

ABSTRACT

The work carried out during this PhD aimed at getting experience on molecular marker techniques and computer software for genome mapping and QTL analysis, and then exploring the possibility of developing a framework map for coconut. A linkage map was developed for Ler x Cvi cross of *Arabidopsis thaliana* with 162 RILs using JoinMap and DrawMap software. A total of 43 QTL (16 for flowering, 19 for leaf characters and 8 for height) were located on all 5 chromosomes of above map using the computer software, QTL Cafe.

A computer simulation was performed using RiceSim computer software to discover the feasibility of combining several F_2 populations together using JoinMap to mimic the real coconut mapping population that we obtained, and found that it was very successful. The mapping population of coconut, consists of 9 different F_2 families, was genotyped using SSR and AFLP markers successfully. However, the mapping population seemed to be adulterated and the attempts taken to sort it out were not so effective. Therefore, the development of a framework map for coconut could not be achieved during this PhD programme. Finally a physical mapping method, known as 'Happy Mapping', was discussed as an alternative to overcome the problems associated with meiotic mapping giving main concern for mapping coconut genome.