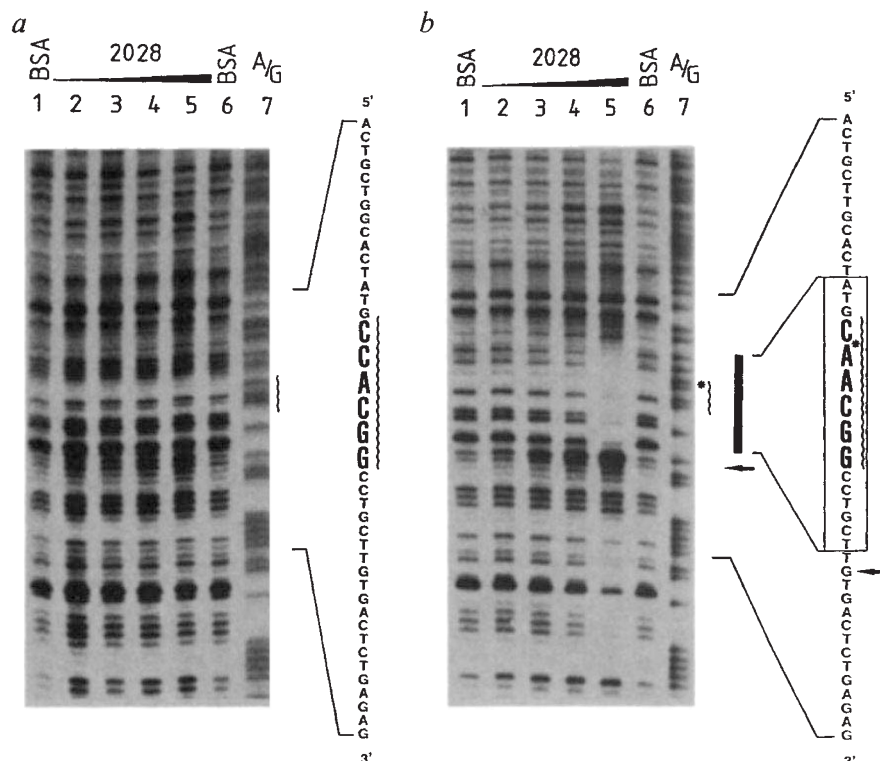


**Fig. 3.** The pyAACG/TG-motif is important for MYB-specific DNA-binding. DNase I footprints of gel-purified full-length v-MYB (2028) bound to a sequence derived from the upstream region of the chicken lysozyme gene (panel *a*) or to a mutated version of this sequence (panel *b*). Approximate amounts 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<sup>20</sup>. 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<sup>12</sup>, and *myb* genes could also be regulatory. Interestingly, the *A1* gene of *Zea mays* is a candidate target gene for the *C1* gene product<sup>22</sup> 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<sup>13</sup> show no significant homology with consensus sequences of either 'helix-turn-helix'- or 'zinc-finger'-type DNA-binding proteins<sup>23,24</sup>, so MYB could exemplify a novel type of DNA-binding protein.

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