into any of the possible outcomes because of the Wada property.

We have verified the Wada property experimentally for our laboratory model by using a beam of 0.48 mm diameter from a 0.95 mW helium–neon laser. If the beam is shone on a boundary point, we find that the laser light can be seen through each of the openings. However, if the beam is aimed at the interior of one of the coloured regions, the light is seen through only one opening, casting a bright spot on the corresponding poster board.

We believe that Wada boundaries should be a typical feature in chaotic scattering systems that have more than two exit modes. We have verified the existence of Wada boundaries in a situation involving chemical reactions[4] with two and three degrees of freedom.

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Rainfall characteristics of hurricane Mitch

The hurricane or tropical storm known as Mitch struck Central America towards the end of October 1998. The subsequent flooding and landslides claimed approximately 11,000 lives. It was the most deadly hurricane to strike the Western Hemisphere in two centuries. We have measured rainfall totals during Mitch (from 1 to 48 hours) and find that they were not exceptional for hurricanes and tropical storms in the Atlantic basin. Rainfall totals and intensities measured over intervals of 1, 2, 5, 10, 30 and 60 minutes were less than values from the updated maximum potential rainfall curve[1,2]. The data suggest that extraneous factors, such as already saturated soils and denuded hillsides, were largely responsible for the damage caused.

Detailed rainfall data from hurricanes are often lacking because rainfall-recording instruments are washed away. The emphasis has been on recording wind strengths, which can underestimate the damage potential.

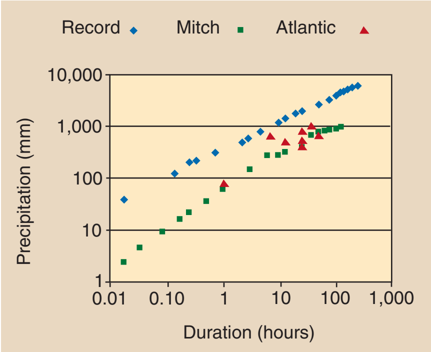

Figure 1 Plot of maximum rainfall amounts (squares) against duration from a rain gauge in southern Honduras during hurricane/tropical storm Mitch ($y=51.64x^{0.674}$, $R^2=0.99$). Also plotted are updated record rainfall events (diamonds) for different durations[12] that define the curve of maximum potential rainfall ($y=353.07x^{0.519}$, $R^2=0.99$) and data (triangles) from recent major Atlantic hurricanes and tropical storms[3–5].

Rainfall distribution is often estimated from radar and satellite data with little ground-truth support. Data from an autographic rain gauge in southern Honduras, where flooding and landslides were extensive, provide a unique insight into the rainfall distribution during Mitch. The tipping-bucket rain gauge (ELE DRG-52) was located at 87° 04′ W and 13° 17′ N on a hill crest (100 m above sea level) in the foothills of Cerro Guanacaure (1,007 m above sea level).

Mitch formed on 21 October 1998 in the southwest Caribbean and reached category 5 hurricane status on the Saffir/Simpson scale as it moved towards northern Honduras. On 29 October, Mitch was downgraded to a tropical storm and moved southwards and inland. The storm was declared to be over on 1 November.

Mitch produced torrential rains despite being downgraded from a hurricane. Between 18:00 (Honduran time, which is 6 hours before GMT) on 27 October and 21:00 on 31 October, there was 896 mm of rainfall. The most intense and prolonged rainfall was between 15:00 on 29 October and 07:00 on 31 October (a total of 41 hours). During this period, 698 mm of rain fell. There were two distinct periods of extreme rainfall intensities: 186 and 245 mm of rain fell during six-hour periods from 16:00 to 22:00 on 29 and 30 October, respectively. Maximum intensities ranged from 138 mm h^{-1} (2-minute period) to 58.4 mm h^{-1} (60-minute period). Landslides affected approximately 20% of surrounding hillsides and typically occurred during the two periods of most intense rainfall. Simultaneously, the Choluteca river flooded adjacent settlements and parts of the city of Choluteca. The river also altered its course.

Although Mitch caused extensive flooding and loss of life, Fig. 1 shows that rainfall in southern Honduras was comparable to the severest hurricanes and tropical storms in the Atlantic basin[3–5]. Rainfall was also substantially less than the updated maximum potential rainfall curve, which is defined largely by rainfall events from La Réunion, Indian Ocean[1,2], where there might be greater topographic forcing. The data suggest that extensive damage in Honduras and Nicaragua was accentuated by several factors: the storm struck at the end of the rainy season when the soil was saturated, resulting in catastrophic flooding and landslides; agricultural extension caused by land pressures had left many hillsides denuded; and the population was ill prepared because, before making landfall, it had been predicted that Mitch would move northwards.

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Analysis of telomere lengths in cloned sheep

The development of nuclear-transfer techniques using cultured somatic cells[1–4] allows animals to be produced without involving germline cells. This enables us to examine the importance of the repair of chromosome ends (telomeres) in the germ line and to test the telomere hypothesis of ageing[5–8].

To investigate whether telomere erosion is repaired after nuclear transfer, the telomere lengths of animals 6LL3 (Dolly)[1], 6LL6 and 6LL7 were compared with age-matched control sheep, donor mammary gland tissue and donor cells before and after culturing (Fig. 1a). Animal 6LL3 was derived from the transfer of a nucleus from sheep (ovine) mammary epithelial (OME) cells from a six-year-old Finn Dorset sheep; 6LL6 was derived from sheep embryonic cells (SEC 1) obtained from day 9 Poll Dorset embryos; and 6LL7 was derived from fibroblasts[1] from a day 25 Black Welsh fetus.

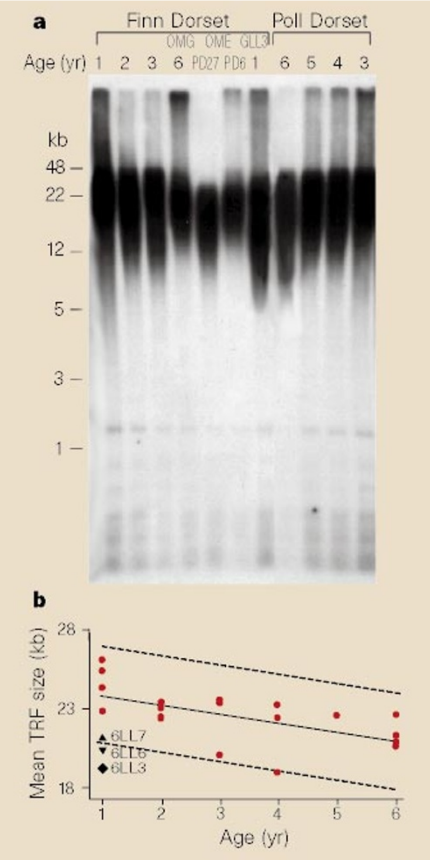

Figure 1 A representative analysis of sheep TRF lengths. **a,** Genomic DNA from Finn Dorset sheep, the six-year-old Finn Dorset ovine mammary gland (OMG) tissue used to provide donor cells for nuclear transfer, OME cell primary cultures derived from the aforementioned tissue, Finn Dorset nuclear-transfer animal 6LL3 (Dolly), and from Poll Dorset animals was analysed by Southern blotting and hybridization with radiolabelled $(TTAGGG)_3$ oligonucleotide. Animal ages are indicated above their respective lanes; the duration in culture for primary cells (OME) is indicated as population doublings (PD). The presence of a consistent signal at approximately 1.5 kb was used as a comparative control for loading and sample integrity. **b,** Regression analysis of mean TRF lengths against age, showing the decline in telomere length with age for the controls (solid circles) together with the fitted line (solid line) and 95% prediction interval for an additional observation at any given age (dashed lines). Comparisons in the text between nuclear-transfer sheep and controls were made by using the prediction intervals from the regression and by Student *t*-tests on 17 degrees of freedom; the control sheep were used to estimate the mean response and its variance. Similar conclusions for 6LL3 were drawn by using a two-sided *t*-test against either the four controls aged 1 year or the four controls aged 6 years, with the use of the appropriate group of four control sheep to estimate the mean response and its variance.

The mean size of the terminal telomere fragment obtained by cutting with restriction enzyme (the mean terminal restriction fragment, or TRF) was found to decrease in control animals with increasing age, at a mean rate of 0.59 kilobases (kb) per year. A linear regression analysis of the sheep DNAs yielded a significant result ($t=3{,}29$; $P<0.01$) (Fig. 1b).

Mean TRF sizes were smaller in all three nuclear-transfer animals than in age-matched controls. DNA in 6LL3 showed the greatest diminution of mean TRF size for a one-year-old animal (19.14 versus 23.9 ± 0.18 kb). The size difference is significant ($P<0.005$) compared with the age-matched control animals. The smaller TRF in 6LL3 is consistent with the age of her progenitor mammary tissue (six years old) and with the time that OME cells derived from that tissue spent in culture before nuclear transfer. 6LL6 also showed a significant decrease in TRF size (20.37 versus 23.9 ± 0.18 kb; $P<0.030$). As the number of animals analysed was small, it is possible that the difference was due to natural variation of the mean TRF size in these individuals, but the statistical significance of the data argues against this.

There was no significant difference between the DNA from the six-year-old progenitor mammary tissue and age-matched control DNA from fresh blood.

The influence of duration in culture, superimposed on the effect of the age of the progenitor tissue, can be gauged from the diminution in mean TRF size of OME cells that have undergone up to 27 population doublings. A decrease in mean TRF size was observed at an average 0.157 kb per population doubling. This is an average derived from replicate experiments and is consistent with results from human somatic cells in culture[9,10].

These observations indicate that the extent of shortening of the TRF might be mitigated, principally by minimizing the duration in culture and by a careful choice of the source of donor cells. This is particularly relevant for 6LL7, for which the use of fetal tissue and minimal culturing yielded an animal in which the mean TRF size was not significantly shorter at 95% confidence limits (21.19 versus 23.9 ± 0.18 kb; $P<0.088$) than age-matched controls. This is in contrast to results from 6LL3 and 6LL6, for which culturing was more prolonged.

The most likely explanation for the shorter mean TRFs in all three nuclear-transfer animals is that the mean TRF size observed in these animals reflects that of the transferred nucleus. Full restoration of telomere length did not occur because these animals were produced without germline involvement. It remains to be determined whether any telomerase activity, or an alternative telomere-lengthening mechanism, is present that could result in some telomere repair during the early development of sheep.

It is not known whether the actual physiological age of animals derived by nuclear transfer is accurately reflected by TRF measurement. Recent veterinary examination of the nuclear-transfer animals has confirmed that they are healthy and typical for sheep of their breeds, despite having a shorter mean TRF length. Furthermore, 6LL3 has undergone two normal pregnancies and has successfully delivered healthy lambs.

Telomere-based models of cellular senescence[5–9] predict that the nuclear-transfer-derived animal 6LL3 would reach a critical telomere length sooner than age-matched controls. However, considering the large size distribution of sheep TRFs, it remains to be seen whether a critical length will be reached during the animal's lifetime. The experimental inactivation of murine telomerase produced a phenotype only after five generations[10], and similar observations have been made in telomerase-deficient yeast cells[11]. Mice have also been sequentially cloned by the transfer of adult cumulus-cell nuclei without any adverse effects[12].

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Did parrots exist in the Cretaceous period?

The timing of the origin of modern birds is much debated. The traditional view, based largely on the fossil record, suggests that most modern groups did not appear until the Tertiary, after the end-Cretaceous extinction event[1], but recent work, based on molecular divergence data, has suggested that most, or all, of the major clades were present in the Cretaceous[2,3]. Verification of the latter proposal awaits the discovery of modern bird fossils in the Mesozoic which can be confirmed on the