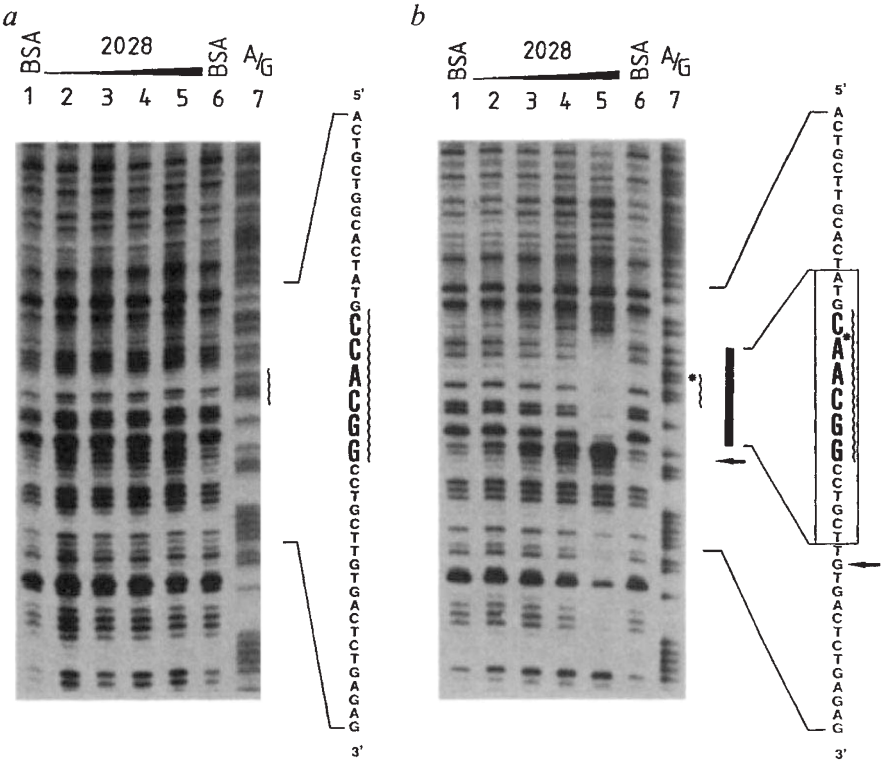

Fig. 3. The pyAACG/TG-motif is important for MYB-specific DNA-binding. DNase I footprints of gel-purified full-length v-MYB (2028) bound to a sequence derived from the upstream region of the chicken lysozyme gene (panel *a*) or to a mutated version of this sequence (panel *b*). Approximate amounts of v-MYB used were: 50 ng (lane 2), 100 ng (lane 3), 250 ng (lane 4) and 500 ng (lane 5). Other lanes represent control reactions containing BSA instead of v-MYB. Lanes marked by *A/G* show the products of (A+G)-specific sequencing reactions of the radiolabelled DNA fragments. The position of a point mutation converting the original CCACGG sequence to the putative v-MYB recognition motif CAACGG is marked by an asterisk. The protected region and an enhancement of DNase I cutting are marked by a bar and an arrow respectively.
Methods. Footprinting analysis was carried out as described in Fig. 2, using a *StuI/BsmI* restriction fragment from about 6 kilobases upstream of the chicken lysozyme gene promoter (see ref. 26 for the exact location of the mutated sequence, designated BS1b).

to sequences found in *myc*-, *fos*- and *jun*-encoded proteins and in the transcription factor C/EBP, and is assumed to mediate protein-protein interaction[20]. We do not know whether or not these similarities reflect comparable modes of action for v-MYB and these other proteins.

At present we can only speculate on the *in vivo* function of MYB. The '*myb*-like' *C1* gene of *Zea mays* controls the expression of genes involved in anthocyanin biosynthesis[12], and *myb* genes could also be regulatory. Interestingly, the *A1* gene of *Zea mays* is a candidate target gene for the *C1* gene product[22] and lies close to a cluster of 12 puAACGT sequences, which is related to the MYB-binding motif. As well as indicating that the MYB recognition motif has been highly conserved during evolution, this observation also supports the idea that v-MYB controls gene expression by direct binding to MYB target genes. Our approach could be used to identify MYB target genes in a collection of DNA sequences. Finally, it is interesting that the amino-acid sequences of the MYB DNA-binding domain at its amino terminal[13] show no significant homology with consensus sequences of either 'helix-turn-helix'- or 'zinc-finger'-type DNA-binding proteins[23,24], so MYB could exemplify a novel type of DNA-binding protein.

We thank H. Arnold for technical assistance, J. Paz-Ares, U. Wienand and H. Saedler for communicating results before publication and C. Bonifer, M. Koenen and A. Nordheim for discussion. This work was supported by the Bundesministerium für Forschung und Technologie.

Received 21 July; accepted 19 September 1988.

1. Klempnauer, K.-H. *et al. Cell* **33**, 345-355 (1983).
2. Boyle, W. J. *et al. Proc. natn. Acad. Sci. U.S.A.* **81**, 4265-4269 (1984).
3. Moelling, K. *et al. Cell* **40**, 983-990 (1985).
4. Klempnauer, K.-H. & Sippel, A. E. *Molec. cell. Biol.* **6**, 62-69 (1986).
5. Klempnauer, K.-H., Bonifer, C. & Sippel, A. E. *EMBO J.* **5**, 1903-1911 (1986).
6. Gonda, T. J. & Bishop, J. M. *J. Virol.* **46**, 212-210 (1983).
7. Gonda, T. J., Gough, N. M., Dunn, A. R. & de Blaquiere, J. *EMBO J.* **4**, 2003-2008 (1985).
8. Rosson, D. & Reddy, E. P. *Nature* **319**, 604-606 (1986).
9. Slamon, D. J. *et al. Science* **233**, 347-351 (1986).
10. Katzen, A. L., Kornberg, T. B. & Bishop, J. M. *Cell* **41**, 449-456 (1985).
11. Peters, C. W. B., Sippel, A. E., Vingron, M. & Klempnauer, K.-H. *EMBO J.* **6**, 3085-3090 (1987).
12. Paz-Ares, J. *et al. EMBO J.* **6**, 3553-3558 (1987).
13. Klempnauer, K.-H. & Sippel, A. E. *EMBO J.* **6**, 2719-2725 (1987).
14. Sap, J. *et al. Nature* **324**, 635-640 (1986).
15. Weinberger, C. *et al. Nature* **324**, 641-646 (1986).
16. Bohmann, D. *et al. Science* **238**, 1386-1392 (1987).
17. Angel, P. *et al. Nature* **332**, 166-171 (1988).
18. Rauscher, F. J. *et al. Cell* **52**, 471-480 (1988).
19. Rauscher, F. J. *et al. Science* **240**, 1010-1016 (1988).
20. Landschulz, W. H., Johnson, P. F. & McKnight, S. L. *Science* **240**, 1759-1764 (1988).
21. Klempnauer, K.-H., Gonda, T. J. & Bishop, J. M. *Cell* **31**, 453-463 (1982).
22. Schwarz-Sommer, Z. *et al. EMBO J.* **6**, 287-294 (1987).
23. Klug, A. & Rhoades, D. *Trends biochem. Sci.* **12**, 464-469 (1987).
24. Pabo, C. O. & Sauer, R. T. *A. Rev. Biochem.* **53**, 293-321 (1984).
25. Hager, D. A. & Burgess, R. R. *Analyt. Biochem.* **109**, 76-86 (1980).
26. Borgmeyer, U., Nowock, J. & Sippel, A. E. *Nucleic Acids Res.* **12**, 4295-4311 (1984).
27. Wessel, D. & Flügge, U. I. *Analyt. Biochem.* **138**, 141-143 (1984).

Errata

Crystal structure of *trp* repressor/operator complex at atomic resolution

Z. Otwinowski, R. W. Schevitz, R.-G. Zhang, C. L. Lawson, A. Joachimiak, R. Q. Marmorstein, B. F. Luisi & P. B. Sigler
Nature **335**, 321-329 (1988).

IN this article the present address of one of the authors was given incorrectly. Rong-guang Zhang's correct address is: Chinese Academy of Sciences, Institute of Biochemistry, Shanghai, The People's Republic of China.

Controls on the structure of subducted slabs

Michael Gurnis & Bradford H. Hager
Nature **335**, 317-321 (1988).

THE above title better reflects the meaning of this article, which appeared in the 22 September issue with the word 'of' instead of 'on'.