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DETERMINATION OF OPTIMUM POPULATION SIZE FOR HIGHER
ACCURACY IN MAPPING QUANTITATIVE TRAIT LOCI

A PROJECT REPORT PRESENTED BY

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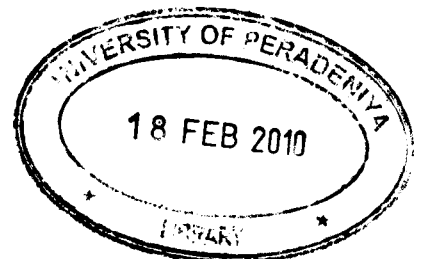
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Priyanka Samani Molligoda

Construction of genetic maps is becoming common in crop improvement programmes. Yet the precision of the maps produced do vary depending on the size of mapping populations. The current study focuses on demonstrating the importance of proper size of the mapping population and determination of the optimum population size for two hypothetical crops by computer simulation. A computer simulation was performed using RiceSim computer software to acquire genotypes of mapping populations for F_1 segregating populations obtained by cross-pollinating parent 1 to self pollinating parent 2, of two hypothetical crop species one with eight haploid chromosomes named as crop A and the other one with ten haploid chromosomes named as crop B, both with two different marker densities, 11 markers per chromosome and 6 markers per chromosome. Five different sizes of populations comprising of 50, 100, 150, 200 and 250 individuals, as progeny members were independently simulated to gain twenty different F_1 progeny for both plants. Mapping populations for all F_1 progenies were successfully produced. JoinMap software was executed to design framework maps for the derived populations. JoinMap was able to map all chromosomes successfully. Stabilization of map occurs with the increase of population size. It is revealed that the size of segregating population with 150 individuals and 100 individuals of the crop A having 8 haploid chromosomes with 6 markers and 11 markers respectively are the optimum population sizes to obtain good linkage map. In crop B comprising 10 haploid chromosomes the size of segregating population with 200 individuals is the optimum population for good linkage map irrespective of marker densities six and eleven. .