

Nagy Sándor (2012)

PICcalc: An Online Program to Calculate Polymorphic Information Content for Molecular Genetic Studies

Absztrakt

Molecular markers have been proved to be valuable tools in the characterization and evaluation of genetic diversity within and between species and populations. The program PICcalc was developed for the simple calculation of polymorphic information content (PIC) and heterozygosity (H). It allows the calculation of these values for an individual locus or for a given number of loci.

Calculate: this type of program was developed for the calculation of H and PIC values information from allelic frequencies which frequencies were calculated by the user.

Calculate from file: this type of program was developed for the calculation of H and PIC information from text files with allelic frequencies in binary format. The program can process large amount of data.