32-kilobase (kb) region on the 5′ side of the δ- globin gene which includes the γ, ε and ψ β_1 genes. Six sites are found in a separate 20kb block across and to the 3′ side of the β gene. Theoretically, the variants at the seven restriction sites might be found in over one hundred different combinations in the 5′ region. Remarkably, only three combinations are common, all of which are distinguished from each other at at least two sites. Similarly, in the 3′ block, only three more combinations are found. This high degree of linkage association would be unsurprising in view of the short distance separating the markers, but for the observation that across an 11 kb region spanning the δ gene, random association between 5′ and 3′ haplotypes is found. However, this recombination hot spot is unlikely to be a function of the δ-globin gene itself, as the flanking blocks include all the other genes in this cluster.

In surveys of the β-globin region, few DNA insertion variants have been found. In contrast, studies of restriction site polymorphism at two genes in *Drosophila* indicate that insertion/deletion events are an important source of variation. In a 12 kb region around the alcohol dehydrogenase (*Adh*) gene in *D. melanogaster*, five insertion/deletion variants were discovered in 18 lines from natural populations (C.H. Langley, NIEHS, North Carolina). However, the commonest restriction map in *D. melanogaster* showed little divergence that could be ascribed to DNA insertion from those obtained for two other species, *D. simulans* and *D. mauritiana*. Similar results are seen for the *87A* heat-shock locus in *Drosophila* (A. Leigh Brown, Imperial Cancer Research Fund). It is not yet known whether these other *Drosophila* species also show insertional variation but it could be that 'the spaces between the genes' are important in as yet undefined ways such that insertions or deletions are generally screened out by natural selection. The strong conservation of the distances between genes in the β-globin cluster of higher primates has prompted similar speculations (Jeffreys).

The *Adh* gene in *D. melanogaster* is also the first nuclear gene to be used for a systematic survey of variation in natural populations using DNA sequencing (M. Kreitman, Harvard University). Of 1,750 bp which have been sequenced in 11 isogenic strains, 36 nucleotide positions are variable. Unlike mtDNA, transitions and transversions are equally frequent. No amino acid substitutions were detected apart from the Thr-Lys substitution which causes the well known 'fast-slow' electrophoretic polymorphism. If it is assumed that the only substitutions permitted are silent ones whch do not result in an amino acid change, the frequency of polymorphic nucleotide sites relative to the number of silent sites in exons is very similar to the total frequency found in the introns. A much lower frequency was found in the 5′-non-coding regions of the transcripts, suggesting that some constraints on nucleotide substitution may be acting upstream of the protein-coding region. However, these apparently do not extend to the transcription start point, around which substitutions were quite frequent.

Finally, population genetics theory is now being applied to the behaviour of transposable elements in eukaryotic populations. A simple mathematical model has been developed that gives the expected frequencies of occupation of a particular chromosomal site by a mobile element in a natural population under the action of random genetic drift (J. Brookfield and C.H. Langley, NIEHS). Testing this model with data on the sites of hybridization to *Drosophila* polytene chromosomes of three mobile elements, *copia*, *412* and *297*, Brookfield and Langley showed that the data give a good fit for a high transposition rate. The result may be unexpected given that some mutations due to *copia* insertions (for example w^a) are very stable. It was also observed that the frequency of co-occupancy of a site by more than one type of transposable element was much higher than expected. This suggests either that insertion is not random and occurs after strand breakage or some similar event, or that the total number of occupable sites is restricted.

The P factor is a transposable element whose movement is responsible for a syndrome of germ-line aberrations in *D. melanogaster* known as hybrid dysgenesis. These aberrations are only found when wild males are crossed to females from long-established laboratory strains. Wild-type strains from the USA almost without exception carry this factor (P strains) while old-established laboratory strains do not (M strains). It had been thought that this loss was a consequence of inbreeding but new data on the relative frequency of such strains in collections from Europe and the Far East give a very different picture (M. Kidwell, Brown University). Here 'Q' strains, which are compatible with both P and M strains but contain many copies of the P element, are common, while M strains are of intermediate frequency and P strains are rare. In addition, some wild M strains are now known to contain some copies of the P element. The P element is known to be highly labile and it is not known whether any of the elements in these strains are functional. This complex pattern suggests that the element is itself undergoing rapid evolutionary change and possibly indicates an invasive rather than a symbiotic history.

Speculation that transposable elements may be involved in speciation has flourished following the discovery of their role in hybrid dysgenesis. If, however, the germ-line incompatibility is a consequence of a transient process of invasion, such involvement is much more difficult to envisage. It is hardly reasonable to propose a new invasion for each speciation event. Similarly, no clear pattern can yet be discerned on the general significance of insertional variation, which is apparently common in *Drosophila*, but is very rare in the human β-globin region. It seems more reasonable that the current difference between the mammalian and *Drosophila* data is due to the particular genes which have been studied in each organism to date [for example, the *dilute* coat colour mutation in the mouse is due to an insertion of retro-viral sequences (Jenkins, N. *et al. Nature* **293**, 370; 1981) and insertional polymorphism has also been found in man (Wyman & White, *PNAS* **77**, 6754; 1980)].

These studies are beginning to reveal some of the processes which take place in the genome during evolution. It should be nevertheless recognized that the pursuit of detail is not a satisfactory end in itself. However much is learnt about a single gene, if the knowledge cannot be generalized we will not have discovered much about evolution. The greatest interest in the new developments stems from the fact that the whole genome has been rendered accessible by these techniques, and that is something that evolutionary biologists have waited a long time for. □

100 YEARS AGO

THE two Swedish gunboats which conveyed the circumpolar observation party to Spitzbergen, have just returned to Tromsö. Capt. Palander states that it was impossible to approach Mossel Bay, he having made two attempts, on account of heavy pack-ice, and that the party had therefore settled on Cape Thordsten as their residence, where observations commenced on the 15th inst. He further reports that all the Norwegian fishermen he met complained of the unfavourable season and the enormous quantity of ice this summer, no vessel having been able to get higher than Amsterdam Island, from where no opening could be seen by telescope in any direction.

The steamer *A.E. Nordenskjöld*, belonging to M. Sibiriakoff, left Tromsö on the 18th inst. for the Jenisei. The vessel has on board a cargo of English merchandise, two steam launches, and an engine for the Siberian gold works. The vessel will attempt to save some of the cargo lost in the *Oscar Dickson* in Gydaviken, and return next year with a full cargo of tea, which will be brought from China across the Baikal sea to Kureika on the Jenisei.

The death is announced of Count Lutke, well known in connection with Russian Arctic exploration, especially in the Novaya Zemlay region.

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