

The pea map - comments from a frustrated Mendelian geneticist

With the advent of DNA markers the construction of a genetic linkage map for a species is becoming almost a routine goal for any geneticist particularly interested in that species. The tomato map now has well over 1,000 markers, a map for slash pine (150 markers) was developed in two months, and grasses such as barley, maize, and rice all have relatively complete maps. Even more exciting is the finding that these maps appear to be relatively stable. The sequence of markers on the potato map is nearly identical to that on the tomato map, and many linkage groups in rice can be found in maize.

Yet, despite a long history of genetic studies in pea, its linkage map still has several regions of uncertainty. The most conspicuous recent evidence of this problem is the article by Ellis et al (1), where the authors are unable to develop a consistent map despite the availability of nearly 200 clearly defined markers. However, many pea geneticists have experienced similar inconsistencies in the position of a gene (for instance, *er* has been mapped to five of the seven linkage groups of pea). This problem is particularly vexing in light of the stability of maps for other species (e.g. tomato/potato) which in the case of tomato was based initially on results from interspecific crosses. Does the pea genome differ fundamentally from tomato or rice with regard to linkage consistency and incidence of chromosome rearrangements? If so, how? (and why do we still find significant blocks of genes conserved between pea and lentil or pea and chickpea?). Do so many chromosomal rearrangements occur in our markers lines that we have been defeating ourselves by using them? The parental lines used by Ellis et al were relatively respectable and thought to contain only one translocation. Whatever is happening, we should get to the bottom of it, and I think putting a little more rigour in mapping analysis might help.

With these thoughts in mind, the members of the Linkage Map Committee (Mike Ambrose, Wojtek Swiecicki, and myself) are going to attempt to establish a set of guidelines for mapping genes in pea to be published in Vol 25 of Pisum Genetics. These criteria are expected to be used by the Editor of Pisum Genetics as well as by reviewers of manuscripts for other journals to evaluate the data and determine if the evidence presented meets a minimum standard for publication. However, it is my hope that the guidelines will be much more useful to researchers performing the mapping experiments by establishing and characterising marker lines, identifying reliable markers, and focusing our thoughts on a problem that affects us all and which may be of fundamental importance. As the guidelines will have an impact on numerous experiments it is important that we receive input from as many scientists mapping genes in pea as possible. A first draft of the guidelines will be sent to the principal researchers mapping genes in pea as soon as the Linkage Committee can agree upon them. Comments from others would be greatly appreciated and can be sent directly to me (Fax: 315-787-2320, email: Norman_Weeden@qmrelay.mail.cornell.edu) or to other members of the Committee.

1. Ellis, T.H.N., Turner, L., Hellens, R.P., Lee, D., Harker, C.L., Enard, C., Domoney, C. and Davies, D.R. 1992. Genetics 130:649-663.

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