RÉSUMÉ

Dead issues

THE idea that some mass extinctions were caused by massive volcanic episodes is undermined by D. H. Erwin and T. A. Vogel in *Geophysical Research Letters* (**19**, 893–896; 1992). The greatest extinction, the Permo/Triassic, has been linked to volcanics in southern China with an estimated volume of 1,000 km^3. For comparison, Krakatau, which erupted just 12 km^3 of magma and raised ash to a height of 30 km, caused global cooling of 0.4 °C for two years. The authors test the idea by reversing it, looking at some of the greatest volcanic episodes (the largest, at Elkhorn Mountains 75–81 million years ago, erupted at least 4,000 km^3 of magma) to see if they coincide with increases over the natural extinction rate. But in none do the authors find any related decrease in biological diversity, even regionally.

Molecular lightning rod

THE pursuit of the magic bullet that will penetrate a cell and strike only its target protein was probably started by Ehrlich. One version depends on bringing a chromophore close to the target protein and exciting it with laser light, thus sensitizing the photochemical destruction of the protein. The dye can be coupled to an antibody or dispersed in a membrane or micelle if the target is a membrane protein. K. G. Linden *et al.* (*Biophys. J.* **61**, 956–962; 1992) have now defined the distance over which the excited chromophore will exert its effect: a labelled antibody, attached to its antigen, β-galactosidase, causes (under given conditions) 75% inactivation of the enzyme. Attached to protein A, which is then bound to the antibody, it destroys 20% of the activity and on anti-protein A, bound to protein A, itself bound to the enzyme-associated anti-β-galactosidase, it can annihilate no more than 4% of the activity.

Cereal success

FOR all its enormous economic importance, wheat has proved a tough subject for the genetic engineer. But the door to the manipulation of its genome springs ajar with a report by V. Vasil *et al.* (*Bio/Technology* **10**, 667–674; 1992) of the production of fertile transgenic plants. The gene involved (*bar*) is selectable because it encodes an enzyme which inactivates the main agent of a broad-spectrum herbicide; it was delivered, in plasmid form, into the cells of an embryogenic callus by microprojectile bombardment. The resulting plants exhibited *bar* activity down to the third generation, and the gene segregated in dominant mendelian form. The success rate of gene transfer was low, but the door to the engineering of drought- and pest-resistant wheat will no doubt be pushed open further in the coming months.

GENE REGULATION

Transcriptional transgressions

Michael R. Green

EUKARYOTIC RNA polymerases, the enzymes that transcribe the genetic information, are unable to initiate the process accurately by themselves; instead, they are directed to the start-site of a gene by a group of auxiliary proteins, dubbed transcription factors. Over the past 15 years some general principles about transcription factors have emerged — or rather we thought they had emerged, for a series of papers[1–5] has now brought three of those principles into question.

Eukaryotic genes can be divided into three classes, according to which RNA polymerase is responsible for transcribing them: thus RNA polymerase I transcribes ribosomal RNA (class I) genes; RNA polymerase II transcribes mRNA-encoding (class II) genes; and RNA polymerase III transcribes class III genes, which encode small RNAs such as 5S RNA and transfer RNAs. The transcription factors for each RNA polymerase were originally defined by chromatographic fractionation.

First principle

One principle to emerge was that each RNA polymerase has its own set of transcription factors. Yet several observations revolving around the transcription factor TFIID have blurred the demarcation between transcription factor classes. TFIID, a multiprotein complex, is the prototype class II transcription factor. It is best known for binding to the TATA box, the major landmark of a minimal (or core) class II promoter. But some class III genes (for example U6 snRNA, 7SK and EBER2) contain an upstream TATA-like element required for full transcriptional activity. Biochemical complementation experiments have verified that the TATA-box binding protein (TBP), a subunit of TFIID, is indeed required for transcription of these class III genes[6–8].

It had been generally assumed, however, that the TATA-containing class III promoters were quirks; the more conventional class III genes (tRNA and 5S RNA, for example) have completely intragenic promoters and lack an upstream TATA box element. Yet White and colleagues[2] have used both biochemical complementation and TATA box oligonucleotide-inhibition experiments to show that TBP is also required for the transcription of these typical class III genes.

But the TBP story does not end here. Comai *et al.*[3] demonstrate that TBP is also involved in RNA polymerase I-directed transcription; specifically, anti-TBP antibodies can deplete the RNA polymerase I transcription factor SL1, thereby abolishing transcription. RNA polymerase I transcription was restored by addition of SL1 but not TBP. This is because SL1 is not just TBP, but rather a complex of TBP and three TBP-associated factors (TAFs). TFIID is also a complex of TBP and several TAFs, but the constellations of TAFs in TFIID and SL1 are completely different[3].

Although the TBP-containing complex involved in RNA polymerase III transcription has not been characterized, several observations suggest that it is TFIIIB, a well-known RNA polymerase III transcription factor. The unifying concept taking shape is that all three RNA polymerases require an essential transcription factor, which is a complex containing TBP and TAFs, the composition of the TAFs differing in the three instances.

These findings explain why TBP does not behave as a single biochemical entity. For example, it is present both in the conventional TFIID fraction and in another abundant complex, designated B-TFIID (ref. 9). It now seems likely that B-TFIID is involved in either class I or class III transcription.

Surprisingly, however, B-TFIID can substitute for the RNA polymerase II transcription factor, TFIID, in a basal transcription reaction[9]. B-TFIID can therefore provide the TBP function of TFIID. Minimally, this means that TBP in B-TFIID can contact the TATA box and several RNA polymerase II trans-

1. Parvin, J. D., Timmers, H. T. M. & Sharp, P. A. *Cell* **68**, 1135–1144 (1992).
2. White, R. J., Jackson, S. P. & Rigby, P. W. J. *Proc. natn. Acad. Sci. U.S.A.* **89**, 1949–1953 (1992).
3. Comai, L., Tanese, N. & Tjian, R. *Cell* **68**, 965–976 (1992).
4. Roy, A. L., Meisterernst, M., Pognonec, P. & Roeder, R. G. *Nature* **354**, 245–248 (1991).
5. Sumimoto, H., Okhuma, Y., Tamamoto, T., Horikoshi, M. & Roeder, R. G. *Proc. natn. Acad. Sci. U.S.A.* **87**, 9158–9162 (1990).
6. Lobo, S. M., Lister, J., Sullivan, M. L. & Hernandez, N. *Genes Dev.* **5**, 1477–1489 (1991).
7. Margottin, F. *et al. Science* **251**, 424–426 (1991).
8. Simmen, K. A. *et al. EMBO J.* **10**, 1853–1862 (**19??**).
9. Timmers, H. T. M. & Sharp, P. A. *Genes Dev.* **5**, 1946–1956 (1991).
10. Stringer, K. F., Ingles, C. J. & Greenblatt, J. *Nature* **345**, 783–786 (1990).
11. Horikoshi, N. *et al. Proc. natn. Acad. Sci. U.S.A.* **88**, 5124–5128 (1991).
12. Lee, W. S., Cheng-Kao, C., Bryant, G. O., Liu, X. & Berk, A. J. *Cell* **67**, 365–376 (1991).
13. Liberman, P. M. & Berk, A. J. *Genes Dev.* **5**, 2441–2454 (1991).
14. Seto, E., Shi, Y. & Shenk, T. *Nature* **354**, 241–245 (1991).
15. Ohkuma, Y., Sumimoto, H., Horikoshi, M. & Roeder, R. G. *Proc. natn. Acad. Sci. U.S.A.* **87**, 9163–9167 (1990).
16. Vaishnav, Y. N. & Wong-Staal, F. *A. Rev. Biochem.* **60**, 577–630 (1991).
17. Tamura, T., Sumita, K., Hirose, S. & Mikoshiba, K. *EMBO J.* **9**, 3101–3108 (1990).
18. McCormick, A., Brady, H., Fukushima, J. & Karin, M. *Genes Dev.* **5**, 1490–1503 (1991).

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