

ANNUAL REPORT  
COMPREHENSIVE RESEARCH ON RICE  
January 1, 2000 - December 31, 2000

PROJECT TITLE: RB-3: Rice Genetics and Germplasm Development  
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LEVEL OF 2000 FUNDING: \$ 16,000

OBJECTIVES AND EXPERIMENTS CONDUCTED BY LOCATION TO ACCOMPLISH OBJECTIVES:

- a) **Molecular markers for disease resistance genes.** The objectives were to apply molecular marker technology to developing rice varieties with resistance to stem rot and blast diseases. (Level of funding: \$5,000)
- b) **Cold tolerance.** The objective was to map genes controlling cold tolerance at the reproductive stage. (Level of funding: \$5,000)

- c) **Interspecific gene introgression.** The objective was to introduce genes controlling advantageous agronomic traits into a California rice variety by backcrossing and molecular marker technology. (Level of funding: \$3,000)
- d) **Seedling traits for stand establishment and weed suppression/competition.** The objective was to evaluate different experimental lines to determine their usefulness for weed suppression through competition and good seedling vigor. These include submergence tolerant lines and high-seedling vigor lines. (Level of funding: \$3,000)

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## SUMMARY OF 2000 RESEARCH (MAJOR ACCOMPLISHMENTS) BY OBJECTIVE

### A. Molecular markers for disease resistance genes.

#### *Rice blast*

Experiments on rice blast included (i) characterization of blast donors and susceptible California varieties for molecular markers linked to known blast resistance genes and (ii) determining the linkage of blast resistance in a rice cross being evaluated at Biggs with molecular markers linked to blast resistance genes. Most blast resistance genes are known to reside in clusters on rice chromosomes 4, 11 and 12. Markers located on these chromosomes were selected to determine if they would be useful for selecting for resistance genes in a breeding program.

The analysis of blast donors is still continuing. Egyptian varieties with good resistance to blast were imported and some were crossed with California cultivars at Biggs. After the F<sub>3</sub> rows were screened for blast resistance, the resistant and susceptible lines were screened with molecular markers linked to blast resistance genes. Some of the markers tested are candidates for linkage to the resistance genes. The results are still being analyzed and confirmed.

The nature of this project has changed, because researchers in Texas have agreed to provide markers linked to blast resistance genes for use in the breeding program in California. Since the Rice Experiment Station can now screen directly for resistance, the use of these markers will be most useful for either determining the nature of unknown resistance genes being used by the breeders or in combining more than one resistance gene into a single variety. While the latter is thought to confer greater durability of resistance, it is not known if the additional effort required is necessary under the relatively low blast pressure in California.

#### *Stem rot*

Resistance to stem rot is difficult to measure due to the large effect of environment and quantitative nature of the resistance. We evaluated several rice populations developed at Biggs to determine if the resistance could be linked to molecular markers. We identified two markers that explained a large percentage of the genetic differences for resistance (Fig. 1). We are now testing these markers to determine if they are present in all the known resistant lines being used in the California breeding program.

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## B. Cold tolerance

The genetics of cold tolerance at the reproductive stage was studied in a cross between a tropical indica variety (IR50R) and a widely-grown California cultivar (M-202). The location of genes conferring cold tolerance in this cross could assist in developing varieties with higher levels of tolerance, especially when using tropical parents in the California breeding program. A large number of traits were scored on plants grown both in the field and in the growth chambers. The data for these experiments is still being analyzed. Three of the most important traits related to cold tolerance are spikelet fertility, panicle exsertion (distance of the panicle node from the flag leaf sheath), and delay in heading under low temperature. Some of the important loci identified for these traits are shown in Fig. 2.

## C. Interspecific transfer of genes

This experiment involves the analysis of the wild species *Oryza nivara* as a source of useful traits for introduction into the California cultivar M-202. Development of the initial population was very laborious and involved crossing this wild species with M-202, making a backcross of the  $F_1$  to M-202, and then backcrossing individual  $BC_1F_1$  plants again to M-202. The resulting  $BC_2F_1$  plants were selfed for three generations and then studied for agronomic traits. Plants were analyzed for yield and yield components in 1998 and 1999 in the field at Davis.

Some of the lines developed with *O. nivara* chromosomal segments equaled the yield of M-202, although none were significantly higher yielding. Some of the lines, however, had significantly higher seedling vigor, as measured by shoot length, than M-202 (Table 1). These lines may have a good source of seedling vigor that can be used in California breeding programs.

The advanced backcross QTL analysis method (ABQTL) was used to identify the chromosomal regions associated with improved agronomic traits. The most important loci are shown in Table 2. In this table, the markers listed all indicate chromosomal segments derived from the wild parent that contributed positively for the trait. Generally, those with probability (P) less than 0.05 are suggestive of loci, and those with  $P < 0.01$  are highly significant. The loci with the largest contributions to the respective trait are the shoot-length loci on chromosomes 5, 6 and 7 and the panicle number locus on chromosome 7. It is interesting that the marker associated with increased yield, RM84 on chromosome 1, was also associated with increased grain weight and increased spikelets per panicle.

Lines with desirable alleles were crossed again to M-202 so that individual loci could be isolated in this genetic background for further studies and applications in the breeding program.

## D. Seedling traits for stand establishment and weed suppression/competition

Herbicide restrictions in California have emphasized a need to search for plant traits that could result in more weed competitiveness. Plant traits related to weed competitiveness include higher seedling height, increased root growth, and increased leaf area index. California cultivars have limited variability for these characteristics. We evaluated lines derived from *O. nivara*

backcrosses (project C above) for leaf area index, root growth, and competitiveness with *Echinochloa*.

The weed *Echinochloa* and a germplasm accession (PI312777) reported to be allelopathic had lower shoot/root ratios compared to the California cultivar M-202 and the southern long-grain Lemont, indicating good root growth (Fig. 3). One line derived from *O. nivara*, DX221-52-4-1 (4233), showed a similar s/r ratio to these two lines. Furthermore, this same line had a relatively high LAI compared to M-202 and other lines (Fig. 4). This line has similar yield potential to M-202 in limited yield tests at Davis over two seasons. Further testing of this line is necessary to determine if it has potential for weed suppression.

*Gift of herbicides from United Agri Products is gratefully acknowledged.*

#### PUBLICATIONS OR REPORTS:

Xu K, Xu X, Ronald PC, Mackill DJ (2000) A high-resolution linkage map in the vicinity of the rice submergence tolerance locus *Sub1*. *Mol Gen Genet* 263:681-689.

Mackill DJ, Nguyen HT, Zhang JX (1999) Use of molecular markers in plant improvement programs for rainfed lowland rice. *Field Crop Res* 64:177-185.

Li L, Yang JB, Xiang TH, Wang XF, Wu D, Colowit PM, Mackill DJ (1999) Identification of the most common Chinese hybrid rice cultivars and their parental lines using RAPD and microsatellite markers. *SABRAO J Breed Genet* 31:83-91.

Neves PC, Colowit PM, Mackill DJ (2000). Transfer of genes from a wild species *Oryza nivara* into the California cultivar M-202. In Rice Field Day, (pp. 31). Biggs, CA:

Xu K, Xu X, Zhang H, Deb R, Ronald PC, Mackill DJ (2000) Fine-scale mapping of the rice submergence tolerance gene. *Plant & Animal Genome VIII* (San Diego, 9-12, 2000):p. 4.

**CONCISE GENERAL SUMMARY OF CURRENT YEAR'S RESULTS:**

The potential of molecular markers for identifying and selecting for blast resistance genes was evaluated. Two molecular markers linked to resistance to stem rot, one on chromosome 2 and one on chromosome 3, were identified. These two loci control much of the resistance, and these markers should be useful for evaluating resistance in the breeding program. Genes associated with cold tolerance in japonica rice were identified through molecular marker mapping. The most important genes controlling spikelet fertility, panicle exertion, and delayed heading under low temperature were located on the genetic map. An attempt will be made to cross these genes into an indica rice variety to develop a cold tolerant indica type. Interspecific progenies derived from the weedy species *Oryza nivara* were evaluated for various agronomic traits. Genes associated with higher seedling vigor and yield were identified. These genes are being backcrossed into the variety M-202 for further exploitation in the breeding program. One of the interspecific backcross lines, DX221-52-4, possessed high yield, high leaf area index, and greater root mass in a pot experiment. This line may have potential in terms of competitive ability against weeds.

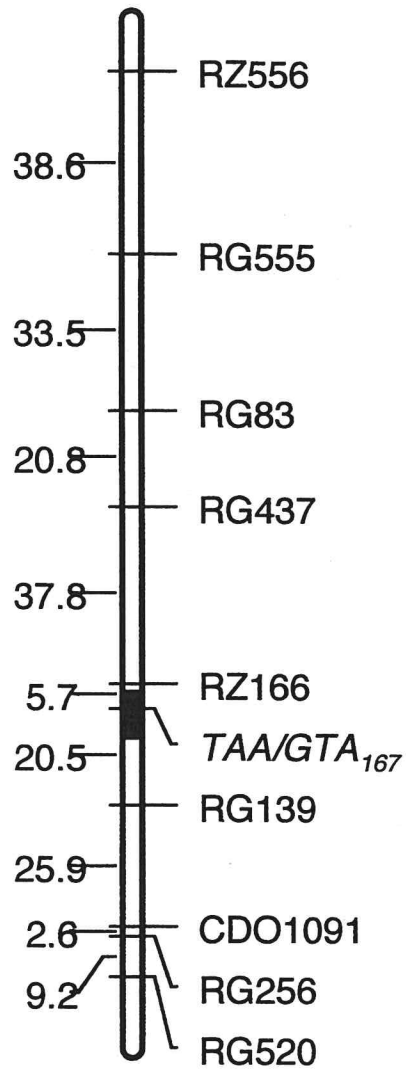
Table 1. Lines derived from *Oryza nivara* X M-202 backcross populations with best seedling vigor (longest shoot length).

Entry	Shoot length (mm)	Plant height (cm)
DX221-48-4-1	52.7	124
DX221-42-5-1	49.3	119
DX221-48-10-1	48.7	94
DX221-58-3-1	45.9	94
DX221-24-1-1	44.4	104
DX221-20-1-1	44.2	86
M-202 (check)	31.9	96
LSD (0.05)	5.8	14.2

Table 2. Molecular markers associated with improved agronomic traits from *Oryza nivara* in the M-202 backcross populations.

Trait/marker	Chromosome	Probability	% of trait explained
<b>Shoot length</b>			
RM212	1	0.0011	8.1
RM267	5	0.0000	14.5
RM176	6	0.0098	12.2
RM234	7	0.0011	13.5
RM258	10	0.0028	6.6
<b>Root length</b>			
RM256	8	0.0016	6.8
RM228	10	0.0060	5.6
<b>Yield</b>			
RM84 (1998)	1	0.0075	3.9
RM201 (1999)	9	0.0220	3.3
RM84 (1998-99)	1	0.0109	4.2
<b>Grain weight</b>			
RM84	1	0.0027	4.9
RM51	7	0.0109	3.7
<b>No. spikelets per panicle</b>			
RM211	2	0.0161	4.6
RM84	1	0.0238	2.8
<b>Panicle no. (tillering)</b>			
RM82	7	0.0000	23.6
RM44	8	0.0077	7.1

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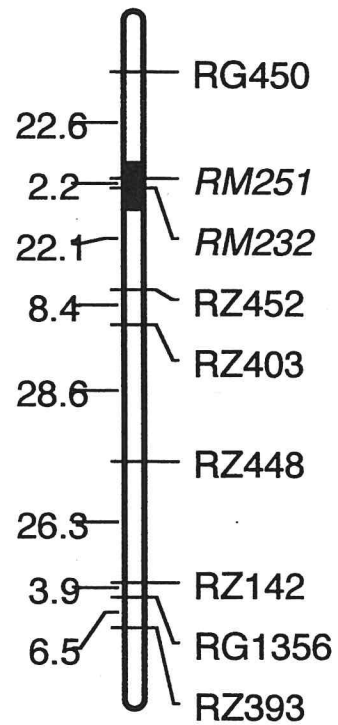


Fig. 1. Two loci control stem rot resistance in the resistant line 87-Y-550.

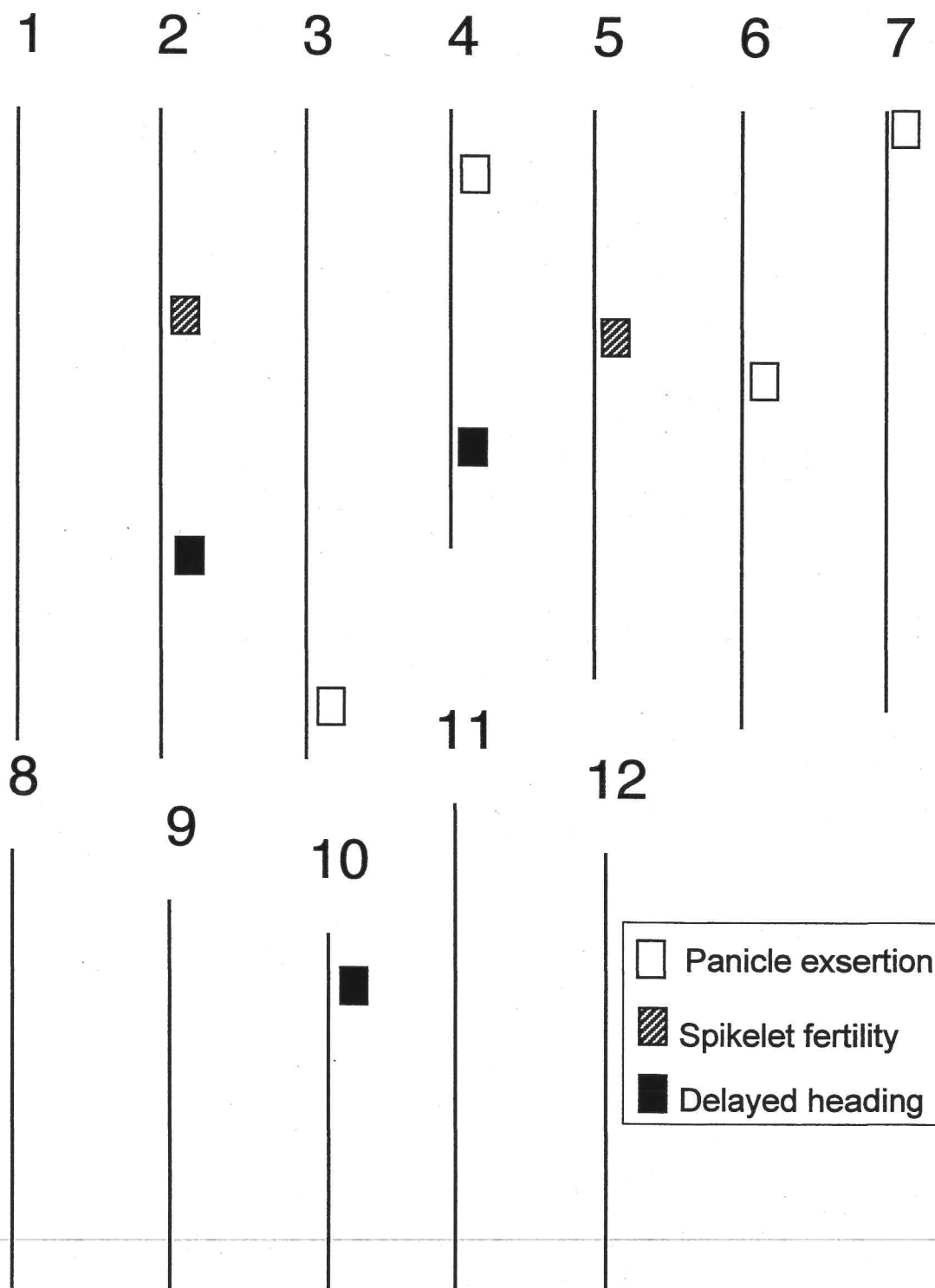


Fig. 2. Chromosome map showing location of most important loci for cold tolerance.



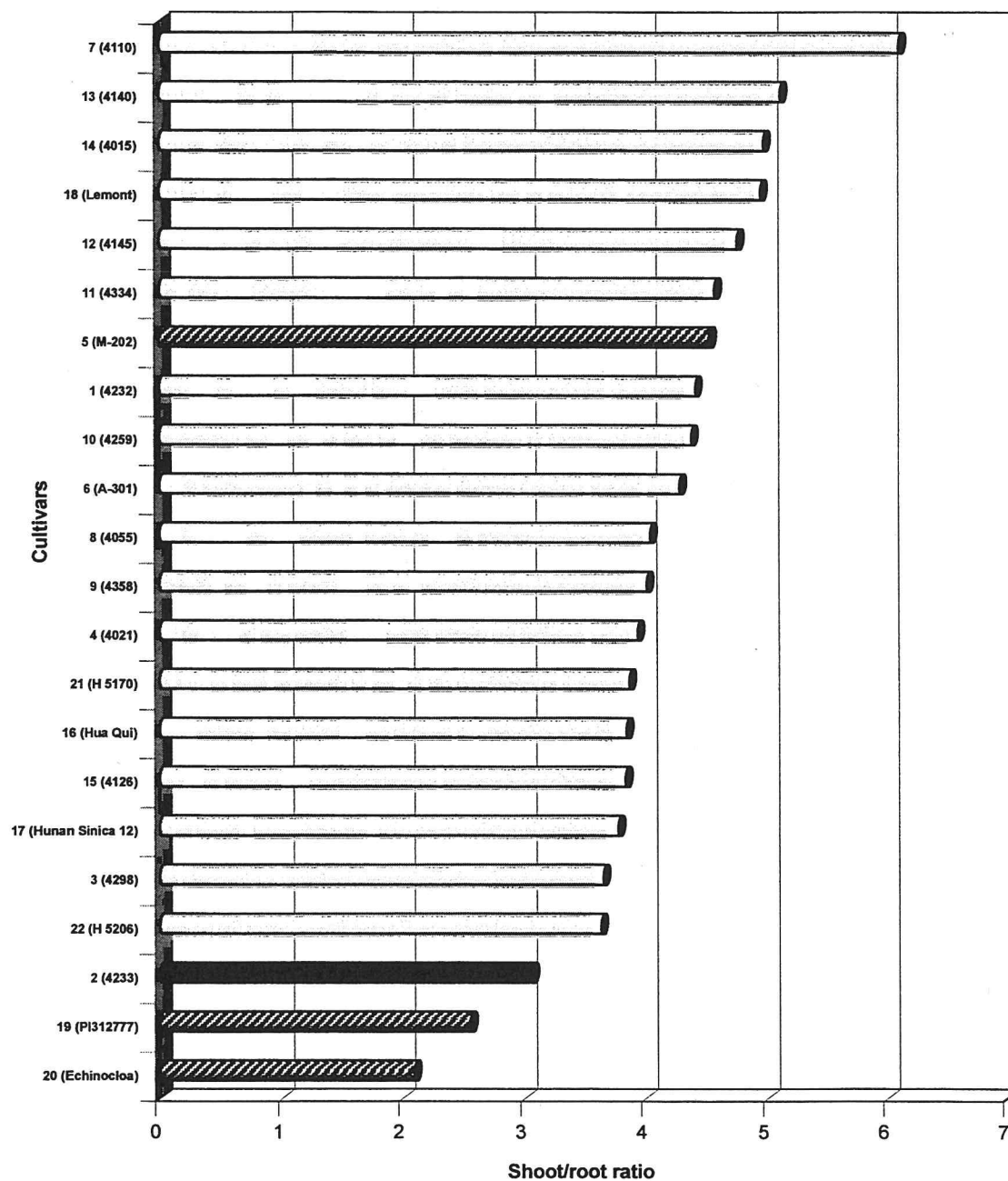
**Fig. 3. Shoot/root ratio of interspecific lines**

Fig. 4. Leaf Area Index of interspecific lines at three growth stages.

