muscle-type acetylcholine receptor[5]. We have found that both cell lines contain an N-*ras* gene that is activated by a point mutation at the third base of codon 61 and, in new cell stocks obtained directly from the American Type Culture Collection, that the majority of marker chromosomes are common to the cell lines. Furthermore, DNA fingerprinting with locus-specific and core probes fails to reveal differences between the two lines.

Both cell lines were derived in the same laboratory but RD was described[6] and submitted to the ATCC before the first report of TE671. When considered together these observations indicate that TE671 is most probably a subline of the rhabdomyosarcoma cell line RD.

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Spectral peaks

SIR—Lutz and Watson[1] discuss the frequency spectrum of the Harland *et al.*[2] geomagnetic reversal record of the past 165 million years. This spectrum has been interpreted as showing a 30-million-year short-term oscillation superimposed on an aperiodic long-term variation. Lutz and Watson argue that the long-term component, $\lambda_L(t)$, dominates the frequency spectrum for periods P up to 40 million years. Here I show that the spectrum in this range is essentially determined by the strong boundary discontinuities introduced by performing a Fourier transform $\lambda_L(t)$ over a finite interval (τ_1, τ_2); that is, these discontinuities dominate over any time variation of $\lambda'_L(t)$ between τ_1 and τ_2.

The influence of discontinuities becomes apparent when the limits of the Fourier transform are extended to $(-\infty, +\infty)$. This leaves all integrals unchanged, provided that the 'extended' function $\lambda'_L(t)$ has the form

$$\lambda'_L(t) = \begin{cases} \lambda_L(t) \text{ for } \tau_1 \leq t \leq \tau_2 \\ 0 \text{ otherwise} \end{cases} \quad (1)$$

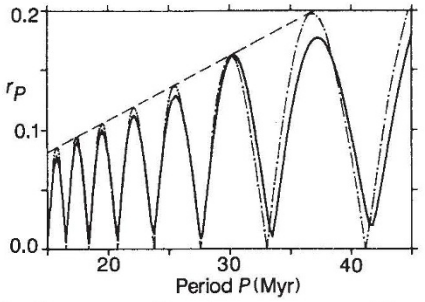
As $\lambda_L(t)$ is largest at the boundaries, $\lambda_L(t)$ exhibits large discontinuities there. The dominance of these discontinuities can be demonstrated by considering a simplified trial function

$$\lambda^0_L(t) = \begin{cases} \lambda_d = \text{constant for } -T/2 \leq t \leq T/2 \\ 0 \text{ otherwise} \end{cases} \quad (2)$$

which retains the two boundary discontinuities (of size λ_d, taken to have the value 5 Myr^{-1}, and separation $T = \tau_2 - \tau_1$) but carries no information on variations in between. The spectrum of this function,

$$R^0_P(T) = N^{-1}\lambda_d (P/\pi) |\sin(\pi T/P)| \quad (3)$$

is compared in the figure with that of $\lambda_L(t)$ obtained by Lutz and Watson[1]. (Here N is the total number of reversals.) We interpret the close correspondence in shape, position and peak heights as verification of our initial claim. The straight dashed line denotes the exact small-P asymptotic envelope for any function $\lambda(t)$ that has the same discontinuities as $\lambda'_L(t)$ and $\lambda^0_L(t)$. The positions of the maxima of $R^0_P(T)$ are given by $P_n \approx T/(n+1/2)$ for integers $n \geq 0$; for all T, they agree well with the values from the numerical Fourier transform of $\lambda_L(t)$ given in Table 1 of ref. 1, for which τ_1 was varied in discrete steps. Therefore, the grouping together there of peak positions with more or less constant period is arbitrary. When $\tau_2 - \tau_1$ decreases continuously, the peak positions do so too.



Fourier spectra of two long-term reversal functions plotted against period $P = 2\pi/\omega$. $R^1_P(\tau_1, \tau_2)$, from ref. 1, is shown as a solid curve, and $R^0_P(T)$ (equation (3)) as a dash-dotted line. The straight dashed line is the exact asymptotic envelope for $P << T$ to both spectra.

The influence of short-term oscillations would thus be seen only as noticeable deviations of the peak heights from those of $R^0_P(T)$, that is, from the envelope of $R_P(\tau_1, \tau_2)$. Using a Poisson process, Lutz and Watson[1] show that the long-term component alone may generate fluctuations in the peak heights that are large enough to account for the spectrum of the total reversal function $\lambda(t)$.

Thus, for periods $\lesssim 40$ Myr, the spectrum $R_P(\tau_1, \tau_2)$ of the total reversal function is determined mainly by the strong discontinuities in $\lambda_L(t)$ at τ_1 and τ_2, and hides any information on short-term variations. These can be reliably detected in the spectrum only if the discontinuous long-term variation can be subtracted before the Fourier transform operation.

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RNP in maize protein

SIR—We wish to point out an interesting feature in the sequence of the abscisic acid-induced glycine-rich protein (AAIP) of maize recently reported by Goméz *et al.*[1]. The protein contains a sequence (see below) which conforms perfectly to the RNP consensus sequence[2–4] that has been found so far in heterogenous nuclear RNA-, messenger RNA-, pre-ribosomal RNA-, and small-nuclear RNA-binding proteins.

Maize AAIP:

$\cdots^{49}$ Arg Gly Phe Gly Phe Val Thr Phe^{56}...

RNP consensus sequence:

... Lys Gly Phe Gly Phe Val Thr Phe...
Arg Tyr Ala Tyr X Tyr

This strongly suggests that AAIP is a single-stranded nucleic-acid binding protein, most probably an RNA-binding protein (RNP). Several other features of the AAIP sequence also resemble those found in some of these proteins. The protein appears to contain two distinct domains: an amino-terminal domain (about 90 amino acids) that contains the RNP consensus sequence, and a carboxy-terminal glycine-rich domain. The amino-terminal domain is the putative RNA-binding domain[4]. There are extensive similarities in the general character of the amino-terminal domain with that of the putative RNA-binding domain of several RNP proteins[4]. A glycine-rich domain is also a feature of some RNP proteins (for example, the hnRNP protein A1 (ref. 5), and the nucleolar protein nucleolin[6]). AAIP may be the first plant protein described so far to contain an RNP consensus sequence. The predicted property of AAIP as an RNA-binding protein can be readily tested, for example, by chromatography on small-subunit DNA columns, on ribohomopolymer columns, and by photochemical crosslinking to RNA.

Abscisic acid is a hormone that appears to modulate the response of plants to adverse conditions, and it seems to also play a role in embryogenesis. Determining if AAIP is indeed an RNA-binding protein, and if so, what RNA it binds to should be important for understanding the mechanism of these important processes.

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