Transformation by the p21^{ras} protein

SIR — Ralph[1] has questioned the validity of certain speculative comments of mine concerning the mechanisms by which p21^{ras} proteins transform mammalian cells. He has obviously misunderstood the point of my remarks.

In my article, I drew an analogy between new findings showing loss of GTPase activity in the transforming protein and the fixation of adenylate cyclase Gs protein in the GTP state after cholera toxin binding. In case it was not made clear in the article, perhaps I should state that there is no evidence of a functional link between the adenylate cyclase system and p21^{ras}, and therefore for a direct role of cyclic AMP regulation in *ras*-mediated transformation. Examples of some of the known effects of cholera toxin on cell physiology and proliferation were mentioned solely to illustrate the profound consequences which result from fixation of the adenylate cyclase G-protein in the GTP form. As stated in my article, which (if any) specific effector systems involve p21^{ras} in signal transduction remains to be established.

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The gyroscope test of relativity

SIR — Your account of the "relativity gyroscope experiment"[1] does not go beyond that of Schiff[2], who proposed that two effects, the geodetic (de Sitter or spin–orbit) and motional (Lense–Thirring or spin–spin) precessions, could be measured separately by the use of at least two gyros in free fall in a perfect polar orbit. An accuracy of 0.3 milliarc-seconds per year is the desired goal. However, there are many other contributions which are well above 0.3 marc s yr^{-1} (for a review see ref. 3).

The goal of the experimentalists is to make a sphere of fused quartz accurate to one part in 10^7, but even a perfect sphere is distorted when set spinning, acquiring a quadrupole moment, which for an altitude of 500 miles, will contribute more than 0.3 marc s yr^{-1} to the gyro drift rate if the spin axis is more than 20 minutes of arc away from either the orbit plane or the perpendicular to the orbit plane[4].

Second, the Earth's quadrupole moment will contribute an amount of 4 marc s yr^{-1}, more than ten times the desired accuracy, and, more subtly, distorts the satellite orbit so that, in averaging over a polar orbit, one obtains an additional "indirect contribution" of 1.33 marc s yr^{-1}.

Third, the contribution due to the Sun will give rise to a geodetic precession of the gyro (due to interaction of the spin of the the gyro with its orbital angular momentum about the Sun), with the relatively large value of 19.2 marc s yr^{-1}, while the deflection of light from the reference star (Rigel in Orion) can cause an apparent drift of the gyroscope of up to14.4 marc s yr^{-1}.

The relativity gyro experiment test of general relativity is thus more complex than originally envisaged. Hence, there is a need for other tests of the geodetic and motional precessions, particularly the latter. A promising suggestion in this direction is the proposal of Scully and co-workers[5,6] to use a ring laser interferometer to test both the geodetic and the motional precessions, which has the attraction that it can be carried out on Earth, while another proposal is to use a Foucault pendulum at the South Pole[7]. Also, the binary pulsar PSR1913+16 may provide a test of the spin–orbit precession and our calculations[8] predict a precession rate for the pulsar spin axis of 1.23° yr^{-1}, based on the data of Taylor and Weisberg[9].

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Mouse Igκ sequence elements in *Drosophila*

SIR — Two sequence elements may be needed for correct transcription of the mouse immunoglobulin κ gene. They are: TNATTTGCAT (dc), its inverted and complementary ATGCAAATNA (cd), upstream of the H-chain gene and TGCA$^{G}_{C}$CTGTGNCCAG (pd)[1]. The same sequences (8 out of 10 base pairs) ATTTGCAT and ATGCAAAT have been found by Parslow *et al.* independently[2]. Sequences related to the above elements were found upstream of all human and mouse κ and λ variable region genes and within the mouse heavy-chain enhancer in a homology of 50–100%. The same elements are present in high homology in chicken ovalbumin gene, sea urchin histone gene cluster and in other genes[1]. I report here that the elements dc and cd are present upstream of the homoeotic gene *ftz*[3] of *Drosophila*.

The element AGGCAAATAC is found upstream the coding region of *ftz* (first nucleotide position −794)[3]. This has 78% homology with the cd element ATGCAAATNA. The sequence ATGTTTGCAT is also found upstream of the coding region of *ftz* (first nucleotide −854)[3] and shares 78% homology with the dc element TNATTTGCAT. Other sequence elements can also be found upstream or within the *ftz* gene with less homology with the dc, cd or pd 50–67%, but this does not seem to be significant since dc, cd or pd can be found in many genes when homology less than 70% is considered (F. G. Falkner and H. G. Zachau, personal communication).

The dc and cd elements are highly conserved among many genes. Their location within the immunoglobulin genes suggests functional relation[1]. The homoeotic gene *ftz* is associated with *Drosophila* development and contains a highly conserved region, the homoeo box, which has been found in other homoeotic genes — *Antp* and *Ulb* of *Drosophila* as well as in a wide spectrum of animals. The relationship of conserved sequences needed for transcription to upstream sequences needed for segmentation during development is unknown. It is, of course, possible that the homologies might be chance events, and more information is needed before evolutionary or functional relationships are considered.

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FAULKNER AND ZACHAU REPLY — We agree that the occurrence of dc-related elements upstream of genes deserves attention. We quote some examples for that in our previous paper[1] and others in a forthcoming one (F. G. F., E. Neumann and H. G. Z., manuscript in preparation). At this point we would like to mention that a sequence fully homologous to dc was found upstream of all or most histone H2B genes[2], a point which we had missed previously. In general, we searched sequence libraries for dc at the 89% homology level since at lower levels too many sequences are picked up. But also dc (and pd) related sequences with lesser homology may be interesting if they can be correlated with putative regulatory functions. One example of this which we recently encountered is the findingof the dc and cd related sequences in the regulatory regions upstream of catabolite-sensitive genes of *Escherichia coli*[3,4].

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