

# Utilization of New Alleles from Wild Rice Species to Improve Cultivated Rice in Latin America

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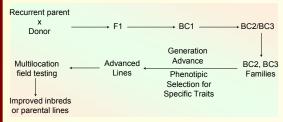
## Introduction

In spite of the great impact made in rice production in Latin America (LAC) there is a need to increase it in a sustainable way. New alleles can provide genetic variability for crop enhancement. The Oryza wild species represent a potential source of new alleles for improving the yield, quality and stress resistance of cultivated rice. The purpose of this paper is to provide increasing evidence that certain regions in O. rufipogon and O. glaberrima harbor genes of interest for the genetic improvement of cultivated rice.

## Materials and Methods

## 1. Breeding Scheme

Improved varieties (Bg90-2, Oryzica 3 and Caiapo) were used as recurrent parents whilst O. rufipogon (IRGC105491), and O. glaberrima (IRGC103544) were used as donors in an interspecific-backcross breeding scheme shown below.



## 2. Replicated yield trials

Twenty eight lines derived from the cross Bg90-2/O. rufipogon were planted in replicated yield trials in six locations under irrigated conditions in Colombia. Transplanting was done in CIAT whilst direct seeding was done elsewhere. A completely randomized design with three reps was used. Data on main agronomic traits, including grain yield, was taken. A two-way analysis of variance was used for the analysis of grain yield, whilst a GEBEI package that implements appropriate clustering and ordination procedures was used in a preliminary analysis of the GxF data

#### 3. Evaluation for tolerance biotic stresses

Advanced breeding lines from the cross Oryzica 3/O. rufipogon were field tested in a "hot spot" for reaction to three diseases in Tolima, Colombia, using the Standard Evaluation System for Rice and three reps.

Doubled-haploid lines derived from the cross Caiapo/O. glaberrima were evaluated in a "hot spot" area in Meta, Colombia, for tolerance to the Rice Stripe Necrosis Virus.

## 4. Selection for grain quality

Advanced breeding lines were evaluated for grain length and translucency in the CIAT Quality Lab.

## Results

## 1. Grain yield

Data are presented in Figure 1. Statistical analysis showed no significant yield difference in grain yield between Bg90-2 and its progenies in each location.

Although none of the interspecific lines was excellent in all locations, a few lines performed better than Bg90-2 suggesting that there was a good genetic variability present in this group of lines. A few lines performed as well as Fedearroz 50, the highest yielding variety planted by farmers in Colombia.

However, the GxE interaction was very high (75%), suggesting that the performance of genotypes was dependent on the climatic/soil conditions found in each location (data not shown).

## 2. Tolerance to biotic stresses

Some fungal diseases, particularly Rhizoctonia solani, Sarocladium oryzae and Bipolaris oryzae, considered of minor importance in the past are now causing yield losses in several areas in LAC. Most commercial varieties grown are susceptible. Results from field tests suggest that lines derived from the cross Oryzica 3/O. rufipogon showed a good tolerance level to these diseases (Table 1).

The fungus Polymyxa graminis transmits the rice stripe necrosis virus (RSNV), disease first reported in Ivory Coast in 1977; it was reported in Colombia in 1991 and now is found in Panama and Brazil. All commercial varieties are susceptible to RSNV (Table 2); however, high level of tolerance was found in O. glaberrima. Our results show that tolerance to RSNV has been successfully transferred to improved varieties.

Figure 1. Performance<sup>1/</sup> of breeding lines derived from Bg90-2 / O. rufipogon in farmers' fields in six locations, 2002.

		Location 2/				Mean Yield (t/ha)				
Line	1	2	3	4	5	6	0 3			6 7.
CT13941-27-M-11-6-M-M	1.13	0.96	1.00						-	ť
CT13941-27-M-11-6-M-M CT13941-27-M-15-2-M-M	0.98	1.03	1.00							+
CT13941-27-M-15-2-M-M CT13941-11-M-25-5-M-M	1.07	1.03	1.00	1.20	0.96	1.52				+
CT13958-13-M-17-5-M-M	1.05	1.02	1.26	1.24	0.98	1.40				
CT13941-11-M-25-1-M-M	1.04	1.20	1.18	1.31	0.83	1.51				
CT13946-26-M-5-3-M-M	1.09	1.11	1.05	0.94	1.01	1.40				
Fedearroz 50	0.97	1.10	1.05	1.52	1.00	1.15				
CT13941-27-M-11-5-M-M	0.98	0.87	0.89							
CT13941-11-M-25-4-M-M	0.98	1.05	1.04	1.37	0.91	1.30				
CT13958-13-M-7-5-M-M	1.11	1.07	1.06	0.87	0.99	1.18				f
CT13956-29-M-29-2-M-M	1.08	1.14	1.01	1.04	0.93	1.27				+
CT13946-26-M-5-6-M-M	1.06	0.89	1.11	1.34	0.82	1.25				+
CT13958-13-M-2-3-M-M	1.06	1.18	1.16	1.19	0.82	1.02				+
CT13956-29-M-14-1-M-M	1.02	1.12	1.10	1.23	0.74	1.38				+
CT13959-3-M-10-5-M-M	1.13	1.03	0.99	0.94	1.02	1.16				1
CT13956-29-M-8-3-M-M	1.02	0.80	1.08	0.94	0.94	1.24				¢
CT13958-12-M-1-7-M-M	1.13	0.85	1.01	0.81	1.02	1.35				þ
CT13941-27-M-15-3-M-M				1.53	1.04	1.16				ġ,
CT13958-13-M-26-5-M-M	1.07	1.11	0.94	1.09	0.87	1.01				1
CT13958-13-M-2-1-M-M	1.04	1.12	1.04	0.76	0.85	1.07				1
Bg90-2	1.00	1.00	1.00	1.00	1.00	1.00				1
CT13958-13-M-2-4-M-M	1.05	1.13	1.02	1.06	0.80	0.93		_		1
CT13958-13-M-26-4-M-M	1.05	1.00	1.03	0.94	0.83	1.13				1
CT13958-13-M-33-1-M-M	1.11	1.01	0.93	0.94	0.80	1.22				
CT13976-7-M-14-1-M-M	1.03	0.98	0.93	0.82	0.97	1.03			_	1
CT13941-27-M-19-1-M-M	0.96	1.00	0.98	1.21	0.76	1.13			_	1
CT13959-3-M-10-4-M-M	1.05	0.79	0.96	0.97	0.93	1.16				1
CT13956-29-M-25-7-M-M	0.99	0.94	1.10	0.77	0.76	1.27				1
Local checks	0.95	0.60	0.87	1.14	0.78	1.16				1
CT13941-27-M-5-4-M-M				1.27	0.89	1.07				1
CT13941-27-M-4-1-M-M				1.08	0.80					L

// Relative value compared to BG90-2
// Relative value compared to BG90-2
// Location 1 = Aceituno 2 = Ciat 3 = Montería
4 = Jamundí 5 = Saldaña 6 = Villavicence

Table 1. Tolerance to several diseases of advanced lines
from the cross Oryzica 3 / O. rufipogon under field
conditions in Saldaña, Tolima. Fedearroz 2002.

Pedigree	R. solani1/	S. oryzae <sup>1</sup> /	B. oryzae1/	B. oryzae <sup>2/</sup>
CT14524-2-M-2-M	3	3	5	15
CT14524-2-M-3-3	3	3	5	15
CT14529-12-M-1-2	3	1-5	5	0
CT14529-12-M-2-3	3	5	7	30
CT14529-18-M-3-M*	3	3-5	3	0
CT14529-18-M-4-M*	3	1-5	3	20
CT14534-12-M-1-3	5	3	7	0
CT14534-12-M-3-4*	3	1	1	0
CT14534-12-M-4-1	5	3	1	0
CT14537-8-M-4-M	3	1	1	0
CT14537-9-M-4-1*	3	5	3	0
CT14537-21-M-6-3	3	3	3	0
CT14539-31-M-1-1*	3	5	3	0
CT14539-34-M-4-M-2*	3	3	3	0
Oryzica 3 (Check)	7-9	5-7	1-3	0-20
CT14524-3-M-2-2	7-9	7	5-7	40

1/ Scale 1-9. IRRI Standard Evaluation System % Panicle neck infection

Lines selected by Fedearroz

Table 2. Tolerance to Rice Stripe Necrosis Virus in doubled-haploid lines derived from the cross Caiapo / O. glaberrima under field conditions. Meta, Fedearroz 2002.

Pedigree	%Diseased Plants
1. CT16322-CA-6	2.4
2. CT16323-CA-3	5.1
3. CT16311(2)-CA-3	5.1
4. CT16318-CA-3	5.8
5. CT16308-CA-3	6.5
6. CT16322-CA-7	7.0
7. CT16313-CA-16	7.3
O. glaberrima (ACC #10354	4) 2.0
CG-20 (O. glaberrima)	2.4
Cimarrón (Check)	40.0
O. Caribe 8 (Check)	14.0

#### 3. Grain quality

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Development of high yielding varieties with tolerance to biotic stresses and excellent grain quality is the main breeding objective of national rice programs in LAC. Both parents, Bg90-2 and O. rufipogon, posses poor grain quality. However, positive transgressive segregation for superior grain quality was observed in the BC2F2 generation which led to the selection of advanced lines with long and slender, translucent grains (Figure 2).

Figure 2. Advanced lines with excellent grain quality were derived from the cross Bg90-2/O. rufipogon



# Discussion

It has been shown (Xiao et al., 1998; Moncada et al., 2001) the Oryza wild species represent a potential source of new alleles for improving the yield, quality and stress resistance of cultivated rice. Our results from evaluations under greenhouse and farmer's fields confirm that O. rufipogon and O. glaberrima posses alleles with positive effects on yield, stress resistance and grain guality. Molecular markers are being used to map the gtl in various crosses and near isogenic lines are being established for further crosses.

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# References

Watson, S. L. DeLacey, I. H. Podlich, D. W. Basford, K. E. 1999. GEBEI: An analysis package using agglomerative hierarchical classificatory and SVD ordination procedures for genotype x environment data. http://biometrics.ag.uq.edu.au/software.htm

Moncada, P. et al. 2001. Quantitative trait loci for yield and yield components in an Oryza sativa x O. rufipogon BC2F2 population evaluated in an upland environment. Theor. Appl. Genet. 102:41-52.

Xiao, J. et al. 1998. Identification of trait-improving quantitative trait loci alleles from a wild rice relative, Oryza rufipogon. Genetics 150:899-909.