T4 phage DNA. Now they have synthesized T4 lysozyme in the same system (*Proc. US Nat. Acad. Sci.*, **63**, 1351; 1969).

β-Glucosyl transferase is an early enzyme appearing in infected cells one to two minutes after infection. The *E. coli* RNA polymerase with the *E. coli* sigma factor transcribes the early genes of T4 *in vivo* and it is not surprising, therefore, that the β-glucosyl transferase gene is read and translated in a cell-free system obtained from uninfected *E. coli*. The successful synthesis of T4 lysozyme in such a cell-free system is, however, more surprising. Lysozyme is allegedly a late protein detectable only eight to ten minutes after infection. But the *in vitro* synthesis of lysozyme was induced by only a slight increase in the concentration of magnesium ions.

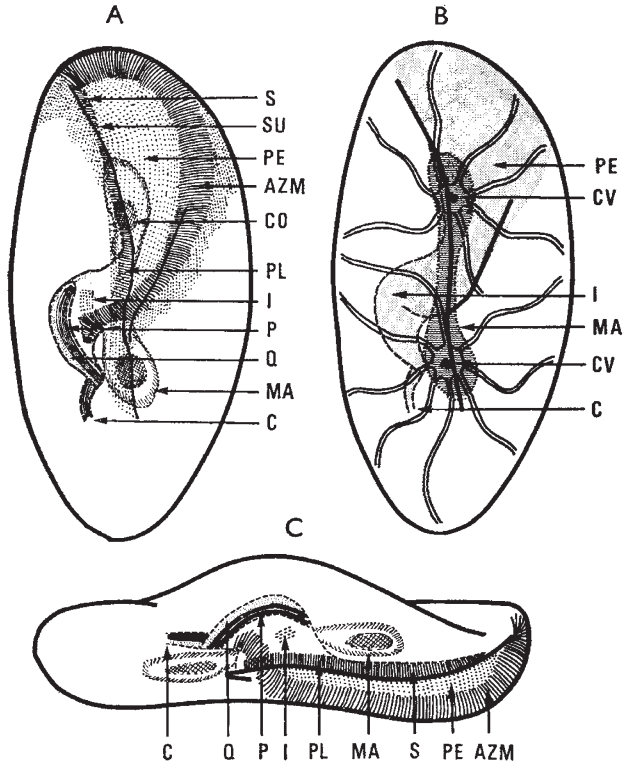
This result adds to the evidence obtained with cells infected with T4 phage, which suggests that the lysozyme gene is not a typical late gene. Apparently it can be transcribed by *E. coli* RNA polymerase programmed with *E. coli* sigma factor, whereas the other late genes of T4 can probably only be transcribed after the synthesis of a new T4 specific sigma factor. But all that aside, having detected *in vitro* synthesis of both lysozyme and β-glucosyl transferase, Schweiger and Gold can boast of perhaps the best recipe yet for making cell-free systems in which transcription and translation of DNA are coupled.

In theory, at least, a cell-free system derived from *E. coli* cells should be able to transcribe the whole of a coliphage genome. It is another matter to expect an *E. coli* cell-free system to transcribe and translate the genome of an animal virus, but Bryan, Gelfand and Hayashi (*Nature*, **224**, 1019; 1969) may well have achieved this. Using a cell-free system from *E. coli*, which was originally developed to study transcription and translation of the coliphage φX174, Hayashi's group seems to have successfully made two of the coat proteins of SV 40 virus, which usually grows in monkey cells. As things are, the identification of two proteins, made when the bacterial cell-free system is programmed with SV 40 DNA, as SV 40 coat proteins rests solely on electrophoretic mobility. But if this claim can be confirmed by fingerprint analysis of the two proteins, Hayashi's work seems to imply at the very least that the initiation signal for the start of translation of mRNA into protein is similar in bacteria, eukaryotic cells and their respective viruses. This is unexpected because the numerous attempts to prove that viruses and eukaryotic cells initiate their proteins with formylmethionine, as do bacteria and phage, have all failed. But if mitochondria are really symbiotic bacteria, would it be so surprising to discover that bacteria and eukaryotes use mutually recognizable signals for initiation of translation?

PROTOZOOLOGY

Structure of a Ciliate

THESE schematic drawings represent *Neobursaridium gigas*, a ciliate related to *Paramecium*. Although the organism was discovered in 1941, the fine structure of *N. gigas* has only recently been described (J. R. Nilsson, *CR Trav. Lab., Carlsberg*, **37**, 49; 1969). Nilsson isolated the ciliate from a papyrus swamp in Uganda in 1955 and has been culturing it ever since. The organism, which averages 550 by 275 microns, has had an interesting taxonomic history; it was first thought to be heterotrichous, but is now recognized as holotrichous. In the drawings, which Nilsson complements with a series of electron micrographs, *A* and *B* show the ventral surface and *C* is a lateral view. The buccal region consists of a peristome (PE) and infundibulum (I) ending at the cytostome (C). The peristome contains two membranellar zones: the pseudo-asoral zone (AZM) and the "septum" (S) on the inner side of the peristomal plate (PL). The infundibulum contains two peniculi (P) and a quadrulus (Q). The macronucleus (MA) contains at least two well defined areas (CO), and two contractile vacuoles have radiating canals (CV).



UNIVERSAL DECELERATION

New Method for Measurement

from our Cosmology Correspondent

DETERMINATION of the universal deceleration parameter (q_0), using the redshift magnitude diagram for the brightest members of clusters of galaxies, suffers considerably from inaccuracies in the allowance made for the evolution of these galaxies in the time it takes for their light to reach the Earth. It is therefore desirable that an alternative method of measuring q_0 should be found, and it seems that this has now been done.

Peach and Beard (*Astrophys. Lett.*, **4**, 205; 1969) have considered the angular diameter/redshift relation for clusters of galaxies in the context of this problem. They found 646 rich clusters from the Abell catalogue which are identifiable with clusters in the Zwicky catalogue, so that for these clusters a combination of the data listed in each catalogue yields both accurate redshifts and angular diameters (defined to an outer isopleth where the surface density of galaxies is twice that in the surrounding field).