

as a natural group. When the chloroplast DNA RFLP data previously obtained in the *Sativa* section (Dally 1988) is considered, the present data support the recognition of the *Oryza* section (*O. sativa*, *O. latifolia* and *O. collina* in the present material) as a natural group within the genus. *Oryza collina* was not included in the study of Dally (1988). It appeared that *O. collina* presents a plastotype not previously observed, with a closest affinity in the *O. officinalis* complex.

The seven genera *Zizania*, *Chikusichloa*, *Rhynchoriza*, *Potamophila*, *Hygroryza*, *Zizaniopsis* and *Luziola*, although generally endemic in different continents, clustered together. The case of *Potamophila*, endemic in Australia, does not favor the hypothesis of Cretaceous breakup of the Gondwanaland being involved in the origin of the pattern of distribution of the tribe because the closest relative (as read in the distance matrix) of *Potamophila* is *Chikusichloa* which is endemic in Asia. A common Asian ancestor more likely migrated from South-East Asia to Australia. Similarly, various *Oryzeae* would have entered America by land from Eurasia, the latest being *Zizania*, the North American "wild rice".

The same material is being studied at the level of nuclear and mitochondrial DNA RFLPs and should allow further phylogenetic relationships to be drawn.

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IV. Segregation distortion

15. Abnormal segregation patterns in crosses between *Oryza sativa* and *O. glaberrima*

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Four progenies of crosses between the two cultivated rice species were obtained by pollinating a common *Oryza glaberrima*/*O. sativa* F₁ hybrid with four different *O. sativa* cultivars. We present here the results on the development of these progenies and on the segregations scored at 6 isozyme loci.

The five parental varieties were: W025 (*O. glaberrima*, Guinea-Bissau), ES70-6 (*japonica*, Tanzania), YS309 and YS45-1 (*japonica*, Guinea), and SS404 (*indica*, Senegal). W025 was provided by the National Institute of Genetics (Mishima,

Japan) while *O. sativa* cultivars were obtained from ORSTOM collection. The 4 crosses studied are presented in Table 1. The F₁ hybrid used as female parent W025/ES70-6 being common, the 4 crosses are designated as//ES70-6,//SS404,//YS45-1 and //YS309, respectively.

The seeds were dehulled, disinfected, rinsed in water and then sown in petri dishes with nutritive solution. After 10 days, seedlings were planted in pots. Plants were grown in glasshouse. Electrophoresis procedures used are described by Second (1982) and de Kochko (1987).

Approximately 40% of the plants were lost during cultivation (Table 1). The first level of loss was observed at seed germination. All progenies showed a similar rate of non-germinated caryopses (<20%), which was about the same as for F₁ seeds of W025/ES70-6. The second level of losses occurred at seedling stage, where significant differences appeared between the progenies. More than 50% seedlings of the cross//ES70-6 died.

Table 1. Development of plants in four *glaberrima/sativa//sativa* backcrosses

Cross	No. of seeds		No. of inviable seedlings	No. of adult plants	Total percent of loss
	Sown	Non-germinating			
W025/ES70-6//ES70-6	35	16 (14%)	16 (53%)	14	60%
" " //SS404	46	4 (9%)	8 (19%)	34	26
" " //YS309	12	2 (17%)	1 (10%)	9	25
" " //YS45-1	27	3 (12%)	7 (29%)	17	37

Table 2 presents the results for segregation of isozyme loci. Note that we have observed the segregations of the female gametes of the F₁ hybrid W025/ES70-6. Four of the 20 observed segregations deviated (at 5% significance level) from the 1:1 Mendelian ratio. The *Est-2* locus was subject to distortion in the crosses//SS404 and //ES70-6. *Sdh-1* segregation was abnormal in the cross //YS309. In these three cases, an excess of the *O. glaberrima* allele was observed. On the other hand, a deficiency of the *O. glaberrima* allele appeared at the *Est-8* locus in the cross //ES70-6.

Sano et al. (1979) proposed the "one-locus sporogametophytic interaction" model to account for the sterility of F₁ hybrids between the two cultivated species (i.e., parents *O. sativa* and *O. glaberrima* are respectively assumed to have $S^a S^a$ and SS ; the presence of the *S* allele in the maternal tissue leads to sterility of gametes S^a). This model explains the distortion observed for *Est-2*, because marker genes linked to the sterility gene will be subject to distortion. Further, because of the chromosomal location of locus *Est-2* and because the *O. glaberrima* parent W025 was used by Sano et al. (1979), it is likely that the sterility gene involved in our experiments is the same as S^a-1 and $S-1$ designated by Sato et al. (1987).

Table 2. Segregation ratios observed at isozyme loci in four cross progenies and test of their conformity to Mendelian 1:1 ratio

Locus ^a	//ES70-6			//SS404			//YS309			//YS45-1		
	G	S	Test(B)	G	S	Test(G)	G	S	Test(B)	G	S	Test(B)
<i>Cat-1</i>	10	4	ns	17	15	ns	7	2	ns	8	7	ns
<i>Est-1</i>	7	7	ns							11	5	ns
<i>Est-2</i>	12	2	**	27	5	***						
<i>Est-8</i>	3	11	*	17	16	ns	6	3	ns	8	9	ns
<i>Pgi-1</i>	6	8	ns	20	14	ns	5	4	ns	7	10	ns
<i>Sdh-1</i>	7	7	ns	18	16	ns	9	0	**	11	6	ns

a: Symbols follow those proposed in RGN 3, p. 15-17.

G: Plants with the allele from *O. glaberrima* parent, W025.

S: Plants with the allele from *O. sativa* parent, ES70-6.

Test(B): Binomial test (Sokal and Rohlf 1981, p. 78).

Test(G): G-test (Sokal and Rohlf 1981, p. 706).

ns: Not significant; * P<0.05; ** P<0.01; *** P<0.001.

The "one-locus sporogametophytic interaction" model cannot explain the observations at the loci *Est-8* and *Sdh-1* because opposite results were observed in different crosses. This means that the genotype of the male *O. sativa* parents has to be considered, in addition of those of W025 and ES70-6. The differential rates of loss during the cultivation could explain the deviation at *Est-8* in the cross //ES70-6. The hypothesis of an early differential zygotic selection, involving an albumen-embryo interaction, seems necessary to account for the distortion of *Sdh-1*. This was suggested by Gadish and Zamir (1987) in an interspecific cross between *Lycopersicum esculentum* and *L. penneli*.

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