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GENETIC STUDIES OF ESTERASES ON THE TAIWAN WILD RICE POPULATION AND CULTIVATED RICE[1]

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Abstract

Genetic analysis of esterase isozymes in Taiwan wild rice (*Oryza perennis* var. *formosana*) and cultivars of rice (*O. sativa* L.) by starch gel electrophoresis shows a total of 9 anodic bands and 3 cathodal bands. The cathodal bands are controlled by a single locus with two codominant alleles. The 3-band zymogram represents heterozygotes. No variant is observed for anodic bands A1 and A4 in wild rice and the cultivars examined. Each of loci A2, A3, A5, A6, and A7 has one null variant. Bands A8 and A9 showed segregation in some families but genetic analysis is incomplete. A2 and A3 loci are linked with 11.3 map units apart. The samll Taiwan wild rice population showed a high proportion of genetic polymorphic loci (75%), and the average heterozygosity was 22.2%. The cultivars examined display fewer bands than wild rice. This could be the result of fixation of various loci for null alleles during development of varieties. Taiwan wild rice is on the verge of extinction; without protection this genetic resource could be lost permanently.

Introduction

A large amount of genetic variation has been found in natural plant and animal populations by electrophoretic studies of isozymes (Lewontin 1974, Ayala *et al.* 1974, Allard *et al.* 1975). Information on genetic structure of economic plant species and their wild relatives is important for genetic improvement programs in crop plants. Many isozyme studies on cultivated plants such as maize (Schwartz and Endo 1966), barley (Kahler and Allard 1970), wheat (Brewer *et al.* 1969) and soybean (Gorman and Kiang 1978) have been reported, but relatively few studies have been reported on rice, one of the most important crops of the world. Enzyme polymorphism in the cultivated rice

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(*Oryza sativa* L.) and its relatives has been studied with acid phosphatase (Pai *et al.* 1975), peroxidase (Pai *et al.* 1973, Endo 1971, Chu 1967, Chu and Oka 1967), and esterase (Nakagahra 1977). Nakagahra *et al.* (1975) reported variation and geographic cline of esterase isozymes in rice varieties of Asian region. To our knowledge there has been no estimate of genetic variation in wild rice populations by isozyme analysis. We studied genetics of esterase isozymes of the Taiwan wild rice population and cultivars, and estimated genetic variation of the population.

The Taiwan wild rice population has become nearly extinct, and the possible causes of its disappearing have been discussed (Kiang *et al.* 1979). During the 1920's and 1930's Taiwan wild rice (*Oryza perennis* var. *formosana*) was growing abundantly in a large number of irrigation ponds and ditches around Sinchu and Taoyuan highland areas in Northwestern Taiwan (Hara 1942). Oka and Chang (1961) visited the area in 1957, and found only three populations, each less than one thousand plants. They reported that the populations showed a great deal of morphological variation, and suggested that they contained much genetic variation (Oka and Chang 1961). In 1976, one of us, Wu, visited the sites studied by Oka and Chang, and found a small population of about 70 plants growing along the edge of a pond on mud which had been brought up from the bottom of the pond. Plants sampled from this small population were used for this study.

We found a great amount of genetic variation in the population, confirming the previous report (Oka and Chang 1961). We also found that the esterase zymograms of wild rice were different from those of the cultivars examined. We made a genetic analysis of esterase isozymes based on the data gathered.

Materials and Methods

In 1976, 23 plants were sampled from the small Taiwan wild rice population found at Patu village, Taoyuan, Taiwan. These plants were maintained in large clay pots and in concrete beds at the Institute of Botany, Academia Sincia, Taipei, Taiwan.

Selfed seeds were collected from each wild rice plant. Crosses between wild rice and cultivars Taichung No. 65 (T65) and Tainan No. 5 (T5) were made. The selfed and intercrossed F_1 seeds were grown, and their selfed seeds (F_2) were harvested from individual plants. Twelve wild rice selfed seeds and twelve hybrid (F_1) seeds were grown in concrete beds. In addition to T65 and T5, 15 cultivars were also grown for esterase isozyme study.

Horizontal starch gel electrophoresis of leaf extracts was used for the esterase isozyme analysis. Gel preparation, buffer systems, and the method of staining for esterase activity were similar to those reported previously (Wu and Kiang 1979).

Results

Esterase zymograms of wild rice and rice cultivars are shown in Fig. 1. A total of 9 anodic bands and 3 cathodal bands was observed.

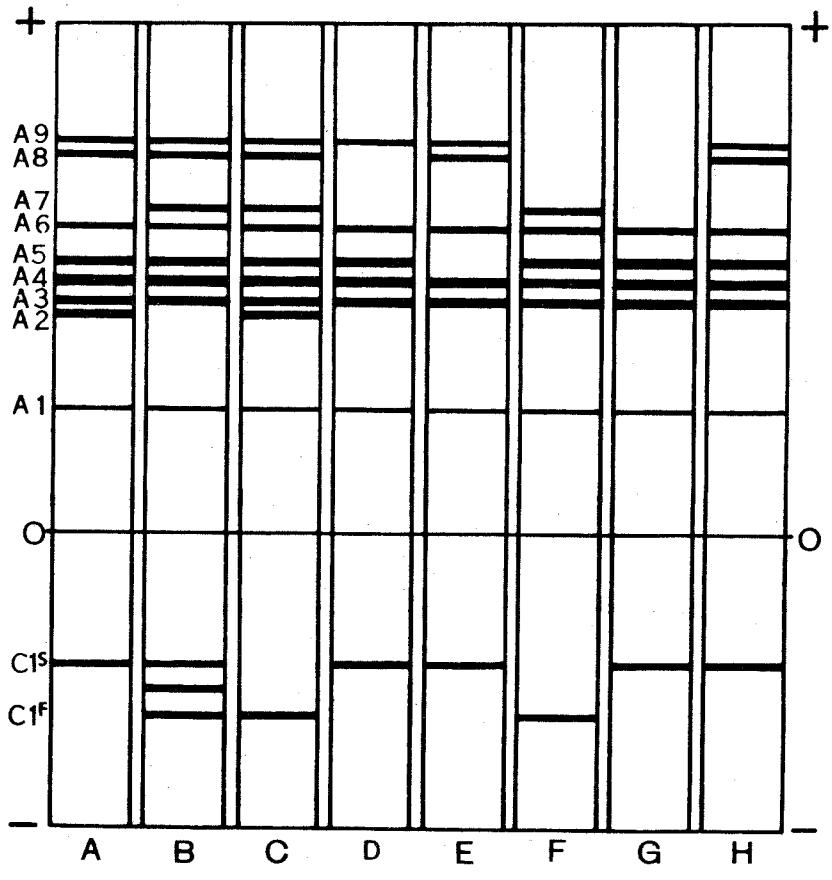

Fig. 1. Zymograms of esterase isozymes in Taiwan wild rice and cultivars. A, B, and C are wild rice P5, P10, and P21 respectively. P10 showing three cathodal bands is a heterozygote at C1 locus. D, E, F, G, and H are cultivars Taichung 186, Taichung 65, Hsien 8, Chia-Hsien 11, and Taichung-Tsai-Lai 1, respectively.

Cathodal bands

Three zymograms were observed: one fast migrating band (F), one slow band (S) and a three-band pattern (See Fig. 1B).

Plants showing the F-band by selfing produced only the F-band offspring, and the progeny of S-band plants were all S-band (Table 1). This observation was also true for the cultivars examined. Progeny of selfed 3-band plants, (e.g. P10), gave S-band, 3-band, and F-band zymograms in a 1:2:1 ratio (Table 1). Both cultivars T65 and T5 showed the S-band, and the progeny of T65 X P10, P10 X T65, and T5 X P10 segregated in a 1:1 ratio for the S-band and 3-band zymograms (Table 2). The F_1 hybrid (T65 X P10) T10-20 and its selfed progeny were all the S-band phenotype (Table 1). Based on the

analyses of the data we conclude that the 3 types of cathodal zymograms are governed by a single locus (C1) with two codominant alleles ($C1^F$, $C1^S$). The 3-band zymogram is

Table 1. *The zymograms of esterase C1 locus in Taiwan wild rice, cultivars and their selfed progeny*

Parent	Zymogram	Progeny S	Progeny 3-band	Progeny F
P2	F	0	0	12
P3	F	0	0	5
P4	F	0	0	6
P5	S	12	0	0
P6	S	9	0	0
P12	S	12	0	0
P14	F	0	0	12
P16	F	0	0	5
T65(1)	S	20	0	0
T5(1)	S	20	0	0
H6(1)	F	0	0	20
KH11(1)	F	0	0	20
T10-20(2)	S	24	0	0
P10(3)	3-band	15	23	8
P11(3)	3-band	2	7	3
P13(3)	3-band	2	7	3

(1) Cultivars: Taichung 65 Tainan 5; Hsien 6; Kaohsiung Hsien 11.
(2) F_1 of T65 X P10.
(3) The segregation of progeny deviating from a 1:2:1 ratio is not significant. (X^2 test).

Table 2. *The zymograms esterase C1 locus in hybrids of Taiwan wild rice and cultivars*

Parent	Progeny S	Progeny 3-banded	Progeny F
T65 X P10(1)	15	7	0
P10 X T65	2	3	0
T5 X P10(1)	5	3	0

(1) The segregation of progeny deviating from a 1:1 ratio is not significant (X^2 test).

formed by intragenic dimerization. Thus, a heterozygote for the $C1^F$ and $C1^S$ will show the 3-band zymogram: the F-band, the S-band and a heterodimer in between. The cultivars were either homozygous for the S allele or the F allele, corroborating their supposed pure-line status.

Anodic bands

a. All of the wild rice and the cultivars examined showed band A1 regardless whether other bands were present. It was a weak band in comparison with others. Since there was no variant observed, genic analysis was not possible. We assume band A1 is governed by a single locus A1.

b. Anodic band A2 is a unique band observed in wild rice. No band A2 was observed in the 17 cultivars examined. One single wild rice plant, P10, did not reveal band A2 (Fig. 1B). Progeny of crosses T65 X P10 and T5 X P10 did not show band A2 either. Progeny of some wild rice plants segregated at band A2 and the ratio of plants with band A2 and without (null) does not deviate from a 3:1 ratio (Table 3). We deduce that band A2 is controlled by locus A2 with allele A2 and a null allele ($A2^\circ$). Thus, P10 and the cultivars are homozygous for the null allele ($A2^\circ A2^\circ$), and wild rice plants exhibiting segregation are likely to be heterozygous at the A2 locus (A2A2).

Table 3. *The zymograms of esterase anodic band A2 (A2 locus) in Taiwan wild rice, Cultivars and their progeny*

Parent	Zymogram	Genotype	Progeny zymogram band A2	Progeny zymogram no band A2	X^2 value(1)
P2	band A2	$A2A2^\circ$(2)	11	4	0.20
P6	band A2	$A2A2^\circ$	10	6	2.08
P8	band A2	$A2A2^\circ$	24	9	0.11
P9	band A2	$A2A2^\circ$	17	7	0.22
P11	band A2	$A2A2^\circ$	13	3	0.75
P13	band A2	$A2A2^\circ$	13	6	0.86
P14	band A2	$A2A2^\circ$	14	2	2.08
P21	band A2	$A2A2^\circ$	10	7	3.31
P23	band A2	$A2A2^\circ$	12	7	2.12
P10	null	$A2^\circ A2^\circ$	0	68	
T65	null	$A2^\circ A2^\circ$	0	20	
T5	null	$A2^\circ A2^\circ$	0	20	
T65 X P10			0	21	
T5 X P10			0	8	

(1) The X^2 value calcualted based on a 3:1 ratio.

(2) $A2^\circ$ null allele.

c. Anodic band A4 was present in all of the samples (including cultivars) regardless of the pattern of zymograms. It was often stained deeper than other bands in wild rice. Genic analysis of band A4 was impossible without a variant. We tentatively assume that band A4 is controlled by a separate locus form others.

d. Anodic bands A3, A4 and A5 were considered together in analysis. Some wild rice showing a 3-band zymogram by selfing produced only the 3-band progeny (e.g. P5, Table 4); others showed segregation among their progeny (e.g. P10, Table 4). The cultivars H6 and TTL1 showed the 3-band zymogram, and their selfed progeny were found to show the 3-band zymogram. The progeny of the 2-band cultivars (T65, T5) all revealed the 2-band zymogram (band A3 and A4) similar to that of their parents. The progeny of P10 segregated for either 3 bands, 2 bands, or 1 band (Table 4). It seems likely that two separate loci are responsible for band A3 and A5. P10 is probably heterozygous for null alleles at both A3 and A5 loci ($A3A3^{\circ}A4A4A5^{\circ}$), and thus selfed progeny will segregate in a 9:6:1 ratio for 3-band: 2-band: 1-band. The observed ratio did not significantly deviate from the expected 9:6:1 ratio. The expected ratio should be 9:3:3:1 for 3-band: 2-band (bands A3, A4): 2-Band (bands A4, A5): 1-band

Table 4. *The zymograms of esterase anodic bands A3, A4 and A5 (A3, A4 and A5 loci) in Taiwan wild rice, cultivars and their progeny*

Parent	Zymogram	Genotype	Progeny zymogram 3-band	2-band	1-band	Expected ratio
P5	3-band	$\frac{A3}{A3}\ \frac{A4}{A4}\frac{A5}{A5}$	12	0	0	
P10[1]	3-band	$\frac{A3}{A3^{\circ}}\ \frac{A4}{A4}\frac{A5}{A5^{\circ}}$[2]	42	25	1	9:6:1
T65	2-band (A3A4)	$\frac{A3}{A3}\ \frac{A4}{A4}\frac{A5^{\circ}}{A5^{\circ}}$	0	20	0	
T5	2-band	$\frac{A3}{A3}\ \frac{A4}{A4}\frac{A5^{\circ}}{A5^{\circ}}$	0	20	0	
H6	3-band	$\frac{A3}{A3}\ \frac{A4}{A4}\frac{A5}{A5}$	20	0	0	
TTLI[3]	3-band	$\frac{A3}{A3}\ \frac{A4}{A4}\frac{A5}{A5}$	20	0	0	
T65 X P10[1]			13	11	0	1:1
T5 X P10[1]			4	4	0	1:1
T65 X P7			7	0	0	

(1) Deviation of the observed from the expected is not significant.
(2) $A3^{\circ}$ and $A5^{\circ}$ are null alleles at loci A4 and A5 respectively.
(3) Cultivar. Taichung Tsai Lai No. 1.

(band A4). In counting, all the 2-band individuals were scored as one class. Another line of evidence also supports the hypothesis. Both T65 and T5 showed bands A3 and A4, but not A5; they are homozygous for alleles A3, A4 and A5° at these three loci (A3A3A4A4A5°A5°). When they were crossed with wild rice P10 (A3A3°A4A4A5 A5°) the F1 progeny segregated in a 1:1 ratio for 3-band: 2-band, as would be expected based on the hypothesis that bands A3 and A5 are governed by two separate loci (A3, A5) and each has two alleles (A3, A3° and A5, A5°) and P10 is heterozygous for both loci (Table 4). The segregation data in the F_2 of T65 X P10 and T5 X P10 also support this hypothesis (Table 5). The F_1 plant T10-4 (progeny of T65 X P10) showed

Table 5. *The zymograms of F_1 and F_2 of T65 X P10 (T10) and T5 X P10 (510) showing segregation of esterase anodic bands A3, A4, and A5*

F_1	Zymogram	Genotype	F_2 zymogram 3-band	2-band	1-band	Expected ratio
T10-4	2-band	$\frac{A3}{A3}\ \frac{A4}{A4}\ \frac{A5^\circ}{A5^\circ}$	0	57	0	
T10-16(1)	3-band	$\frac{A3}{A3}\ \frac{A4}{A4}\ \frac{A5}{A5^\circ}$	15	3	0	3:1
T10-20	3-band	$\frac{A3}{A3}\ \frac{A4}{A4}\ \frac{A5^\circ}{A5^\circ}$	15	8	0	3:1
T10-14(1)	3-band	$\frac{A3}{A3^\circ}\ \frac{A4}{A4}\ \frac{A5}{A5^\circ}$	19	14	1	9:6:1
510-3(1)	3-band	$\frac{A3}{A3}\ \frac{A4}{A4}\ \frac{A5}{A5^\circ}$	19	11	0	3:1

(1) By the X^2 test deviation of the observed from the expected is not significant.

a 2-band zymogram (bands A3 and A4), and its selfed progeny (F_2) all showed the zymogram similar to their parent (Table 5). The F_1 plants T10-16, T10-20 (progeny of T65 x P10) and 510-3 all showed the 3-band zymogram and their F_2 segregated in a 3:1 ratio for 3-band: 2-band (bands A4 and A5). These observations indicate that the F_1 plants T10-16, T10-20 and 510-3 were heterozygotes for the null allele at A5 locus. The F_1 plant T10-14 (Progeny of T65 X P10) displayed the 3-band zymogram and its progeny segregated by 19 3-band, 14 2-band and 1 1-band, which does not deviate from the expected ratio (9:6:1) significantly (Table 5). Thus, T10-14 is a double heterozygote for A3 and A5 loci, and its genotype is similar to one of its parents P10.

e. Anodic bands A6 and A7 were considered together. The wild rice plants all displayed only band A6, except P10 and P21 which showed both bands A6 and A7. The selfed progeny of those individuals showing band A6 all showed band A6 only (e.g. P17, P18, P19 Table 6). Cultivars showing band A6 produced selfed progeny

showing band A6 only (e.g. T65, T5 Table 6) and those displaying both bands A6 and A7 produced progeny displaying both bands.

The wild rice P10 selfed progeny segregated as 6 band-A6, 24 Band-A6 band-A7, and 3 band-A7, which does not significantly deviate from a 9:3:3:1 ratio (Table 6). The progeny of P21 segregated in 9 band-A6 band-A7 and 6 band-A6 (Table 6). The deviation from a 3:1 ratio is not significant. Based on the data we deduce that bands A6 and A7 were governed by two separate loci, each having two alleles. Genotypes of P17,

Table 6. *Zymograms of esterase anodic bands A6 and A7 in Taiwan wild rice, cultivars and their progeny.*

Parent	Zymogram (band)	Probable genotype	Progeny A6	Zymogran A6, A7	(band) A7
P17	A6	$\frac{A6}{A6}\ \frac{A7^{\circ}}{A7^{\circ}}$	12	0	0
P18	A6	$\frac{A6}{A6}\ \frac{A7^{\circ}}{A7^{\circ}}$	13	0	0
P19	A6	$\frac{A6}{A6}\ \frac{A7^{\circ}}{A7^{\circ}}$	16	0	0
P10[1]	A6, A7	$\frac{A6}{A6^{\circ}}\ \frac{A7}{A7^{\circ}}$	6	24	3
P21[2]	A6, A7	$\frac{A6}{A6}\ \frac{A7}{A7^{\circ}}$	6	9	0
T65	A6	$\frac{A6}{A6}\ \frac{A7^{\circ}}{A7^{\circ}}$	20	0	0
T5	A6	$\frac{A6}{A6}\ \frac{A7^{\circ}}{A7^{\circ}}$	20	0	0
H6	A6, A7	$\frac{A6}{A6}\ \frac{A7}{A7}$	0	20	0
TTL1	A6, A7	$\frac{A6}{A6}\ \frac{A7}{A7}$	0	20	0
T65 X P10[3]			11	10	
T5 X P10[3]			6	2	

(1) Deviation from a 9:3:3:1 (bands A6, A7: band A6: band A7: no band) ratio is not significant.
(2) Deviation from a 3:1 (bands A6, A7: band A6) ratio is not significant.
(3) Deviation from a 1:1 (bands A6, A7: band A6) ratio is not significant.

P18, P19, T65 and T5 are probably homozygous at A6 locus (A6A6), and homozygous for the null allele at A7 locus ($A7^{\circ}A7^{\circ}$). P10 is most likely a double heterozygote for null alleles at both A6 and A7 loci ($A6A6^{\circ}A7A7^{\circ}$), since selfed progeny segregated 9:3:3:1.

Further evidence seems to support this hypothesis. The progeny of T65 X P10 segregated as 11 band-A6 and 10 band-A6 band-A7. This observation is in agreement with the expected 1:1 ratio (Table 6). Further evidence obtained from the F_2 of T65 X P10 crosses also supports this hypothesis. The F_1 T10-4 displayed band-A6 without band-A7, and its progeny all showed band-A6 only (Table 7). The F_1 plants T10-14 and T10-20 showed both bands A6 and A7. Their progeny approximated a 9:3:3:1 ratio for band-A6 band-A7: band-A6: band-A7: no band (Table 7). Thus, plants T10-14 and T10-20 were likely dihybrids for loci A6 and A7. The progeny of T10-19, which showed both bands A6 and A7, segregated in 8 band-A6 band-A7: 3 band-A6. Although the number of progeny is rather small, the ratio does not deviate from the 3:1 ratio. Therefore, T10-19 was probably heterozygous for the null allele at locus A7 (Table 7). The presence, or absence of band-A6 or band-A7, or both bands did not associate with the presence or absence of any other particular bands.

f. We observed segregation of bands A8 and A9 in some of the families but the genetic analysis is incomplete because of insufficient data.

Table 7. *F_1 and F_2 of T65 X P10 showing segregation of esterase anodic bands A6 and A7 (A6 and A7 loci).*

F_1	Zymogram (band)	Probable genotype	F_2 zymogram (band) A6, A7	A6	A7	on band
T10-4	A6	$\frac{A6\ A7^{\circ}}{A6\ A7^{\circ}}$	0	57	0	0
T10-14(1)	A6, A7	$\frac{A6^{\circ}\ A7^{\circ}}{A6\ A7}$	19	6	4	1
T10-20(1)	A6, A7	$\frac{A6^{\circ}A7^{\circ}}{A6\ A7}$	17	2	3	1
T10-19(2)	A6, A7	$\frac{A6\ A7^{\circ}}{A6\ A7}$	8	3	0	0
T10-21(1)	A6, A7	$\frac{A6^{\circ}A7^{\circ}}{A6\ A7}$	16	4	2	0

(1) Deviation from a 9:3:3:1 (bands A6, A7: band A6:band A7:no band) ratio is not significant.
(2) Deviation from a 1:1 (bands A6, A7: band A6) ratio is not significant.

Linkage

Wild rice plants showing bands A2, A3, A4 and A5 produced 4-band, 3-band, and 2-band progeny (Table 8). The 2-band progeny all showed bands A4 and A5. The ratio of 4-band to 2-band approached a 3:1 ratio (Table 8). Based on the data, we hypothesize

Table 8. *Zymograms of Taiwan wild rice and their selfed progeny showing segregation for esterase anodic bands A2, A3, A4 and A5*

Parent	Zymogram	Progeny zymogram 4-band	3-band	2-band (A4 A5)
P2	4-band	11	2	2
P6	4-band	10	3	3
P8	4-band	24	4	5
P9	4-band	17	2	5
P11	4-band	13	1	2
P13	4-band	13	4	2
P14	4-band	14	1	1
P20	4-band	6	0	4
P23	4-band	12	1	7
P21	4-band	10	3	4
Total		130	21	35

that the plants are heterozygous for nullalleles at A2 and A3 loci, and that the two loci are linked.

Some progeny showing a 3-band zymogram were observed. These 3-band individuals were probably the products of crossing over between loci A2 and A3. If this hypothesis is correct, the frequency of crossover between A2 and A3 loci is 21/186 X 100 = 11.3%. A larger number of offspring from crosses involving those putative double heterozygotes with homozygotes null at loci A2 and A3 is necessary to make a better estimate of linkage strength.

Polymorphism and average heterozygosity

A total of 8 esterase loci were examined in the Taiwan wild rice population. Six out of 8 loci were found to be polymorphic (0.75). The average heterozygosity was calculated by the method of Nei (1975). At a given locus the homozygosity is estimated by $j_i = \Sigma X_i^2$ and the heterozygosity is $h_i = 1 - j_i$, where X_i is the frequency of the ith allele. Average heterozygosity (H) is the average of h_i over all loci examined. H is not related to the frequency of heterozygotes in populations, but it is a useful measure of gene diversity (Nei 1975). Two polymorphic loci among the 8 loci examined did not have sufficient data to allow estimating allele frequencies. These two loci (A6, A7) were excluded from calculation of average heterozygosity. The average heterozygosity based on the six esterase loci was estimated to be 0.222.

Discussion

A small sample from a small Taiwan wild rice population was studied. Unfortunately the population is nearly extinct (Kiang *et al.* 1979), and we were unable to examine a larger sample size to make a better estimate of the average polymorphic loci and heterozygosity. Based on the information gathered in this study the average polymorphism for esterase loci is high (0.75). The average heterozygosity is in the range of heterozygosity reported for most natural populations (Lewontin 1974). The average frequency of heterozygotes was 0.27 which supports the previous report that Taiwan wild rice populations had a high frequency of heterozygotes (Oka and Chang 1961). Although cultivated rice is self-pollinating, Taiwan wild rice had 30.7% outcrossing (Oka 1956). Hybridization between wild rice and cultivars has occurred (Oka and Chang 1961, Kiang *et al.* 1979), and by virtue of vegetative propagation, the wild rice can retain alien genes from cultivars even though those genes may decrease fertility. Through outcrossing, hybridization with cultivars, and vegetative propagation, the wild rice population can maintain a high proportion of polymorphic loci and heterozygosity.

The esterase cathodal bands in rice were not reported previously. The cathodal bands are controlled by a single locus (Cl) with two codominant alleles. Since the three genotypes of locus Cl can be readily identified by zymograms, it is a good marker for genetic studies. In anther culture of wild rice we demonstrated that the Cl locus could be successfully used as a marker for screening for pollen derived plants (Wu and Kiang 1979).

We observed a total of 9 anodic bands. Using the agar-gel thin layer method Nakagahra *et al.* (1975) reported 14 esterase anodic bands. Since they used agar-gel it is difficult to compare their observations with ours. Katayama and Chern (1973), using starch gel, reported 8 esterase anodic bands. Our observation on anodic bands is comparable to theirs, but they did not report genic analysis.

The wild rice showed more anodic bands than the 17 cultivars examined (Fig. 1). *Oryza perennis* is considered to be the progenitor of the cultivated rice *O. sativa* L. (Oka 1974). During breeding and selection each variety of cultivated rice is fixed for different alleles at different loci, and some of the loci are probably fixed for null alleles. This process would reduce the number of bands.

The number of individuals examined from some of the families was small. Individuals of various zymograms should be included in crosses, and more F_2 families should be examined. Backcrosses of F_1's to cultivars could give better information as to the genetic basis of the various isozyme bands. Unfortunately the study was discontinued and the genetic models in this report were based on the data gathered during summer 1977 through spring 1978. Until more information becomes available alternative genetic models of esterase isozymes in cultivated rice and its wild relatives cannot be completely ruled out. This study clearly suggests that Taiwan wild rice contains considerable variability which can be useful in rice improvement. The species is on the verge of extinction. To preserve genetic resources, Taiwan wild rice should be restored and protected in its natural habitat.

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台灣野生稻與栽培稻酯化同位酵素 (Esterase isozymes)之遺傳分析

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使用澱粉膠電泳法 (Starch gel electrophoresis) 對台灣野生稻(*Oryza Perennis* var. *formosana*) 和栽培稻(*O. Sativa* L.)做酯化同位酵素的遺傳分析，觀察 9 個陽極酵素帶和 3 個陰極酵素帶。此 3 個陰極酵素帶代表一異型結合子(Heterozygotes) 並受單一基因座(locus)控制。關於 9 個陽極酵素帶中，A_1 及 A_4 在野生稻和所檢驗的栽培稻中均未發現變異性。每一 A_2 ，A_3 ，A_5 ，及 A_7 等基因座均發現一不存 (null)相對因子 (allele)。A_8 和 A_9 基因座雖顯示變異性，但遺傳分析上的證據尚不完全。A_2 和 A_3 二基因座連鎖間的距離爲 11.3單位 (map unit) 此一小集團的台灣野生稻具有高度的多型態遺傳基因座 (genetic polymogrphic loci) (75%) ，以及平均 22.2%的異型結合子(heterozygosity) 。栽培稻比野生稻顯示較少數的酵素帶，此結果可能由於在馴化過程中，不同的不存相對因子被固定的原故。台灣野生稻正處於絕滅的邊緣，若不及時加以保護，該一自然資源將永遠地遺失。