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**GENETIC DIVERSITY AND POPULATION STRUCTURE OF WILD
BANANA (*Musa balbisiana*) POPULATIONS IN SRI LANKA**

**A PROJECT REPORT PRESENTED BY
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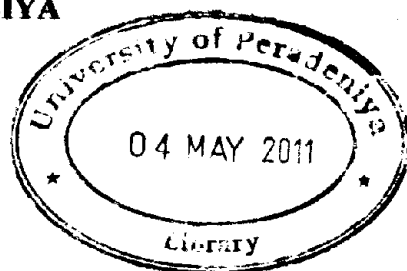
to the Board of Study in Biochemistry and Molecular Biology of the
POST GRADUATE INSTITUTE OF SCIENCE

in partial fulfillment of the requirement
for the award of the degree of

MASTER OF SCIENCE IN EXPERIMENTAL BIOTECHNOLOGY

of the

**UNIVERSITY OF PERADENIYA
SRI LANKA
2010**



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Musa balbisiana Colla [(BB) (2n=22)] locally known as 'Eti kesel' is a wild progenitor of banana and plantain. Its genetic diversity is very useful for crop improvement and conservation programs, to ascertain future global food security. Explorations have been recorded earlier, but study on genetic diversity has not been done in Sri Lanka.

In this experiment, *M. balbisiana* populations were surveyed and morphological and genetic diversity was assessed in the field and laboratory. DNA extracted from 23 samples was amplified using eight SSR primers (MaSSR9 a/b, MaSSR24 a/b, MaSSR18 a/b, AGMI95/96, AGMI103/104, Mb1-113, Mb1-134 and Mb1-69). Bands were visualized on 8% polyacrylamide gels, alleles were scored and evaluated using SPSS10 and GenAIEx6 software packages to generate a dendrogram, genetic diversity and population structure information.

The populations were located in wet zone of the country in protected as well as in unprotected areas and were under threat due to various reasons. Morphological variations were not observed among samples of different locations or while, the molecular diversity of the populations was substantial. Primers generated 3–6 alleles/locus and total of 34 alleles. Mb1-113 and MaSSR24 were the best primers for genetic diversity assessments.

The highest genetic distance was recorded in between Hangarapitiya-Malalpola and Gonbaddala-Malalpola samples. Three populations defined based on geographical distribution namely, Population 1 (individuals in Nuwara Eliya, Kegalle and Ratnapura), Population 2 (Kandy) and Population 3 (Matara and Kalutara) have shown 95.85% of mean polymorphic loci percentage leading to high genetic diversity. Population 1, 2 and 3 possessed 31.03%, 18.18% and 5.26% of population specific alleles respectively while, 44.12% of common alleles. There were 2 rare alleles found in Population 1. The

mean H_e (0.4966) was higher than the mean H_o (0.4119). Results indicated high gene flow values and low F_{st} values, representing an increase in out breeding nature. An AMOVA analysis showed 6% of variance among populations while 94% of variance within populations.

The distinct and rare alleles possessing populations are recommended to be conserved for the future benefits.