



Changes in genetic diversity in the Japonica rice region of Taiwan

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Abstract. Crop genetic diversity is an important consideration for plant breeders, since genetic uniformity makes plants potentially and identically vulnerable to unexpected epidemics. The coefficients of parentage in combination with hectareage data were used as indices for the field uniformity in the Japonica rice (*Oryza sativa* L.) regions. Field uniformity increased considerably in the early 1980s, but has decreased in recent years. The highest score occurred in 1982, when a single variety accounted for 77% of the total hectareage. Field uniformity between time periods also increased during 1980s. These estimates indicate continuous culture of closely related genotypes and repeated use of similar germplasms for variety development. Recent efforts to introduce diverse sources of germplasm into variety development should continue to alleviate the increasing genetic vulnerability due to continuous monoculture.

Key words: Germplasm; *Oryza sativa*; Pedigree analysis.

Introduction

Genetic vulnerability has been one of the major concerns in crop improvement since the 1970s. Although genetic uniformity in crops does not necessarily lead to immediate epidemics, it makes plants identically vulnerable to disaster. Traditional hybridization breeding programs may unintentionally result in a narrow genetic base of self-pollinating cultivars (Delanay *et al.*, 1983; Dilday, 1990; Lin, 1992). A knowledge of genetic relationships among released germplasm allows plant breeders to monitor the genetic structure of the germplasm pool and optimize breeding strategies, thereby avoiding a reduction in genetic diversity.

Biochemical and morphological markers have been used to measure genetic diversity (Cox *et al.*, 1985; Souza and Sorrells, 1991), but the coefficient of parentage (r) (Kempthorne, 1969), based on pedigree analysis, provides an estimate of the overall genetic relationship between the genotypes of crops such as soybean (*Glycine max* (L.) Merr.) (Cox *et al.*, 1985), wheat (*Triticum aestivum* L.) (Cox *et al.*, 1986), peanut

(*Arachis hypogaea* L.) (Knauff and Gorbet, 1989), and oat (*Avena sativa* L.) (Souza and Sorrells, 1989). Cowen and Frey (1987) further indicated that crosses between oat parental lines with low r values had, on the average, a higher genetic variance of quantitative traits than those between parents with high r values. Therefore, r values are useful in selecting mates for crosses that would optimize genetic variation in subsequent inbred generations.

Recent variety development has not alleviated the problems of a narrow genetic base in the Japonica rice (*Oryza sativa* L.) region (Lin, 1991). The objectives of this study were 1) to compute r values between Japonica rice varieties released in Taiwan, and thus to provide a theoretical basis for rice breeders wishing to cross highly adapted yet genetically diverse cultivars, and 2) to evaluate the changes in field uniformity over time, based on r values in combination with variety-hectareage data.

Materials and Methods

A total of 99 Japonica rice varieties released in

Taiwan from 1940 to 1987 were included in the study (Table 1). These varieties were developed through artificial hybridization, except for three varieties which were released as selections from plant introductions. To simplify the analysis of genetic diversity over time, the varieties were grouped by time of release in 10-year intervals. There were 30, 30, 16, 12, and 11 varieties released in the periods of 1940-1949, 1950-1959, 1960-1969, 1970-1979, and 1980-1987, respectively. Pedigree information and release dates for the varieties were obtained primarily from the Council of Agriculture *et al.* (1987).

Coefficients of parentage for all pairwise combinations of varieties were calculated as defined by Kempthorne (1969). The r value between two varieties is the probability that a random allele at a given locus in one variety is identical by descent to a random allele at the same locus in the other variety. Assumptions for the calculations were the same as those used by Murphy *et al.* (1986). Hence, these estimates do not reveal true nuclear compositions, but merely statistical representations. While conducting pedigree analysis, all plant introductions and indigenous varieties of unknown ancestry were considered to be ancestors and were assumed to be unrelated to each other.

Two estimates (r_3 and r_4) of genetic diversity described by Cox *et al.* (1986) were used to evaluate the changes in field uniformity in the Japonica rice regions. The r_3 value is the sum over all r values between varieties, weighted by the product of two hectare proportions on which the varieties were grown in a year. Thus, it is an estimate of field uniformity in a given year. The r_4 value is the sum over all r values between varieties from different years, weighted by the product of two hectare proportions on which the varieties were grown in their respective years. It is an estimate of field uniformity over years. Previous data revealed that as few as three varieties represented more than 70% of the Japonica rice sown from 1971 to 1987, and that since 1980, over half of the hectare has been covered by a single variety (Lin, 1991). Also, due to the incomplete documentation of the planting areas covered by individual varieties, only the three most widely grown varieties in each year since 1971 were used to calculate these two estimates of field uniformity, and hence, both values are underestimated. The r_3 values were computed for each year between 1971 and 1989, and the r_4 values were computed for five-year intervals

between 1971 and 1986, plus 1989.

Results and Discussion

Genetic Diversity between Varieties

The number of ancestors involved in varietal parentages provides a crude estimate of the genetic base for individual varieties (Table 1). These numbers increased considerably since the issue of genetic vulnerability was raised in the 1970s. Of the 60 varieties released before 1960, only 17 had more than 4 ancestors in their parentages. Since 1970, all but 2 varieties have between 6 and 30 ancestors in their respective parentages. These scores are not unusual, since elite genotypes developed in the early period were used to derive new varieties.

The increasing number of ancestors in variety development did not, however, ensure an increase in the genetic diversity among varieties. The average r values between varieties of 1940s, 1950s, 1960s, 1970s, and 1980s were 0.22, 0.13, 0.19, 0.11, and 0.23, respectively. The greatest genetic diversity observed in the 1970s was due mainly to the unique genetic status of 'Kaohsiung Sel. 1' and 'Taichung 188'. 'Kaohsiung Sel. 1' was a selection from a Japanese introduction, 'Tokai 26', and was related to only three of its derivatives: 'Kaohsiung 141', 'Kaohsiung 142', and 'Tainan 9'. 'Taichung 188' was related only to 'Taichung 180', which was a selection from 'Yubo Asahi', also from Japan. The exclusion of 'Kaohsiung Sel. 1' and 'Taichung 188' increased the average r value for the 1970s from 0.11 to 0.18. 'Tainung Sel. 3', released in 1964, was another source of unique germplasm. It was selected from a Japanese introduction, 'Nohrin 65', and was not related to any other varieties. The exclusion of this selection increased the average r value for the 1960s from 0.19 to 0.22. Based on these estimates, the genetic diversity among the majority of the varieties did not increase over the five time periods. The average r value among all 99 varieties was 0.19, indicating little change in use of the germplasm pool for variety development. The extensive use of the superior genotypes from common sources, such as 'Taichung 65', explains why the genetic diversity among modern varieties did not increase as the genetic base of individual varieties increased. 'Taichung 65' and its derivatives were most frequently used as parents in hybridization for variety development. 'Taichung 65' was related to 83 varieties

Table 1. Japonica rice varieties included in the study and the time periods of their release

Time periods	Abbreviation	Variety	Ancestors ^a	Abbreviation	Variety	Ancestors ^a
1940–1949	CN1	Chianan 1	4	KS18	Kaohsiung 18	6
	CN2	Chianan 2	4	KF1	Kwangfu 1	6
	CN3	Chianan 3	4	KF401	Kwangfu 401	4
	CN4	Chianan 4	4	TC145	Taichung 145	3
	CN5	Chianan 5	4	TC150	Taichung 150	3
	CN6	Chianan 6	4	TNG37	Tainung 37	2
	CN7	Chianan 7	4	TNG38	Tainung 38	3
	CN8	Chianan 8	4	TNG40	Tainung 40	4
	CN9	Chianan 9	4	TNG45	Tainung 45	4
	CN10	Chianan 10	4	TP7	Taipei 7	4
	CN11	Chianan 11	4	TP8	Taipei 8	4
	CN12	Chianan 12	4	TP9	Taipei 9	4
	CN13	Chianan 13	4	TP10	Taipei 10	2
	HC4	Hsinchu 4	4	TP17	Taipei 177	2
KS12	Kaohsiung 12	3	TP301	Taipei 301	3	
1950–1959	CG242	Chianung 242	9	KS53	Kaohsiung 53	4
	HC24	Hsinchu 24	3	KS64	Kaohsiung 64	7
	HC50	Hsinchu 50	2	TC170	Taichung 170	4
	HC51	Hsinchu 51	2	TC172	Taichung 172	7
	HC52	Hsinchu 52	2	TC176	Taichung 176	3
	HC53	Hsinchu 53	3	TC178	Taichung 178	5
	HC54	Hsinchu 54	2	TC179	Taichung 179	8
	HC55	Hsinchu 55	5	TN1	Tainan 1	5
	HC56	Hsinchu 56	5	TN2	Tainan 2	4
	HC57	Hsinchu 57	4	TN3	Tainan 3	10
	HC60	Hsinchu 60	4	TP111	Taipei 111	3
	KS22	Kaohsiung 22	7	TP139	Taipei 139	3
	KS24	Kaohsiung 24	7	TP306	Taipei 306	4
	KS25	Kaohsiung 25	7	TT16	Taitung 16	6
KS27	Kaohsiung 27	8	TT24	Taitung 24	5	
1960–1969	HC62	Hsinchu 62	4	TN4	Tainan 4	5
	HL18	Hualien 18	10	TN5	Tainan 5	8
	KS136	Kaohsiung 136	7	TNG60	Tainung 60	4
	KS137	Kaohsiung 137	10	TNGS3	Tainung Sel 3	1
	TC180	Taichung 180	1	TP309	Taipei 309	6
	TC181	Taichung 181	3	TP311	Taipei 311	4
	TC184	Taichung 184	3	TT25	Taitung 25	6
	TC186	Taichung 186	3	TT26	Taitung 26	6
1970–1979	KS139	Kaohsiung 139	15	TNG61	Tainung 61	9
	KS140	Kaohsiung 140	9	TNG62	Tainung 62	6
	KSS1	Kaohsiung Sel 1	1	TNG67	Tainung 67	20
	TC187	Taichung 187	15	TT27	Taitung 27	6
	TC188	Taichung 188	2	TT28	Taitung 28	16
	TN6	Tainan 6	10	TT29	Taitung 29	13
1980–1987	HC64	Hsinchu 64	8	TN9	Tainan 9	15
	KS141	Kaohsiung 141	21	TNG68	Tainung 68	14
	KS142	Kaohsiung 142	30	TNG69	Tainung 69	12
	TC189	Taichung 189	20	TNG70	Tainung 70	25
	TC190	Taichung 190	21	TNG72	Tainung 72	18
	TN7	Tainan 7	17			

^aThe number of ancestors involved to derive individual varieties.

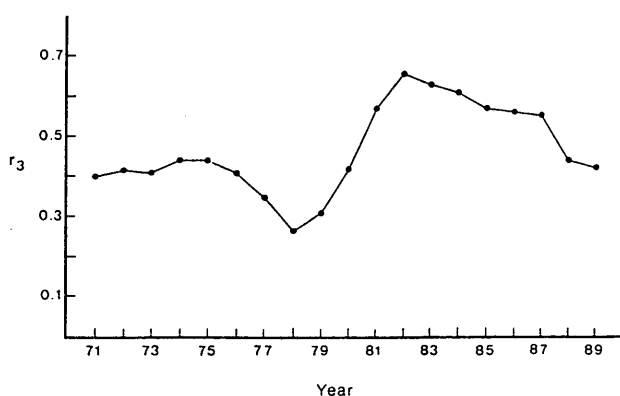


Fig. 1. Mean degree of relationship among leading varieties weighted by proportional hectareage between 1971 and 1989.

Table 3. Mean coefficient of parentage (r_4) among leading varieties from different years, weighted by the product of the proportional hectareages

	1976	1981	1986	1989
1971	.39	.25	.23	.19
1976		.23	.20	.17
1981			.55	.48
1986				.48

and appeared in 80 parentages of the 99 varieties released between 1940 and 1987. The r values between 'Taichung 65' and these 83 varieties varied from 0.12 with 'Tainung 72' to 0.98 with 'Taichung 186'. The varieties without 'Taichung 65' in their genetic background were either less-related or unrelated to most of the other varieties.

Field Uniformity

There have been more than 100 Japonica rice varieties developed in the last 50 years, but only a small number of superior varieties were grown and they covered a relatively large proportion of the primary production region. Table 2 shows the r values between 30 primary varieties that had been grown on more than 10,000 hectares in a year. The average r value between these varieties was 0.22. The three most prominent varieties ('Chianan 8', 'Tainan 5', and 'Tainung 67') since 1960 were related to Taichung 65 and were closely related to each other. The r values for all three pairwise comparisons varied from 0.33 between 'Tainan 5' and 'Tainung 67' to 0.57 between 'Chianan 8' and

'Tainan 5'. For those varieties of unique genetic status, three ('Kaohsiung Sel. 1', 'Taipei 306', and 'Taitung 27') were listed among the primary varieties. And only 'Kaohsiung Sel. 1' was ranked among the three leading varieties between 1974 and 1980 (Lin, 1991). Excluding these three, the average r value among the other 27 primary varieties increased from 0.22 to 0.27. These data reveal that Japonica rice growing regions were covered mainly by closely interrelated varieties. The genetic uniformity actually encountered in the field may be higher than these estimates show. Thus, it is important to periodically examine the relationships between released germplasm, and precaution should be taken to avoid a reduction in genetic diversity.

Although the genetic diversity among released germplasm changed little over the five time periods, field uniformity (r_3) increased considerably in the early 1980s but has decreased in recent years (Fig. 1). A dramatic increase in field uniformity occurred in 1982 when 'Tainung 67' alone accounted for 77% of the total hectareage. The most recent outbreak of leaf blast also occurred in 1982 (Huang, 1987). More than 30,000 hectares were infected by this disease. Since 1980, 'Tainung 67' (a variety susceptible to leaf blast) has predominated, accounting for more than 54% of the total hectareage. Greater field diversity was observed between 1976 and 1979 when 'Kaohsiung Sel. 1' was ranked among the three leading varieties.

The r_4 value measures field uniformity over years. It is expected that the estimates of uniformity between consecutive dates will be somewhat greater than those between nonconsecutive dates (Table 3), because of the overlap of the varieties and germplasm in use. The r_4 values varied from a low of 0.17 for 1976 vs. 1989, to a high of 0.55 for 1981 vs. 1986. Continuous culture of closely related genotypes and widespread popularity of a single variety resulted in considerably greater estimates between years of the 1980s. These estimates further reaffirm that similar germplasms were utilized repeatedly for variety development in recent time periods. The r_4 values for the year 1976 were consistently smaller than for other years, attributable to 'Kaohsiung Sel. 1' being a leading variety in this year.

Among the hundreds of varieties developed, a few (such as 'Tainung 67') remained predominant for years. Periodical examination of relatedness between germplasm is beneficial to breeders when choosing mates for crosses to optimize the genetic variance in subse-

quent inbred generations. Recent efforts to introduce diverse sources of pest resistance should continue to alleviate the increasing genetic vulnerability due to continuous monoculture.

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稈稻栽培區遺傳變異性之演變

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維持適當的遺傳變異性，可預防田間作物，大規模地被病原菌所感染。本研究係以稈稻品種之譜系為材料，利用親緣係數 (coefficient of parentage) 及品種之栽培面積，來估算台灣稈稻栽培區之遺傳變異性。田間之遺傳變異性，於 1980 年代初期，急劇下降，在 1982 年降至最低點，該年單一品種 (台農 67 號) 即佔稈稻栽培面積的 77%，即至近年來，遺傳變異性才逐漸增加。數據顯示，這二十年來，所栽培之主要稈稻品種，大部份血緣都非常接近。爾後育種，應考慮採用不同來源的種源，以避免遺傳變異性降低所可能帶來的問題。