

## CHAPTER 5

### GENERAL CONCLUSION

Our investigation indicated the phylogenetic utility of chloroplast and nuclear DNA sequences to infer evolutionary history of banana cultivars and hybrids. Despite low diversity, the sequences addressed clearly that the genome designation suggested by Simmonds and Shepperd (1955) is mostly applicable. An interesting result from this study is that the ABB triploid hybrids are highly variable due to maternal ancestral lineages. To indicate this newly found fact, we proposed the genome designation BBA to be used specifically for the 'Namwa' group of cultivars. The genetic labeling of the 'Hin' and 'Saba' cultivars (ABB/BBA) required special attention because they consist of different clones with distinct maternal origins.

Results from the study of *GBSS* gene identified one B allele among the three found in the BBA hybrids, 'Namwa'. This *GBSS* data could be used to detected levels of ploidy in banana cultivars.

From the DNA sequence data we obtained, several molecular makers could be developed in order to ease the identification and selection in breeding, genetic engineering, collection, and conservation programs.

The results from our study suggested low genetic diversity in *M. balbisiana* as formerly postulated. However, significant contribution of the B genome in hybrid cultivars is apparent and urged further study. Banana species, cultivars, and hybrids may serve as an excellent model for studying the patterns of evolution in polyploids. Nevertheless, more sampling of a wider range of subspecies, cytological characteristics, ploidy, and geographic origins will be necessary in future studies to identify diploid progenitors and genome constitutions of cultivars and hybrids.