at really short distances. The conclusion drawn from this experiment is that for distances down to the order of 10^{-15} cm there is no evidence whatsoever for a primitive acausal (in the sense of special relativity) region or fundamental length.

It has been known for some years (R. Oehme, *Phys. Rev.*, **100**, 1503; 1955) that the existence of an acausal region of space time (across which signals might be propagated at velocities exceeding that of light) leads to a failure of forward dispersion relations for elastic scattering. These relations, which are based only on very general theoretical considerations, state that apart from various subtraction constants and kinematical terms the real part the elastic scattering amplitude (say, for pion–proton scattering) is given by an integral over energy of the total cross section for the process multiplied by well defined functions of this energy. Thus if the real part of the scattering amplitude can be measured (and this is the difficult part) for some simple elastic process where the total cross sections are well known, a critical test of our space–time concepts becomes available.

Lindenbaum and his colleagues have carried out elastic pion–proton scattering experiments in the momentum region 8–26 Bev/c using an impressive array of counter equipment linked directly to computers to provide both permanent record and immediate on-line analysis of data. Although two amplitudes are required to describe this process in general (corresponding to the possibility of reversing the spin of the proton) only one is of significant magnitude at small scattering angles and the experiment is correspondingly performed at angles less than 25 mrad. The real and imaginary parts of this amplitude can be separated by examining in detail the small interference effect (in the differential cross section) between the dominant strong interaction and the much weaker electromagnetic one. It is the very small magnitude of this effect coupled with both theoretical and experimental uncertainties as to form factor and multiple scattering corrections which make this such a hard experiment.

The interference has been found to be destructive for negative pion scattering and construction when positive pions are used. In the former case the ratio of the real to imaginary parts of the amplitude is almost constant at $-0{\cdot}13$ throughout the measured range, and in the latter case rises smoothly from $-0{\cdot}22$ at 8 Bev/c to $-0{\cdot}14$ at 20 Bev/c. By comparing these results with the measured total cross sections (the authors have also remeasured these, but have not yet published their results) integrated in the dispersion relations, it has been established that good agreement exists at least up to values of 20 Bev/c for the pion momenta.

Experiments which test such basic concepts are quite rare, and ones which combine such powerful techniques in both theory and experiment are rarer still. It is a welcome change in these days of the mass production of resonances to see one of the largest machines used in this thoughtful manner.

Cytochrome c

from a Correspondent in Molecular Biology

CYTOCHROME *c* is an interesting protein for a number of reasons, not least because it offers an unrivalled opportunity for observing biochemical evolution. Cytochrome *c*s have been isolated from vertebrates, invertebrates, micro-organisms and plants, and through the efforts of E. L. Smith, Margoliash and their associates, the amino-acid sequences of a wide range of these have been determined. The most recent study, by Stevens, Glazer and Smith (*J. Biol. Chem.*, **242**, 2764; 1967), gives the first sequence of a plant cytochrome *c*—that from wheat germ—and therefore represents a particularly interesting addition to the series.

The polypeptide chain consists of 112 residues, compared with 104 for all vertebrate pigments. It differs from the other cytochrome *c*s of known sequence (considering only the first 104 residues) in 35–46 amino-acids, and actually shows fewer differences from the human heart protein than that from a fungus. It is extraordinary to discover that between all the known sequences the number of positions in the chain which remain invariant is now reduced to 35. It is true that in many of the variable positions the substitutions are limited to amino-acids of similar kind, for example, that of one non-polar residue for another, but this is by no means always the case. Only one uninterrupted sequence of more than two residues is present in all cytochrome *c*s, namely, the eleven residues, 70–80. In addition, two of the constant residues are cysteines 14 and 17, which are covalently linked to the haem group, and the two residues now generally supposed to act as ligands for the iron on either side of the haem plane, histidine-18 and methionine-80. All known cytochrome *c*s appear to be capable of interacting with mammalian cytochrome oxidase, and the steric requirements for this recognition process evidently therefore involve only a minority of the residues. One may perhaps speculate that the long invariant sequence is in some manner involved in this aspect of the function.

It is a happy circumstance that at the same time the first report has appeared from Dickerson's laboratory (*J. Biol. Chem.*, **242**, 3015; 1967) of the X-ray structure of horse heart cytochrome *c* at 4 Å resolution. This is sufficient to define many of the structural features of the molecule. Cytochrome *c* appears to possess little or no α-helix. From the distribution of electron density it appears that the molecule conforms well with the principle that the hydrophobic side chains are packed into the interior of the molecule, while the polar side chains coat the exterior. The two cysteine residues attached to the haem, and one of the ligands, histidine-18, can be identified with certainty. The haem group lies in a long crevice down the long axis of the molecule, with one edge only exposed. The chain appears to be in a largely extended state, and the structure is very different from those of the other haem proteins, myoglobin and haemoglobin.

It is to be hoped that as more details become available it will soon be possible to identify the invariant positions in the chain, which must be supposed necessary to define the structure as that of a functional cytochrome *c*.

Fungal Morphogenesis

from a Correspondent in Microbiology

ONE of the most exciting challenges of contemporary biology is the interpretation in biochemical terms of morphological change. Studies of biochemical differen-