

## Linkage relationship of genes *curl* and *His1* is conserved in *Pisum sativum* and *P.fulvum*

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The genus *Pisum* comprises only two true species: *P. sativum* L., including several subspecies, and *P.fulvum* Sibth. et Smith. The latter species is well adapted to the arid habitat of the Near East and should carry many genes useful for constructing new cultivars of pea. In spite of several chromosome rearrangements that took place during the divergent evolution of both species (1), their hybrids can give a few seeds. Therefore, the transfer of genes between the two *Pisum* species can be performed quite easily. The problem is how to trace the fate of the segments of the *P. fulvum* genome in the series of back-crosses to *P. sativum*. Recently we have undertaken a search for mutations marking the genome of *P.fulvum*.

500 seeds of *P. fulvum* (accession VIR6070, received from VIR, St Petersburg) were treated for 24 h with a 0.15% EMS solution. Several dozen mutations (mostly affecting chlorophyll pigmentation) were found in the M<sub>2</sub> generation. One morphological mutant we called *curl* because it was phenotypically very similar to the mutation *curl* of *P. sativum* (3). The interspecific F<sub>1</sub> hybrids of a cross between *P. sativum* SGE689, *curl*, (used as female) and the *curl* mutant of *P.fulvum* also exhibited a *curl* phenotype indicating homology of the genes affected.

The gene *curl* of *P. sativum* occupies a locus in linkage group V 4 cM from locus *His1* encoding the major fraction of the histone H1 proteins (2). Among four *P. fulvum* accessions available from the VIR, two (namely, VIR2523 and VIR3397) possess the fast variant of the *His1* histone fraction whereas two others (VIR6070 and VIR6071) have the slow variant. The alleles encoding these variants are referred to as *His1<sup>F</sup>* and *His1<sup>S</sup>*, respectively. The mutant (*curl*, *His1<sup>S</sup>*) was crossed with a plant from accession VIR2523 (*Curl*, *His1<sup>F</sup>*). F<sub>1</sub> plants were heterozygous for *His1* and had the *Curl* phenotype, F<sub>2</sub> segregation data (Table 1) confirm that *curl* is a recessive mutation and indicate fairly strong linkage between the *curl* and *His1* loci (recombination fraction  $10.3 \pm 3.7\%$ ). This result shows that the linkage relationships of these two loci are conserved in the segments of the genomes of both *Pisum* species.

Table 1. Joint segregation of phenotypes *curl* and *His1* in the F<sub>2</sub> of the cross between *P. fulvum* lines VIR6070 (*curl His1<sup>S</sup>*) and VIR2523 (*Curl His1<sup>F</sup>*).

	<i>His1<sup>S</sup></i>	<i>His1<sup>S/F</sup></i>	<i>His1<sup>F</sup></i>
<i>Curl</i>	4	33	21
<i>curl</i>	13	3	0

Joint segregation  $\chi^2 = 39.72$ ,  $P < 0.0001$ , Recombination fraction  $10.3 \pm 3.7\%$ .  $\chi^2$  (3:1 for *curl*) = 0.45 ( $P > 0.7$ );  $\chi^2$  (1:2:1 for *His1*) = 0.49 ( $P > 0.5$ ).

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