tion of worker polymorphism and foraging strategies in leaf-cutting ants[1,10], and may be significant in other ant genera.

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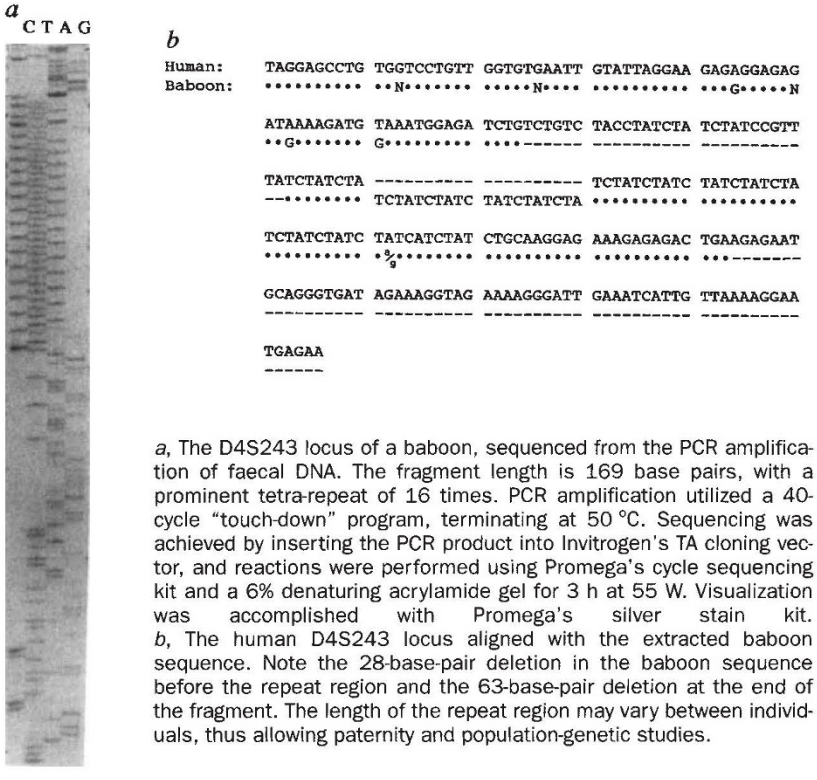
Nuclear DNA from primate dung

SIR — Although hypervariable DNA markers have revolutionized the study of kinship patterns and mating systems in the wild[1,2], these techniques have largely been restricted to species that can be easily captured and handled. Where handling is either unsafe or impracticable, DNA must be obtained non-invasively[3]. Collecting hair or buccal cells can be difficult or impossible in many species, so the ideal system should be based on material that is both plentiful and can be attributed unambiguously to a specific individual. Following the extraction of mitochondrial and chloroplast DNA from bear dung, by Höss *et al.*[4], we investigated whether useful samples of nuclear DNA could be obtained from the faeces of wild primates.

We collected dung from individually recognized olive baboons in the Gombe Stream National Park, Tanzania[5,6], and stored it first in liquid nitrogen, then in a −20 °C freezer. We modified a protocol for extracting mitochondrial DNA from chimpanzee dung[7], combining the techniques of Pääbo[8] and Boom[9] with a phenol/chloroform extraction with hexadecyltrimethylammonium bromide (CTAB) and collagenase. CTAB was added to the overnight incubation in order to break down ingested plant compounds that would inhibit subsequent PCR reactions. Extracted DNA was amplified using human nuclear microsatellite primer D4S243 (ref. 10) and PCR. As a control, we used chelex[3] to extract DNA from hair of several of the same individuals. PCR products were inserted into TA cloning vector (Invitrogen) and transformed into *Escherichia coli*. Colonies were grown overnight, plasmids were isolated and sequenced with the M13 forward primer.

Nuclear DNA extracted from dung and hair reveals that the baboon sequence at the D4S243 locus aligns with the human sequence, exhibiting three base substitutions, four ambiguous codes, and deletions of 28 and 63 base pairs (see figure). Human microsatellite primers successfully amplify baboon DNA in a significant number of cases (J. Rogers, personal communication), and paternity exclusions can usually be achieved by amplifying six polymorphic loci. PCR amplification has been successful in 39 out of 40 faecal samples tested so far. The ability to amplify microsatellite regions from faecally extracted nuclear DNA opens a new realm of possibilities for studying organisms that are difficult to catch or handle[11]. Dung should be considered essential material for paternity and population genetic studies of arboreal or endangered mammals.



a, The D4S243 locus of a baboon, sequenced from the PCR amplification of faecal DNA. The fragment length is 169 base pairs, with a prominent tetra-repeat of 16 times. PCR amplification utilized a 40-cycle "touch-down" program, terminating at 50 °C. Sequencing was achieved by inserting the PCR product into Invitrogen's TA cloning vector, and reactions were performed using Promega's cycle sequencing kit and a 6% denaturing acrylamide gel for 3 h at 55 W. Visualization was accomplished with Promega's silver stain kit. *b*, The human D4S243 locus aligned with the extracted baboon sequence. Note the 28-base-pair deletion in the baboon sequence before the repeat region and the 63-base-pair deletion at the end of the fragment. The length of the repeat region may vary between individuals, thus allowing paternity and population-genetic studies.

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Comparison of deep ice cores

SIR — Comparison of the GRIP and GISP2 deep ice cores from central Greenland[1,2] has confirmed the occurrence of exceptionally large, rapid changes in many climatic indicators over approximately the past 100,000 years[3,4]. Similar rapid changes occur within deeper ice with a warm isotope signature (identified as the Eemian, Sangamonian, or stage 5e[3,4]), but differences in their patterns between the two cores raise the possibility that at least one record was disturbed by ice-flow processes[1,2]. Disturbances might include boudinage, open folding or similar processes that would distort the time-depth relation but leave layers in stratigraphic order, or overturned folding that would disturb stratigraphic order. The GRIP and GISP2 steering bodies have initiated comparative studies of the two cores, including visible stratigraphy and crystal fabrics in selected sections of both cores, which are reported here. The most important results of these studies include the following.

(1) The small diameters of the cores and the lack of any highly reliable stratigraphic 'up' indicators prevent us from distinguishing overturned from right-side-up layers in structures much larger than the core diameter (13 cm for GISP2 and 10 cm for GRIP before sampling). We thus cannot invalidate or confirm the instability of the Eemian record.

(2) Both cores contain structures above the Eemian (which was identified as 2,790–2,865 m at GRIP[3,4]) that are larger than the core diameter and that could represent inverted strata. A 10–20-cm long region of layers dipping 20 ° relative