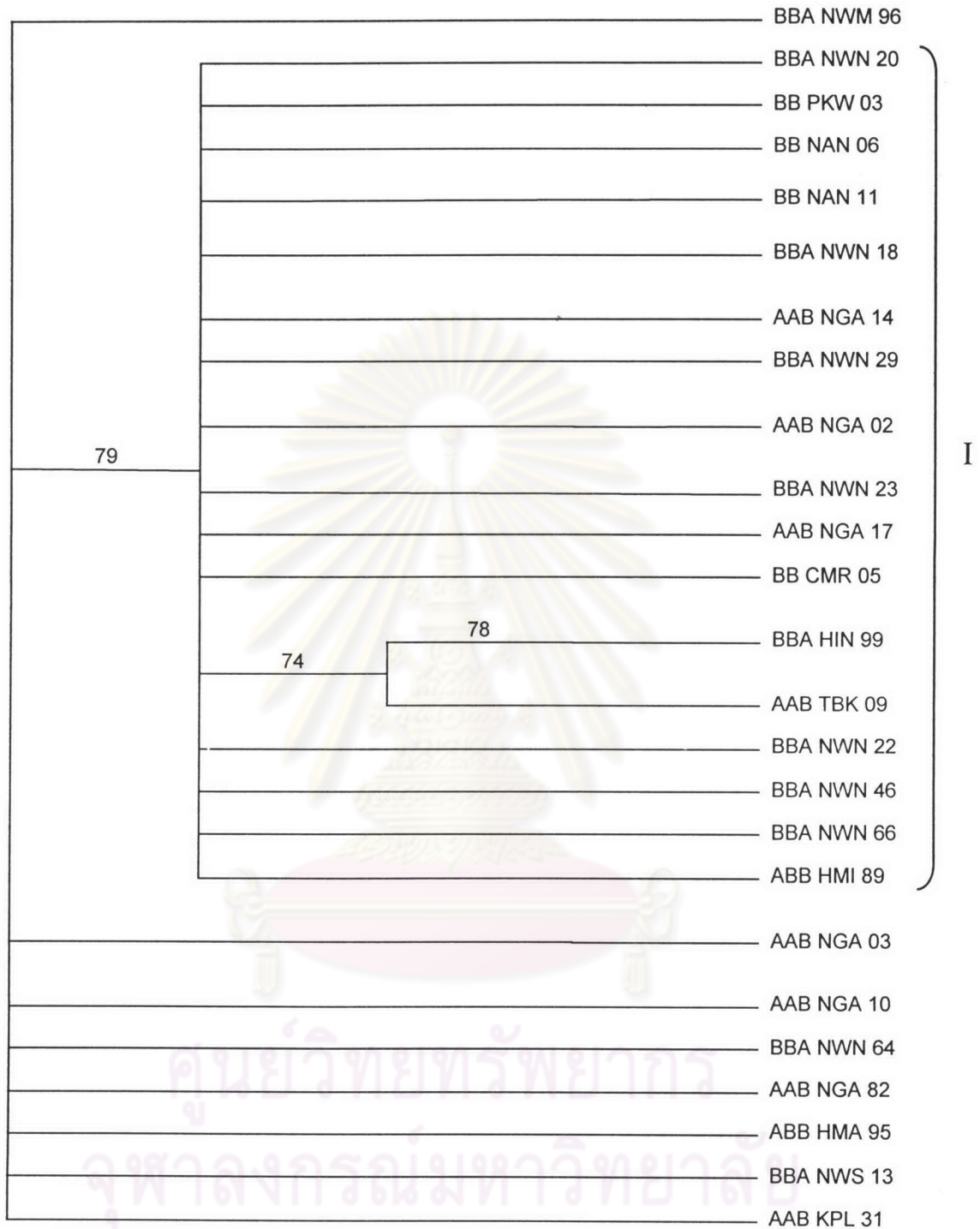


# CHAPTER 1

## INTRODUCTION

Banana, along with taro and yam, is one of the earliest cultivated plants in Southeast Asia and the Pacific Islands as supported by linguistic and archaeological evidence. Almost all known, non-seeded, edible cultivars of bananas are derived either from 'Kluai Pa' *Musa acuminata* Colla (AA) or 'Kluai Tani' *M. balbisiana* Colla (BB), or are hybrids of these two seeded wild species. *M. balbisiana* has the widest geographical distribution of all bananas, though, as many scientists believe, its variation is minimal. It has been postulated that, along with other agricultural commodities, Neolithic Austronesian-speaking voyagers were the carriers of this wild species, from mainland Southeast Asia, throughout the Pacific. Surprisingly, it is believed that *M. balbisiana* is not native to Thailand, though its cultigens generally called 'Kluai Tani', have long been grown for its leaves, used as wrappings and linings, and young inflorescences as food. It is unclear whether wild *M. balbisiana* is not distributed in the forest of Thailand or it is in the process of extinction. Though until today, there is no paleobotanical data to support the ancient presence of *M. balbisiana* in Thailand, the words for bananas, their leaves, and male buds have long been used in the Austro-Tai language family from which Thai evolved. It should be noted that somatic variations of 'Kluai Namwa', BBA hybrids, are found nowhere else except in this country. However, ancestors of these *M. balbisiana*-genome containing bananas are still unknown. It is our inquest therefore using modern molecular techniques, to reveal the evolution of *M. balbisiana* group of relatives.



**Fig. 4.3** A 50% majority-rule consensus tree of 34,775 most parsimonious trees from the analysis of *GBSS* non-coding regions of *Musa* with gaps coded as missing. Number above branch represents bootstrap values. Name of taxa appear according to Table 4.1, number behind name indicated clone number.

Though DNA sequences have been used widely to infer evolutionary history at lower taxonomic levels in several plants, they have not been applied in bananas. Our investigations are the first to report the new access to genetics of the *Musa* cultivars and hybrids through polymorphism of chloroplast and nuclear DNA sequences.

The result of the study provides the first information on the actual genome constitution of some banana hybrid cultivars in Thailand and Southeast Asia. It also suggests the molecular makers for the selection of proper parents in breeding and genetic engineering programs. The evolutionary history that is inferred from this investigation is profoundly useful for the collection and conservation management of traditional banana cultivars, which will be invaluable in future sustainable food production in tropical areas.



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