Theor Appl Genet (1991) 83:115–118

THEORETICAL AND APPLIED GENETICS

Field uniformity of the Japonica rice region of Taiwan as estimated by relative genetic contribution *

Maw Sun Lin
Department of Botany, National Chung-Hsing University, Taichung 40227, Taiwan, Republic of China

Received February 8, 1991; Accepted May 16, 1991
Communicated by A. R. Hallauer

Summary. Despite the concerns for genetic vulnerability that were raised in the 1970s, the field uniformity of the Japonica rice (*Oryza sativa* L.) region in Taiwan has increased since 1980 with over 82% of the cultivated areas being covered by as few as three varieties and over half of this hectarage by a single variety. Japanese plant introductions are the major ancestral contributors of genetic constituents for varieties released in Taiwan. The main constitution of the genetic base present in the field has changed little since 1971. Six common ancestors comprised 60%, 55%, 78%, and 77% of the genetic constituents present in the field in 1971, 1976, 1981, and 1986, respectively. These estimates revealed that at least 55% of the genes utilized in the last 15 years came from the same sources. Recent efforts in introducing new germ plasm sources to variety development should continue to alleviate the possible crop loss due to continuous monoculture.

Key words: *Oryza sativa* L. – Genetic diversity – Germ plasm

Introduction

Extensive genetic uniformity in the field could lead to devastating yield losses as those experienced with the southern corn (*Zea mays* L.) leaf blight epiphytotic in the USA. St. Martin (1982) reported that genetic improvement in soybean (*Glycine max* (L.) Merr.) productivity and stability was accomplished by a reduction in genetic variation. Knowledge of the genetic diversity among released germ plasm is important to plant breeders for their understanding of germ plasm usage and the genetic structure of the germ plasm pools. In this way the development of cultivars with a narrow genetic base can be avoided.

Coefficient of parentage (Kempthorne 1969) has been used as an indicator of genetic diversity between genotypes for autogamous crops such as soybean (Cox et al. 1985), wheat (*Triticum aestivum* L.) (Murphy et al. 1986), oat (*Avena sativa* L.) (Souza and Sorrells 1989), and peanut (*Arachis hypogaea* L.) (Knauft and Gorbet 1989). Dilday (1990) computed relative genetic contributions as estimates of the genetic base for rice (*Oryza sativa* L.) cultivars released in the USA and concluded that these cultivars were derived on a narrow base. However, superior varieties are often grown on larger hectarages in the primary production regions. Thus, it is questionable whether estimates of genetic variability among released germ plasm are applicable to those encountered in the field. Cox et al. (1986) used the coefficient of parentage, weighted by the percentage of the acreage on which the cultivars were grown in a year, to measure field uniformity. They found that genetic diversity in the red winter wheat regions of the USA was increasing.

Pedigree analysis in combination with variety-hectarage data were used in the research reported in the present article to study the changes in the genetic constituents of Japonica rice varieties grown in Taiwan, and thus to provide indirect estimates of genetic uniformity in the rice-growing region.

Materials and methods

Pedigree analyses were conducted to identify the ancestors of the leading Japonica rice varieties that are widely grown in Taiwan. Due to the incomplete documentation of planting areas covered

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* Research supported by National Science Council
(NSC 78-0211-B005-14)

Table 1. Percentage of area covered by the top three leading Japonica rice varieties between 1971 and 1987

Year	Percentage[a] of area in three leading varieties			
	Rank 1	Rank 2	Rank 3	Total
1971	56.3 (Tainan 5)	7.7 (Hsinchu 56)	7.1 (Chianan 8)	71.1
1972	58.5 (Tainan 5)	7.0 (Hsinchu 56)	6.2 (Chianan 8)	71.7
1973	58.4 (Tainan 5)	7.6 (Hsinchu 56)	5.4 (Chianan 8)	71.4
1974	64.2 (Tainan 5)	6.5 (Hsinchu 56)	5.9 (Kaohsiung Sel 1)	76.6
1975	64.7 (Tainan 5)	5.8 (Kaohsiung Sel 1)	5.4 (Hsinchu 56)	75.9
1976	58.4 (Tainan 5)	8.0 (Tainan 6)	5.9 (Kaohsiung Sel 1)	72.3
1977	48.7 (Tainan 5)	14.6 (Tainan 6)	7.4 (Kaohsiung Sel 1)	70.7
1978	43.6 (Tainan 5)	15.6 (Tainung 67)	7.5 (Kaohsiung Sel 1)	66.7
1979	34.3 (Tainung 67)	32.5 (Tainan 5)	9.7 (Kaohsiung Sel 1)	76.5
1980	53.7 (Tainung 67)	21.5 (Tainan 5)	6.9 (Kaohsiung Sel 1)	82.1
1981	68.8 (Tainung 67)	12.7 (Tainan 5)	6.1 (Kaohsiung 141)	87.6
1982	76.8 (Tainung 67)	7.5 (Tainan 5)	5.5 (Kaohsiung 141)	89.8
1983	75.8 (Tainung 67)	7.6 (Hsinchu 64)	5.0 (Kaohsiung 141)	88.4
1984	74.2 (Tainung 67)	8.9 (Hsinchu 64)	3.7 (Kaohsiung 141)	86.8
1985	68.9 (Tainung 67)	10.3 (Hsinchu 64)	4.5 (Tainung 70)	83.7
1986	61.8 (Tainung 67)	14.7 (Tainung 70)	8.9 (Hsinchu 64)	85.4
1987	53.6 (Tainung 67)	24.2 (Tainung 70)	9.7 (Hsinchu 64)	87.5

[a] Percentage was computed on the basis of the total area on which Japonica varieties were grown

by individual varieties, only the first three leading varieties in each year after 1970 were included in this investigation. Records covering 1971, 1976, 1981, and 1986 (5-year intervals) were utilized to study the changes in the genetic base of Japonica rice varieties. Sources of pedigree information and release dates for the varieties were primarily obtained from the Council of Agriculture (1987). Indigenous varieties of unknown ancestry were considered to be ancestors and were assumed to be unrelated to each other. All plant introductions were also considered to be ancestral parents, although they might be related to some degree at the primary origin where they were derived.

Relative genetic contributions of different ancestors to individual leading varieties were computed as described by Delannay et al. (1983), except that these estimates were weighted by the proportion of the hectarage upon which a leading variety was grown in a given year. Proportions of the hectarage were computed based on the total areas covered by Japonica varieties. The mean genetic contribution of a given ancestor was the sum over all of the weighted genetic contributions of this ancestor to all leading varieties grown in a certain cear. The weighted mean relative genetic contribution, therefore, partitions the whole genetic constituents present in the field into theoretical percentages attributable to each ancestor in a given year. The successive summation of the mean relative genetic contributions generated cumulative relative genetic contributions over time. A computer program written in PASCAL was used in calculating relative genetic contributions. For computation, it is assumed that a variety derived from a cross obtains half of its genes from each parent. Hence, these estimates are not real nuclear compositions but merely statistical representations.

Results and discussion

There have been hundreds of rice varieties and land races cultivated in Taiwan during the last 50 years. Of these, only a small number have been grown in the primary production areas. Japonica rice varieties are grown extensively and in recent years cover nearly 90% of all of the rice-planting area. Percentage of area covered by leading Japonica varieties, thus, provides a rough estimate of field uniformity (Table 1). As few as three varieties were grown on more than 70% of the Japonica rice-growing areas from 1971 to 1987, with the exception of 1978, with 66.7%. In addition, only nine varieties were ranked among the top three leading varieties in this period. From 1971 to 1978 'Tainan 5' was the most prominent variety; in 1979 it was replaced by 'Tainung 67', and Tainung 67 has remained the most popular variety to date. Percentages of areas covered by the first leading variety varied from 34.3% in 1979 to 76.8% in 1982. Despite the concerns for genetic vulnerability raised in the 1970s, field uniformity has increased since 1980 with over 82% of the areas cultivated being covered by the three leading varieties and over half of this hectarage by a single variety. The greatest uniformity was observed in 1982 when three varieties accounted for approximately 90% of the hectarage. Such continuous monoculture provides the potential for the outbreak of pests, particularly since 'Tainung 67' is susceptible to blast and brown planthopper (*Nilaparvata lugens* Stål), the vector for the grassy stunt virus.

On the basis of the pedigree information presented in Table 2, all but 'Kaohsiung Sel 1', which since 1971 ranks among the top three leading varieties, can be seen to be closely interrelated. For example, the coefficient of parentage between 'Tainan 5' and 'Tainung 67' equals 0.33. And, the average coefficient of parentage between the top three leading varieties (excluding 'Kaohsiung Sel

Table 2. Pedigrees of the top three leading Japonica rice varieties between 1971 and 1987

Variety	Pedigree[a]
Chianan 8	Taichung 65//Mitsui/Oloan-chu
	Teichung 65 is from Shinriki/Kameji
	Mitsui is from Shinriki/Aikoku 1
Hsinchu 56	Chinan 2//Taichung 64/Tainung 21
	Chinan 2 is from Taichung 65//Mitsui/Oloan-chu
	Taichung 64 is from Shinriki/Kameji
	Tainung 21 is from Shinriki/Hinode
Hsinchu 64	Taichung 65/NC 4//Tainan 5
Kaohsiung 141	KSEY21/KSY973//Kaohsiung 139
	KSEY21 is from Akinishiki/Taichung 186//Kaohsiung Sel 1
	Taichung 186 is from Taichung 65(6[b]) Kanto 55
	KSY973 is from Kaohsiung 53(2)//Kaohsiung 135/Taichung 65
	Kaohsiung 53 is from KF401/Taichung 65
	KF401 is from Taichung 150//I-kung-pao/Taichung 65
	Taichung 150 is from Taichung 65/NC 4
	Kaohsiung 135 is from Kaohsiung 24/Li-chi-hung
	Kaohsiung 139 is from CNG242//Tainan 5/Kuni Katsu
	CNG242 is from Tainung 45/Taipei 7//CNGY65
	Tainung 45 is from Taichung 65/Tainung 16
	Tainung 16 is from Iyosengoku/Iwata Asahi
	Taipei 7 is from Meijiho/Yokichi//Osaka Asahi/Kyonishiki
	CNGY65 is from Taichung 150/Hsinchu 4
	Hsinchu 4 is from Taichung 65/Tainung 16
Kaohsiung Sel 1	A selection from Tokai 26
Tainan 5	Chinan 8//Taichung 114/Kaohsiung 10
	Taichung 114 is from Taichung 65/NC 4
	Kaohsiung 10 is from Kaohsiung 6/Kairio Aikoku
	Kaohsiung 6 is from Kinai Chiushio 76/Takenari
Tainan 6	Li-chi-hung/Kaohsiung 24//Tainan 5
	Kaohsiung 24 is from Taichung 158/Kaohsiung 18
	Taichung 158 is from Mejinishiki/Taichung 114
	Kaohsiung 18 is from Taichung 114/Kaohsiung 10
Tainung 67	Tainung 61(2)/TCT138
	Tainung 61 is from Chianan 8/NG 61-1
	TNG 61-1 is from Taichung 153//Takenari/Erteng-ishihsing
	Taichung 153 is from Taichung 114//Taichung 65/TC116-1
	TC116-1 is from Shinriki//Wu-chien/Miyako
	TCT138 is from TN1-1/CNG242//Taichung 178/TCC15
	TN1-1 is from Taichung 65/Taichung Native 1
	Taichung Native 1 is from Dee-geo-woo-gen/Tsai-yuan-chon
	Taichung 178 is from Taichung 65/TCG35//Yoshino 1
	TCG35 is from Shinriki//Chento-oloan-chu/Miyako
	TCC15 is from TN1-1/TCC15X-1
	TCC15X-1 is from Taichung 65/CNG242//TCC15X-2
	TCC15X-2 is from Taichung 65(2)/Cutsugulucle
Tainung 70	Tainung 67//Tainung 62/CNGY243
	Tainung 62 is from Hsinchu 56(2)/CI 5309
	CNGY243 is from Tainan 5(2)/Mudgo

[a] A slash (/) denotes the first cross and two slashes (//), the second cross

[b] The number of cross to the recurrent parent

1') is 0.34. Such relatedness between varieties could result in great genetic uniformity over a number of years. Tables 3–6 present the ten most important ancestral contributions, weighted by the proportion of hectarage, of the leading varieties in 1971, 1976, 1981, and 1986, respectively. There were only nine ancestors present in the pedigrees of the three leading varieties in 1971. Nine or ten of the most important ancestors of the three leading varieties collectively contributed from 71% to 78% of the genetic constituents in these 4 years of investigation. It must be stated here that these values are somewhat underestimated considering that these ancestors might also contribute their genes to varieties other than the three leading ones that were grown in each year. The main constitution of the genetic base present in the field has changed little since 1971. Among the important ancestors listed in Tables 3–6, six ('Aikoku', 'NC 4', 'Kameji', 'Oloan-chu', 'Shinriki', and 'Takenari') were consistently present. All of these six common ancestors were Japanese plant introductions, except for 'Oloan-chu', which is a waxy land race from Taiwan. Six ancestors comprised 60%, 55%, 78%, and 77% of the genes of the leading varieties grown in 1971, 1976, 1981, and 1986, respectively. These estimates revealed that a few ancestors account for an increasingly greater proportion of the genetic base observed in the field, which results in a higher degree of genetic uniformity over this 15-year period.

'Shinriki' and 'Kameji' were predominant in the mean genetic contributions. They accounted for more than 30% of the genetic constituents in each year. The large contribution of these two introduction was due to the success of 'Taichung 65', which was derived from the cross of 'Shinriki' × 'Kameji'. 'Taichung 65' and its derivatives were the most frequently used parents in hybridization programs for variety development. Although diverse sources of plant introductions have been integrated into recent breeding programs, they generally have contributed few genetic constituents to modern rice varieties. Most of them have been used as donors of genes for pest resistance and specific grain quality. Thus,

Table 3. Mean genetic contributions, weighted by hectarage, of ancestors for the top three leading Japonica rice varieties grown in 1971

Ancestor	Mean genetic contribution	Cumulative genetic contribution
Shinriki	0.202	0.202
Kameji	0.143	0.345
Oloan-chu	0.098	0.443
NC 4	0.070	0.513
Kairio Aikoku	0.070	0.583
Aikoku	0.049	0.632
Kinai Chiushio 76	0.035	0.667
Takenari	0.035	0.702
Hinode	0.010	0.712

Table 4. Mean genetic contributions, weighted by hectarage, for the ten most important ancestral contributors of the top three leading Japonica rice varieties grown in 1976

Ancestor	Mean genetic contribution	Cumulative genetic contribution
Shinriki	0.173	0.173
Kameji	0.128	0.301
NC 4	0.083	0.384
Oloan-chu	0.082	0.466
Kairio Aikoku	0.081	0.547
Aikoku	0.042	0.589
Kinai Chiushio 76	0.041	0.630
Takenari	0.041	0.671
Tokai 26	0.028	0.699
Li-chi-hung	0.020	0.719

Table 5. Mean genetic contributions, weighted by hectarage, for the ten most important ancestral contributors of the top three leading Japonica rice varieties grown in 1981

Ancestor	Mean genetic contribution	Cumulative genetic contribution
Shinriki	0.232	0.232
Kameji	0.170	0.402
Oloan-chu	0.082	0.484
Takenari	0.074	0.558
Erhteng-ishihsing	0.065	0.623
NC 4	0.059	0.682
Aikoku	0.043	0.725
Yoshino 1	0.022	0.747
Kairio Aikoku	0.017	0.764
Dee-geo-woo-gen	0.016	0.780

their genetic contributions were diluted after several cycles of backcross.

Whenever only a few superior varieties are grown over a large proportion of hectarage, a high level of field uniformity results. There is little that breeders can do to control field uniformity except to develop varieties with a broad genetic base. A broad genetic base within varieties provides some protection against the unexpected outbreak of pests. The recent trend towards introducing new germ plasm sources to variety development is promising, as the genetic base of individual Japonica rice varieties has widened since 1970 (M. S. Lin, unpublished data). Such efforts should continue to alleviate possible crop losses due to continuous monoculture.

Table 6. Mean genetic contributions, weighted by hectarage, for the ten most important ancestral contributors of the top three leading Japonica rice varieties grown in 1986

Ancestor	Mean genetic contribution	Cumulative genetic contribution
Shinriki	0.230	0.230
Kameji	0.165	0.395
Oloan-chu	0.078	0.473
NC 4	0.070	0.543
Takenari	0.070	0.613
Erhteng-ishihsing	0.065	0.678
Aikoku	0.039	0.717
Yoshino 1	0.021	0.738
Tsai-yuan-chon	0.016	0.754
Dee-geo-woo-gen	0.016	0.770

Acknowledgements. The author thanks Drs. Chen-Seng Huang, Cheng Chen, and Randall L. Nelson for their critical reading of this manuscript. The author is solely responsible, of course, for any error in it.

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