

and the chance lying of one strand on top of another normally seen in the electron microscope.

Detection of such short inverted repeats will be made much easier by the recognition by Broker *et al.* (*J. molec. Biol.* **112**, 579; 1977) that following denaturation and reannealing they give rise to a characteristic structure which they call an 'underwound loop.' When a single molecule containing two short inverted repeats anneals with itself it forms a structure with a single-stranded loop and two single-stranded tails (like an α). If the DNA is left to reanneal long enough the loops of separate molecules will come together in complementary pairs. But this pairing must be incomplete. This is because each of the loops in the two interacting molecules is topologically equivalent to a circle (because of the base pairing at the cross-over point), and two circles, unlike two linear strands, are topologically unable to undergo the high degree of winding necessary to make a complete double helix. Some pairing is possible at the expense of twisting and tangling the rest of the molecule; the 'underwound loop' that results therefore contains both double-stranded and single stretches of DNA which are clearly visible in the electron microscope. Broker *et al.* use this method to reveal the short inverted repeats at the ends of the Mu G segment (presumably the G segment is a transposon since an identical sequence is present in phage P1, where it has much longer terminal inverted repeats), those at the ends of adenovirus-2, and at the two ends of the $\gamma\delta$ segment (a 5,700-base-pair sequence found at the boundary between F (sex factor) DNA and chromosomal DNA).

This technique will be valuable for detecting short inverted repeats separated by a spacer. I suspect that it will not be long before they are reported in eukaryote DNA. The fact that in *E. coli* the G segment can have either short terminal repeats (as in Mu) or long ones (as in P1) suggests that there is no fundamental functional difference between the long inverted repeats that abound in eukaryotes and the short ones which have so far been reported only in bacteria.

So far, ideas as to the function of palindromic sequences in eukaryotes are very vague (see *News and Views* **262**, 255; 1976). One possibility is that they have no function for the organism as a whole; they may even be disadvantageous 'selfish genes' maintained by strong positive selection at the level of the individual gene balanced by negative selection at the level of the organism; this would be entirely consistent with their tendency to trans-

The Sun and the weather

from Roger H. Olson

OVER the past few years, research into the relationships between solar activity (such as sunspots, flares and sector boundaries) and various climate and weather parameters has become more respectable. Although the search for mechanisms has as yet yielded few results, the number of impressive statistical correlations is steadily increasing. One of the best examples is the work of J. M. Mitchell, senior climatologist with the National Oceanic and Atmospheric Administration (NOAA). Mitchell has been looking at the correlation between sunspot activity and periods of drought in the Western United States, particularly since AD 1700, established from tree ring analysis.

Mitchell has worked with C. W. Stockton and D. M. Meko of the University of Arizona Tree Ring Laboratory, in studying the size of the area covered by drought in the Western United States. First, tree ring patterns, based on several types of trees, over the past 40 years were compared with well-known periods of drought. Once this standard correlation had been established it was possible to trace periods of drought back to AD 1700. A variety of sophisticated techniques were used to compare the period and geographical extent of the drought with the sunspot cycles, which have been observed reasonably consistently back to the beginning of the period.

No evidence was found for any influence of the 11-year cycle, but there is a very strong match between periods of drought and the 22-year double sunspot cycle (the Hale magnetic cycle). The area covered by drought tended to reach a maximum about 3 years after every other minimum in the 11-year cycle, with the most recent well-documented drought being that of the mid-1950s, correlat-

ing with the sunspot minimum of 1954. (The drought of the 1970s seems to be correlating with the sunspot minimum of 1976.)

The time between droughts averaged 20.4 years, whereas the average double sunspot cycle is 22 years. The reason for this apparent discrepancy is that the best coherence between drought area and sunspots comes during times when the sunspot maxima are high. It is during such periods that the time between successive maxima and minima tends to be smaller. When the sunspot numbers are small, the period of the cycle increases, and the correlation with drought area becomes weak.

Another tree ring series, dating back to AD 1600, was made available to Mitchell by H. C. Fritts. Although this series is not amenable to the statistical treatment mentioned earlier, it does contain one additional bit of information worthy of comment. During the Maunder minimum (see *News and Views* **236**, 405; 1977), when sunspots were virtually absent from the Sun during a 70-year period, the drought periodicity persisted in the Western United States. This suggests that the visible sunspot may not be the best parameter of solar activity to be used in the study of Sun-weather relationships.

A lesson to be learnt from Mitchell's work is that different meteorological parameters may behave in dramatically different ways. His study uses the area covered by drought, rather than the amount of rainfall or some other more arbitrary parameter. Rainfall statistics are notoriously hard to work with, because of their variability and dependence on topography. □

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locate and cause mutations. A more attractive proposition is that they may be the key to understanding the mechanism of cell determination. An important feature of determination is its great stability, inheritable over many cell generations. Although in principle this is explicable in terms of an association between DNA molecules and controlling proteins (and/or RNA) which is so stable that it can persist during replication and division, I think that the idea of a semi-permanent change in the DNA itself has been unduly neglected. Holliday and Pugh (*Science* **187**, 226; 1975) have put forward a most attractive mechanism involving

methylation of short palindromic sequences. Yet another possibility would be a change in the primary sequence of the DNA mediated by insertion sequences. Such a change would be inherited automatically by daughter cells, but would in principle be perfectly reversible (for example, when the nuclei of differentiated cells are transplanted into oocytes). Such changes could be inversions, deletions, duplications or translocations and could switch genes on and off by creating or destroying the recognition sites for controlling proteins. If the IS-mediated events commonly occurred only during DNA replication and were specifically