

苏铁属植物 RAPD 反应体系的优化 及部分种类亲缘关系的探索

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摘 要: 通过优化苏铁属植物的 RAPD 反应体系, 进而探讨苏铁属部分种类的亲缘关系。结果表明, Mg^{2+} 、dNTP、*Taq* 酶及随机引物浓度在 RAPD 反应中有重要影响, 而模板 DNA 浓度有一个很大的适应范围。适合苏铁属植物 RAPD 分析的反应体系: 20 μ L 反应体系中, 含有 10 mmol/L Tris-HCl(pH8.3)、50 mmol/L KCl、2.0 mmol/L $MgCl_2$ 、200 μ mol/L dNTP、0.3 μ mol/L 随机引物、模板 DNA 50ng、*Taq* 酶 1.0 U。聚类分析结果基本反应了苏铁属各个种间的亲缘关系, 证明了 RAPD 适用于苏铁属种间亲缘关系分析。RAPD 聚类分析结合形态学研究表明: 海南苏铁、台湾苏铁、广东苏铁、滇南苏铁和仙湖苏铁之间的亲缘关系较远, 支持各自成为独立的种。

关键词: 苏铁属; RAPD; 亲缘关系

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Improving of RAPD reaction system in *Cycas* and studies on the genetic relationships of some species

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Abstract: In this paper, the reaction system of RAPD in *Cycas* had been established and applied to discuss the relationships among *C. hainanensis*, *C. taiwaniana*, *C. guangdongensis*, *C. diannanensis* and *C. fairylakea*. The results showed that RAPD was affected by the concentrations of four components i. e. Mg^{2+} , dNTP, *Taq* DNA polymerase and primers. The optimal reaction system was as follows, 20 μ L reaction volume, including 10 mmol/L Tris-HCl(pH 8.3), 50 mmol/L KCl, 2.0 mmol/L $MgCl_2$, 200 μ mol/L dNTP, 0.3 μ mol/L primers, 50 ng template DNA, 1.0 U *Taq* DNA polymerase. The reflection of RAPD cluster to the genetic relationship of all the species showed that RAPD was suitable for analysis of interspecific genetic relationship in *Cycas*. Genetic relationship analysis by RAPD markers showed that five defined species had far genetic relationships each other, combining with the analysis of morphological traits, it's concluded that they were five independent genetic units at species level.

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Biography: HUANG Yu-Yuan(1959-), male, born in Qin Zhou of Guangxi, professor, Ph. D., mainly engage in studies of plant systematics, evolution and ecology.

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Key words: *Cycas*; RAPD; genetic relationships

Lots of studies of cycads which is known as "living fossil" for human being, have been carried out to discuss the evolutionary relationships among different cycads species, origin and immigration of existing cycads, and its mechanism adapted to various environments (Huang, 2001). However, the classification of some species is still obscure, and there is a dispute on whether the taxa of some species were credible or not (Huang, 2001), especially on the *Cycas hainanensis*, *C. taiwaniana*, *C. guangdongensis* or "Guangdong cycad" (local name), *C. diannanensis*, *C. fairylakea* and so on. It has become a barrier for the utilization and conservation of *Cycas*. Studies had showed that RAPD was suitable for the analysis of interspecific genetic relationship (Lanner *et al.*, 1996; Zhou, 1999; Wang *et al.*, 2003; Ding *et al.*, 2005; Xiao, 2006; Chen *et al.*, 2007; Wang & Ding, 2007; Wang *et al.*, 2008; Zhang & Huang, 2008). However, no study on *Cycas* by RAPD marker was reported in former researches. In this research, we try to establish an optimized reaction system of RAPD in *Cycas* and to clear

some problems of species at molecular level, thereby, provide reference for setting up the molecular biology basis in evolution investigation, and provide theories basis for further study on the taxonomy, propagation, utilization and conservation of cycads.

1 Materials and methods

1.1 Experimental materials

Six species of *Cycas* had been collected (Table 1), 7—15 samples for each. The leaves of *Cycas* were dried with silica gel right after being collected from the plant (Chase & Hills, 1991). The samples which DNA couldn't be extracted immediately were stored at -70 °C refrigerator.

In order to ascertain optimum reaction system, *Cycas balansae* O. Warburg was used as the experimental material to carry out the comparative study. Other five defined species were carried out for the molecular evolutionary relationships research.

Table 1 Colony and its origin of six species

No.	Species	Source site	Collection site	Time	Collector & voucher specimens No.	^A Lodged
1	<i>C. balansae</i> O. Warburg	Yunnan Province of China	Cycad Garden of Qingxiushan Garden, Nanning of China	May 24, 2004	Huang Y. Y, Nong B. X 356	GXAC
2	<i>C. hainanensis</i> C. J. Chen	Hainan Province of China	South China Botanical Garden, Guangzhou of China	May 31, 2004	Huang Y. Y, Nong B. X 363	GXAC
3	<i>C. taiwaniana</i> Carruthers	Hainan Province of China	Shenzhen Fairy Lake Botanical Garden, Shenzhen of China	Jun 1, 2004	Huang Y. Y, Nong B. X 364	GXAC
4	<i>C. guangdongensis</i>	Guangdong Province of China	Shenzhen Fairy Lake Botanical Garden, Shenzhen of China	Jun 1, 2004	Huang Y. Y, Nong B. X 368	GXAC
5	<i>C. diannanensis</i> Z. T. Guan et G. D. Tao (♀)	Yunnan Province of China	Shenzhen Fairy Lake Botanical Garden, Shenzhen of China	Jun 1, 2004	Huang Y. Y, Nong B. X 370	GXAC
6	<i>C. diannanensis</i> Z. T. Guan et G. D. Tao (♂)	Yunnan Province of China	Shenzhen Fairy Lake Botanical Garden, Shenzhen of China	Jun 1, 2004	Huang Y. Y, Nong B. X 365	GXAC
7	<i>C. Fairylakea</i> Wang DY	Guangdong Province of China	Shenzhen Fairy Lake Botanical Garden, Shenzhen of China	Jun 1, 2004	Huang Y. Y, Nong B. X 358	GXAC

GXAC, Herbarium of the Agricultural College of Guangxi University.

1.2 DNA extraction

Every individual of species was mixed in equal weight respectively, then the DNA of these samples were extracted by using CTAB method (Doyle JJ & Doyle JL, 1987).

1.3 PCR reaction

121 pieces of primers were purchased from Shang-

hai Sangon Biological Engineering Technology & Services Company Ltd., China. And dNTP, Taq DNase were bought from TaKaRa Biotechnology (Dalian) Company Ltd., Dalian of China.

A series of concentrations and volumes of each factor were designed as follows: DNA (10, 25, 50, 75, 100 ng DNA in every tube, respectively); Mg²⁺ (0.5, 1.0, 1.5,

2.0, 2.5, 3.0 mmol/L); dNTP (50, 100, 150, 200, 250, 300 μ mol/L); Taq DNase (0.2, 0.6, 0.8, 1.0, 1.4 U). The primer concentrations were 0.1, 0.2, 0.3, 0.4, 0.5, 1.0, 2.0 μ mol/L. The reaction was conducted in Biometra Tgradient PCR apparatus. The optimal PCR amplification procedure was as follows: Pre-denaturation at 94 $^{\circ}$ C for 5 min and 35 cycles of denaturation at 94 $^{\circ}$ C for 30 s, annealing at 37 $^{\circ}$ C for 40 s, lengthening at 72 $^{\circ}$ C for 110 s; then lengthening at 72 $^{\circ}$ C for 7 min again. The final product was kept at 4 $^{\circ}$ C. The production of PCR was isolated by electrophoresis on an agarose gel (1%) and dyed with ethidium bromide (EB), then were observed and photographed through the Imagine Master VDS.

1.4 Data analysis

Every reaction was repeated for three times. It was labeled with 1 or 0, respectively, according to whether it had RAPD band or not. The data were used to generate Jaccard similarity coefficient and to construct a dendrogram according to unweighted pair-group arithmetic average clustering (UPGMA) in NT-SYS programs.

2 Results and analysis

2.1 RAPD reaction system of *Cycas*

2.1.1 The effect of template DNA concentrations

The bands showed clearly when the template DNA ranged from 25 — 75 ng, but obscurely when DNA less than 10 ng or more than 75 ng (Fig. 1). It's indicated that the range of DNA concentrations was not severely affected in the RAPD. Given the suitable range of DNA concentrations, it could obtain stable amplified production. But to avoid the influence of excessive DNA, every tube (20 μ L reaction solution) contained 50 ng DNA was better.

2.1.2 The effect of Mg^{2+} concentrations Mg^{2+} plays an important role in the PCR reaction, Fig. 2 showed the results of treatments with different Mg^{2+} concentrations. When the Mg^{2+} concentration was 0.5 mmol/L, only one band was produced; when it was 3.0 mmol/L, the darken background was serious; when it was in the range from 1.0 — 2.5 mmol/L, similar bands could be seen, and when the concentration was 2.0 mmol/L, the

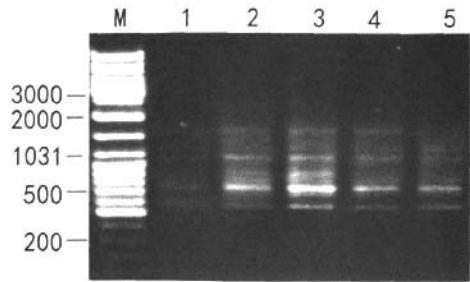


Fig. 1 Comparison of amplification effects of template DNA with different concentrations.

From left to right (Primer S404), 10, 25, 50, 75, 100 ng;
M: Gene Ruler DNA Ladder MIX

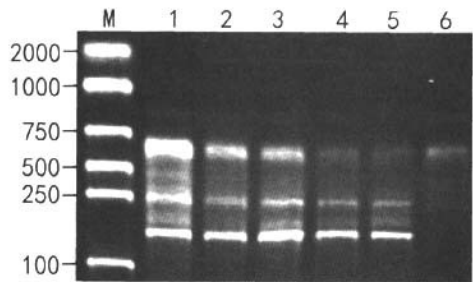


Fig. 2 Effects of Mg^{2+} concentrations on amplified results

From left to right (Primer S216), 3.0, 2.5, 2.0, 1.5,
1.0, 0.5 mmol/L; M: DNA Marker DL2000

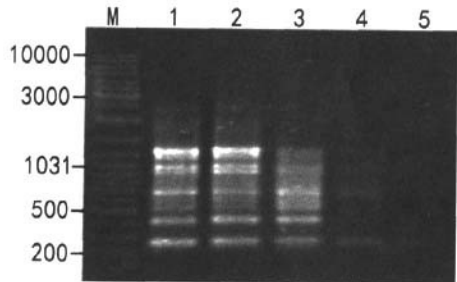


Fig. 3 Effects of dNTP concentrations on amplified results

From left to right (Primer S347), 50, 100, 150, 200,
250, 300 μ mol/L; M: Lambda DNA/HindIII.

bands were clearest. So we selected the 2.0 mmol/L of Mg^{2+} as the best concentration.

2.1.3 The effect of dNTP concentrations The amplified production were basically similar when the concentrations of dNTP ranged from 50 — 200 μ mol/L (Fig. 3), but it was clearer when the concentrations was 200 μ mol/L; when it was 250 μ mol/L, the bands couldn't be

seen clearly,when it was 300 $\mu\text{mol/L}$,there wasn't any band. So we selected 200 $\mu\text{mol/L}$ dNTP as the best content for RAPD reaction.

2. 1. 4 The effect of *Taq* DNA polymerase Fig. 4 indicated that when the *Taq* DNA polymerase ranged from 0. 8—1. 4 U/ μL ,the amplified bands were almost consistent,when it was less than 0. 6 U/ μL ,the bands were getting more and more obscure. Considering the stability and cost,we selected 1. 0 U/ μL *Taq* DNase for RAPD reaction.

2. 1. 5 The effect of primers concentrations The research results showed that when the primer concentrations ranged from 0. 2—0. 5 $\mu\text{mol/L}$,it could produce basical similar bands,when it was 0. 3 $\mu\text{mol/L}$ (Fig. 5), the bands were particularly clear,the primer concentrations was less than 0. 2 $\mu\text{mol/L}$ or more than 0. 5 $\mu\text{mol/L}$,the amplified bands increased and got obscure. So we selected 0. 3 $\mu\text{mol/L}$ primer for RAPD reaction.

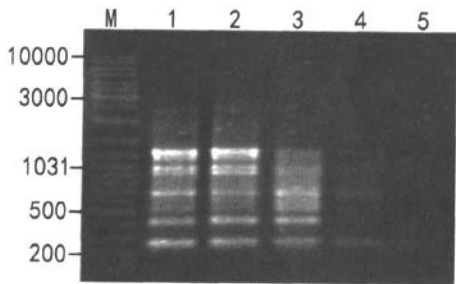


Fig. 4 Effects of *Taq* DNA polymerase concentrations on amplified results
From left to right(Primer S24),1. 4,1. 0,0. 8,0. 6, 0. 2 U/ μL , M, GeneRulerTMDNA Ladder MIX.

2. 2 Primers selection, DNA amplified and clustering analysis

2. 2. 1 Primers selection 3 significant different species in morphologic were amplified with 121 primers to screen polymorphic markers for clustering analysis. 21 pieces of primer produced stably, clearly and polymorphic bands were selected (Table 2) and applied to the further analysis of five species. Total 202 DNA bands had been amplified from 21 primers with an average of 9. 6 bands per primer, while there were 170 bands of the polymorphic DNA occupying 84. 16 % of total, showing there were great diversity in *Cycas* interspecies, the band ranged from 200 — 3 000 bp. Fig. 6

showed the amplified bands of primer S 380.

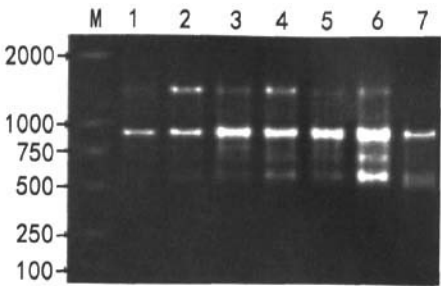


Fig. 5 Effects of primer concentrations on amplified results
From left to right(Primer S216),0. 1,0. 2,0. 3,0. 4, 0. 5,1. 0,2. 0 $\mu\text{mol/L}$, M, DNA Marker DL2000.

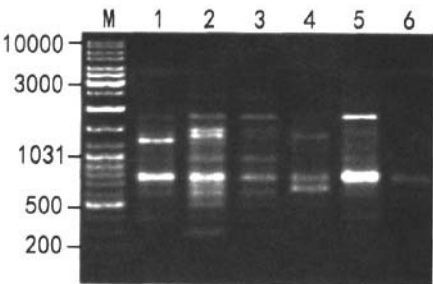


Fig. 6 Amplified bands of primer S380 for five species
1. *C. fairylakeae*; 2. *C. hainanensis*; 3. *C. taiwaniana*; 4. *C. guangdongensis*; 5. *C. diamanensis*(♀); 6. *C. diamanensis*(♂); M, GeneRulerTMDNA Ladder Mix.

Table 2 21 primers used in analysis

No.	Sequence (5'-3')	Amplified loci	Polymorphic loci	Percentage of polymorphic loci (%)
S8	GTCCACACGG	11	11	100.0
S22	TGCCGAGCTG	10	10	100.0
S29	GGGTAACGCC	12	9	75.0
S31	CAATCGCCGT	11	9	81.8
S32	TCGGCGATAG	14	13	92.9
S36	AGCCAGCGAA	8	7	87.5
S38	AGGTGACCGT	11	7	63.6
S40	GTTGCGATCC	9	7	77.8
S41	ACCGCGAAGG	6	4	66.7
S102	TCGGACGTGA	7	6	85.7
S107	CTGCATCGTG	5	3	60.0
S132	ACGGTACCAG	10	9	90.0
S151	GAGTCTCAGG	10	9	90.0
S156	GGTACTGTG	11	9	81.8
S198	CTGGCGAACT	7	7	100.0
S216	GGTGAACGCT	9	8	88.9
S380	GTGTCGCGAG	13	12	92.3
S404	GGCGTTGT	9	8	88.9
S410	TCTGGCGCAC	7	4	57.1
S464	GTGTCTCAGG	11	10	90.9
S1427	GTGGCCGATG	11	9	81.8

It was labeled 1 or 0, respectively, according to whether there was RAPD band or not. The data were analyzed by NTSYS software, we adopted Jaccard coefficient and drew the clustering map using UPGMA(Fig. 7).

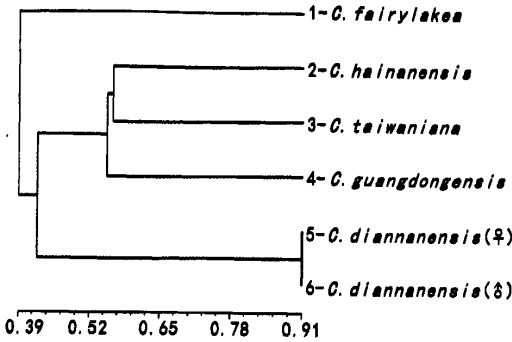


Fig. 7 Dendrogram generated by Jaccard coefficient of similarity

Table 3 Similarity coefficient and genetic distance among 6 taxa

Sequen- ce number	1 C. fairylakea	2 C. hainanensis	3 C. taiwaniana	4 C. guangdongensis	5 C. diannanensis (female)	6 C. diannanensis (male)
1	1.0000					
2	0.3878	1.0000				
3	0.4121	0.5597	1.0000			
4	0.3636	0.5476	0.5504	1.0000		
5	0.3987	0.4351	0.4395	0.4133	1.0000	
6	0.3671	0.4118	0.4167	0.4082	0.9098	1.0000

2.2.2 Clustering analysis The similarity coefficient between every two species ranged from 0.3636—0.5597 (Table 3), showed that they had a far genetic relationship each other. The biggest similarity coefficient was 0.5597, which located in *C. hainanensis* and *C. taiwaniana*, indicating that they had closest genetic relationship. The similarity coefficient of *C. fairylakea* and *C. guangdongensis* was the smallest among all species, it showed that there were farthest genetic relationship between them. The similarity coefficient of different sex colony in a same species; *C. diannanensis* was 0.9098, which was the biggest datum of the all materials, they clustered first of all, showing the closest genetic relationship in all materials. The results of RAPD cluster that reflected the genetic relationship of all the species showed that RAPD was very suitable for interspecies ge-

netic relationship analysis of cycad.

3 Discussions

3.1 Several factors affecting the RAPD reation and RAPD essentiality to plant taxonomy

Template DNA, Mg^{2+} , dNTP, *Taq* DNA polymerase and the primers were the main factors affecting the RAPD reaction, if one of them was changed, the stability of whole reaction system could be influenced greatly. So it is important to ascertain the reaction parameters for RAPD analysis.

To summarize above results and analysis, the optimal reaction system of RAPD was as follows, 20 μ L reaction volume including 10 mmol/L Tris-HCl (pH8.3), 50 mmol/L KCl, 2.0 mmol/L $MgCl_2$, 200 μ mol/L dNTP, 0.3 μ mol/L primers, 50 ng template DNA, 1 U *Taq* DNA polymerase.

Many results of comparative studies on RAPD with ISSR methods to many families of plants showed that the results were very high coherence. Such as correlation analysis among genetic similarities based on RAPD, ISSR markers and phenotypic data showed the correlation coefficient of RAPD and ISSR marks were 0.932, indicating they were significantly correlated. The number of fragments per primer, the percentage of polymorphic loci was in turn 9.09%, 83.73 % for RAPD markers, and 5.88%, 79.79 % for ISSR markers. It's showed that these indexes of RAPD were higher than ISSR. Although ISSR had higher percentage of polymorphic loci in *C. annum* than RAPD, and effective number of alleles(Ne), Shannon's Information index(I), heterozygosity(Ht), the genetic differentiation coefficient (Gst) based on ISSR markers were bigger than those based on RAPD as well. But these indexes had very small difference, the number commonly was the scope in 0.01—0.04, whereas some numbers were RAPD higher than ISSR(Chen *et al.*, 2007).

In another study, for RAPD analysis, 13 random primers were identified with polymorphism among the entries; in total, 167 bands were produced, of which 50 bands were polymorphic; percentage of polymorphic bands was 29.9%. For ISSR analysis, 7 primers were

identified with polymorphism among the entries; in total, 96 bands were produced, of which 44 bands were polymorphic; percentage of polymorphic bands was 45.8% (Xiao, 2006).

Study results from Zhang *et al.* (2007) showed that 225 and 196 bands were amplified by 12 RAPD primers and 12 ISSR primers respectively. There were 215 and 196 polymorphic bands amplified by RAPD and ISSR primers respectively, and the percentages of polymorphic bands were 95.56% and 100.00% respectively. The gene diversity among species (H_t) and within species (H_s) were 0.3689, 0.3575 and 0.1077, 0.1380, respectively.

Hereinbefore these results indicated that polymorphic bands amplified, percentages of polymorphic bands general were higher RAPD than ISSR, in the gene diversity among species (H_t) and within species (H_s) Ne, I, H_t and G_{st} , RAPD and ISSR were very appropinquity, and some species had higher ISSR than RAPD, some species had higher RAPD than ISSR, but their number difference was very small.

These studies fully proved that RAPD method was a very trusty and stabilization to analysis plant relationship between species, subspecies, variation and form, even variety (Wang *et al.*, 2003; Qi *et al.*, 2003, 2004; Ding *et al.*, 2005; Xiao, 2006; Chen *et al.*, 2007; Wang & Ding, 2007; Xiao *et al.*, 2007; Zhang *et al.*, 2007; Jia *et al.*, 2008; Pan *et al.*, 2008; Wang *et al.*, 2008; Zhang *et al.*, 2008). After some scholars had completed the comparative studies RAPD and ISSR, proved RAPD a very and exact method to research the relationships between species, subspecies, variation and form, they continue to use RAPD for the farther studies on some species in same genera, such as Zhang *et al.* had made the studies which comparative studies RAPD and ISSR on *Iris* L. Plants and published (2007), then they continued to carry out RAPD studies on other species of *Iris* L. plants (2008).

The improving of RAPD reaction system for *Cycas* in this study was significant to afford right and effective method on analysed the relationship between species, subspecies, variation and form in Cycadopsida.

3.2 Evolutionary relationships of five species

Researchers have been disputed on the taxon of *C.*

fairylakea, *C. hainanensis*, *C. taiwaniana*, *C. guangdongensis*, *C. diamanensis* for a long time. Both Huang (2001) and Wang *et al.* (1996) considered that *Cycas guangdongensis* (the brand hang in the sample tree located in Shenzhen Fairy Lake Botanical Garden) and *C. taiwaniana* were different names of a same species. Chen pointed that *C. hainanensis* distinguished from *C. taiwaniana* by megasporophyll with less lateral segments, and so on (Hill, 1994). Wang *et al.* (1996) made wide investigation in Hainan Province, finding that Megasporophyll terminal segments shape of type form of *C. taiwaniana* and *C. hainanensis* were broad deltoid, furthermore, it had a series of variation from deltoid to subulate-lanceolate, numbers of later segments also had a certain range of variation, so *C. hainanensis* was a modified form, and should be merged into the latter. Huang (2001) considered that characteristics of *C. hainanensis* had been mistakenly included in the morphologic illustrating of *C. taiwaniana* by Wang, Wang (1996) thought *C. taiwaniana* had many varieties, because he had illustrated characteristics of *C. taiwaniana* including all the megasporophyll shapes of *C. hainanensis*. Chen (1999) merged *C. diamanensis* and *C. fairylakea* into *C. taiwaniana*, then renamed *C. taiwaniana*'s while Chinese name as *C. guangdongensis*. Anatomical research showed that micro-shapes were apparently different between *C. taiwaniana* and *C. hainanensis*, they were two independence species (Huang, 2001).

In this research, different sexes of *C. diamanensis* were clustered in the first group, their similarity coefficient was 0.9098, and it was the biggest one of all the species, *C. taiwaniana*, *C. hainanensis* and *C. guangdongensis* were clustered together, the similarity coefficient between each other of them ranged from 0.5476—0.5597. It indicated that *C. hainanensis* was closer genetic relationship to *C. taiwaniana*, and *C. hainanensis* and *C. guangdongensis*, *C. taiwaniana* and *C. guangdongensis* also had closer genetic relationship. The similarity coefficient among *C. fairylakea*, *C. diamanensis* and *C. taiwaniana* ranged from 0.3671—0.4395, and it showed that they had a far genetic relationship each other.

According to the common view (Lane, 1993), those

species which their similarity coefficients each other was more than 0.90 could be merge to the same species, those which similarity coefficients ranged from 0.67—0.90 were different subspecies and variations, the similarity coefficients being less than 0.67 was at the species level. In present study, the similarity coefficients of 5 defined species of *Cycas* were all less than 0.67, therefore, the authors supported that they were established as five independent species.

Analyzing the results of molecular mark, the similarity coefficient was very high (more than 0.90) between male and female of *C. diamanensis*, other similarity coefficient of defined species each other was lower and very low (all were less than 0.687), it was approximately coincident with the classical taxon by other research methods. It indicated that RAPD was a propitious way to study *Cycas* taxonomy. Present research is useful for further research on the evolutionary relationships of every taxon of *Cycas* and afforded effectively using molecular marker method.

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