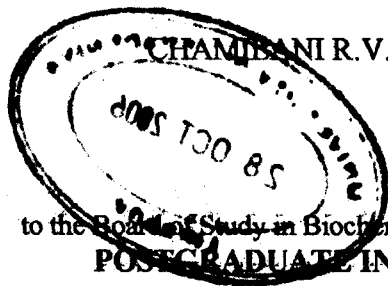# ESTIMATION OF THE EFFECTIVE POPULATION SIZE FOR COCONUT GENOME MAPPING USING COMPUTER SIMULATION

A PROJECT REPORT PRESENTED BY

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ABSTRACT

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This research project carried out during this MSc was aimed at estimating an effective population size for coconut genome mapping by computer simulation.

Computer simulation was performed using RICESIM software to create several gradually increasing cross pollinated populations to mimic real coconut mapping populations. The method was found to be effective.

Separate chromosomal maps were developed for each of above obtained populations using the second software JOINMAP. Both software RICESIM and JOINMAP found to be helpful as well as reliable for generating linkage maps for coconut.

It was noticed during this study, mapping populations which consists of individuals below fifty members are not suitable for genome mapping in coconut. It was also understood as the size of the mapping population increases there is a gradual establishment of chromosomal maps.

However from this study it was not possible to decide the exact population size which is suitable for mapping the coconut genome. But it was concluded a population above four hundred individuals would be suitable to develop a reliable map with a higher resolution.