

have already become locally extinct when a tidal wetland area was converted into prawn culture. Other wild rice populations are threatened by the encroachment of small irrigation tanks, freshwater aquaculture, and a change in the cultivation system from broadcasting to transplanting.

In situ conservation of these important genetic resources must be initiated and complement ex situ conservation efforts. These measures could include

- *Integration into conservation programs of tidal and freshwater swamps.* For example, the Karnataka State Forest Department has a program to conserve mangrove

swamps at Kundapur in Dakshina Kannada and a freshwater wetland at Gudwi Pakshidham in Shimoga. Other wetlands, such as those in Bharatpur in the state of Rajasthan, are being protected under the Ramsar Convention. Special attention should be paid to in situ conservation, including deliberately introducing into the wetlands appropriate indigenous wild rice species.

- *Integration into ecotourism-based conservation programs.* One of the study sites, Gudwi, is a bird sanctuary close to the tourist attraction of the Gerusoppa Waterfalls. Conservation

of wild rices, along with environmental awareness programs, could be effectively integrated with the tourist attraction of aquatic birds.

- *Use of indigenous knowledge.* Some local indigenous communities, such as the Mushahars of eastern Uttar Pradesh and Bihar, depend on wild rice grain and other wild foods for survival. These people have an intimate knowledge of the distribution and habitat requirements of wild rices. It would be highly useful to involve these communities in situ conservation programs.

Panicle culture and karyotype analysis from callus cells of a diploid wild rice, *Oryza meyeriana*

Xiao-Ling Wang, Li-Hui Shu, Wen-Jing Yuan, and Lan-Jie Liao, School of Life Science, Wuhan University, Wuhan, Hubei 430072, China

The genus *Oryza*, to which the cultivated rice (*O. sativa* $2n=24$) belongs, has 20 wild species with $2n=24$ or 48 chromosomes. *Oryza meyeriana* ($2n=24$) is highly resistant to bacterial blight. The karyotype of this species has not been well documented and only a few tissue culture studies have been made. We report the results of in vitro culture of young panicles and karyotype analysis of this species.

Embryogenic calli with high plant regeneration ability. We obtained embryogenic calli with high plant regeneration ability using N6 and MS

culture media alternately. The N6 medium contained $2\text{ mg } 2,4\text{-D L}^{-1}$ and 4.5% sucrose while the MS medium was supplemented with $2\text{ mg kinetin L}^{-1}$, 0.5 mg NAA L^{-1} , and 3.0% sucrose. Green plant regeneration frequency of the selected calli was up to 76% , but that of the unselected calli was only 33% after the 10th culture. The free amino acids in the calli were determined. The methionine glutamic acid and the total amino acid contents in the selected calli were lower than those in the control, while the alanine and phenylalanine contents in the selected calli were higher than those in the control. The main components of the free amino acid pool in the selected calli were alanine, glutamic acid, and phenylalanine, which together constituted 65.8% of the total amino acids.

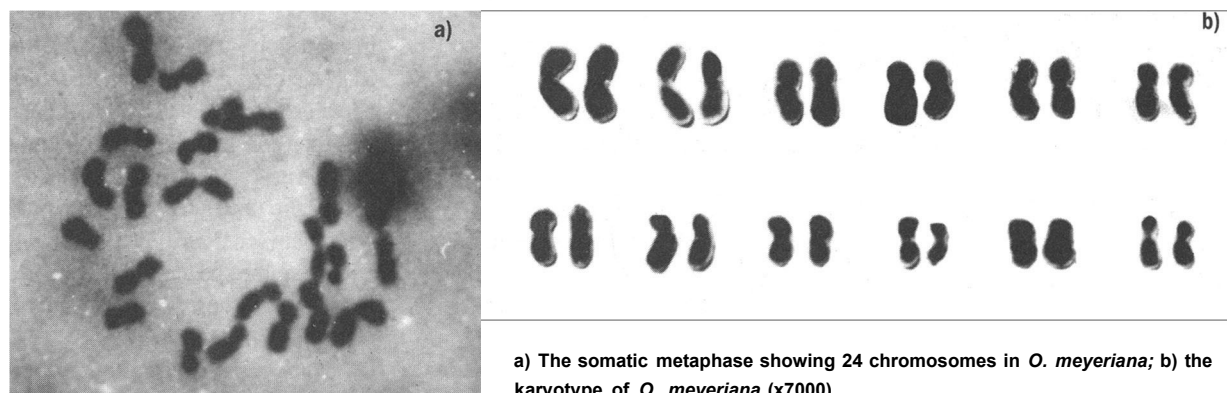
It appears that alanine, glutamic acid, methionine, and phenylalanine occupy a key position in amino acid metabolism and influence the regeneration capacity of calli.

High IAA oxydase activity was helpful in regenerating the calli.

The regenerated plants were tested for reaction to three bacterial blight strains: PXO61, T7174, and Jiang Ling 691. Fifty regenerated plants were inoculated with the three strains on different tillers of the same plant. The regenerated plants were resistant to the strains, but the degree of resistance differed among the plants.

Karyotype analysis. *O. meyeriana* has strong seed shattering and low seed fertility, making karyotype analysis using seed difficult. So instead, we used the method of Kurata et al to conduct karyotype analysis using calli.

The *O. meyeriana* had $2n=24$ (see figure). Based on the arm ratio, the karyotype of *O. meyeriana* consisted of 4 pairs of metacentrics, 7 pairs of submetacentrics, and a pair of satellite-submetacentric chromosomes (see table). ■



a) The somatic metaphase showing 24 chromosomes in *O. meyeriana*; b) the karyotype of *O. meyeriana* (x7000).

Relative length, arm ratio, and classification of the chromosomes of *Oryza meyeriana*.

Chromosome number	Relative length (%)	Arm ratio (short/long)	Classification ^a
1	11.80	0.82	M
2	11.48	0.90	M
3	9.87	0.67	SM
4	8.80	0.70	SM
5	8.69	0.73	SM
6	8.31	0.69	SM
7	8.11	0.73	SM
8	7.26	0.63	SM
9	6.97	0.93	M
10	6.79	0.88	M
11	6.17	0.69	SM
12	5.74 ^b	0.37	SAT

^aM = metacentric, SM = submetacentric, SAT = satellite. Arm ratio: M = (1.0–0.76), SM = (0.75–0.25). ^bThe length of the satellite is not included in the length of the chromosome.



A study of Neolithic carbonized rice grains excavated from Hemudu, China

Shengxiang Tang and Hanyong Yu, China
National Rice Research Institute, Hangzhou
310006, China

Rice grains excavated from Hemudu, China (6950±130 BC) are known to be some of the world’s oldest remains of rice cultivation. We studied the variation in

these grains to improve our understanding of the origin and domestication of cultivated rice in China.
The length and width of 105 of the grains were measured using an enlarged photograph. About half of the grains were awnless. The grain length ranged from 5.2 to 8.6 mm, with an average of 7.1 mm, and the grain width ranged from 2.1 to 3.2 mm, with an average of 2.8 mm. The grain length-width ratio (L:W) was 1.7-3.2. with an average of 2.6. These findings suggest

Length, width, and shape distribution of 105 rice grains excavated from Hemudu, China.

Grain	trait	Distribution														
Length	(mm)	<5.4	5.6	5.9	6.2	6.5	6.8	7.9	7.4	7.7	8.0	8.3	8.6			
	(no.)	1	2	3	6	7	21	29	11	9	11	4	1			
	(%)	0.9	1.9	2.9	5.7	6.7	20.0	27.6	10.5	8.6	10.5	3.8	0.9			
Width	(mm)	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2			
	(no.)	2	3	3	1	5	9	20	24	18	15	4	1			
	(%)	1.9	2.9	2.9	0.9	4.8	8.6	19.0	22.9	17.1	14.3	3.8	0.9			
L-W ratio		1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	>3.1
	(no.)	1	0	1	2	5	7	5	12	12	16	13	5	16	4	6
	(%)	0.9	0	0.9	1.9	4.8	6.6	4.8	11.4	11.4	15.2	12.4	4.8	15.2	3.8	5.7



Classification of A genome species in the genus *Oryza* using nuclear DNA markers

K. Doi, A. Yoshimura, M. Nakano, and N. Iwata, Plant Breeding Laboratory, Faculty of Agriculture, Kyushu University, Fukuoka 812-81, Japan; and D. A. Vaughan, National Institute of Agrobiological Resources, Tsukuba 305, Japan

We did a new analysis of the restriction fragment length polymorphisms (RFLPs) of 67 accessions of A genome species in the

genus *Oryza*, which contains *O. rufipogon*, *O. nivara*, *O. glaberrima*, *O. barthii*, *O. longistaminata*, *O. glumaepatula*, and *O. meridionalis*, and of the materials previously analyzed by Nakano et al (1992) (see figure). A total of 192 accessions of the A genome species were analyzed.
RFLPs were detected for combinations of *Dra*I-digested total DNA and 21 single copy genomic clones. Genetic distances between accessions were quantified as

D = -ln [2Mxy/(Mx+My)]

where Mx and My were the total fragments in accessions X and Y, respectively, and Mxy were the common fragments observed between accessions X and Y. A dendrogram was then constructed by the UPGMA method using 64 of the 67 new accessions and 12 previously analyzed accessions as a reference (see figure).
A genome species were classified into five major groups: Asian (*O. sativa*, *O. rufipogon*, and *O. nivara*), *O. glumaepatula*, *O. glaberrima*-*O. barthii*, *O. longistaminata*, and *O. meridionalis*. *O. glumaepatula* had

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Multiple submissions. Normally, only one report for a single experiment will be accepted. Two or more items about the same work submitted at the same time will be returned for merging. Submitting at different times multiple notes from the same experiment is highly inappropriate. Detection will result in the rejection of all submissions on that research.