity scale of 1–5: 1 = no infection, 2 = outer leaf sheaths attacked, 3 = all leaf sheaths penetrated, 4 = culm infected, and 5 = culm severely diseased (disease index based on rating 10–30 tillers of each of nine to 18 plants grown in a greenhouse).
[b] PI numbers are USDA plant introductions and A numbers are International Rice Research Institute accessions.
[c] $LSD_{0.05 \text{ and } 0.01}$ = 0.5 and 0.6, respectively.
[d] $LSD_{0.05 \text{ and } 0.01}$ = 0.6 and 0.8, respectively.
[e] $LSD_{0.05 \text{ and } 0.01}$ = 0.4 and 0.5, respectively.
[f] Genotypes that did not flower.

Table 2. Effect of flowering on disease index of eight of the more stem rot-resistant *Oryza* species entries plus two *O. sativa* cultivars

Genotype	Disease index[a]	
	Flowered[b]	Not flowered[b]
O. rufipogon A100912	3.0	2.9
O. nivara A101524	2.9	3.0
O. nivara A101512	3.2	3.0
O. spontanea A100943	3.0	3.1
O. fatua PI 239671	3.1	3.7
O. rufipogon A100923[c]	3.4	3.5
O. rufipogon A100946	3.8	3.1
O. rufipogon A100945	3.5	3.7
Average of wild species	3.2	3.2
O. sativa 'Colusa'	3.8	3.8
O. sativa 'M-101'	3.9	3.9

[a] Disease severity scale of 1–5: 1 = no infection, 2 = outer sheaths penetrated, 3 = all leaf sheaths penetrated, 4 = culm infected, and 5 = culm severely diseased (disease index based on rating 10–30 tillers of each of nine plants grown under short-day or long-day conditions in a greenhouse).
[b] $LSD_{0.05 \text{ and } 0.01}$ = 0.3 and 0.4, respectively.
[c] Only genotype that flowered in the initial screening experiment.

flowered and *O. fatua* PI 239671 showed significantly less disease when flowered (Table 2). These two genotypes possibly carried impurities because off-types were occasionally noticed in them. Averaged over the eight wild species entries, there was no difference in disease index between the flowered and nonflowered groups. Therefore, it does not appear that the higher disease index scores observed in the reevaluation experiment, compared with the initial screening experiment, can be ascribed solely to flowering differences. Other unknown factors must have been responsible.

The best overall stem rot resistance in these experiments was in entries of *O. officinalis, O. punctata, O. eichingeri, O. Paraguayensis, O. stapfii*, and *O. latifolia*, all of which possess genomes different from that of cultivated rice (Table 1). Investigations by other workers (summarized by Nayar [9]) indicate that the chances of transferring characters from most of those species are minimal. Selected entries of three A genome species, *O. rufipogon, O. nivara*, and *O. spontanea*, however, had disease indices that generally were significantly more stem rot resistant than Colusa (mean disease index = 3.7). These entries should be useful donors for interspecific transfer of stem rot resistance to *O. sativa*.

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