practical conclusions emerge from our studies. First, whenever feasible, large segments of DNA should be amplified as we found five out of five DNA segments > 700 bp to be highly susceptible to ultraviolet inactivation in contrast to only one of four segments < 250 bp. Second, ultraviolet inactivation is much less effective in elminating dried DNA, suggesting that decontamination of laboratory equipment may require the aid of a photosensitizer or even a completely different approach.

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Repetitive orbital damage

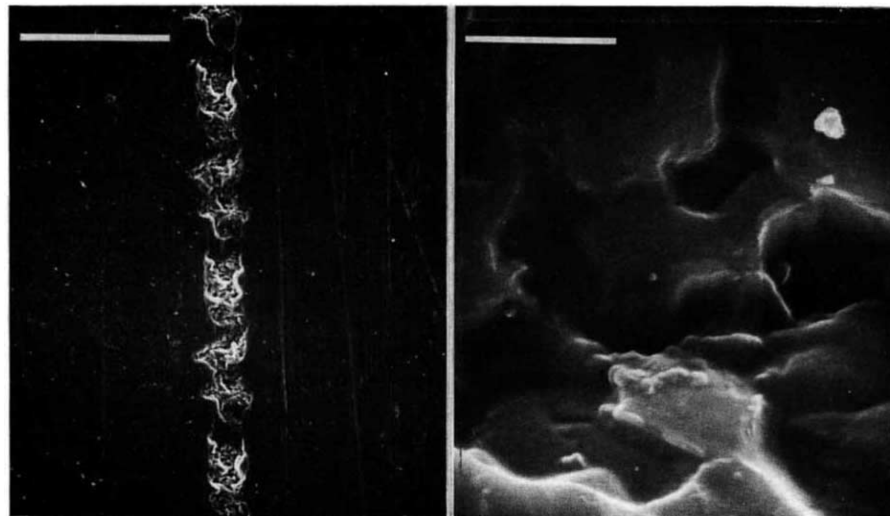
SIR—In the course of a preliminary routine search for micrometeoroid strikes on an experiment tray on a low-Earth orbit satellite we observed several long strings of repetitive indentations which, on detailed examination in the electron microscope, demonstrate similarities of structure down to an extremely fine scale. The experiment panel was flown for 5.8 years in circular Earth orbit at altitudes of 333 to 481 km. The plane of orbit of the vehicle was approximately 5° from the ecliptic. The orientation of the normal to our panel ranged during each passage around the Earth through an arc from 87.25° to the plane of the ecliptic to 77.25° in the opposite direction.

We cut a 20 × 15 mm sample of the outer exposed surface from the aluminium frame and mounted it next to a 20 × 8 mm sample cut from the same piece of the frame containing the under (unexposed) side of the frame. The material of both samples was structural aluminium (2024-T3) clad with commercially pure aluminium. After the mounted specimens were vacuum-coated with approximately 20 nm of gold, we examined them in a Hitachi CS-800 field-emission scanning electron microscope at 15 kV.

The left-hand side of the figure shows a short segment from a string about 6 mm long, incorporating five individual units. From the top down, units, 1, 3 and 5 are the same and units 2 and 4 are the same. This sequence continues perfectly throughout almost all the 6-mm length, except that at the ends the indentations become less distinct. The right-hand side of the figure is a detail from unit 2.

We do not know the source of the indentations. We have observed 10 separate strings on the exposed surface examined, all having a level of replication quality similar to the string shown here. Of the ten strings examined, eight have only one kind of repeating unit, while two have an alternating sequence such as those shown here. We have not found any string that bears any resemblance to any other, but all individual units are 20–60 μm in size.

We suggest that the features observed were not produced during fabrication or handling of the aluminium frame. Because the experiment tray was either protected in a clean room or in orbit from the time NASA mounted it on the satellite until it was returned to us, the evidence indicates that the observed indentations were likely to have been created during the 5.8-year mission.



Left, scanning electron micrograph of five units of a 6-mm-long string. Scale line is 75 μm long. Up is away from the Earth, left is the direction of velocity of the experiment tray. Right, portion of the lower left extension of unit 2 (counting from the top). Scale, 1.76 μm.

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Origin of *vpx* in lentiviruses

SIR—Primate lentiviruses have been classified into four groups on the basis of similarity of their Pol gene products, as discussed by Desrosiers' News and Views[1]. All these viruses have five genes that are essential, in the cases examined, for propagation *in vitro*: the structural genes *gag*, *pol* and *env*, and the regulatory genes *tat* and *rev*. Five other genes, not essential *in vitro*, are found in various combinations: *vif* and *nef* are invariably present but *vpu* is found only in the HIV1/SIV_{CPZ} group; *vpr* is found in all viruses except those of the SIV_{AGM} group; and *vpx* is found in only two groups — SIV_{AGM} and HIV2/SIV_{SMM}/SIV_{MAC}.

We suggest that the *vpx* gene in the HIV2/SIV_{SMM}/SIV_{MAC} group arose by duplication of the *vpr* gene. The strongest support for this proposal lies in the alignment of the Vpr and Vpx proteins from various prototype isolates shown in Fig. 1. All the Vpr and Vpx proteins share regions of similarity with each other, suggesting critical residues whose mutation may help to elucidate their functions.

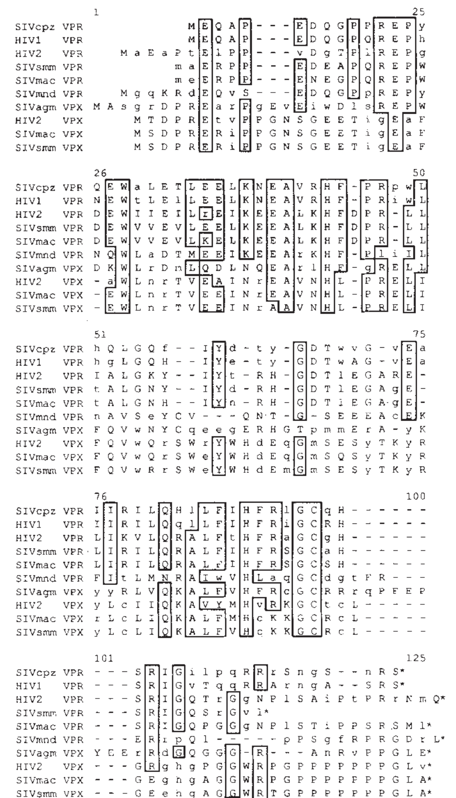

FIG. 1. Comparison of the deduced amino-acid sequences of *vpx* and *vpr* genes from primate lentiviruses. The following isolates were used in the comparison: $HIV1_{BRU}$, SIV_{CPZ}, $HIV2_{ROD}$, SIV_{SMMH4}, $SIV_{MACMM142}$, SIV_{MNDGB1}, $SIV_{AGMTYO\text{-}1}$. Sequences obtained from the Human Retroviruses and AIDS Database[3,4]. Capital letters, conserved amino acids between isolates; amino acids boxed when identical in six or more cases. Dashes, gaps introduced in the sequences to allow optimal alignment. Sequences aligned both by eye and with the programs AMPS[5] and HOMED[6].

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