3-ii) Assessment of genetic diversity among the major Myanmar banana landaces.

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Introduction

- Bananas (*Musa spp.*), native to Southeast Asia and the western Pacific, are a major common food for millions of people in the tropical world. Cultivated clones are widely distributed throughout the subtropics and are spread by vegetative propagation for their characteristics of polyploidy and parthenocarpy.
- In this research, thirteen common landraces of banana from different regions of Myanmar (provided by VFRDC) were used to detect polymorphism and eleven international standard cultivars supplied by Singapore were used for comparison.

Materials

Accession number at GRCUT	Original name	Skin color	Origin
MS2-1	Thanda sein	Green	VFRDC, Myanmar
MS2-2	Thanda sein	Green	VFRDC, Myanmar
MS4-2	Low BNN-1	Yellow	VFRDC, Myanmar
MS5-1	Shwe Ni	Red	VFRDC, Myanmar
MS8-2	Wet Ma Lot	Yellow	VFRDC, Myanmar
MS9-1	Khin Wa	Yellow	VFRDC, Myanmar
MS10-1	Khin Wa-2	Yellow	VFRDC, Myanmar
MS10-2	Khin Wa-2	Yellow	VFRDC, Myanmar
MS11-1	Yatana	Yellow	VFRDC, Myanmar
MS11-2	Yatana	Yellow	VFRDC, Myanmar
MS13-2	Ind	Yellow	VFRDC, Myanmar
MS17-1	LKB-II	Yellow	VFRDC, Myanmar
MS19-2	Khun War II	Yellow	VFRDC, Myanmar
SFC02		Yellow	Singapore
SFC03		Yellow	Singapore
SFC06		Yellow	Singapore
SFC13		Yellow	Singapore
SFC15		Yellow	Singapore
SFC29		Yellow	Singapore
SFC33		Yellow	Singapore
SFC36		Yellow	Singapore
SFC37		Yellow	Singapore
CARDAVA		Yellow	Singapore
SABA#1		Yellow	Singapore

Methods

- **P450 based analogues (PBA) markers**
  - PBA marker technology was based on specific multi-gene family and composed of 15 pair-sets including three forward primers and five reverse primers. It is a useful tool for rapid, simple and precise evaluation of genetic diversity in most plant and animal organisms, which reflects both functional and genome-wide regions (Yamanaka et al., **Theor. Appl. Genet.** Vol.**108** p1–9, 2003).

Primer	Sequence (5` to 3`)
CYP1A1F	GCC AAG CTT TCT AAC AAT GC
CYP2B6F	GAC TCT TGC TAC TCC TGG TT
CYP2C19F	TCC TTG TGC TCT GTC TCT CA
CYP1A1R	AAG GAC ATG CTC TGA CCA TT
CYP2B6R	CGA ATA CAG AGC TGA TGA GT
CYP2C19R	CCA TCG ATT CTT GGT GTT CT
Heme2B6	ACC AAG ACA AAT CCG CTT CCC
Heme2C19	TCC CAC ACA AAT CCG TTT TCC

Methods

- **Data analysis**
  - The genetic distance among landraces and cultivars was calculated according to the Jaccard’s coefficient. Clustering analysis was based on UPGMA method. Dendrograms were then constructed.
  - Principal component analysis (PCA) was also adopted to show multiple dimensions of the distribution of the landraces or cultivars in a scatter-plot.

Results

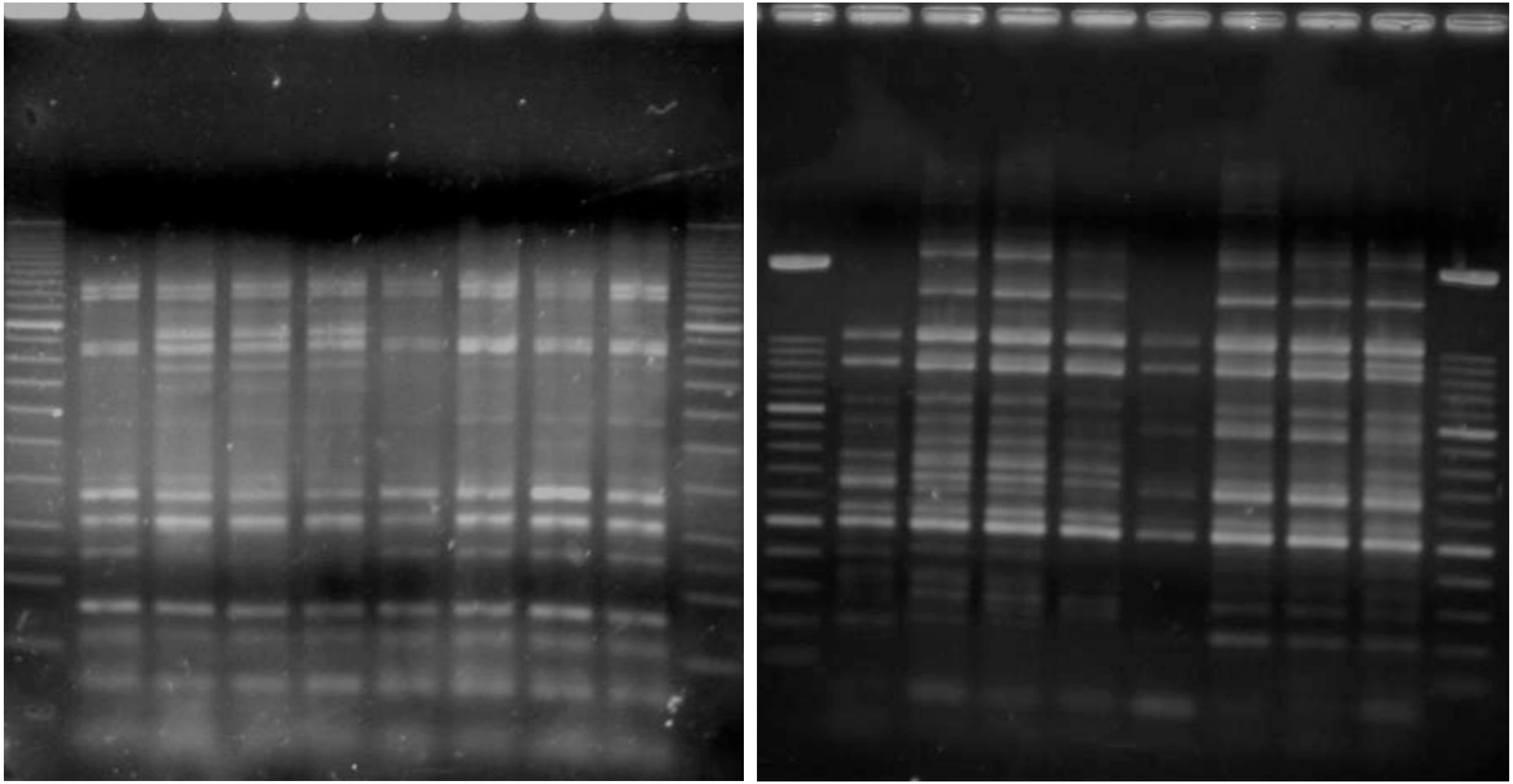
- For thirteen banana landraces from Myanmar, six pairs of primers got total 46 scorable bands include 30 polymorphic bands; and the frequency of polymorphism was 65.2%.
- For eleven banana cultivars from Singapore, 5 pairs of primers got total 39 scorable bands, 26 polymorphic bands; and the frequency of polymorphism was 66.7%.
- For all materials, 5 pairs of primers got total 42 scorable bands, 27 polymorphic bands; and the frequency of polymorphism was 64.3%.

Table Genetic diversity of banana genetic resources estimated by PBAs

Primer Sets	Genetic diversity[1]		
	Myanmar landraces (n=13)	International standard cultivars (n=11)	All (n=24)
CYP1A1F/CYP1A1R	0.363	0.485	0.435
CYP1A1F/CYP2C19R	0.325	0.307	0.366
CYP1A1F/heme2B6	0.281	0.217	0.298
CYP2B6F/CYP2B6R	0.292	0.422	0.389
CYP2B6F/heme2B6	0.343	0.248	0.326
Average	**0.321**	**0.336**	**0.363**

1: From Nei (1973)

Figure DNA polymorphism of PBA markers in banana



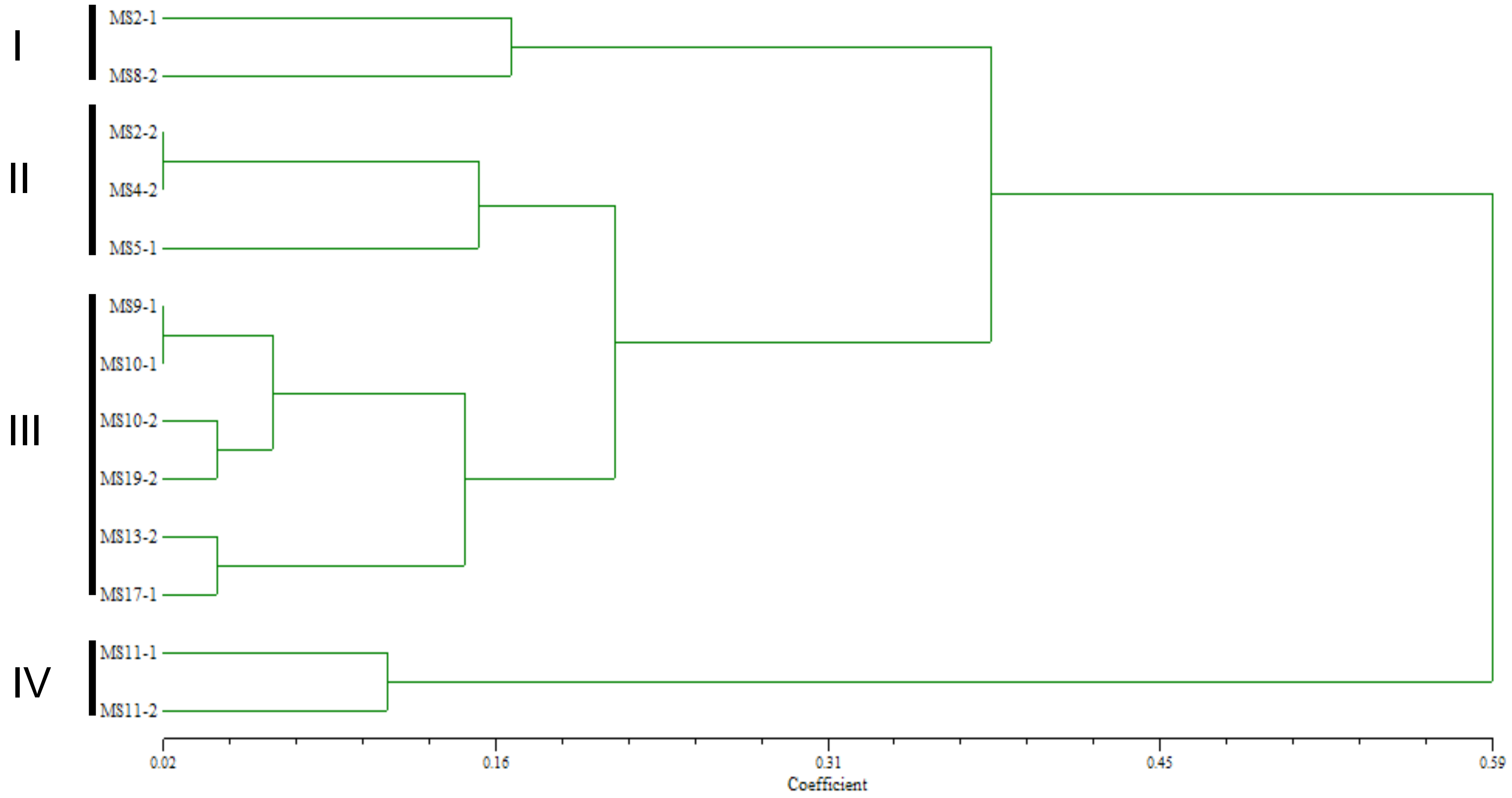
CYP1A1F/ CYP1A1R

CYP2B6F/ CYP2B6R

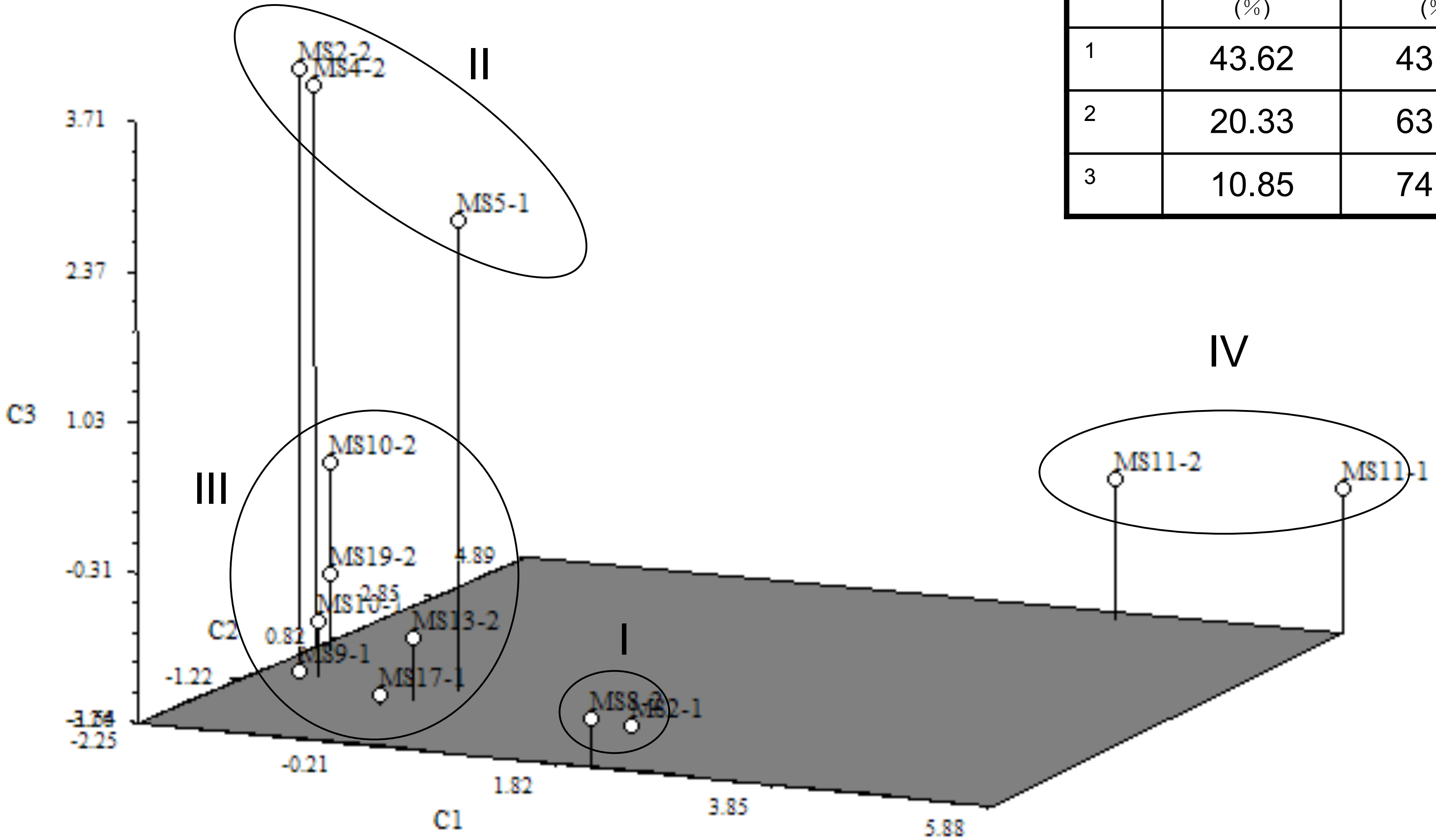
Results – Myanmar materials

- UPGMA clustering analysis showed that 13 landraces from VFRDC were divided to 4 groups.
- Principal components analysis scatter-plot showed that these landraces were also divided to 4 major groups, the results were well matched to that of UPGMA clustering. The cumulative contribution rates up to the third component were 74.8%.

Dendrogram of banana landraces from Myanmar



PCA scatter-plot of banana landraces from Myanmar

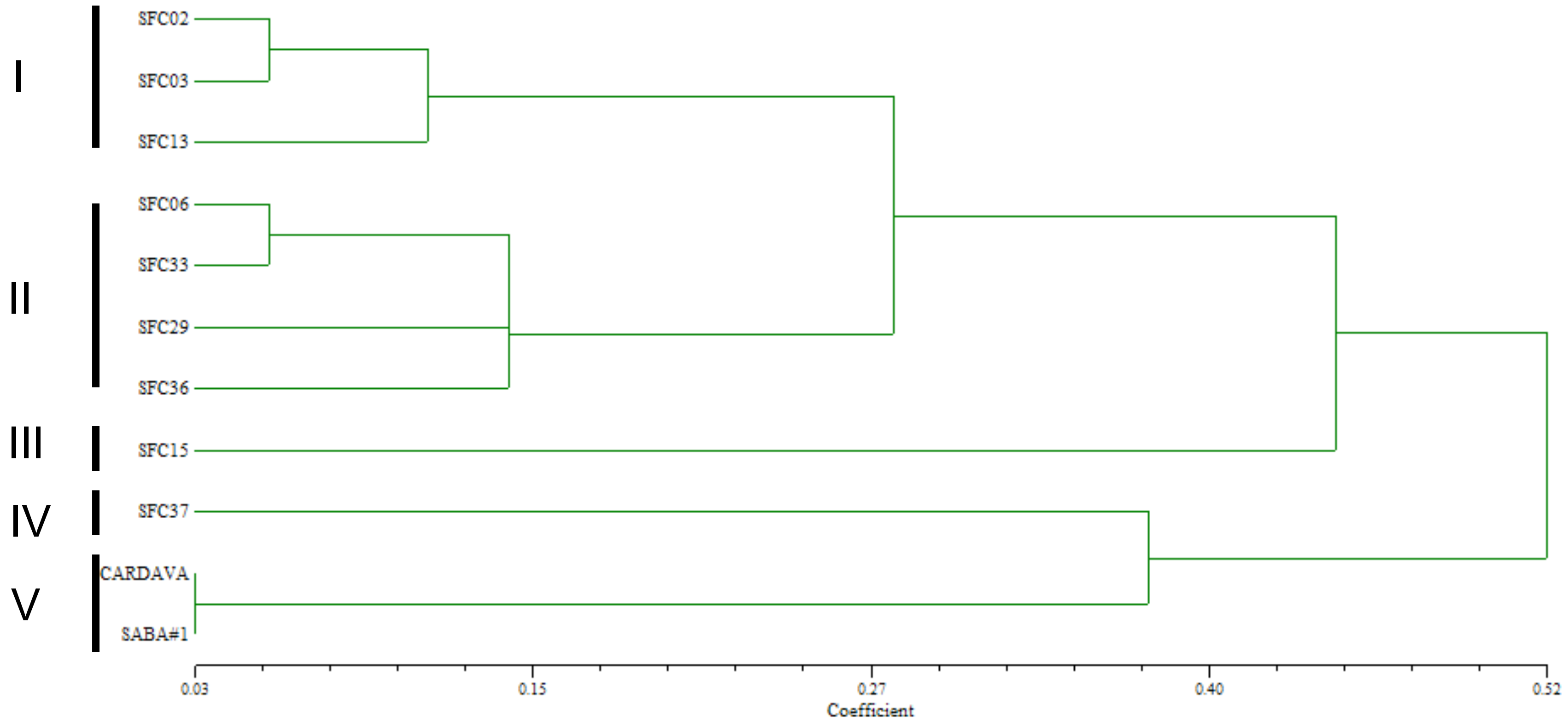


PC	Contribution (%)	Accumulation (%)
1	43.62	43.62
2	20.33	63.95
3	10.85	74.80

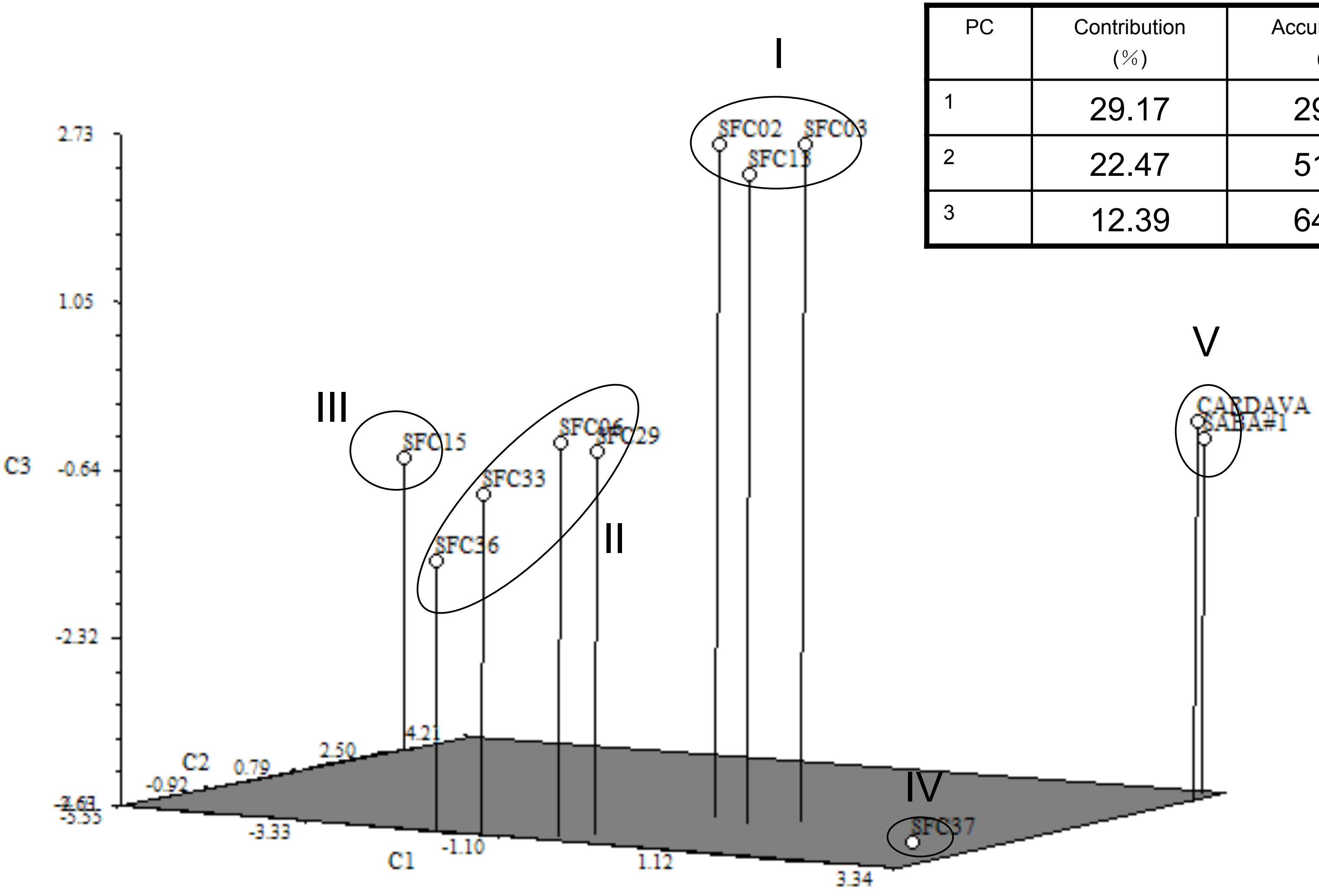
Results – International standard materials

- UPGMA clustering showed that 11 international standard cultivars supplied from Singapore were divided to 5 groups.
- Principal components analysis scatter-plot also showed the same results. The cumulative contribution rates up to the third component were 64.0%.

Dendrogram of banana cultivars from Singapore



PCA scatter-plot of international standard banana cultivars

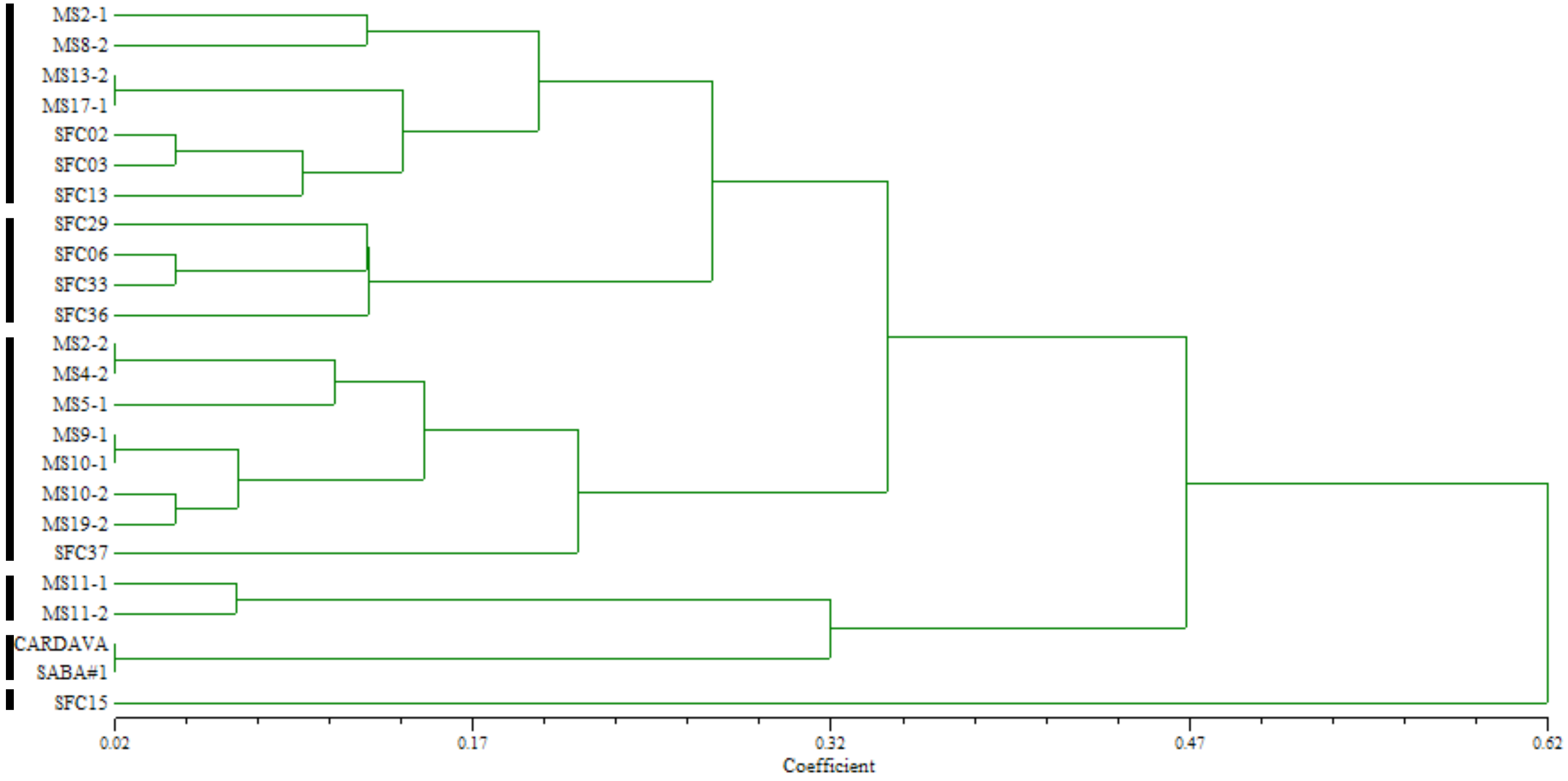


PC	Contribution (%)	Accumulation (%)
1	29.17	29.17
2	22.47	51.64
3	12.39	64.03

Results – Combined materials

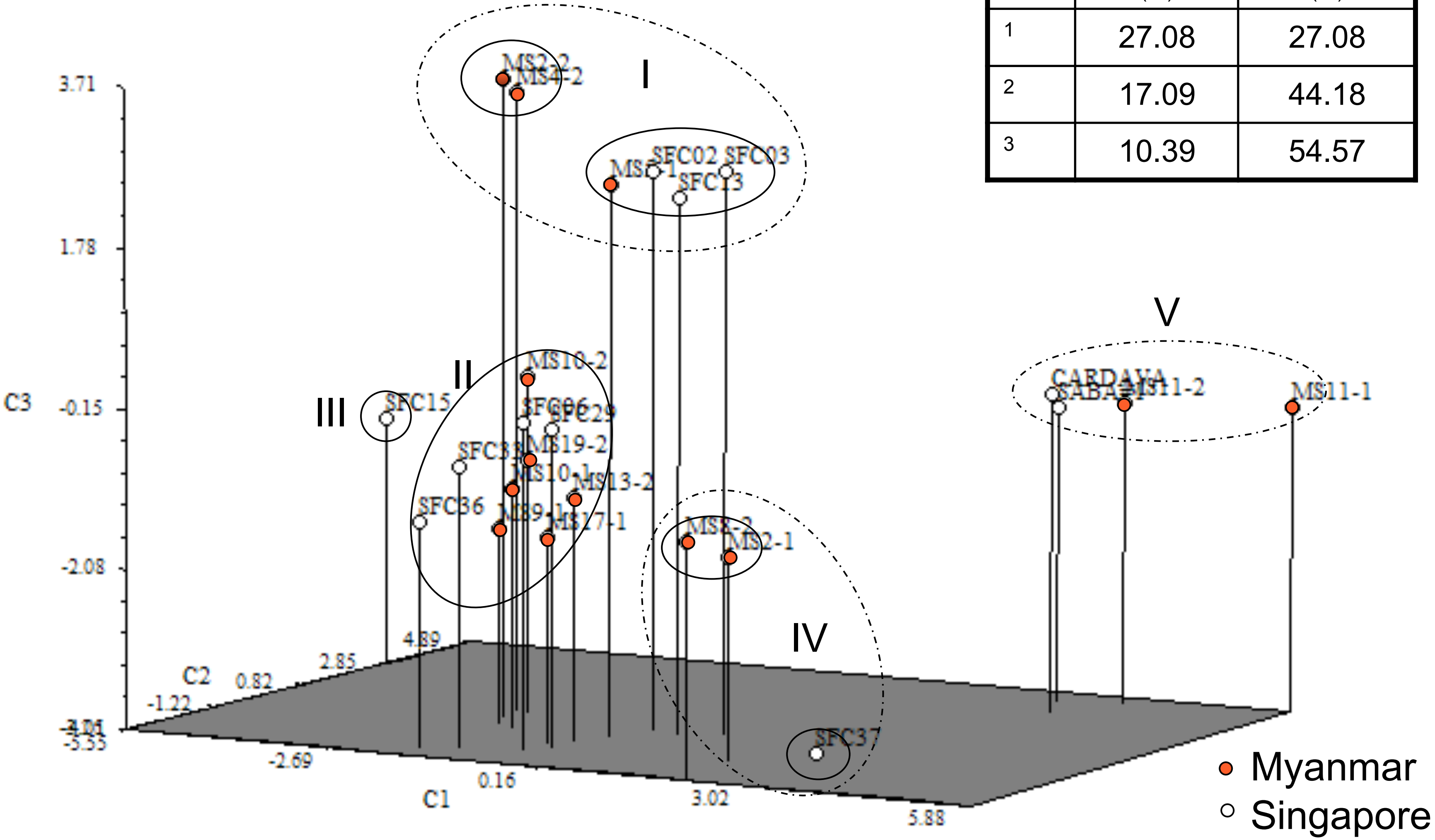
- UPGMA clustering divided all materials to 6 groups.
- PCA scatter-plot showed that international materials were divided to 5 groups, and Myanmar landraces distributed in the 4 groups of them. The cumulative contribution rates up to the third component were 54.6%.

Dendrogram of combined banana materials



PCA scatter-plot of combined banana materials

PC	Contribution (%)	Accumulation (%)
1	27.08	27.08
2	17.09	44.18
3	10.39	54.57



Discussion

- The genetic diversity of Myanmar materials was almost same with International standard materials. PCA also showed that four groups of Myanmar landraces were correspondent to the specific group of International materials.
- According to PCA, although almost half of Myanmar materials (6 landraces in 13) were grouped together, some landraces with more genetic variation were also found.
- Some landraces, such as MS2-1 and MS2-2, MS11-1 and MS11-2, although have the same original name, were not genetic identical according to DNA marker information.

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