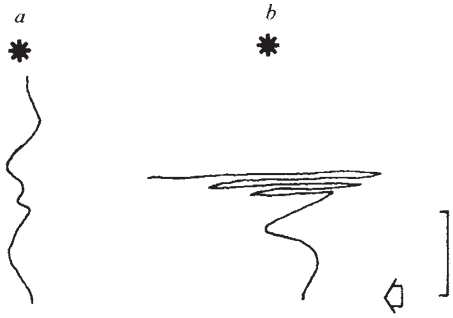

Two 3 s flight tracks (based on videotape records) of the same male *Cadra cautella* after its arrival by upwind flight at a point 0.50 m from a source of female scent. To the left (*a*): the source remained throughout the upwind position marked by the star. To the right (*b*): the source was removed as soon as the male reached the level of the arrowhead so that the male entered unscented air after travelling approximately 0.15 m further upwind. (Scale: 0.15m.)

movement of black and yellow stripes on the floor. If the stripes were stationary the males flew upwind against the stream of odour from the female; if the stripes moved downwind above a certain velocity the flying male also was carried downwind. If the odour was suddenly removed while the male was in flight, but the odourless air stream continued, the male arrested its upwind flight and flew at right angles to the air stream, casting to and fro over a progressively widening band (see figure). This response was unchanged if one antenna was removed, which would not have been the case if a chemotropotactic mechanism were involved.

It seems, therefore, that an odour-controlled optomotor anemotaxis is still the most plausible mechanism to account for the response of the male moth to the sex pheromone of the female; and that the side to side casting when the odour trail is lost, which had been noted in the past, is an important element in the optomotor reaction.

Anchoring the Ig molecule

from a Correspondent

IT is generally accepted that immunoglobulin (Ig) acts as the antigen recognition unit at the surface of bone marrow-derived (B) lymphocytes. The chemical homology between the membrane-bound Ig and the molecules secreted by the activated antibody-forming B cell is unknown although this must be considerable since the surface-bound Ig component can be detected if serum reagents specific for both variable and constant regions of the soluble secreted molecules are used. This raises the problem of how a soluble Ig glycoprotein molecule is adapted to perform a function which requires firm attachment to the cell surface membrane. In many integral membrane proteins and glycoproteins a small hydrophobic segment of peptide anchors the rest of the molecule into the lipid bilayer of the membrane. It is possible certainly that the polypeptides of surface Ig contain an extra stretch of amino acids suitable for this purpose. If the two or three well studied examples of membrane proteins are considered, these amino acids would be located at the carboxyl terminal of heavy chains in the constant (Fc) portion of the molecule.

An alternative method for anchoring an essentially water soluble component to a membrane involves attachment to an integral membrane component with a recognition site for some part of the soluble protein. This method is favoured by Ramasamy *et al.* (*Nature*, **249**, 573; 1974) for surface-bound Ig.

B lymphocytes as well as macrophages, mast cells and polymorphonuclear cells possess surface receptors for the constant (Fc) portion of Ig. It is proposed that these receptors tightly bind Ig molecules to the B cell surface in such a way that the antigen binding sites of the variable region of Ig extend into the extracellular space and are available to specific antigen. The murine plasma cell tumour MOPC 21 (P3) secretes IgG1 kappa molecules in culture, a small proportion of which may be assumed to bind to and saturate the putative Fc surface receptors. Indeed, no Fc receptors are detectable on these cells. Mutants blocked in Ig secretion, however, can be obtained and these also carry no surface Ig molecules. Ramasamy *et al.* argue that in these cells the Fc surface receptors should be demonstrable and this proved to be the case. That is to say there is in general an inverse correlation between the presence of surface Ig and Fc receptors.

The surface Ig of mouse B lymphocytes is probably monomeric IgM, and it seems that the secreted pentameric IgM may have decreased affinity for Fc receptors since secreted IgM only weakly inhibits Fc rosettes on B cells. The interaction of Ig with Fc receptors also seems in some cases to require intact Ig carbohydrate units. Williams *et al.* (*J. Immunol.*, **111**, 1690; 1973) have treated rabbit IgG preparations with an endo-β-N-acetylglucosaminidase from *Diplococcus pneumaniae*. About a half of the carbohydrate, present largely in the Fc portion of the Ig molecule, is removed. The bacterial agglutinating activity of anti-pneumococcal IgG was unaffected by this treatment whereas complete loss of opsonic activity occurred. Similarly several treated IgG preparations had markedly decreased ability to inhibit rosette formation between human monocytes (carrying surface Fc receptors) and IgG-coated erythrocytes. Not all IgG preparations were affected in this way, however, (for example, anti-streptococcal), although similar amounts of carbohydrate were removed by the glycosidase.

The reason for this finding is not clear. Since it cannot yet be excluded that the detailed carbohydrate structure of Ig molecules may differ according to species or possibly with the particular cell clones activated to produce antibody, it seems likely that the type of carbohydrate structure left behind on the treated Ig molecule may also vary. In some cases the biologically relevant sugar sequences might not be removed by glycosidase treatment. Further work using additional enzymes will be required to remove more than half of the carbohydrate, leaving the Ig polypeptide chains intact. Only then will it be feasible to decide if significant differences in the mechanisms for oponisation and phagocytosis of different bacteria exist rather than the simpler explanation that differences in carbohydrate structure occur in Ig molecules of different specificities.

Terminal sequences of animal virus RNAs

from Alan E. Smith

To date, attempts to sequence the RNA of animal viruses have lacked the spectacular success of bacteriophage RNA sequence work. This is largely because of the difficulties encountered with animal viruses in obtaining either highly labelled RNA for analysis by the Sanger technique or large amounts of RNA for sequence determination by more classical methods. Nevertheless, methods are being developed to overcome these problems and among the most successful are the techniques for the enzymatic introduction of radioactive phosphate into specific positions within viral RNA molecules.

Silkworm cytoplasmic polyhedrosis virus (SCPV) contains ten pieces of genomic double-stranded RNA, and in this and other respects it is very similar to the more familiar reoviruses. Some time ago the nucleotides present at the ends of reovirus double-stranded RNA were determined by isolating ^{32}P-labelled viral RNA and subjecting this to Sanger RNA sequencing techniques. All ten fragments of reovirus were found to have a 5′ terminal guanosine 5′ diphosphate followed by a pyrimidine residue (*J. molec. Biol.*, **61**, 643–653; 1971) and a 3′ terminal cytosine (*Nature new Biol.*, **232**, 114–115; 1971). Each genome fragment therefore