

**Fig. 3** Sequence analysis of the termini of insertions associated with eye mutants. Left and right ends of each insertion are shown aligned above and below the wild-type sequence, respectively. Sequences from the insertions are in lower-case letters. Duplicated target sequences are shaded (see text). The *fa<sup>De</sup>* insertion is 127 bp to the right of the *Pst*I site in *D. simulans* at coordinate -15.0. This site is also found in *D. melanoaster*. Restriction-site coordinates are from ref. 2. The *fa<sup>fs</sup>* insertion is 230 bp to the right of the *Pvu*I site at -13.8, *fa* is 157 bp to the left of the *Bgl*II site at -11.2, and *fa<sup>8</sup>* is 25 bp to the left of the *Hind*III site at -9.4. All these distances are measured from the 5' nucleotide of the duplicated target sequence to the 5' end of the restriction site. We cloned restriction fragments for sequencing into M13, mp18 or mp19 (ref. 9), and grew and sequenced them as described elsewhere<sup>10,11</sup>

<i>fa<sup>De</sup></i>	CCCTTAAAGGCAGCAAAACATACATATA	acttacgtagttatta		
<i>Notch<sup>+</sup></i>	CCCTTAAAGGCAGCAAAACATACATATATGTGGGATCTCTCGATCTTCTGCAAAC		<i>Notch<sup>+</sup></i>	
	atattatgctac	ATATATGTGGGATCTCTCGATCTTCTGCAAAC	<i>fa<sup>De</sup></i>	
<i>fa<sup>fz</sup></i>	GGATTTTATTGGGTTGTATATATAT	gtaagattgt		
<i>Notch<sup>+</sup></i>	GGATTTTATTGGGTTGTATATATATAAATTTTTTATATCTGGCATCTGTGTTT		<i>Notch<sup>+</sup></i>	
	ccttactccatgttac	ATATATATAAATTTTTTATATCTGGCATCTGTGTTT	<i>fa<sup>fz</sup></i>	
<i>fa<sup>g58</sup></i>	TTTTTCTTATATACGATGTTATGTATATATATCTCTTCATATATGTTAT	gtaaga		
<i>fa</i>	TTTTTCTTATATACGATGTTATGTATATATATATAGTTCACCTTGCATCAGGTTCTCG			
<i>fa<sup>g</sup></i>	TTTTTCTTATATACGATGTTATGTATATATA	aaattaattaagtgtatgtg		
<i>fa<sup>g62</sup></i>	TTTTTCTTATATACGATGTTATGTATATATAT	gtaagattg		
<i>Notch<sup>+</sup></i>	TTTTTCTTATATACGATGTTATGTATATATATATCTCTTCATATATGTATAGGCT		<i>Notch<sup>+</sup></i>	
	gcttactccatgttac	ATATATATCTCTTCATATATGTATAGGCT	<i>fa<sup>g62</sup></i>	
	ccggttaacttagttaact	TATATATATCTCTTCATATATGTATAGGCT	<i>fa<sup>g</sup></i>	
	agaagagggttcttaact	TATATATCTCTTCATATATGTATAGGCT	<i>fa<sup>g</sup></i>	
		gcttactccatgttac	ATGTTATAGGCT	<i>fa<sup>g58</sup></i>
<i>fa<sup>g</sup></i>	CATGGGAATCCCAAGCAAAAAAAAAAAAAAAAAATATATATATATATATATATAGT	gtaagattgttt		
<i>Notch<sup>+</sup></i>	CATGGGAATCCCAAGCAAAAAAAAAAAAAAAAAATATATATATATATATAGT	TTAATGAGAG	<i>Notch<sup>+</sup></i>	
		ccttactccatgttac	ATATATATAGT	<i>fa<sup>g</sup></i>

it is reasonable to conclude that deletions, point mutations and even  *copia-like*  transposable-element insertions with the same transcriptional orientation as *Notch*, do not give eye phenotypes of this sort when they break *Notch* intervening sequences. The phenotypic effect of deleting a portion of an intervening sequence is unknown, but one  *copia-like*  insertion in this region (in intervening sequence 1), a *B104/roo* insertion associated with a recessive lethal phenotype 1(1)N, is transcribed in the same direction as *Notch* (ref. 2). Also, an FB-transposable element (not a  *copia-like*  element) insertion has been detected in this intervening sequence in a wild-type strain of *Drosophila*<sup>3</sup>. Thus, the aberrant eye phenotypes do not seem to result from simply dissociating eye-specific control regions of a *Notch* intron.

Second, the *glossy-like* mutations are found only in conjunction with insertions of members of a single transposable-element family, *flea*. Presumably, a *glossy-like* phenotype cannot be produced by association with any other element. The dependence of the *glossy-like* phenotype on *flea* is also evident from sequencing insertion sites. The insertion sites occupied by *fa* and *fa<sup>g62</sup>* differ by one nucleotide, whereas the *fa<sup>g62</sup>* and *fa<sup>3</sup>* insertion sites differ by only three nucleotides (Fig. 3), yet *fa* and *fa<sup>3</sup>* give a *facet* phenotype and *fa<sup>g62</sup>* produces a *glossy-like* eye. Clearly the differences in the phenotypes of these mutants reflect special properties of the associated transposable elements rather than where within *Notch* the elements have been integrated.

The insertions associated with *facet* and *glossy-like* mutations probably interfere with *Notch* expression to generate aberrant eye phenotypes because temperature-sensitive, lethal mutations that map to *Notch* protein-coding regions produce similar eye phenotypes following temperature pulses early in pupation<sup>2,4,5</sup>. Also a short deletion *strawberry*, near the 5' end of *Notch* produces a related mutant phenotype, presumably by altering the level of *Notch* locus transcription<sup>5</sup>. It is possible that insertions associated with *facet* and *glossy-like* mutations only differ in the time or degree to which they interfere with *Notch* activity. Analysis of phenotypes of *fa* and *fa<sup>3</sup>* mutants at different temperatures provides support for this notion. At 25 °C both mutants produce a *facet* phenotype, whereas at 29 °C the eyes of these mutants tend toward to *glossy-like* (J. Renvall and S.K., unpublished). The most likely source of any interference with *Notch* locus activity is the expression of the transposable elements themselves, and the elements *flea*, *opus*, *hopper* and *springer* do show different patterns of transcription during *Drosophila* development (Fig. 2). In contrast, analysis of *glossy-like* and *facet* mutations does not suggest a major role for specific sequences within *Notch* introns in the generation of wild-type eye phenotypes. If the interactions of *Notch* and these transposable elements are typical for complex loci in *Drosophila*, it seems likely that the variety of insertion-associated mutant phenotypes

observed for such loci does not accurately reflect the level of informational complexity to be found within corresponding wild-type genes.

We thank Laurel Eckhardt, Peter Model and Norton D. Zinder for comments on the manuscript. We also thank M.M. Green, O. G. Fahmy, P. Portin, W. Welshons and R. Woodruff for supplying *facet* and *glossy-like* mutants, and J. Renvall for assistance in cloning some of the mutants. This work was supported by grants to M.W.Y. from the National Institutes of Health and the Andre and Bella Meyer Foundation.

Received 30 April; accepted 19 June 1986.

- Lindsley, D. L. & Zimm, G. *Drosophila Information Service* **62**, 114-116 (1985).
- Kidd, S., Lockett, T. J. & Young, M. W. *Cell* **34**, 421-433 (1983).
- Grimwade, B. G., Muskavitch, M. A. T., Welshons, W. J., Yedvobnick, B. & Artavanis-Tsakonas, S. *Devl Biol.* **107**, 503-519 (1985).
- Shellenbarger, D. L. & Mohler, J. D. *Devl Biol.* **62**, 432-446 (1978).
- Kidd, S., Kelley, M. R. & Young, M. W. *Molec. Cell. Biol.* **6**, 3094-3108 (1986).
- Welshons, W. J. *Genetics* **76**, 775-794 (1974).
- Karlik, C. C. & Fyrberg, E. A. *Cell* **41**, 57-66 (1985).
- Melton, D. A. et al. *Nucleic Acids Res.* **12**, 7035-7056 (1984).
- Norrander, J., Kempe, T. & Messing, J. *Gene* **26**, 101-106 (1983).
- Sanger, F., Coulson, A. R., Barrell, B. G., Smith, A. J. H. & Roe, B. A. *J. molec. Biol.* **143**, 161-178 (1980).
- Biggin, M. D., Gibson, T. J. & Hong, G. F. *Proc. natn. Acad. Sci. U.S.A.* **80**, 3963-3965 (1983).

## Corrigendum

### DNA fingerprint analysis in immigration test-cases

W. G. Hill

*Nature* **322**, 290-291 (1986).

IN this Matters Arising item, the equation in the footnote to Table 1 should read:

$$\ln L = \sum_i \sum_j \sum_k n_{ijk} [\ln p_{ijk} - \ln (1 - p_{000})]$$

In the calculations as published a correct version of the formula was used.

## Errata

### Increased levels of myelin basic protein transcripts in virus-induced demyelination

K. Kristensson, K. V. Holmes, C. S. Duchala, N. K. Zeller, R. A. Lazzarini & M. Dubois-Dalq

*Nature* **322**, 544-547 (1986)

IN the title of this letter the word 'gene' was incorrectly included. The title is correct as above.