was seen about the time the blast wave should have crossed the magnetic field line intersecting the payload. Nearly coincident with this, electron fluxes of 2-kV were seen moving up and down the field lines, but the electrons did not actually seem to reach the atmosphere. The currents generated by the electric field apparently set up reflecting electric shocks both above and below the burst point, and the electrons were probably trapped between them.

The discrete auroras are believed to be caused by electrons accelerated through similar shocks, or double layers, also set up by currents flowing parallel to magnetic field lines; but although the current-driven shocks play roles in both the natural aurora and the Trigger experiment, their roles are quite different.

The instrument package also observed electron fluxes with energies greater than 40 kiloelectron volts (keV). There was a prompt burst followed a second later by sustained fluxes of electrons. Fluxes greater than 40 keV are believed to be responsible for the patchy and pulsating aurora seen in the early morning hours in the diffuse aurora (see review by A.D. Johnstone *Nature* **119**, 274; 1978). The natural precipitation is also accompanied by electromagnetic wave emissions called chorus. The chorus emission is in the audio frequency range, 0.5 to 2 kHz, and when amplified sounds like the chirping of birds. The precipitation can be enhanced by increasing the ambient ionization because the ambient ionization makes the trapped electrons more unstable to precipitation caused by the electromagnetic emissions.

It is tempting to attribute the delayed precipitation of electrons of energy greater than 40 keV in Trigger to the enhanced ionization density left by the caesium in the wake of the Trigger blast wave. The delayed fluxes were accompanied by wave emissions, but the emissions were electrostatic, rather than electromagnetic, and so would not probably be able to cause precipitation of trapped fluxes. Moreover, the Trigger fluxes were primarily field aligned, which is again inconsistent with a wave-particle diffusion process. The experimenters attribute most of the enhancement to noise contamination of the magnetic field-aligned detector. However, an X-ray detector suspended from a parachute that was deployed by a second rocket did observe 0.13-Hz pulsations in X-ray fluxes some two minutes after the event. This frequency is comparable with pulsation frequencies observed in natural aurora.

The prompt energetic electron fluxes are believed to be real, and they are accompanied by an electromagnetic pulse. However, as the electron fluxes are also primarily field aligned, the acceleration mechanism would have to be a stochastic process, since the electric potentials generated by the explosion are considerably less than the observed electron energies.

The Trigger experiment initiated a number of interesting plasma processes, some of which are similar to those responsible for the aurora. However, the natural aurora and the events observed in Trigger are not similar enough for the Trigger results to be applied in a direct way towards understanding the aurora; but after further theoretical interpretation it may turn out that the experiment has provided a number of useful clues to understanding processes in the natural aurora.

Certainly, the concept of the Trigger experiment is very appealing. Not only does the technique of artifically perturbing the ionosphere or magnetosphere allow the study of a wide range of general plasma processes, it also makes it possible to separate cause and effect, an often serious problem in the interpretation of auroral observations.

The use of chemical releases in space research will increase; groups from many countries are now proposing that such release experiments be conducted from a 'chemical release module' which will be be launched through the US space shuttle programme sometime in the mid-eighties. □

Are membrane proteins introverted?

from N. Michael Green

THE PURPLE MEMBRANE of *Halobacterium halobium* has become a test bed for sophisticated new techniques. These, in turn, have given exciting new information about the structure and function of the major protein of the purple membrane, bacterial rhodopsin. The most recent technique, neutron diffraction, shows that rhodopsin is an "inside-out" protein. Six years ago a combination of novel electron microscopic techniques with X-ray diffraction gave a picture of the structure at 7 Å resolution (Henderson and Unwin *Nature* **257**, 28; 1975). Then last year, a correlation of the electron density distribution with the amino acid sequence of appropriate helical segments produced a tentative model structure (Engelman *et al. Proc. natn. Acad. Sci. U.S.A.* **77**, 2023; 1980). It is this model which now receives strong support from some elegant neutron diffraction experiments (Engelman and Zaccai *Proc. natn. Acad. Sci. U.S.A.* **77**, 5894; 1980). This method, based on the great difference between neutron scattering by protons and deuterons, has also been used to show that there are no detectable aqueous channels in the membrane (Zaccai *J. molec. Biol* **132**, 181; 1979; Rogan and Zaccai *J. molec. Biol.* **145**, 281; 1980.).

Purple membranes were prepared in which all of either the valine or the phenylalanine residues had been replaced by their fully deuterated analogues and the neutron diffraction patterns were compared with that from normal membrane. From the latter a neutron density map was constructed which closely resembled the electron density map. Difference Fourier maps relative to the deuterated preparations were computed and showed that valine and phenylalanine residues were concentrated in different regions. This was to be expected, since these residues have rather different distributions both between the seven transmembrane helices and azimuthally within each helix. The peak density differences for both valine and phenylalanine side chains were off the helix axes, as would be expected, but whereas the valine peaks were displaced towards the exterior of the molecule those of phenylalanine were nearer to the interior, in the region where many of the charged groups had been placed in the tentative structure of Engelman *et al.* This differential distribution was consistent with the relative azimuthal distributions of valine and phenylalanine derived from the sequences of the previously assigned helices.

Comparison of the sequence-based azimuthal distributions with those of the charged residues confirms that valines (17 out of 19) are on the opposite sides of helices from phenylalanines (9 out of 11), and that the buried charged groups go with the phenylalanines. Moreover, the previously assigned locations of helices rich in valine or phenylalanine were consistent with the Fourier difference maps derived from neutron scattering, though the authors refrain from any detailed interpretation of this at the moment. The consistency of these new results with the earlier model is impressive and gives confidence in the validity of the arguments used in support of the previous assignments.

A firm picture is beginning to emerge of an 'inside-out' protein molecule with buried polar and charged groups located predominantly between helices and with most of the interface between lipid methylene groups and the protein being occupied by hydrophobic aliphatic chains. The authors suggest that in addition to a possible role in providing sites for proton translocation, the charged and polar groups would be an important stabilizing element in such a predominantly hydrophobic structure, since in their absence interactions between hydrophobic helices immersed in a hydrophobic solvent are very weak. □

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