

Linkage groups of pea

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(N.F. Weeden, W.K. Swiecicki, M. Ambrose and G.M. Timmerman)

Well over 500 loci (classical markers, protein polymorphisms, and RFLPs of known genes or cDNA sequences) have been identified in pea. Unfortunately, a considerable number of these have not been mapped relative to classically defined markers, making it difficult to combine them into a general linkage map. In some instances conflicting reports in the literature make it impossible to identify the precise location of a locus. For instance, the *rugosus* locus, *rb*, and the closely linked vicilin sequence, *Vc-5*, have recently been placed near *M* (6) and near *b* (1). Both reports appear to be based on strong evidence, yet the same locus cannot be assigned to both ends of linkage group m on the standard map.

In the construction of the map on the cover of this issue, the Linkage Committee has maintained a very conservative approach, starting with well known and easily scored markers such as *a*, *i*, *k*, *wb*, *M*, etc. Other markers were added only when the evidence for linkage with the primary markers was strong and ambiguities as to the location of the marker relative to flanking markers did not exist. This latter requirement forced many of the markers to be placed in parentheses, either near the primary markers to which they show linkage or at the base of the linkage group if the location of that marker is less clear. Only just over 300 markers could be assigned to linkage groups using this approach, and the Committee extends apologies to those investigators whose markers (usually RFLPs) were not included in the map. The omissions reflect difficulties in combining maps, not judgements of scientific merit. The Committee did not attempt to use statistical programs such as Joinmap to combine maps because of the known variability in linkage intensities between the same markers in different crosses.

Several of the classical linkage groups (e.g. linkage groups I and IV) were split because serious questions regarding their integrity have developed (see 2, 4 and 5). Despite the recent confirmation of linkage between the *oh*—*Cab* region and *Rrn-2* (3), linkage group VII is presented as two segments to encourage further investigation of this region. Finally, the *wsp*—*Alat-p* group tentatively has been placed with group IVA because *wsp* is believed to be on the alternate satellite chromosome to that containing *oh-wa* (2).

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