CHAPTER 2

AN OVERVIEW OF Musa balbisiana AND THE CLASSIFICATION OF EDIBLE BANANAS

Bananas are one of the earliest cultivated crops and is of considerable importance to the economies of many tropical countries. Almost all known edible cultivars of the bananas are derived either from Musa acuminata Colla (A genome) or Musa balbisiana Colla (B genome), or are hybrids of these two seeded wild species (Cheesman 1947; Simmonds and Shepherd 1955; Shepherd 1990). Both species are diploid with 2n = 22. Parthenocarpy and seed sterility in M. acuminata, under human selection in Southeast Asia, gave rise to edible diploid cultivars (AA) and, subsequently, triploids (AAA) (Simmonds and Shepherd 1955). Based on a scoring method for 15 diagnostic morphological characters and cytological determination of the chromosome number, Simmonds and Shepherd (1955) developed a genomic classification system of cultivated bananas. They suggested seven natural genomic groups: AA, BB, AB, AAA, AAB, ABB, and ABBB. They also assumed that parthenocarpy does not occur in M. balbisiana since no edible diploid BB has been found. However, a group of edible BBB bananas was later found in the Philippines (Valmayor 1979) and Thailand (Chomchalow and Silayoi 1984).

B genome is important in banana improvement for assorted quality characteristics as well as for providing hardiness and disease resistance. In general, the B genome gives starchiness and acidity to the fruit, characters commonly considered as cooking quality. Argent (1977) noted that *M. balbisiana* grows in areas of lower rainfall than other wild *Musa*

species, which is in agreement with Simmonds' observations. Simmonds (1987) noticed that *M. balbisiana* is more tolerant to drought and flooding and more resistant to Panama disease, leaf spot, or nematodes than *M. acuminata*. Cultivars containing the B genome are weaker than wild species (BB) itself but they are relatively superior in those aspects than AA or AAA clones, and the ABB group is certainly hardy.

Though none of the B genome-containing bananas is significant in the world trade, they are invaluable for rural people in Thailand and other tropical countries. 'Kluai Namwa' (BBA), a prime example in this case, is the most important banana for domestic consumption in Thailand. Though total export amount including all banana cultivars from Thailand was only 5,213 tons, about one million tons of 'Kluai Namwa' was produced in 2002. In the same year, only 87,674 tons of 'Kluai Khai' (AA) and 134,067 tons of 'Kluai Hom' (AAA) were produced (DOAE, 2004).

It is apparent that *M. acuminata* and *M. balbisiana* have played dominant roles in the evolution of edible clones. However, there is still inadequate data about the role which diversity within both species has played in the evolution of hybrid types, or where and when these ancestral hybridizations occurred (Jarret 1990). Variation of isozymes, i.e. malate dehydrogenase (MDH), phosphoglucose isomerase (PGI) and phosphoglucomutase (PGM), suggested that *M. acuminata* and *M. balbisiana* have diverged significantly and *M. balbisiana* is a polymorphic species (Lebot et al., 1993). In agreement, Kaemmer et al. (1997) found that the B genome present in plantains (AAB) and the B genome detected in ABB bananas came from different *M. balbisiana*

donors. Shepherd (1990) had already suggested that AAB and ABB cultivars evolved in different areas at different times.

Distribution areas of *M. acuminata* range from southern China to northern Australia and from India to the Philippines, while M. balbisiana distribution area is from Sri Lanka and eastern India to southern China (Simmonds 1962). Centers of hybrid origin were proposed differently by Simmonds (1962) and De Langhe and De Maret (1999). Simmonds (1962) suggested that India was a center of origin of AB, AAB, and ABB hybrids, while eastern Malaysia was the second center of triploid hybrids, and ABBB originated from Indochina. On the other hand, De Langhe and De Maret (1999) proposed that AAB hybrids probably originated in Papua New Guinea and then moved to southern India and to East Africa, based on the fact that M. balbisiana was found 'wild' in the Pacific Islands where M. acuminata ssp. banksii was found. The wild M. balbisiana species found in natural habitats in Philippines, Bismarck Archipelago and Hawaii forms the basis of the theory that M. balbisiana was carried by Austronesian-speaking people from Mainland Southeast Asia to the Philippines and afterward to the Pacific Islands (Simmonds 1962, 1995; Argent 1977; De Langhe and De Maret 1999). Linguistic and archeological evidences supported the route of these Neolithic voyagers (Benedict 1975; Bellwood 1991; Blust 1995; Oppenheimer 1998; Gray and Jordan 2000). It is doubtful, however, that no wild hybrids between M. balbisiana and other wild species was found in Papua New Guinea where Argent (1977) observed that M. balbisiana populations were ecologically isolated from other wild Musa species. Moreover, traditional AAB and ABB hybrids are almost completely absence in New Guinea and the Philippines (Simmonds 1962; De Langhe and De Maret 1999).

Simmonds (1962) suggested that *M. balbisiana* is not native to Thailand, Malaysia, and Indonesia, but was introduced and perhaps locally naturalized in these countries. The report has profound implication that AAB and ABB cultivars are not likely to have been generated in Thailand. On the other hand, somatic mutations in ABB group of 'Pisang Awak' or 'Kluai Namwa' has been recorded only from Thailand, e.g. 'Kluai Namwa Daeng' with pink flesh; 'Kluai Namwa Khao' with more waxy fruits than usual; and 'Kluai Namwa Khom' is a dwarf mutant (Chomchalow and Silayoi 1984). De Langhe et al. (1998), therefore, recommended further investigation on the possibility that AAB/ABB evolved from hybridization where *M. balbisiana* is cultivated in the presence of edible AA. *M. balbisiana* is believed to have been present for a very long time in Thailand considering its importance in Thai cultures and beliefs (Moonchinda 1995).

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