Corrigenda

Thyroid hormone receptor α isoforms generated by alternative splicing differentially activate myosin HC gene transcription

Seigo Izumo & Vijak Mahdavi

Nature 334, 539-542 (1988).

IN the typing of the derived amino-acid sequence of $rTR\alpha 1$ and $rTR\alpha 2$ cDNAs, the sequence for amino acids 401-410 were inadvertently swapped between the two isoforms. The correct sequence reads: FLEVFEDQEV for $rTR\alpha 1$ and QLLGMHVVQG for $rTR\alpha 2$.

T-cell antigen receptor genes and T-cell recognition

Mark M. Davis & Pamela J. Bjorkman

Nature 334, 395-402 (1988).

IN this Review Article, the colour-coding given in the legend to Fig. 4 relates to an earlier version of the figure, not the one in the final version of the manuscript. The legend is reprinted here in full with the correct colour coding:

Fig. 4 Representations of the structures of a, the immunoglobulin combining site; b, the peptide-binding site of an MHC molecule; and c, the alignment of CDRs in a hypothetical TCR over a peptide-MHC complex. a, The arrangement of CDRs in an immunoglobulin antigen-binding site (Fab J539)¹²² viewed from above (from the position of the antigen). The carbon- α backbone of $V_{\rm H}$ and $V_{\rm I}$ is shown in blue with van der Waals' surfaces highlighting the three CDRs from each domain (CDR1: blue, CDR2: yellow, CDR3: pink). The first and second CDRs from one variable domain (for example, immunoglobulin V_1 or TCR V_{α} or $V_{\rm v}$) are separate from their counterparts on the partner variable domain (immunoglobulin $V_{\rm H}$ or TCR V_{β} or V_{δ}). The space between them is occupied by the third CDR from each V domain. The similarities between immunoglobulins and TCRs suggest that TCRs may have a combining site that preserves these same general features (see text for details). b, Top surface of an MHC molecule with a (hypothetical) bound peptide. The carbon- α backbone of the α_1 and α_2 domains of HLA-A2 (ref. 40) is shown in blue with van der Waals' surfaces highlighting the two α -helices (yellow). Van der Waals' surface of a hypothetical bound peptide (a 12-mer polyvaline α -helix) that has been fitted between the HLA α -helices is shown in pink. The putative recognition site for processed foreign antigens is shown in pink. The pinkive recognition such that processed to each of the human located on the top surface of the molecule between two α -helices for the human class I histocompatibility molecule HLA-A2^{40,41}. The N-terminal α_1 and β_1 domains of class II MHC molecules are predicted to have a similar tertiary structure and peptide-binding site⁴². Note that the distance between the MHC α -helices, and the separation of the first and second CDRs of each V-region in the combining site shown in part a are very similar. (Figures are to scale with respect to each other). c, Model for TCR interaction with a peptide-MHC complex. The combining site CDRs (a) are shown aligned over the peptide-MHC complex (b). The molecules in this figure are rotated $\sim 90^{\circ}$ with respect to their orientations in (a) and (b). V domains of Fab J539 (ref. 122; top of figure) here represent the V domains of a TCR bound to a peptide-MHC complex (bottom of figure). The carbon- α backbone of V_L and V_H (blue) is shown with main and side-chain atoms of CDR1 and CDR2 (yellow) from each domain. The main and side-chain atoms of the CDR3s of each domain are shown in pink. The carbon- α backbone of the α_1 and α_2 domains of HLA-A2 (blue) is shown with the main and side-chain atoms of the two α -helices in yellow and the main and side-chain atoms of a hypothetical peptide bound between the two helices in pink. The relatively flat surface of the V-region combining site is complementary to the flat surface of the MHC-peptide complex, with CDR1 and CDR2 of each V domain 'fitting' over an MHC α -helix. The CDR3s from each V domain are then aligned over the peptide (see text for details). Because the antibody (and presumably TCR) V regions pair with approximate twofold (dyad) symmetry^{9,10}, a similar interaction of CDR1 and CDR2 with the MHC α -helices and CDR3 with peptide would be accomplished if the $V_{\rm H}$ - $V_{\rm L}$ dimer shown in this figure were rotated by 180° about the pseudo-dyad axis between the two V regions (axis is vertical in this figure). Note that the relative sizes of the combining site (a) and the peptide-binding site of the MHC molecule (b) would allow TCRs to be bound in different registers along the MHC α -helices, depending on the particular peptide bound to that MHC protein. Thus the V genes employed by different T cells restricted to the same MHC molecule would not be expected to be identical. Furthermore, the C-terminal few amino acids encoded by a V gene are part of the V-J or V-D-J junction, and would be predicted by this model to interact primarily with peptide rather than MHC determinants.

In addition, in Table 1 on page 397, the penultimate column should be headed γ rather than ν .

The molecular genetics of embryonic pattern formation in *Drosophila*

P. W. Ingham

Nature 335, 25-34 (1988).

THE labels were omitted from Fig. 2 in this Review Article, and are shown below in a black-and-white version of the figure.



Errata

Sensory transmitters regulate intracellular calcium in dorsal horn neurons

M. D. Womack, A. B. MacDermott & T. M. Jessell Nature 334, 351-353 (1988).

In this letter, the two sentences beginning on line 29 on page 353 should read: "Both classes of transmitters appear to regulate $[Ca^{2+}]_i$ in these neurons, albeit by many different mechanisms. Substance P increases $[Ca^{2+}]_i$ in many dorsal neurons by mobilizing intracellular Ca^{2+} stores.

Global fire at the Cretaceous–Tertiary boundary

W. S. Wolbach, I. Gilmour, E. Anders, C. J. Orth & R. R. Brooks *Nature* 334, 665–669 (1988).

ON page 666, the third line from the bottom should read: "The soot content rises even more sharply across the boundary: 11, 1930 and 97 p.p.m."