Ser appears to be the serrate leaflet locus mapped on linkage group III

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Lamprecht (3) identified three types of leaflet serration present in the *Pisum* germplasm: 1) *scalaris forma,* or 'step-form' 2) *serratus,* or saw-form and 3) *incisus* or deeply cut. These types are believed to be controlled by three distinct loci: *Td, Ser* and *Inci,* respectively (3, 9). The JIC pgene collection website (www.jjc.bbsrc.ac.uk/cgi-bin/germplas/geneID) lists the type lines for these genes as follows: *Ser*: JI 2781 (= WL 1414), *Td*: JI 2679 (= WL 6) and *Inci*: WL 1292 or Wt 16 155. According to Lamprecht (3), *Td* is normally found in European germplasm, whereas *Ser* is typical of *P. sativum* ssp. *abyssinicum* and a line from Afghanistan (WL 1414) and *Inci* is limited to lines from south Israel. Lamprecht (2) found that *Td* displayed linkage with *Fa* and assigned it to the *N-Z-Fa* group now forming the upper portion of LG IV (10). However, several other investigators have reported linkage between *Td* and markers on LG III (4, 5, 6), and Marx (5) questioned which linkage group actually contained *Td*. We believe that *Ser* is located on LG III, and that further studies are necessary to determine where *Td* is located.

The confusion appears to have developed when Marx reported linkage between the serrate leaflet phenotype, which he believed to be produced by *Td,* and the LG III marker *b* (5). Marx used line A 886-193 as his source of *Td*, a line for which the serrate leaflet phenotype could be traced back to a "*Pisum abyssinicum*" line obtained from Dr. K. Dobbs (5). Grajal-Martin and Muehlbauer (1) used a related Marx line (A778-26-6) to map *Td* to LG III near *Lap1*. Polans (5) further established the linkage between serrate leaflets and markers in the middle of LG III using two lines (Marx' A 778-26-6 and Weeden's 82-14n). The line 82-14n is actually a sample of PI 268480, a *P. sativum* ssp. *sativum* line from Afghanistan. Smirnova (6) reported linkage between weakly serrate leaflets (lines WIR 4907 and WIR 319) and *Le*, another LG III marker. Finally, Lorenzi et al. (3) found that the serrate leaflet gene in *P. s.* ssp. *abyssinicum* was tightly linked to Cipor, a DNA marker approximately midway between *Lap1* and *Le*.

Except for Smirnova (6), all the *'Td'* lines used in the above studies were either *P. sativum* ssp. *abyssinicum* (4), derived from this source (A 886-193 and A 778-26-6) or from a line from Afghanistan (6). According to Lamprecht (3), all these lines possess *Ser* rather than *Td*. In order to test this possibility, allelism was examined between the serrate leaflet phenotype in WL 1414 (type line for *Ser*) and a line carrying the serrate leaflet phenotype derived from *P. sativum* ssp. *abyssinicum*. All of the approximately 100 F_2 plants examined exhibited the serrate phenotype (N.F. Weeden, unpublished), confirming that the two genes were allelic or controlled by very closely linked loci.

At present we are unable to distinguish between the "allelic" and "closely linked" alternatives because the third gene discussed by Lamprecht, *Inci,* appears to map very near *Ser*. Lorenzi et al. (4) indicated that their *"Td"* (now known to be *Ser*) mapped to LG III between *Lap1* and *Np*. Święcicki (9) also found linkage between *b* and the serrate leaflet phenotype in line Wt 702, although he was uncertain of the gene involved, referring to it tentatively as "*Inci*" based on its phenotype. Subsequently, Smirnova (8) mapped *Inci* in WIR 2521 to LG III between *B* and *Np*. Although the linkage value between *B* and *Np* was smaller than expected, the position assigned for *Inci* was indistinguishable from the position Lorenzi et al. (4) assigned to *Ser*. An allelism test is clearly required between *Inci* and *Ser*, for these two may represent the same locus.

We suggest that the gene that has been mapped in most of the above studies is *Ser*, and that the consensus map be changed to reflect this conclusion. The position of *Td* is uncertain, although

Lamprecht's data placing it on LG IV remains the most relevant. The sample of WL 6 that we had available did not exhibit strongly serrate margins, and we were not able to confirm a LG IV location.

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Note:
PI 268480 was also described in a previous Pisum Genetics paper (N.F. Weeden and B. Wolko, 2001. Pisum Genetics 33: 21-25). The accession was described as a *P. sativum* ssp. *elatius* line from Syria, in contrast to the description "*P. sativum* ssp. *sativum* line from Afghanistan" given in the present paper. The passport data on this accession was corrected in 1993, but I used the original data in the 2001 article. On examining the accessions, I agree that the *P. sativum* ssp. *sativum*. is much more appropriate for PI 268480 and that its morphology and allozyme genotype are consistent with an Afghanistan origin. I apologize for my oversight.
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