A GENOMIC DIVERSITY MEASURE IN DOUBLE HAPLOID QTL POPULATION

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Prediction of performance of lines obtained through Marker assisted selection based on the Genome-wise Genetic diversity estimates assumes importance, particularly when phenotyping the population is costly. A simple but useful method for estimation of genetic diversity of the lines developed based on marker assisted double-haploid population is proposed. The procedure is to obtain the orthonormalised matrices representing the k genomes and p phenotypic characters of a standardised matrix derived from an observational matrix using generalised Singular Value Decomposition technique. A measure of genomic diversity is obtained by a functional relationship of Row and Column matrices. The diagonal elements of the resultant matrix give the diversity indices for each genome and the off-diagonal elements give the affinities between genomes. The index is compared with other similar index. The genotypes are clustered based on the affinities.