Genetic variation of *Musa formosana* (Warb.) Hayata native in Taiwan using microsatellite markers

[1] Agricultural Research Institute, Taichung, 413, Taiwan
[2]Department of Agronomy,Taiwan University, Taipei, 106, Taiwan
[3]Department of Horticulture, Taiwan University, Taipei, 106, Taiwan
*chl@wufeng.tari.gov.tw

Abstract

Genetic variations of *Musa formosana* were assessed using molecular markers. Genetic variation analysis in collected 8 populations, included 100 individual clones, was detected with *M. acuminata*-specific intra-simple sequence repeat (intra-SSR) markers. Results from analysis of molecular variation (AMOVA) indicated that significant difference ($p<0.001$) were found among populations (23.10 % of total variation) and within populations (74.60 % of variation). However, no significant difference ($p=0.2048$) showed between regions (2.29 % of variance). Cluster analysis revealed two major groups diverged at 0.22 units of genetic distances (GD). One group was comprised of the populations that collected at the mountain areas of east-northern Taiwan; the other group was that at southern part of Taiwan and included two additional highly divergent populations collected at Shihzih Township, Pingtung County (GD=0.64) and at Shihjhuo, Chiayi County (GD=0.36).

Introduction

Musa formosana (Warb.) Hayata (Musaceae) (Fig. 1) is a wild banana native in Taiwan. They distribute from southern to northern mountain areas below 1,400m altitude in Taiwan. Facing the problem of habitat destruction and fragmentation, the effective and efficient conservation practices become a central concern. Molecular markers, such as microsatellites and ITS, have proved to be valuable help to this situation. The identification of genetic variation provides useful information for making conservation strategies on *M. formosana*.

Fig. 1. *Musa formosana* (Warb.) Hayata

Materials and Methods

- 8 populations, including 100 individual clones, of *Musa formosana* collected from Taiwan islands were joined.
- 16 informative *M. acuminata*-specific intra-simple sequence repeat (intra-SSR) markers were chosen.
- Genetic variation was analyzed by analysis of molecular variation (AMOVA) and NT-SYS software.

Results

- Significant difference were found among populations and within populations. No significant difference showed between regions (Table 1).
- Cluster analysis revealed two major groups diverged at 0.22 units of genetic distances (GD) and two additional highly divergent populations collected at Shihzih Township, Pingtung County and at Shihjhuo, Chiayi County (Fig. 2 and 3).

Source of variation	df	SS	MS	Variance component	% Total variation	*P* value*
8 populations						
Among populations	7	3.7581	0.537	0.0379	24.78	<0.001
Within populations	92	10.598	0.115	0.1152	75.22	<0.001
2 regions						
Among regions	1	1.0702	1.070	0.0035	2.29	0.2048
Among populations within regions	6	2.6879	0.448	0.0357	23.10	<0.001
Within populations	92	10.598	0.115	0.1152	74.60	<0.001

*After 1000 random permutations.

Table 1. Hierarchical analysis in molecular variance (AMOVA) of *Musa formosana* mediated SSR analysis

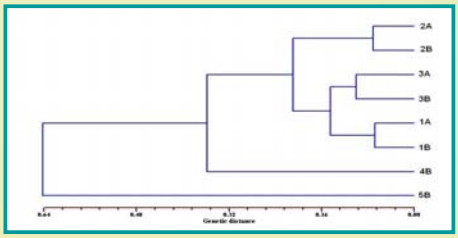

Fig. 3. Dendrogram based on 8 populations of *Musa formosana* using SSR data. The units of the scale are relative levels of branching of nodes based on populations distance (The code and distribution area of each population see Fig. 2).

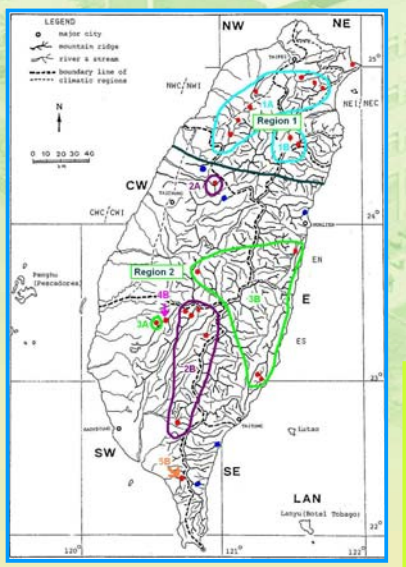

Fig. 2. Map with information of the distribution and diversity areas of *Musa formosana* populations.

Conclusion

- In term of *in situ* conservation of *Musa formosana*, we proposed the diversity areas in Hsinch-Chilian and Chiayi-Kaohsiung were the best choice.
- In term of *ex situ* conservation, we need to take more individuals from the diversity areas and these individuals from isolated populations in shihjhuo and shihzih-township if we plan to construct a repository to preserve their diversity for the future.

行政院農業委員會農業試驗所
Agricultural Research Institute, COA