often thought to be genetically inert, is stained selectively by the fluorochrome. Chromosomes of *Scilla sibirica*, however, also had a characteristic fluorescent pattern, but these chromosomes do not respond to cold in the same way as do those of *Vicia* and *Trillium*, though they possess heterochromatin as judged by other criteria (La Cour, *Heredity*, **5**, 37; 1951).

Exactly how quinacrine mustard binds to the chromosomes is not known, although it has been suggested that it binds to guanine molecules. Clearly, the pattern of fluorescence reveals something about the chemistry of the chromosome. It is interesting that ethidium bromide gives the opposite pattern of fluorescence from quinacrine mustard. In spite of these uncertainties, this new technique could allow separate identification of morphologically similar chromosomes (such as in the human complement) as well as being a step towards an understanding of the chemistry of the genes as they are arranged along the chromosome.

BACTERIA

## Mesosomes and Biosynthesis

from our Microbiology Correspondent

THE notion that some bacteria contain organelles which are the sites for the synthesis of cell wall components has now been strengthened. Mesosomes, invaginations of the protoplasmic membrane of Gram-positive and Gram-negative bacteria, have been endowed with various functions including an involvement in nucleoid separation, cell division and endosporulation. Although a role in cell wall synthesis has been proposed by many groups during the past decade, evidence has been slow to emerge. But recently K. J. I. Thorne and D. C. Barker of the Dunn Nutritional Research Laboratory in Cambridge have obtained data which strongly support the idea. The starting point for their investigations was the finding that mevalonic acid could replace acetate in the growth of lactobacilli, and that the acid was channelled into the synthesis of the isoprenoid alcohol, bactoprenol.

Cells of *Lactobacillus casei*, labelled by incubation with $^{14}$C-mevalonic acid, were treated with a combination of trypsin, EDTA and lysozyme and 60 per cent of the label was released. A large proportion of this material was bactoprenol which was bound to protein in a complex with a molecular size of $3{\cdot}5 \times 10^7$, containing an estimated forty molecules of bactoprenol. After negative staining Thorne and Barker examined the bactoprenol–protein complex in the electron microscope and found vesicles approximately 0·1 micron in diameter. These had resisted ammonium sulphate precipitation and gel filtration of the bactoprenol–protein complex. Thin sections of *Lactobacillus casei* before and after digestion with lysozyme revealed that the vesicles were of cellular origin and, furthermore, were derived from the mesosome. Such an origin for the extracellular vesicles is fully supported by previous ultrastructural studies of species of *Bacillus* and *Lactobacillus*.

Material released from *Lactobacillus casei* by enzyme treatment included ATPase and the acetate activating enzymes acetokinase and phosphotransacetylase. The kinetics of the release of enzymes and bactoprenol were not identical, but all were precipitable by 80 per cent ammonium sulphate saturation. Disc electrophoresis and gel filtration confirmed that the enzymes were not attached to the vesicular material, but it could be argued that these activities represent soluble mesosome components which are released when the mesosome is converted to vesicles. Thorne and Barker propose that the bactoprenol entity, in contrast, might represent the outer membrane of the vesicles. The most interesting feature of these results, however, is that the acetate activating enzymes could be involved in fatty acid biosynthesis. Thus, the correlation between bactoprenol as a carrier in peptidoglycan synthesis and its location in the mesosome is an important step forward in the understanding of cell wall synthesis, and weighty support for the idea that mesosomes are involved in the process.

VIRUSES

## Subunits Explored

from our Molecular Biology Correspondent

THE laying bare of the architectural principles of virus structure has without doubt been one of the most aesthetically satisfying achievements of molecular biology. A tenet which might reasonably be based on the structure of tobacco mosaic virus is the structural equivalence of identical subunits. The long rod-like particles are made up of identical protein subunits disposed in a regular helix of 23 Å pitch, such that there are forty-nine subunits in every three turns. In the common strain of the virus (*vulgare*), all subunits (apart from those at the ends of the particle) are strictly equivalent. This principle seemed, however, not to be upheld in certain mutant forms, of which the best characterized is the dahlemense strain. The long-awaited and definitive article on the structure of this form has now appeared (Caspar and Holmes, *J. Mol. Biol.*, **46**, 99; 1969), and contains lessons of the widest relevance to subunit-based structures in general.

The X-ray pattern of the dahlemense strain shows the same helix pitch as the *vulgare*, but also an additional set of reflexions, which signify a perturbation of the regular structure. The near-meridional position of the new reflexions indicates a distortion of the helix in the axial direction, which involves a deformation near the surface of the particle, permitting the pairwise approach of subunits from adjacent turns. The interior part of the helix is rigid and unchanged, so that the deformation is confined to a region of the protein monomers near their outer edge. This distorted structure repeats every six turns. Caspar has termed the type of relationship between subunits seen here "quasi-equivalent". In the dahlemense structure there are ninety-eight such sterically distinguishable quasi-equivalent environments for the identical subunits. Since the spatial relation between side-to-side neighbours is unchanged, it is clear that only the axial distortion within each subunit is sufficiently cheap energetically to make the extra contact worth the price. A curious feature of the structure is that the distortion does not extend throughout the length (3000 Å) of the particle, but occurs in domains some 500 Å long. The reasons for this are by no means obvious, although Caspar and Holmes offer a rationalization on entropic grounds. They suggest that quasi-equivalence is likely to be the prevalent condition not only in TMV strains, but also in many fibrous structures, where it could