



Pedigree analysis of soybean varieties

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Abstract. The genetic diversity among twenty-six released soybean (*Glycine max* (L.) Merr.) varieties was examined by means of pedigree analysis. The coefficients of parentage (r) between genotypes were computed and used as indices of genetic diversity. The pedigrees of the twenty-six varieties were traced to eighteen ancestors from five geographic regions, with Japanese germplasm forming the major portion (64%) of the genetic constituents of these varieties. Wakashima (23%) and the land race Japan Ching-pi-dow (16%) were predominant in mean relative genetic contribution. The average r between varieties was 0.09. This relatively small value results from the use of diverse germplasm for variety development. Cluster analysis based on r produced six groups of varieties, but three varieties were not members of any cluster. The average r within clusters ranged from 0.33 to 0.50. Little relationship was found between clusters. Although cluster and pedigree analyses revealed that individual soybean varieties are not broadly based, reasonable genetic diversity occurs among these genotypes.

Keywords: Ancestor; Cluster analysis; Coefficient of parentage; Genetic diversity; *Glycine max*; Pedigree.

Introduction

Despite the concerns for genetic vulnerability that were raised in the 1970s, the loss of Japonica rice (*Oryza sativa* L.) field diversity has accelerated, due partly to the greater popularity of modern cultivars over old varieties and land races (Lin, 1991). Although genetic uniformity in crops does not necessarily lead to epidemic, it makes plants identically vulnerable to disaster. To sustain genetic variability and genetic gain, breeders must carefully select parents for hybridization to optimize genetic variation in subsequent inbred generations. Knowledge of the nuclear composition and cytoplasmic relationship between varieties is useful when selecting parents for crosses and when optimizing breeding strategies.

Biochemical and morphological markers have been used to measure genetic diversity (Cox et al., 1985; Souza and Sorrells, 1991). While these markers reflect limited samples of the genome, the coefficient of parentage (r) (Kempthorne, 1969) provides an estimate of overall genetic relationship among genotypes in 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) indicated that crosses between oat parental lines with a low r had higher genetic variance of quantitative traits, on the average, than did those

between parents with a high r . Relative genetic contributions, described by Delannay et al. (1983), quantify the genetic base of individual varieties and provide indirect information about the relatedness of varieties. Such examinations were reported for soybean (Delannay et al., 1983), rice (Lin, 1992), and peanut (Knauff and Gorbet, 1989).

There was virtually no available systematic information on genetic uniformity among the soybean varieties of Taiwan, and so our research objectives were to determine the ancestry of soybean varieties, to compute relative genetic contributions and quantify the genetic base of individual varieties, and to compute coefficients of parentage between genotypes to measure the overall relationships among soybean varieties.

Materials and Methods

Twenty-six soybean varieties were evaluated, of which all but four were developed through artificial hybridization. Kaohsiung 1 was selected from Chu-tzu-dow (a land race from Taiwan), Mao Kaohsiung Sel. 1 was selected from Ohkachi Shirakei Edamamei (a Japanese introduction), Tainung 1 (R) was derived from Sankoku through thermal-neutron mutagenesis, and Tainung 2 (R) was developed from Wakashima through X-ray irradiation. Sixteen varieties were developed from single crosses and contained only two ancestors in their respec-

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Table 1. Ancestral contribution (%) to soybean varieties.

Varieties ^b	Ancestors ^a																	
	Waka	JCPD	PI	Sank	JIK	CTD	PCPD	HPC	SHIM	OHKA	SYDD	YONE	SRF	HaDa	Fort	DLD	Acad	RYOK
CH1	-	-	-	-	-	-	50	50	-	-	-	-	-	-	-	-	-	-
CH2	-	-	-	-	-	-	50	50	-	-	-	-	-	-	-	-	-	-
CH3	-	-	-	-	-	-	-	-	-	50	50	-	-	-	-	-	-	-
HL1	50	-	-	-	-	-	-	-	-	25	25	-	-	-	-	-	-	-
HL2	50	-	-	-	-	-	-	-	-	-	-	-	-	-	50	-	-	-
KS1	-	-	-	-	-	75	-	-	-	-	-	-	-	-	-	-	-	-
KS2	-	-	-	-	-	50	-	-	-	-	-	-	-	-	-	-	50	-
KS3	-	-	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KS8	25	25	50	-	50	-	-	-	-	-	-	-	-	-	-	-	-	-
KSS10	-	-	-	-	50	-	-	-	-	-	-	-	50	-	-	-	-	-
MKSS1	-	-	-	-	-	-	-	-	75	-	-	-	-	-	-	-	-	-
MKS2	12.5	12.5	25	-	-	-	-	-	-	-	-	-	-	-	-	-	-	50
MKS3	12.5	12.5	25	-	-	-	-	-	-	-	-	-	-	50	-	-	-	-
TNG1R	-	-	-	75	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TNG2R	75	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TNG3	-	-	50	25	-	-	-	25	-	-	-	-	-	-	-	-	-	-
TNG4	-	-	50	25	-	-	-	25	-	-	-	-	-	-	-	-	-	-
TNG15	-	-	-	50	-	-	-	50	-	-	-	-	-	-	-	-	-	-
TNS1	-	-	-	-	50	-	-	-	-	-	-	-	-	-	50	-	-	-
TUKS1	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TUKS2	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TUKS3	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TUKS4	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TUKS5	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TUKS6	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TUKS7	50	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

^aAbbreviations of ancestors: **Waka**, Wakashima; **JCPD**, Japan Ching-pi-dow; **PI**, PI200.492; **Sank**, Sankoku; **JIK**, Jikkoku; **CTD**, Chu-tzu-dow; **PCPD**, Pingtung Ching-pi-dow; **HPC**, Huang-pao-chu; **SHIM**, Shimota Sirazu; **OHKA**, Ohkachi Shirakei Edamamei; **SYDD**, Shin-yin-da-dow; **YONE**, Yoneidakei; **SRF**, SRF400; **HaDa**, Hanhung Daelip; **Fort**, Forrest; **DLD**, Dah-lien-dow; **Acad**, Acadian; **RYOK**, Ryokuko.

^bAbbreviations of varieties: **CH1-3**, Chunghsing 1-3; **HL1-2**, Hualien 1-2; **KS1-3**, Kaohsiung 1-3; **KS8**, Kaohsiung 8; **KSS10**, Kaohsiung Sel 10; **MKSS1**, Mao Kaohsiung Sel 1; **MKS2-3**, Mao Kaohsiung 2-3; **TNS1**, Tainan Sel 1; **TNG1R**, Tainung 1R; **TNG2R**, Tainung 2R; **TNG3-4**, Tainung 3-4; **TNG15**, Tainung 15; **TUKS1-7**, NTU-Kaohsiung 1-7.

Table 2. Relative genetic contributions (RGC) and the number of occurrences for ancestors of the soybean varieties.

Ancestor	Origin	Mean RGC	Cum. RGC	Num. occur.
Wakashima	Japan	0.23	0.23	13
Japan Ching-pi-dow	Japan	0.16	0.39	10
PI200.492	USA	0.10	0.49	6
Sankuo	Japan	0.07	0.56	4
Jikkoku	Japan	0.06	0.62	3
Chu-tzu-dow	Taiwan	0.05	0.67	2
Pingtung Ching-pi-dow	Taiwan	0.04	0.71	2
Huang-pao-chu	China	0.04	0.75	2
Shimota Sirazu	Japan	0.04	0.79	3
Ohkachi Shirakei Edamamei	Japan	0.03	0.82	1
Shin-yin-da-dow	Taiwan	0.03	0.85	2
Yoneidakei	Japan	0.03	0.88	2
SRF400	Taiwan	0.02	0.90	1
Hanlung Daelip	Korea	0.02	0.92	1
Forrest	USA	0.02	0.94	1
Dah-lien-dow	China	0.02	0.96	1
Acadian	USA	0.02	0.98	1
Ryokuko	Japan	0.02	1.00	1

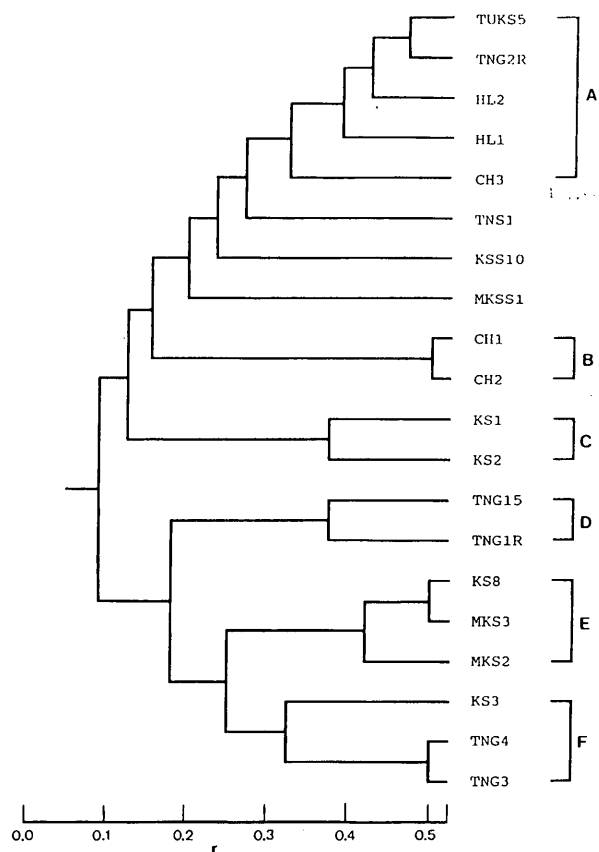


Fig. 1. Clustering dendrograph of the coefficients of parentage between soybean varieties. Abbreviations: **CH1-3**, Chunghsing 1-3; **HL1-2**, Hualien 1-2; **KS1-3**, Kaohsiung 1-3; **KS8**, Kaohsiung 8; **KSS10**, Kaohsiung Sel 10; **MKSS1**, Mao Kaohsiung Sel 1; **MKS2-3**, Mao Kaohsiung 2-3; **TNS1**, Tainan Sel 1; **TNG1R**, Tainung 1R; **TNG2R**, Tainung 2R; **TNG3-4**, Tainung 3-4; **TNG15**, Tainung 15; **TUKS1-7**, NTU-Kaohsiung 1-7.

itive parentages. The other six varieties had either three or four ancestors in their respective parentages. Pedigree analysis was used to identify the ancestry of these varieties. Indigenous varieties of unknown ancestry were considered ancestors, and were assumed to be unrelated to each other. Plant introductions were also considered ancestors even though they may have been related to some degree at their primary origin.

The *r* for all pairwise combinations of varieties were calculated as defined by Kempthorne (1969). The *r* between two varieties is the probability that a randomly selected allele at a given locus in one variety is identical by descent to a randomly selected allele at the same locus in the other variety. The relative genetic contributions (Delannay et al., 1983) of different ancestors to a given variety were computed using path coefficients. Both calculations were performed using a computer program developed by Lin and Wu (1994). Relative genetic contribution partitions the theoretical proportion of genes coming from an ancestor. The mean genetic contribution of a given ancestor is the mean of the relative genetic contributions of this ancestor to all varieties. The successive summation of the mean relative genetic contributions generates cumulative relative genetic contribution. Detailed pedigree information of soybean varieties is required for these computations. The assumptions used in the algorithm are the same as those described by Cox et al. (1986): **1)** a cultivar derived from a cross obtains half of its genes from each parent; **2)** all lines used in crossing are homozygous and homogeneous, in other words the *r* between a cultivar and itself is 1.0; **3)** all ancestors are unrelated to each other; **4)** the *r* between a cultivar and a selection from that cultivar is 0.75. Thus, the estimates are not real nuclear compositions but merely statistical representations. The contradiction between assumptions 2 and 4 is necessary to account for those few varieties from which variants have been selected. A computer program (Lin and Lo, 1992) was used to identify the donors of cytoplasm to individual varieties and to determine the uniformity of cytoplasm distribution among released germplasm.

Cluster analysis was performed on the matrix of *r* between survey varieties and ancestral parents, employing the unweighted pair-group mean method of the Proc Cluster program (SAS, 1985). This hierarchic, non-overlapping clustering method computes the mean similarity between all varieties within a cluster. A dendrograph (McCammom, 1968) was drawn based on the cluster analysis. A dendrograph, similar to a dendrogram in its treelike structure, adds another dimension to the diagram by spacing varieties according to the relationships between varieties and clusters.

Results

The ancestry of the twenty-six soybean varieties is shown in Table 1. Overall, the parentages of soybean varieties were simpler than those of Japonica rice vari-

Table 3. Coefficients of parentage between 26 soybean varieties^a

	CH1	CH2	CH3	HL1	HL2	KS1	KS2	KS3	KS8	KSS10	MKSS1	MKS2	MKS3
CH1	1.000	0.500	-	-	-	-	-	-	-	-	-	-	-
CH2	0.500	1.000	-	-	-	-	-	-	-	-	-	-	-
CH3	-	-	1.000	0.250	-	-	-	-	-	-	-	-	-
HL1	-	-	0.250	1.000	0.250	-	-	-	0.125	-	-	0.063	0.063
HL2	-	-	-	0.250	1.000	-	-	-	0.125	-	-	0.063	0.063
KS1	-	-	-	-	-	1.000	0.375	-	-	-	-	-	-
KS2	-	-	-	-	-	0.375	1.000	-	-	-	-	-	-
KS3	-	-	-	-	-	-	-	1.000	0.250	0.250	-	0.125	0.125
KS8	-	-	-	0.125	0.125	-	-	0.250	1.000	-	-	0.500	0.500
KSS10	-	-	-	-	-	-	-	0.250	-	1.000	-	-	-
MKSS1	-	-	-	-	-	-	-	-	-	-	1.000	-	-
MKS2	-	-	-	0.063	0.063	-	-	0.125	0.500	-	-	1.000	0.250
MKS3	-	-	-	0.063	0.063	-	-	0.125	0.500	-	-	0.250	1.000
TNG1R	-	-	-	-	-	-	-	-	-	-	-	-	-
TNG2R	-	-	-	0.375	0.375	-	-	-	0.188	-	-	0.094	0.094
TNG3	-	-	-	-	-	-	-	0.250	0.250	-	-	0.125	0.125
TNG4	-	-	-	-	-	-	-	0.250	0.250	-	-	0.125	0.125
TNG15	-	-	-	-	-	-	-	-	-	-	-	-	-
TNS1	-	-	-	-	-	-	-	0.250	-	0.250	-	-	-
TUKS1	-	-	-	0.250	0.250	-	-	-	0.250	-	-	0.125	0.125
TUKS2	-	-	-	0.250	0.250	-	-	-	0.250	-	-	0.125	0.125
TUKS3	-	-	-	0.250	0.250	-	-	-	0.250	-	-	0.125	0.125
TUKS4	-	-	-	0.250	0.250	-	-	-	0.250	-	-	0.125	0.125
TUKS5	-	-	-	0.250	0.250	-	-	-	0.500	-	-	0.250	0.250
TUKS6	-	-	-	0.250	0.250	-	-	-	0.250	-	-	0.125	0.125
TUKS7	-	-	-	0.250	0.250	-	-	-	0.250	-	-	0.125	0.125

	TNG1R	TNG2R	TNG3	TNG4	TNG15	TNS1	TUKS1	TUKS2	TUKS3	TUKS4	TUKS5	TUKS6	TUKS7
CH1	-	-	-	-	-	-	-	-	-	-	-	-	-
CH2	-	-	-	-	-	-	-	-	-	-	-	-	-
CH3	-	-	-	-	-	-	-	-	-	-	-	-	-
HL1	-	0.375	-	-	-	-	0.250	0.250	0.250	0.250	0.250	0.250	0.250
HL2	-	0.375	-	-	-	-	0.250	0.250	0.250	0.250	0.250	0.250	0.250
KS1	-	-	-	-	-	-	-	-	-	-	-	-	-
KS2	-	-	-	-	-	-	-	-	-	-	-	-	-
KS3	-	-	0.250	0.250	-	0.250	-	-	-	-	-	-	-
KS8	-	0.188	0.250	0.250	-	-	0.250	0.250	0.250	0.250	0.500	0.250	0.250
KSS10	-	-	-	-	-	0.250	-	-	-	-	-	-	-
MKSS1	-	-	-	-	-	-	-	-	-	-	-	-	-
MKS2	-	0.094	0.125	0.125	-	-	0.125	0.125	0.125	0.125	0.250	0.125	0.125
MKS3	-	0.094	0.125	0.125	-	-	0.125	0.125	0.125	0.125	0.250	0.125	0.125
TNG1R	1.000	-	0.188	0.188	0.375	-	-	-	-	-	-	-	-
TNG2R	-	1.000	-	-	-	-	0.375	0.375	0.375	0.375	0.375	0.375	0.375
TNG3	0.188	-	1.000	0.500	0.250	-	-	-	-	-	-	-	-
TNG4	0.188	-	0.500	1.000	0.250	-	-	-	-	-	-	-	-
TNG15	0.375	-	0.250	0.250	1.000	-	-	-	-	-	-	-	-
TNS1	-	-	-	-	-	1.000	-	-	-	-	-	-	-
TUKS1	-	0.375	-	-	-	-	1.000	0.500	0.500	0.500	0.500	0.500	0.500
TUKS2	-	0.375	-	-	-	-	0.500	1.000	0.500	0.500	0.500	0.500	0.500
TUKS3	-	0.375	-	-	-	-	0.500	0.500	1.000	0.500	0.500	0.500	0.500
TUKS4	-	0.375	-	-	-	-	0.500	0.500	0.500	1.000	0.500	0.500	0.500
TUKS5	-	0.375	-	-	-	-	0.500	0.500	0.500	0.500	1.000	0.500	0.500
TUKS6	-	0.375	-	-	-	-	0.500	0.500	0.500	0.500	0.500	1.000	0.500
TUKS7	-	0.375	-	-	-	-	0.500	0.500	0.500	0.500	0.500	0.500	1.000

^aAbbreviations of varieties: CH1-3, Chunghsing 1-3; HL1-2, Hualien 1-2; KS1-3, Kaohsiung 1-3; KS8, Kaohsiung 8; KSS10, Kaohsiung Sel 10; MKSS1, Mao Kaohsiung Sel 1; MKS2-3, Mao Kaohsiung 2-3; TNS1, Tainan Sel 1; TNG1R, Tainung 1R; TNG2R, Tainung 2R; TNG3-4, Tainung 3-4; TNG15, Tainung 15; TUKS1-7, NTU-Kaohsiung 1-7.

Table 4. Mean coefficients of parentage within and between clusters A to F (refer to Fig. 1) of soybean varieties.

	A	B	C	D	E	F
A	0.325					
B	—	0.500				
C	—	—	0.375			
D	—	—	—	0.375		
E	0.264	—	—	—	0.417	
F	—	—	—	0.225	0.250	0.333

Table 5. Cytoplasmic parents and their relative genetic contributions (RGC) to soybean varieties.

Variety	Cytoplasmic parent	RGC
Chunghsing 1	Huang-pao-chu	0.50
Chunghsing 2	Huang-pao-chu	0.50
Chunghsing 3	Shin-yin-da-dow	0.38
Hualien 1	Shin-yin-da-dow	0.19
Hualien 2	Dah-lien-dow	0.50
Kaohsiung 1	Chu-tzu-dow	0.75
Kaohsiung 2	Chu-tzu-dow	0.50
Kaohsiung 3	PI200.492	0.50
Kaohsiung 8	PI200.492	0.50
Kaohsiung Sel 10	Jikkoku	0.50
Mao Kaohsiung Sel 1	Ohkachi Shirakei Edamamei	0.75
Mao Kaohsiung 2	Ryokuko	0.50
Mao Kaohsiung 3	Hanhung Daelip	0.50
Tainan Sel 1	Forrest	0.50
Tainung 1R	Sankoku	0.75
Tainung 2R	Wakashima	0.75
Tainung 3	Shimota Sirazu	0.25
Tainung 4	Shimota Sirazu	0.25
Tainung 15	Shimota Sirazu	0.50
NTU-Kaohsiung 1	Japan Ching-pi-dow	0.50
NTU-Kaohsiung 2	Japan Ching-pi-dow	0.50
NTU-Kaohsiung 3	Japan Ching-pi-dow	0.50
NTU-Kaohsiung 4	Japan Ching-pi-dow	0.50
NTU-Kaohsiung 5	Japan Ching-pi-dow	0.50
NTU-Kaohsiung 6	Japan Ching-pi-dow	0.50
NTU-Kaohsiung 7	Japan Ching-pi-dow	0.50

eties (Lin, 1991). The pedigrees of the twenty-six varieties could be traced to eighteen ancestors from five geographic regions (Table 2). Half of the ancestors came from Japan; their germplasm was a large fraction (64%) of the genetic constituents of released varieties. Wakashima (23%) and Japan Ching-pi-dow (16%) were the direct parents of seven varieties, NTU-Kaohsiung 1 through NTU-Kaohsiung 7, and also appeared frequently in varietal parentages. Wakashima was present in thirteen of the pedigrees, and Japan Ching-pi-dow occurred in ten. Those ancestors present only once in twenty-six pedigrees had smaller mean genetic contributions, yet they were used as direct parents for varietal development and were present in 50% of the final genotypes. For instance, half of the genes of Kaohsiung 2 come from Acadian. The mean relative genetic contribu-

tions presented here reflect the relative importance of individual ancestors in the gene pool for all varieties.

Although as much as 67% of the genetic base for our released soybean germplasm was attributed to as few as six ancestors, the interrelationships between varieties were not as closely related as those between Japonica rice varieties (Lin, 1991). The coefficients of parentage for all pairwise combinations of the varieties are presented in Table 3. The average r is 0.09. The largest r is 0.5 for varieties derived from the same crosses. This relatively small value results from the use of diverse germplasm in variety development conducted in various regional breeding stations.

The genetic diversity among varieties can be more clearly shown by cluster analysis. Arbitrarily selecting a minimum within-cluster mean r of 0.3, cluster analysis produced six groups of varieties, designated A to F (Fig. 1). Three varieties (Kaohsiung Sel. 10, Mao Kaohsiung Sel. 1, and Tainan Sel. 1) were not members of any cluster. Of these three, Mao Kaohsiung Sel. 1 was not related to any others. Since NTU-Kaohsiung 1 through NTU-Kaohsiung 7 were developed from the same cross, only one (NTU-Kaohsiung 5) is shown in the dendrogram. Cluster A is the largest, containing eleven varieties. The smallest groups contain only two varieties. The predominant ancestors were Wakashima and Japan Ching-pi-dow in cluster A, Pingtung Ching-pi-dow and Huang-pao-chu in cluster B, Chu-tzu-dow in cluster C, Sankuo in cluster D, and PI200.492 in clusters E and F. The three nonclustered varieties were excluded from the data set. Average r s within and between clusters are presented in Table 4. The r within clusters ranged from 0.325 for cluster A to 0.5 for cluster B. No relatedness between varieties from different clusters was found, except between A and E, D and F, and E and F. Such little relationship between the groups results in a high degree of overall genetic diversity among the twenty-six released varieties.

The ultimate cytoplasm donors were traced to four-teen ancestors from five different geographic areas (Table 5), indicating that diverse sources of cytoplasm were used in variety development. Considerable genetic diversity of cytoplasm and nuclear composition was found among these soybean varieties. Japan Ching-pi-dow is the most important donor of both nuclear and cytoplasmic genes.

Discussion

In Taiwan, soybean is a less important crop than is rice. Early soybean breeding programs focused on plant introductions and on acclimation of foreign germplasm to select suitable elite genotypes that suited the local environments. Relatively little effort has been put into genetics and hybridization breeding research, resulting in simpler soybean pedigrees. Variety development involves at most three crosses, and matings between close-

ly related elite genotypes are unlikely to occur. Thus, genetic diversity between released varieties is maintained to some extent.

The coefficient of parentage is a direct measurement of the relationship between varieties, whereas relative genetic contribution estimates the relationships between ancestors and their derivatives and provides indirect information about the relatedness of varieties. These estimates can be used with caution to predict genetic variability. Although it was assumed that the plant introductions were unrelated, many have virtually no documentation and could be related. While a low r does not ensure that a particular cross will produce desirable segregates, such crosses generally exhibit higher genetic variances, thus raising heritability and the frequency of transgressive segregates. Cluster analysis based on r divides varieties into different groups according to their overall genetic relationship. Breeders, who desire to increase genetic diversity among new varieties while maintaining the complex of desired agronomic and quality traits that are present in existing elite varieties, may benefit from these estimates.

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大豆品種之譜系分析

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以台灣所育成之 26 個大豆品種為材料，來進行譜系分析，並計算親緣係數 (coefficient of parentage)，以估算大豆品種間之遺傳變異性。這 26 個大豆品種，可追溯至 18 個原始祖先 (ancestor)，來自日本的種源提供了 64% 之遺傳組成份 (relative genetic contribution)，其中又以和歌島及日本青皮豆所佔比例最高，分別提供了 23% 及 16% 之遺傳組成份。這 26 個品種之平均親緣係數為 0.09，根據親緣係數所做之分群分析 (cluster analysis) 發現，26 個品種可分成六群，群內之平均親緣係數從 0.33 至 0.50，而群間之關係極低。根據譜系分析及分群分析顯示，台灣大豆品種之育成，雖然不是建立在廣汎的遺傳背景上，但品種間仍維持著相當之遺傳變異性。

關鍵詞：原始祖先；分群分析；親緣係數；遺傳變異性；大豆；譜系。