Computer Note

GGT: Software for the Display of Graphical Genotypes

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A graphical representation of molecular marker data can be an important tool in the process of selection and evaluation of plant material. A computer program was developed that enables representation of molecular marker data by simple chromosome drawings in several ways. Commonly used marker file types that contain marker information serve as input for the GGT program. Besides representation, GGT can also be used for selection.

The widely used molecular marker techniques that were developed in the last decade have introduced a new, valuable source of data (Tanksley 1993). Polymorphisms at the molecular level are widely used to analyze differences between individual plants, populations, and species. Combined analysis of marker and trait data can lead to the unraveling of genetic factors, underlying observable traits (e.g., Lander and Botstein 1989). Visualization of marker data can play an important role in selection for individuals containing positive genome regions or, reversely, against individuals that are carrying negative genome regions. The concept of graphical genotypes was first described by Young and Tanksley (1989) and graphical representation of genetic data has been applied frequently in the case of QTL fine mapping. Another application can be found in backcross breeding programs, where it is important to reduce, as quickly as possible, the amount of donor genome, except for the region of interest. A clear overview of the (estimated) genetic descent of genome regions, covered with markers, can be of great help to breeders and researchers. My computer program (GGT) produces a display of molecular marker data.

GGT brings graphical genotyping to the widely used windows platform. Besides graphically representing marker data, GGT can also be used to select individuals with a preferred genotype. GGT was written in Borland Delphi and runs under Microsoft Windows or Windows 95/98.

Required Data

GGT requires input in the form of GGT data files. GGT data files are derived from two sources of data: a locus file, containing marker names and raw marker scores, and a linkage map file, specifying marker positions on a linkage map. The locus file is a plain text file. It contains data on marker alleles using the MapMaker/JoinMap type of coding (Lander et al. 1987; Stam 1993). A separate locus file is required for each linkage group. The map file is a text file listing, in two columns, markers and their map positions. GGT needs information on both the alleles of a locus as well as the map position. A GGT data file, which contains this information, can be constructed by merging a locus and a map file. This can either be done by hand or automatically, using the Build GGT-file option of the GGT program.

Viewing the Graphical Genotypes

When a GGT dataset has been constructed it can be opened by GGT. Several linkage groups can be opened simultaneously. GGT draws a graphical representation of the data in two ways: arranged by linkage group or arranged by individual. In both viewing modes, the user has the option to draw color or black-and-white linkage-group representations. Colors and hatch patterns are configurable.

When the data indicate that a crossover event has occurred in between two markers, the exact location of the crossover is unknown. GGT uses the most probable position for the crossover, exactly in the middle of the two markers, to change the color coding.

Statistics about the estimated proportion of the genome that has descended from either parent are calculated. A detailed list of individual (plant/line/marker) statistics is available.

The screen image of the graphical genotype can be printed, copied to the Windows clipboard, or saved to a disk as a bitmap file.

Selection

GGT has the option to specify a desired (marker) genotype for several linkage groups. Only the graphical genotypes of individuals that match this genotype are drawn and a list of these individuals is presented. Selection is done by demanding specific markers to carry a specific allele. By gradually increasing the stringency of selection a population can be screened very efficiently for regions of interest.

Availability

The GGT software is available for IBM-compatible PCs running Microsoft Windows (version 3.1 and higher). GGT can be obtained free of charge by sending a blank, DOS formatted floppy disk to the author. GGT can also be downloaded from the website of the Laboratory of Plant Breeding of the Wageningen Agricultural University (http://www.spg.wau.nl/pv/pub/GGT/). The distribution package contains the executable program, help file, a manual document, sample data files and a list of frequently asked questions.

References

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