polymerase itself, as would be the case if the enhancer segment served as a very efficient entry site for initial polymerase binding, or whether the enhancer acts solely via its influence on the conformation of an upstream polymerase binding site. The latter interpretation presumes the existence of a promoter-like element upstream of the transcriptional initiation site, which would be susceptible to *cis* regulation by the enhancer. It is already known that *V* genes have TATA box elements in the necessary upstream position; now Parslow *et al.* and Falkner and Zachau (*op.cit.*) have identified a second set of upstream sequences that may be essential for promoter function.

An alignment of the sequences that flank the transcriptional initiation site of a relatively large number of mouse and human V_κ genes as well as the mouse V_λ genes has revealed a very highly conserved octanucleotide, ATTTGCAT, located about 60–80 nucleotides upstream of the initiation site. Moreover, gene transfer experiments in which deletion mutants of a functional κ gene were integrated into the genomes of plasmacytoma cells that were not producing immunoglobulin have demonstrated that the region containing this octanucleotide is essential for effective transcription (Falkner & Zachau, *op. cit.*). Remarkably, the V_H genes do not contain this sequence but its inverted complement (ATGCAAAT) at precisely the same location relative to their transcriptional start site. These octanucleotide elements may have a role analogous to the various similarly located sequences that have been shown to be important for the transcription of other genes; together with the TATA box, they may comprise the functional promoters of immunoglobulin genes. Although a more narrowly defined set of mutants will be needed to establish whether the octanucleotide is a critical part of the promoter, its almost ubiquitous occurrence in all *V* genes makes it a most attractive candidate. Indeed, for this gene family, its conservation greatly exceeds that of the TATA box. Interestingly, there is a perfect ATTTGCAT sequence in a region of the J_H–C_μ intron where some of the germ-line (sterile) heavy-chain transcripts are initiated and an almost perfect inverted sequence (ATGTAAAT) upstream of the site where germ-line κ transcripts are initiated. It is conceivable that these sequences help define the 'pseudopromoters' that are used in the generation of germ-line transcripts.

The difference in transcriptional competence between unrearranged *V* and *C* regions suggests that some type of regulatory hierarchy between enhancer and promoter elements is maintained throughout the course of B-lymphocyte development. The recent finding of a heavy-chain gene that presumably lacks its normal enhancer and yet still produces heavy-chain mRNA has been interpreted to mean that the enhancer function is not obligatory for expression (Wabl, M.R. & Burrows, P.D. *Proc. natn. Acad. Sci. U.S.A.* **81**, 2452; 1984). However, it is difficult to evaluate the significance of this observation because the gene has not yet been sequenced; conceivably the enhancer function has been taken over by some surrogate sequence element, just as the pseudopromoters can substitute for the proper *V*-region promoters.

The enhancer element seems to require a tissue-specific *trans*-acting factor, the activity of which is subject to induction by external stimuli during the early (pre-B-cell) maturation stages and becomes constitutive in later (B-cell and plasma-cell) stages (Nelson, K.J. *et al. Nucleic Acids Res.* **12**, 1911; 1984). The promoter may also be regulated by *trans*-acting factors. If so, such factors might be responsible for the increased rate of transcription that is characteristic of terminally differentiated plasma cells. □

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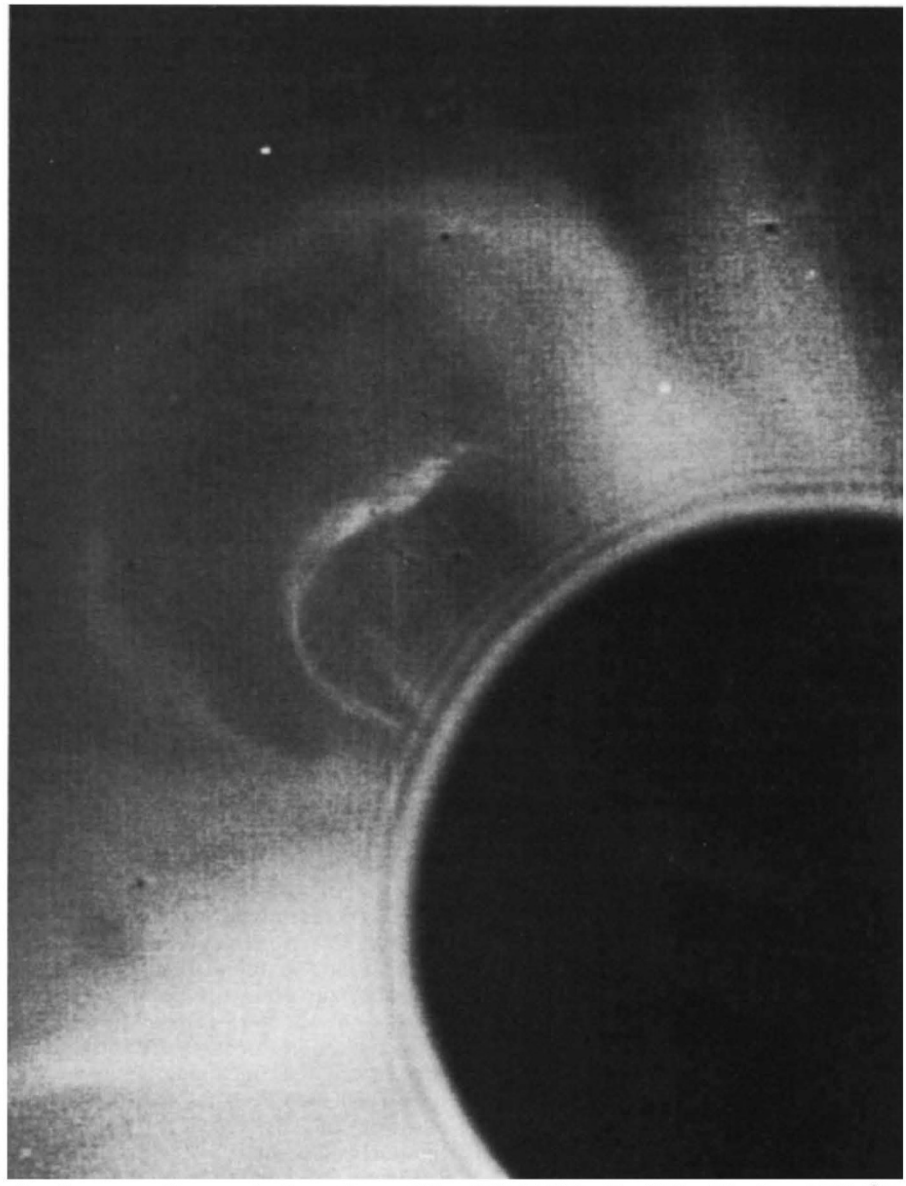

A solar coronal mass ejection observed in white light by the Solar Maximum Mission coronograph. The axis of solar rotation runs from the upper left (north) to the lower right; the Sun-centred occulting disc has a radius of 1.6 times the radius of the Sun. The outward velocity was 200 km^{-1}. The ejection is typical of 65 observed during the Solar Maximum Mission between March and September 1980 in that it has a three-part structure: an inner bright loop sometimes seen in Hα and thus probably the material from an emptying prominence; a 'dark' shell surrounding the loop, probably identifiable with the cavity seen around prominences in the low corona; and an outer 'rim' of displaced coronal material. Such ejections, representing a discrete addition of material to the solar wind, were detected on average 0.9 times per day during the 1980 Solar Maximum Mission sampling period — 20 per cent more often than detected by Skylab in the declining phase of the previous sunspot cycle in 1973–4. (From Hundhausen, A.J., Sawyer, C.B., House, L., Illing, R.M.E. and Wagner, W.J. *Journal of Geophysical Research* 89, 2639; 1984.)