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^{Ds} insertion is 127 bp to the right of the PstI site in D. simulans at coordinate -15.0. This site is also found in D. melangoaster. Restriction-site coordinates are from ref. 2. The fa^{fx} insertion is 230 bp to the right of the PvuI site at -13.8, fa is 157 bp to the left of the Bg/II site at -11.2, and fa^{g} is 25 bp to the left of the HindIII 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^{10,11}

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 eve 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 Drosophila³. Thus, the aberrant eve 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^{g62} differ by one nucleotide, whereas the fa^{g62} and fa^3 insertion sites differ by only three nucleotides (Fig. 3), yet fa and fa^3 give a facet phenotype and fa^{g62} 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 eve phenotypes because temperature-sensitive, lethal mutations that map to Notch protein-coding regions produce similar eye phenotypes following temperature pulses early in pupation^{2,4,5} Also a short deletion strawberry, near the 5' end of Notch produces a related mutant phenotype, presumably by altering the level of Notch locus transcription⁵. 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^3 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 intereference 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

No

fa No

fa ^{Ds} Notch ⁺	CCCTTAAAAGGCAGCAAACATACATATAC ttacgtagttatta CCCTTAAAAGGCAGCAAACATACATATATGTGCGATCTCTCTGGATCTTCTGCAAA atattatgctactATATATGTGCGATCTCTCTCGATCTTCTGCAAA	C Notch ⁺ C fa ^{Ds}
fa ^{fz} Notch ⁺	GGATTTTATTTGGGTTGTATATATATATgtaagattgt GGATTTTATTTGGGTTGTATATATATATATATATTTTTTT	ΓNotch ⁺ Γfa ^{fx}
f a ^{g 5 8} f a g f a ^g 6 2 Notch ⁺	TTTTTCTTATATACGTATGTTATGTATATATATATATCTCTTTCATATATGTATgtaaga TTTTTCTTATATACGTATGTTATGTATATATATATATATCTCTTCTTATATACGTATGTTATGTATATATA	Notch ⁺ fa ^{g 82} fa ^g fa fa ^{g 58}
fa ^g Notch ⁺	CATGGGAATCCCCAAGCAAAAAAAAAAAAAAAAATATATAT	Notch ⁺ fa ^g

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

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Corrigendum

DNA fingerprint analysis in immigration test-cases

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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-Dalcq

Nature 322, 544-547 (1986)

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