

**Determination of Population Structure of Yellow Dwarf
Coconut Population in Sri Lanka**



By

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**Thesis submitted to the University of Sri Jayewardenepura for
the award of the Degree of Master of Philosophy in Botany on
25th of September, 2014**

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Abbreviations

APS	Ammonium persulfate
AFLPs	Amplified Fragment Length Polymorphisms
ANOVA	Analysis of Variance
Bp	Base pair
CGRD	Coconut Genetic Resources Database
COGENT	Coconut Genetic Resources Network
CGIAR	Consultative Group on International Agricultural Research
CRISL	Coconut Research Institute of Sri Lanka
DNA	Deoxyribonucleic Acid
DW	Dry Weight
DL	dwarf-like
EDTA	Ethylenediaminetetraacetic acid
EC	Equatorial Circumference
FNW	Fresh Nut Weight
G20	Girth at 20 cm Height
G150	Girth at 150 cm Height
GT	Gon Thembili
HW	Husk Weight
HNW	Husked Nut Weight
IL	intermediate-like
IPGRI	International Plant Genetic Resources Institute
ISSR	Inter Simple Sequence Repeat
ISG	Isolated Coconut Seed Garden
KW	Kernel Weight
LL	Leaflet Length
LW	Leaflet Width
WW	Liquid Endosperm Weight
μl	Micro Litre
NFF	Number of Female Flowers
Y02-NI	Number of Inflorescences

NL	Number of Leaflets
NC	Nut Count
Y02-FF	Annual Female Flower Production
PD	Peduncle Diameter
PL	Peduncle Length
PtL	Petiole Length
PT	Petiole Thickness
PW	Petiole Width
PAGE	Polyacrylamide Gel Electrophoresis
PC	Polar Circumference
PCR	Polymerase Chain Reaction
PIC	Polymorphic Information Content
PCA	Principal Component Analysis
RL	Rachis Length
RAPDs	Random Amplified Polymorphic DNA
RFLPs	Restriction Fragment Length Polymorphism
Y02-SF	Settings Flowers
SW	Shell Weight
SSRs	Simple Sequence Repeats
SNPs	Single Nucleotide Polymorphisms
SNW	Split Husked Nut Weight
SWFF	Spikeletes with Female Flowers
SWWFF	Spikeletes without Female Flowers
SG	Stalk Girth
SH	Stem Height
SLGD	Sri Lanka Green Dwarf
SLT	Sri Lanka Tall
SD	Stranded Deviation
TL	tall-like

Acknowledgements

I would like to express my deepest gratitude to my supervisor Dr. (Ms) S.A.C.N. Perera, Principal Research Officer of the Genetics & Plant Breeding Division of the Coconut Research Institute of Sri Lanka, for her invaluable guidance, immeasurable support and cooperation provided to make this project success. I am also greatly indebted to my supervisor, Dr (Mrs.) Nilanthie Dassanayaka, Senior Lecturer of the University of Sri Jayawardenepura for valuable guidance, immense support and important advices kindly provided throughout this project.

I would like to express my sincere gratitude to Mr. Nandika Perera, Senior Scientist, Parentage Analysis Division, Genetech Molecular Diagnostics, Colombo 08, for his encouragement, guidance and support throughout the project which helped me immensely to complete the project successfully.

I am grateful to Dr. J.M.D.T. Everard, the former Deputy Director (Research) of the Coconut Research Institute of Sri Lanka for his valuable guidance, immense support and important advices kindly provided throughout this project.

I gratefully acknowledge Dr. Lalith Perera, Head of the Genetics and Plant Breeding Division of CRI and Mr. Dhammika N. Gunsekera, Owner, Genetech Molecular Diagnostics, Colombo 08, for granting permission to carry out this study as my M. Phil research at the Coconut Research Institute and Genetech respectively.

I would like to express my sincere gratitude to Mrs. Sandya Fernando, Experimental Officer, Mr. Gamini Jayawardana, CRI and all the pollination workers at Ambakelle.

A special word of thanks goes to all the staff members at Parentage Analysis Division, Genetech, Colombo 08, for their valuable support throughout the project.

I would like to acknowledge the financial assistance of the National Research Council, Sri Lanka under grant number 11-042.

Finally, I express my heartfelt gratitude to my parents and brother for their immeasurable love and care bestowed to me throughout my life.

This thesis is dedicated to my loving parents

groups based on the presence or absence of an apparent root bole. Furthermore, the selected palms were divided into three groups based on the appearance of crown: tall-like (TL) group, dwarf-like (DL) group and intermediate-like (IL) group. Analysis of variance and multivariate data analytical methods were performed in SAS and MINITAB software for the analysis of morphology data. Out of these palms, 51 palms were selected randomly for the molecular characterization and a total of 30 microsatellite primer pairs were used for genotyping. Genotypic data were analysed by PowerMarker and STRUCTURE software to determine the genetic diversity and the population structure of Yellow dwarf coconuts.

Individual palm data, when subjected to multivariate discrimination did not reveal clear groupings within the sample population resulting in many overlapping groups. However, when the data of different morphology based groups were analysed the results indicated a separate TL group within this population and it was distant from DL and IL groups. DL and TL groups clearly separated out with different morphological features defining them. However even with this analysis intermediate group could not be defined with clear morphological features.

In PowerMarker dendrogram two major clusters and three sub cluster in one major cluster, resulting four clusters were observed. In STRUCTURE analysis four sub populations ($K = 4$) were identified with the highest probability values concluding four groups within SLYD population.

The population structure of Yellow dwarf coconut form was clearly revealed by the molecular data. Considering both morphological and molecular analysis, the SLYD population was categorized into pure SLYD, Yellow semi tall (new coconut form) and a further mixed two groups.

The semi tall coconut form should be included in the coconut classification in Sri Lanka and should be conserved in *ex-situ* field gene banks of coconut to be utilized in the coconut breeding programmes. Pure SLYD should be used as the female parent in the improved and recommended coconut hybrid CRIC65 (Yellow) to extract the maximum hybrid vigour. This needs to be carefully considered in planting parent populations at the development and upgrading of coconut seed gardens for mass production of the hybrids including SLYD as a parent.

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