

CHAPTER SIX
SUMMARY

The present studies were initiated to characterize the variability present in different wild banana populations of *Musa acuminata* in peninsular Malaysia.

Forty-five morphological characters were used and large amount of variability was observed for most of these characters studied. However these characters have been shown to be variable due to mutations. Bract imbrication on the other hand was found variable among different populations but is attributable to developmental factors and thus cannot be used for taxonomic purposes. Most of the quantitative characters were found to be very variable however they depended on the environmental variability. Qualitative characters were found to be the most useful for characterization of *Musa acuminata*.

Samples belonging to two lowland forms i.e. *ssp. siamea* and *ssp. malaccensis* were found to be overlapping as a result of large morphological similarities and no distinctive grouping was observed. However the highland banana form could be differentiated from lowland accessions based on several morphological characters.

Ploidy level determined through flow cytometry (FCM) appeared similar. The analysis confirmed that all *M. acuminata* accessions had similar chromosome numbers ($2n = 22$).

High performance liquid chromatographic (HPLC) analysis of anthocyanins in *M. acuminata* bracts was able to differentiate all accessions based on geographical distribution i.e. lowland and highland. No variation was observed within the individuals of a population compared to those among different populations. Anthocyanin composition was found to be very stable in the same male bud and results were shown to be highly reproducible. The six compounds studied were present in different proportions. All lowland accessions showed similar anthocyanin patterns with the exception of Flava. The chemotype observed for highland banana was clearly differentiated based on the large accumulation of a new compound (Cyd), which was present in a very little amount in

lowland accessions. Similar results were observed for petunidin accumulated in a high percentage in highland banana compared to peonidin.

Flow cytometric analysis of genomic DNA content of *M. acuminata* samples was able to demonstrate significant variation among the populations compared to those within the populations. The lowland samples both from *ssp. siamea* and *ssp. malaccensis* did not show significant variation in their DNA content (1.194 to 1.244 pg), whereas a significant variation was observed for highland banana (1.277pg).

Different suckers screened in the 'Hot Spot' infested with *Fusarium oxysporum* f. *sp. cubense* Race 4 showed very high resistance as they were found surviving for more than two years. Similarly observations made on different wild *Musa acuminata* populations *in situ* did not reveal susceptibility to FOC attack.

Seed populations were raised through *in vitro* zygotic embryo culture as greenhouse seed germination was found to be difficult. *In vitro* germination was affected by different cultural conditions. *In vitro* embryo culture had increased the germination rate from 2% in greenhouse grown seeds after 40-50 days to 90% germination observed after one week.

Five seed populations of *ssp. malaccensis* were raised through *in vitro* zygotic embryo culture. One of the populations was found to be segregating for albinism (166 green: 23 albino) compared to normal green seedlings observed in other four populations.

Five *Musa acuminata ssp. malaccensis* seed populations were screened for Fusarium wilt Race 4. Seed populations were screened by using double tray technique and were found to be segregating for resistance and susceptibility with 3:1 and 13:3 genetic ratios. The response to FOC varied between and within the seed populations. The resistance of the inoculated seedlings was observed to be durable when these seedlings were found to be surviving for more than one year planted in the 'Hot Spot'.

RAPD markers were used to further characterize the susceptible and resistant seedlings. A total of 96 banding patterns were scored from fifteen primers used. Only 10 out of 96 bands were monomorphic thus suggesting a large genetic variability among the seedlings. Five primers revealed banding patterns, which were specific to either of resistant or susceptible progenies. Four primers produced banding patterns specifically found in susceptible seed progenies while one showed a banding pattern, specific to resistant progenies. A tetraploid was induced in *Musa acuminata ssp. malaccensis* seed progeny found resistant to Fusarium wilt Race 4 and confirmed by chromosomal counting. Morphologically diploid, tetraploid and mixoploids were also found to be distinct.

These studies has opened up the opportunities for future molecular research in *Musa* i.e. linkage mapping, DNA markers linked to disease resistance and subsequently gene cloning for molecular banana breeding.