

### A brief synopsis of the current status of pea cytogenetics

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Lamm (14) and Folkesson (5,6) summarised most of the recent cytological studies in *Pisum*, and much of the following discussion is based on these papers. Some of the cytogenetic findings disagree with the standard linkage map of *Pisum* as developed by Lamprecht (16) and Blixt (3). Certain of these possible alterations also have been supported by linkage studies with molecular markers and have been incorporated into more recent versions of the pea linkage map (20). To complement the revised linkage map published on the cover of this volume of *Pisum Genetics*, we summarize here the cytogenetic data currently available for *Pisum*. For more details on the tester lines used and the appearance of the chromosomes the reader is referred to Table 1 and Fig. 1 in Lamm (14).

Chromosome 1 is defined cytogenetically as one of the short metacentric chromosomes, lacking a satellite (2). This chromosome is involved in several translocations showing linkage between breakpoints and markers of linkage group IV. The T-point of line L-114 displayed linkage with *n* (12) and linkage also was found between the genes *le* and *v* and the T-point of line WL-58 (17). Folkesson (4) demonstrated that neither the translocation in line L-114 nor that in WL-58 involved a satellite chromosome, indicating that *le*, *v* and *n* are not syntenic with a 45S ribosomal array (e.g. *Rrn-1*). According to the standard linkage map of Blixt (3) as well as revised maps of Weeden and Wolko (20) and Weeden et al. (21), a satellite [the ribosomal array *Rrn-1* of Polans et al. (18)] is part of this linkage group. However, Polans et al. (18) report linkage between *Rrn-1* and the *was—fa* segment of this linkage group, not with either *le* or *v*. Although the independent assortment of *le* and *Rrn-1* could be attributed to the large distance between the two loci on the standard linkage group IV, the alternative explanation, that the *z—was—Rrn-1—fa* region is on different linkage group, now appears to be correct, because more detailed mapping has failed to provide compelling evidence for a linkage between *Np* and *Rrn-1*. The location of *n* also may require further investigation.

Chromosome 2 appears to be the same as linkage group VI. One breakpoint (line WL-58), located on the short arm of this chromosome, exhibits linkage with *Pl* (2). The T-point on the long-arm (line L-108) shows weak linkage with *p* and *wlo* (13), but this result requires confirmation. Molecular markers have been able to confirm the synteny of *Pl* and *wlo* in several crosses (19, 22).

Chromosome 3 also appears to be clearly associated with a linkage group, in this case linkage group V. There are two regions on this chromosome that appear to be particularly fragile (often involved in rearrangements). One is in the *cri—gp* segment near the centromere, and the other is the *r—tl* region on the long arm of the chromosome. In addition to line L-112, there are two other lines with interchange points closely linked to *r*: L-25 and A583-139. L-25 has the same structural type as L-112 (i.e. T(3-4)). The second chromosome affected in line A583-139 has yet to be identified (N.F. Weeden unpub.).

Chromosome 4 is one of the two satellite chromosomes. Folkesson (6) demonstrated that the markers *wsp* and *sil* must be placed on one of the satellite chromosomes and *oh—wa* on the other. Unfortunately, neither of these marker pairs has been clearly assigned to a specific chromosome. If we assume that the *oh—wa* linkage group is on chromosome 7 (see below) the *wsp—sil* pair must be on chromosome 4 and be syntenic with the *Rrn-1* linkage group.

Chromosome 5 has been paired with linkage group in by means of translocations with breakpoints near *b* (L-III and L-180) on the short arm and near *st* (L-83) on the long arm of this chromosome (14). This linkage group was established relatively early (see 3) and has been verified by most analyses using molecular markers.

The well known Hammarlund's K-line or L-84 contains a translocation between chromosomes 6 and 3. Recently, the T-points of L-84 were localised more precisely: between genes *cri* and *gp* on chromosome 3 and very close to the histone H1 genes and gene *a* near the centromere of chromosome 6 (1). A new translocation marked by dominant gene *Twt* has its T-point very near *lf* (8). However, the linkage between *a* and *d* has been questioned (11). Thus, the constitution of the corresponding linkage group (beyond the *Aat-p—His-7* segment) is uncertain.

Chromosome 7 is the other satellite chromosome, and is defined as that involved in translocation L-108. The T-point of this translocation displays linkage with *oh* and *wa* (13), indicating that the corresponding linkage group is linkage group VII, which contains the *Pgd-p--Rrn-2--oh* linkage as confirmed by Folta and Polans (7). However, as the two satellite chromosomes can be difficult to distinguish cytologically, this assignment is not particularly useful except as a bookkeeping device.

As can be surmised from the above statements, considerable work is still required before a clear coupling of chromosomes and linkage groups can be made. Fortunately, many more markers are now available for mapping the translocations. Thus, the use of the standard tester set (15), as well as several other lines [e.g. Gorel et al. (8); Klein (9,10)], should permit the resolution of many of the uncertain linkage relationships in the standard karyotype.

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