affinities with *A. afarensis* from Belohdelie, Ethiopia[4], Allia Bay[7] and Tabarin[8], Kenya, and Fejej, Ethiopia[9,10], which suggests the likelihood of several contemporary species. It thus appears that the phylogeny of hominids, like that of many other mammalian groups is very bushy at its base

John Kappelman
Department of Anthropology and Center for Asian Studies,
The University of Texas at Austin,
Austin, Texas 78712-1086, USA
John G. Fleagle
Department of Anatomical Sciences,
State University of New York,
Stony Brook, New York 11794, USA

WOLDEGABRIEL *ET AL.* REPLY — Our first published chronological assessment was made on the basis of stratigraphy, structural relationships, biochronology, $^{40}Ar/^{39}Ar$ dating and palaeomagnetic data[3]. Regional dip, coupled with stratigraphic and structural coherence, indicated that the Aramis strata were deposited well below the VT-1/Moiti tuff (3.89 ± 0.02 Myr). Biochronological comparisons with fauna from Maka/Belohdelie provided the first clue that the Aramis hominids were older than those from east of the modern Awash River.

These relationships were confirmed by $^{40}Ar/^{39}Ar$ dating combined with palaeomagnetic data. The palaeomagnetic sampling was not an attempt at "reversal stratigraphy" (an absurdity if based on two samples), but rather at testing for consistency with the $^{40}Ar/^{39}Ar$ results. We reported initial dating results of 4.387 ± 0.031 Myr for the Gàala Vitric Tuff Complex (GATC), providing a maximum age for the *A. ramidus* fossils[3]. As we stated, the palaeomagnetic data are consistent with the *A. ramidus* fossils being between 4.29 and 4.48 Myr old, based on the astronomically calibrated geomagnetic polarity reversal timescale[11]. This likelihood seems to us far stronger than the younger age that Kappelman and Fleagle suggest.

Kappelman and Fleagle's conjecture would require that at least 210 kyr (from the GATC to above the top of the Cochiti subchron) be compressed into a thin stratigraphic section of less than 4 m without the trace of an unconformity. During this extended period the Aramis landscape in this tectonically unstable area is required to have remained virtually featureless. This is because the superposed Daam Aatu Basaltic Tuff (DABT) maintains a uniform thickness across 4 km along strike of modern outcrop, indicating no subjacent topography. Furthermore, Kappelman and Fleagle's scenario implies that the entire thick succession of sediments (>121 m) above the DABT and below the VT-1/Moiti was then deposited within the next 290 kyr (from <4.18 Myr, the top of the Cochiti subchron, to 3.89 Myr, the age of VT-1/Moiti). There is no stratigraphic evidence for such an abrupt and profound increase in sediment accumulation rate (from <2 to >41 cm kyr^{-1}).

Due to the paucity of cognate feldspar phenocrysts in distal tuffs overlying the hominid fossils[3], we have begun $^{40}Ar/^{39}Ar$ dating of fresh juvenile glass lapilli from the DABT and another, similar basaltic tuff (the Kullunta Tuff) located 63 m above it. Incremental laser-heating analyses of the DABT from two different locations yield plateau ages of 4.390 ± 0.068 and 4.384 ± 0.086 Myr, with a weighted mean of 4.388 ± 0.053 Myr, indistinguishable from our date of 4.387 ± 0.031 Myr for the GATC 4 m below it. The stratigraphically younger Kullunta Tuff yielded a plateau age of 4.289 ± 0.055 Myr. The results are in direct opposition to Kappleman and Fleagle's hypothesis that the age of *Aridipithecus ramidus* was overestimated

G. WoldeGabriel
Los Alamos National Laboratory,
Los Alamos, New Mexico 87545, USA
P. Renne
Berkeley Geochronology Center,
Berkeley, California 94709, USA
T. D. White
Department of Integrative Biology,
University of California, Berkeley,
California 94720, USA
G. Suwa
Department of Anthropology,
University of Tokyo, Bunkyo-ku,
Hongo, Tokyo 113, Japan
J. de Heinzelin
Institut Royal des Sciences Naturelles
de Belgique, 1040 Brussels, Belgium
W. K. Hart
Department of Geology,
Miami University, Oxford, Ohio 45056, USA
G. Heiken
Los Alamos National Laboratory,
Los Alamos, New Mexico 87545, USA

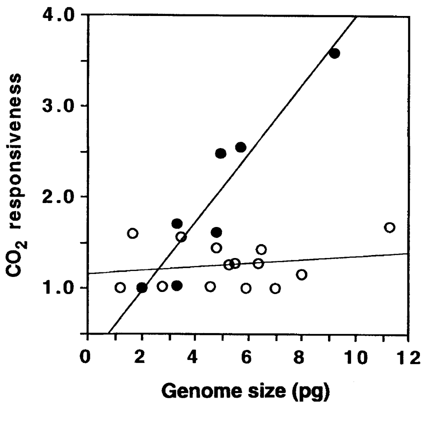
1. White, T. D., Suwa, G. & Asfaw, B. *Nature* **371**, 306–312 (1994).
2 White, T.D., Suwa,G., & Asfaw, B. *Nature* **375**, 88 (1995)
3. WoldeGabriel, G. *et al. Nature* **371**, 330–333 (1994).
4. White, T. D. *et al. Nature* **366**, 261–265 (1993).
5. Cande, S. C. & Kent, D. V. *J. geophys. Res.* **97** (B10), 13917–13951 (1992).
6. Cande, S. C. & Kent, D. V. *J. geophys. Res.* **100** (B4), 6093–6095 (1995)
7. Coffing, K. *et al. Am. J. phys. Anthrop.* **93,** 55–65 (1994).
8. Ward, S. & Hill, A. *Am. J. phys. Anthrop.* **72,** 21–37 (1987).
9. Fleagle, J. G. *et al. J. hum. Evol.* **21,** 145–152 (1991).
10. Kappelman, J. *et al. J. hum. Evol.* (in the press).
11. Hilgen, F. *J. Earth planet. Sci. Lett.* **107**, 349–368 (1991).

Genome size and high CO_2

SIR — Genome size, as measured by the content of nuclear DNA per cell, varies over 2,500-fold among species of angiosperm plants[1]. As genome size is positively correlated with cell size and with the duration of cell cycle[2], it may have direct effects on the evolutionary strategy[3], life history, phenology and distribution of species[2,4,5]. Plant species with large genomes have longer generation times and can start growth at colder temperatures[2,5]. Within species, smaller genomes are frequently associated with stressful or short-duration environments, whereas more beneficial conditions or cultivation lead to an increase in genome size[6]. Thus DNA content may evolve or be directly induced under novel environmental conditions.

A rise in the atmospheric concentration of carbon dioxide is an important component of global changes in climate. The frequently reported enhancement of growth of vegetation under higher CO_2 levels[7] seems to be primarily due to increased availability of CO_2 for photosynthesis or to modulation in the enzymatic activity[8]. We present a survey which suggests that genome size can potentially both influence the responsiveness of a plant species to CO_2 and be affected by elevated CO_2.

Among grasses, the potential advantage of a large genome exists only in the annual species ($n = 7$, $r^2 = 0.876$, $P = 0.002$) and not in the perennial species ($n = 14$, $r^2 = 0.049$, $P = 0.45$)(see figure). Annual grasses not only had greater average enhancements of growth (ratios of 2.01 compared with 1.27; $P = 0.01$), but also the enhancements were positively correlated with the amount of nuclear DNA. It is not clear why perennial species with large genomes do not show pronounced growth enhancements. Physio-



Relationship between responsiveness to elevated CO_2 and haploid nuclear genome size among annual (black circles) and perennial (open circles) species of grasses. CO_2 responsiveness is calculated as the ratio of average final biomass attained at elevated and ambient CO_2. Linear regression slopes differ significantly (analysis of covariance; $P < 0.0001$); average genome size was similar in both groups. The analysis is limited to grasses due to paucity of the published estimates of both CO_2 effects[7,10] and measurements of DNA amounts[1] in plants.