Matters Arising

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values are for several of the largest species in the group, all from the genus *Papio*. With the extra neurone index (N_c), Jerison[2] reported that elephants have a value twice that of humans and porpoises have about the same values as we do. At the other end of the scale, the small South American squirrel monkey, *Saimiri sciureus*, was grouped with lemurs and marmosets rather than with more closely related, but larger, New World monkeys. Jerison himself noted that "If we demand that the values of N_c correspond to an ordering in terms of behavioural capacities we must assume either that the assumptions used in determining N_c are insufficient or that we grossly underestimate the behavioural capacities of the elephant and porpoise. I would guess that both types of error occur, but I would prefer, for the present, to emphasize the second."

If, as these results suggest, there is a tendency for CC and N_c to be underestimated for small species within a taxon, our suspicions of increased encephalization in *P. africanus* remain plausible. For both CC and N_c, the values for *P. africanus* listed by Leutenegger are close to the highest values for all monkeys and the monkeys with the higher values are also considerably larger than *P. africanus* in body size. *P. africanus* has lower values than the extant great apes, but also has a much smaller body size than these.

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RECENTLY Toh *et al.*[1] reported the existence of amino acid sequence similarity between the reverse transcriptase of certain retroviruses and the DNA polymerases of cauliflower mosaic virus (CaMV) as well as a region of hepatitis B virus (HBV) that probably encodes a DNA polymerase. For completeness, we draw attention to other regions of protein similarity between retroviruses (human T-cell leukaemia virus, HTLV; Moloney murine leukaemia virus, Mo-MuLV; and Rous sarcoma virus, RSV), HBV and CaMV that were not reported by Toh *et al.*

The sequences are presented in Table 1 and the relative positions of the similar regions indicated in Fig. 1. The common set of amino acids discussed by Toh *et al.* is conserved in the amino-terminal region of all retrovirus reverse transcriptases studied (regions I–III). These common sequences are located near the amino-terminus of the HBV protein and the centre of the CaMV polymerase. Another region of similarity, IV, not discussed by Toh *et al.*, is also found in all retroviruses and is present in the CaMV protein. Region V, reported by Toh *et al.*, to be present in Mo-MuLV and RSV, is also found on HTLV. We also draw attention to sets of amino acids that are conserved with respect to sequence and relative position between the reverse transcriptases of HTLV and Mo-MuLV (M1–M4) and HTLV and RSV (R1–R4).

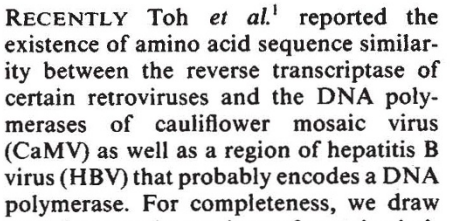

Fig. 1 Alignment of the polymerase gene products among five different viruses, depicting the regions shown in Table 1.

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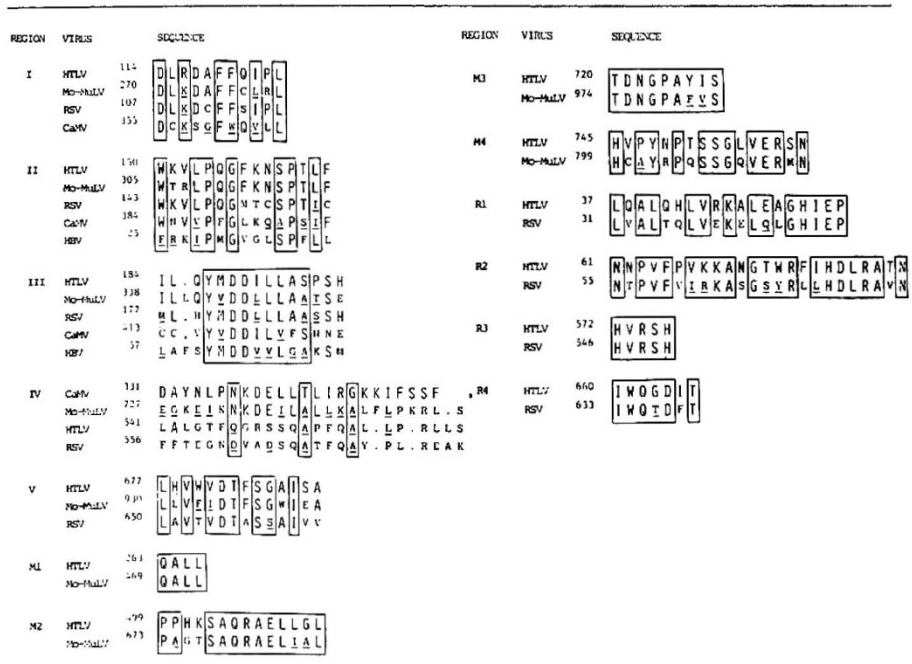
Table 1 Alignment of the similar regions in polymerase gene products among different viruses



Moloney murine leukaemia virus, Mo-MuLV[2]; human T-cell leukaemia virus, HTLV[3]; Rous sarcoma virus, RSV[4]; cauliflower mosaic virus, CaMV[5]; and hepatitis B virus, HBV[6]. Common amino acids are boxed and conservative substitutions with respect to HTLV are underlined. For each sequence, the first amino acid is numbered.