

news and views

Are earthquakes a major cause of the Chandler wobble?

from Hiroo Kanamori

WHETHER or not earthquakes are a major cause of the Earth's free Eulerian nutation (period of 14 months), widely known as the Chandler wobble, has been a controversial issue. The present consensus seems to be that the crustal deformation associated with earthquakes is much too small to explain the amplitude of the Chandler wobble. O'Connell and Dziewonski (page 259 of this issue of *Nature*), however, suggest that earthquakes represent the major factor in the wobble excitation. Since their analysis is very direct and unambiguous, it is important to examine what makes their conclusion distinct from others'.

At one time, there were significant disagreements between theoretical results concerning the excitation of the Chandler wobble obtained by different investigators. This controversy, however, seems to have been completely settled, and the theory is now formulated in a rigorous framework. Observationally, the overall pattern of polar motion seems to be well established, although the data may not be good enough to allow correlation of the fine structure of the trajectory with individual earthquakes.

The physical size of great earthquakes has only recently been measured very accurately. Traditionally, the earthquake magnitude M_s (often called the Richter scale) is determined at periods of about 20 s, but it does not necessarily represent the total crustal deformation associated with earthquakes. In fact, the M_s scale is saturated at a magnitude of about 8 or when the fault length becomes about 100 km. Any earthquake whose fault length exceeds 100 km has M_s of 8.3 ± 0.3 regardless of whether the fault length is 100 or 1,000 km. This does not mean that other measures of earthquake "size" such as energy or seismic moment are similarly bounded. In order to measure accurately the physical size of great earthquakes, precise measurements of long-period seismic waves are necessary. The amount of the overall crustal deformation is best expressed by the seismic moment M_0 , which is proportional to

the product of the fault area and the average displacement on the fault. With the recent progress in long-period seismology, the seismic moment has been determined for many great earthquakes. The fault geometry of great earthquakes is also important. With the advent of plate tectonics, it is reasonable to assume a fault geometry which is consistent with the contemporary plate motion.

In these circumstances, the paper by O'Connell and Dziewonski represents a very timely contribution. Most discussions in the past have dealt with either statistical correlations or correlations between an individual break in polar motion and a particular earthquake. The statistical arguments are somewhat indirect, and the arguments on individual events are hampered by the poor quality of the data. In order to circumvent these shortcomings, O'Connell and Dziewonski used geometries of great earthquakes predicted by plate

tectonics, and computed the cumulative effects of earthquakes on polar motion rather than the effect of individual events.

Since the seismic moment M_0 is not known for most old earthquakes, O'Connell and Dziewonski estimated it by using the relation $\log M_0 = 8.8 + 2.5 M_s$ which is obtained from the work of Chinnery and North (*Science*, **190**, 1197-1198; 1975). The M_s scale used in the above formula is based on Gutenberg and Richter (*Seismicity of the Earth*, Princeton University Press, 1954) and is very close to what is called the 20 s surface-wave magnitude. On the other hand, O'Connell and Dziewonski used the magnitude scale adopted in Duda's catalogue (*Tectonophysics*, **2**, 409-452; 1965) to estimate M_0 . The magnitude scale used in Duda's catalogue is, however, different from Gutenberg-Richter's M_s ; the former is systematically larger than the latter, a fact which is not widely recognised.

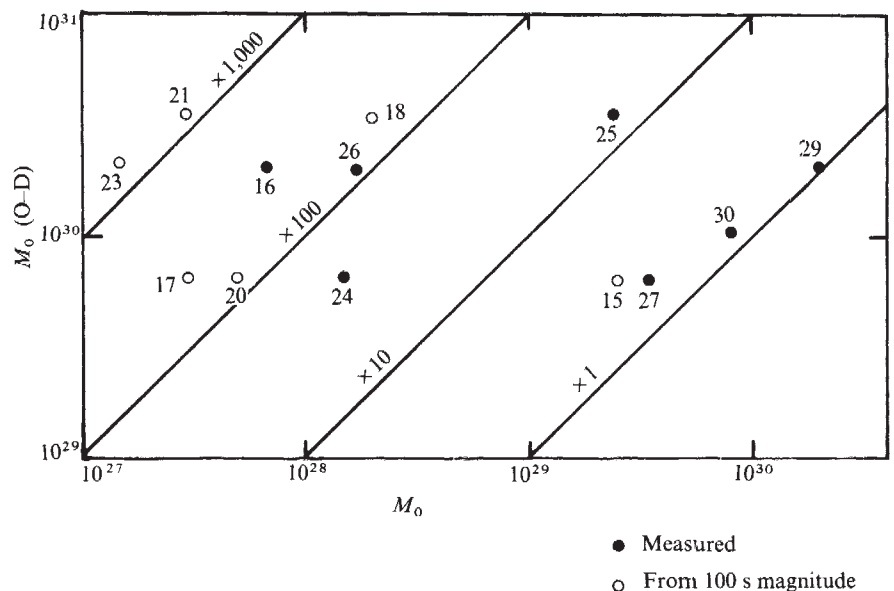


Fig. 1 Measured seismic moment M_0 versus seismic moment M_0 (O-D) assigned by O'Connell and Dziewonski for thirteen earthquakes. Closed circles indicate earthquakes for which M_0 is directly determined (from Kanamori and Anderson, *Bull. Seismol. Soc. Am.*, **65**, 1073-1095; 1975; Ben-Menahem, Aboodi, and

Schild, *Phys. Earth planet. Int.*, **9**, 265-289; 1974), and open circles are for earthquakes for which M_0 is estimated from the 100 s magnitude (Brune, and Engen, *Bull. Seismol. Soc. Am.*, **59**, 923-933; 1969). Numbers refer to those in Table 1 of O'Connell and Dziewonski.

For shallow ($H \leq 60$ km) earthquakes for the period from 1905 to 1952 listed in Table 1 by O'Connell and Dziewonski, the average difference between the two scales is 0.3. Thus, the use of Duda's values in the above M_0 versus M_s relation results in an over-estimate of M_0 by a factor of 5.6. Since the polar shift is linear with the seismic moment, this difference would mean that the effect on the Chandler wobble computed by O'Connell and Dziewonski is, on the average, 5.6 times too large. However, it is more important to note that because of the saturation of the M_s scale beyond 8, any M_0 versus M_s relation is useless for earthquakes of $M_s \geq 8$. For these large earthquakes direct determinations of M_0 are essential. Fortunately, for seven earthquakes listed in Table 1 of O'Connell and Dziewonski, a direct determination of M_0 has been made, and for six other earthquakes the 100 s magnitude (from which M_0 can be estimated fairly accurately) has been determined. In

Fig. 1, these seismic moments are compared with those estimated by O'Connell and Dziewonski from Duda's catalogue through the M_0 versus M_s relation. For earthquakes with very large rupture dimensions such as the Chilean (No. 29), the Alaskan (No. 30) and the Kamchatka (No. 27) earthquakes, the agreement is very good, but for many earthquakes with smaller rupture dimensions, M_0 seems to be overestimated by more than two orders of magnitude. For most events before 1923 no direct determination of M_0 has been made, but it seems almost certain from the above comparison that M_0 is overestimated in a similar manner.

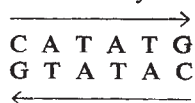
O'Connell and Dziewonski, in fact, considered most of these problems carefully in their article, but in view of the good accuracy of moment determinations even for relatively old earthquakes it appears that the direct effect of earthquakes is about one order of magnitude too small to explain the

Chandler wobble. But as they suggest, it is possible that earthquakes accompany very large aseismic deformation which has not been detected by existing seismological instruments. Then the fact that O'Connell and Dziewonski could explain the temporal behaviour of the Chandler wobble amplitude by using the mechanisms of earthquakes derived from plate motion may suggest that accelerated, but aseismic, plate motions are associated with great earthquakes (Anderson, *Science*, **182**, 49–50; 1974). Although such aseismic deformation has been suggested from several independent observations (of tsunami earthquakes, slow pre- and post-seismic deformations, disparity between plate motion and seismic slip rate for example), the details are at present unknown. With world-wide deployment of high-quality ultra-long period instrumentation (see Agnew *et al.*, *EOS*, **57**, 180–188; 1976), it is hoped that the nature of such aseismic deformation will be revealed in the near future. □

Long palindromes in eukaryotic DNA

from T. Cavalier-Smith

ONE of the most fascinating differences in the organisation of DNA in eukaryotic cells (those with a distinct nucleus) from that in prokaryotes (bacteria and blue-green algae) is the abundant occurrence—in higher eukaryotes at least—of long palindromes. When applied to nucleotide sequences in double-stranded DNA the word 'palindrome' usually means regions of DNA with an axis of two-fold rotational symmetry which would be read the same in both directions by the cell's transcription machinery:



would for example, be transcribed to give an RNA molecule with the sequence C A U A U G whichever end

the RNA polymerase started, because the polarity of the transcript (shown by the arrow) is always antiparallel to that of the template strand.

(A few authors call sequences like



"palindromes", but though when no account is taken of polarity each individual strand appears palindromic, the sequence does not show two-fold symmetry, and if it were read in both directions by RNA polymerase two quite different RNA sequences would

be made—its biological meaning is quite different when read backwards. Here I use 'palindrome' only for sequences with two-fold symmetry.)

Since palindromes are inverted repeats they can be easily identified because the two strands are self complementary. If denatured to separate the strands and then returned to renaturing conditions each strand will rapidly fold back on itself to form a double-stranded hairpin loop:



These can be separated from non-palindromic DNA because they bind strongly to hydroxylapatite. Wilson and Thomas (*J. molec. Biol.*, **84**, 115; 1974) found numerous almost perfect palindromes in *Drosophila*, *Xenopus* and human DNA. Usually 300–1,200 nucleotide pairs long, they form several percent of the total DNA and like non-inverted medium repetitive sequences, are widely dispersed in the DNA and not clustered in some special fraction. Such long palindromes are absent in prokaryotes and may be of profound significance for the organisation of eukaryote chromosomes. In searching for explanations one must bear in mind that not all eukaryote palindromes are perfect. Many are not or have impaired terminal loops (Schmid *et al.*, *Cell*, **5**, 159; 1975; Perlman *et al.*, *Cell*, **8**, 33; 1976).

Palindromes could have many func-

tions. Short ones can serve as recognition sites on the DNA for proteins which themselves have two-fold rotational symmetry. Such short palindromes do exist in prokaryotes: the recognition sites for the *lac* repressor and several bacterial restriction nucleases are palindromes, but these are too short to be detected by hydroxylapatite which in conditions usually used only binds double strands of over 50 base pairs. Another suggestion is that palindromes form pairs of lateral hairpin loops in the DNA which could be important for recombination or other functions. (Sobell, *Prog. Nucl. Acid Res. molec. Biol.*, **13**, 153; 1973). Such paired loops have not been found in isolated DNA, though they can be generated *in vitro* (Karrer and Gall, *J. molec. Biol.*, **104**, 421; 1976). A looped secondary structure (like that of tRNA on a larger scale) would be expected in RNA transcripts of palindromic DNA and has been found in nuclear RNA, including both heterogeneous nuclear RNA and low molecular weight nuclear RNA, though not in cytoplasmic mRNA; however, the length of these loops (which could have an important role in regulation of transcription or RNA processing or transport) is generally shorter than the palindromes seen in the DNA.

Recent studies in *Xenopus* (Perlman *et al.*, *op cit.*) argue against a specific control function for long palindromes. It appears from renaturation kinetic