A Lotus 1-2-3 macro system to analyze a cross of haploid individuals

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The use of RFLPs to construct saturated genetic maps results in the generation of very large sets of data. The management of these data, and the calculations needed to test for linkage relationships, is greatly facilitated by the use of an electronic spreadsheet on a personal computer. Using the spreadsheet Lotus 1-2-3TM (Lotus Development Corp., Cambridge, MA), we have found that the raw data can very efficiently be entered, viewed, edited, sorted, searched, and printed. We have written a program, utilizing Lotus 1-2-3 macro subcommands, that analyzes segregation data from a cross of haploid individuals in several ways.

The occurrence of phenotypes across progeny for each marker is tested for randomness by generating a chi-square statistic measuring deviation from a 1:1 ratio of the two parental phenotypes for each marker.

Markers are tested for linkage in all possible combinations by generating a chi-square statistic measuring the degree of departure from a random assortment. An example of the output generated from this procedure is shown in Table 1. Upper and lower 95% confidence limits of the recombination fraction are calculated according to the formulae of Mason, Gunst and Hess (1989, Statistical design and analysis of experiments with applications to engineering and science. Wiley Press, NY. pp. 417-419). These formulae differ slightly from those used by Bronson et al. in their program (1989, Fung. Genet. Newslet. 36:41-42).

A computation of double crossover frequencies is also available for any number of markers the operator selects (e.g. a linkage group). All possible three-way comparisons are made within the selected group. The output from this procedure includes the names of the markers and their associated single and double crossover frequencies, the most likely gene order (or orders in the event of equal probabilities), and an estimate of interference.

All output is written into the spreadsheet, thus allowing examination with the Lotus searching features as Reeves (Biotechniques 6:12-14, 1988) has suggested. Printouts of all or selected data are available with the Lotus print commands. The program was written in Lotus 1-2-3 version 2.1 and will run on any computer which supports this software. The program is available from either author - please provide a 5.25" diskette. Computational details and printed copies of the program are available from the first author.

Table 1. Example of output from segregation analysis

Marker 1	Marker 2	Total	Nonpar- ental	Parental	%Recom- bination	Chi square	95% confidence limits	
21	4-045	47	5	42	10.6	13.8	1.8	19.4
21	4-145	47	1	46	2.1	20.6	0.7	6.2
21	4-163	43	5	38	11.6	11.9	2.0	21.2