

### **Guidelines for future mapping studies in *Pisum***

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Markers and genes are being placed on linkage maps of complex organisms at an ever accelerating pace. The pea genome is no exception, and numerous programs throughout the world are involved in mapping experiments in this organism. In order to facilitate communication among workers on these programs, minimize ambiguities or uncertainties when identifying linkage groups, and move towards the resolution of a number of contradictions presently in the literature, the members of the Linkage Committee propose the following set of guidelines for researchers performing experiments with the primary goal of locating a gene(s) on the pea linkage map.

- (1) The location of a gene should be made with reference to standard markers (listed in Table 1, with those indicated as "primary" being preferred). Evidence for linkage with the standard marker should be compelling. "Compelling" will be defined on the basis of a probability statistic (P), giving the probability that such a result could have been obtained by chance. We recommend that for publication a  $P < 0.0001$  and/or  $LOD > 4.0$  be expected, and that  $P < 0.001$  and/or  $LOD > 3.0$  be the minimum acceptable evidence for linkage. Linkage to a standard marker can be made through a chain of one or more 'non standard' markers (such as RAPDs, RFLPs not widely available, or other mutants with which the investigator has considerable experience), but each link in the chain must meet the above requirement for linkage ( $P < 0.0001$ ). The product-ratio method is preferred for linkage calculations.
- (2) In most instances, we recommend confirmation of the linkage in a second cross using at least one different parent. This check is particularly important if an obvious or particularly close standard marker was not segregating in the initial mapping population. For instance, if gene X was mapped to the 'upper' portion of linkage group III, but *M* was not segregating in this initial cross, then *M* would be an obvious marker to use in the second cross.
- (3) Pollen fertility should be 90-100% in the  $F_1$  and there should be no indication of seed abortion as might be caused by differences in karyotype between the parents. The karyotype of at least one of the parents should be compared with the standard karyotype represented by line W-110.
- (4) Previous results published by other researchers which are consistent with the new data need to be discussed to such an extent that the reader can appreciate what problems may have been associated with the previous results and what makes the new data more rigorous.

A list of standard marker lines and recombinant inbred lines available for linkage analyses is given in Table 2.

Table 1. Recommended standard reference genes for mapping studies.

Linkage group	Primary markers	secondary markers	DNA markers
I upper	<i>Aat-p, a</i>	<i>lf, His2-5, His7</i>	<i>Lg-J</i>
I lower	<i>d, Idh, af, i, Pur</i>	<i>am-1, o</i>	<i>Lghb</i>
II	<i>wb, k, Pgm-p, Fum</i>	<i>s, orp</i>	<i>Cvc</i>
III	<i>Aat-c, Adh-1, M, st, b, Lap-1</i>	<i>Lap-2, tac</i>	<i>5S/2, cMH69, Vc-5, Pea-2</i>
IVA upper	<i>was</i>	<i>z, Tra</i>	<i>Rrn-1, cMH41</i>
IVA lower	<i>wsp</i>	<i>sil, Alat-p</i>	
IVB	<i>le, v</i>	<i>Np, Tpi-p, Lox</i>	
V upper	<i>r, tl, det, coch<sup>het</sup></i>	<i>bt, Est-4, His-1</i>	<i>Lg-1, cMH71</i>
V lower	<i>gp, Px-1, Pgd-c, Fs, creep</i>	<i>cp, Acp-1, art-2, U, cov</i>	<i>Rbcs, Vc-2, 5S/1</i>
VI	<i>wlo, Prx-3, na, p, Pl, Arg</i>	<i>Acp-4, Gty, art-1</i>	<i>Rpl-22, pI49, Gs-p, Fed, 5S/3</i>
VII upper	<i>Pgm-c, Pgd-p</i>	<i>Pep-3</i>	<i>Rrn-2, cMH58</i>
VII lower	<i>oh, Skdh, Aat-m, wa, Est-2, def, Amy</i>	<i>Aldo, chi-5</i>	<i>Cab, cMH34</i>

Table 2. Standard marker lines and recombinant inbred lines available.

## Standard marker lines

JI15  
 JI73 (=WL1238)  
 JI1794(=Zohary716)  
 Slow  
 Fast  
 WL110 (= standard karyotype)

## Recombinant inbred lines available

JI1794 x Slow (51 F<sub>7</sub> + lines); data on approximately 400 markers  
 Sparkle x JI73 (approximately 64 F<sub>6</sub> lines); data on about 50 markers  
 JI15xJI399 (92 lines); data on 79 markers  
 JI281 x JI399 (71 F<sub>12</sub> lines); data on over 200 markers\*

\*This cross may involve an aberrant chromosomal arrangement since an association was observed between markers *i* (group I) and *le* (group IV) by Ellis et al. (1992; Genetics 130:649-663). The possibility that one or both parental lines carry a translocation is being investigated (T.H.N. Ellis, pers. comm.).