In the field of molecular theory, Professor R. G. Parr (Johns Hopkins University) presented some novel relations between the vibrational force constant k of diatomic molecules and the atomic numbers Z_a, Z_b of the component atoms. These relations, of the type $\ln(k/Z_a)=AR+B$ (A, B constants, R=equilibrium interatomic distance) reflect the exponential decay of the radial wavefunctions. Other contributions carried previous calculations to higher approximations, for instance Dr C. W. Haigh (University College of Swansea) and Dr R. B. Mallion (University of Oxford) on the perturbation of a π-electron cloud by a magnetic field, or Dr M. Thomas (University of Oxford) on the explanation of why the apparent bond length measured by X-rays is less than measured by electron or neutron diffraction.

One of the most interesting sessions was that on the hydrogen bond. The problem of its nature has not yet been fully solved. A discussion of the various contributions to the H-bond energy was presented by Dr L. C. Allen (Princeton University) and Dr P. A. Kollman (University of Cambridge): a molecular orbitals calculation could predict, at least qualitatively, the energy of the bond in H_2O-HF dimers, though the value was very sensitive to the choice of the basis set. Professor M. Kasha (Florida State University) succeeded in unravelling the complicated phenomena (charge transfer, simultaneous transitions, successive excitations, and the like) which occur when molecular oxygen absorbs radiation.

There were also contributions on scattering theory, band theory, polarons, algebra on computers. It was altogether a most enjoyable meeting, demonstrating clearly, as remarked by Professor J. H. van der Waals (Leiden University), the stout trees that have grown from the seeds sown by Coulson perhaps twenty years ago.

SINGLE CELL PROTEIN

Doing the Sums

from our Microbiology Correspondent

PROTEIN shortages of 10 and 22 million tons are predicted by the Food and Agriculture Organization by the years 1980 and 2000 even if all present resources are fully exploited. Such statistics have induced a spectacular response from biologists who see microbiologically produced protein—the now familiar single-cell protein (SCP)—as the prime hope for making good this deficit. The big attraction of SCP is the possibility of utilizing cheap raw materials as fermentation substrates and these include hydrocarbons, molasses, whey, sulphite waste liquor and other wood products. A major uncertainty surrounding the development of SCP, however, is one of economic feasibility; the base line against which to make an economic assessment is about ten cents per pound for cotton seed, soy and peanut proteins. The appraisal of microbial protein by Vilenchich and Akhtar (*Process Biochem.*, **6**, 41; 1971) is therefore timely and should help to orientate both academic and commercial groups interested in this project.

SCP has several advantages over traditional animal and plant proteins; the higher nutritional status and very much shorter time required to double the mass of the product are two of the most important. Offsetting these advantages is the question of market acceptability, especially when a product for direct human consumption is considered. The cost of processing SCP for human diets is high and the final product is likely to be three to four times more expensive than plant proteins. But when petroleum is used as the raw material little processing is required to produce animal feed supplement and the cost can be as little as six cents per pound.

Vilenchich and Akhtar point out that single-cell protein research has centred so far on three basic problems —searching for the cheapest suitable fermentation substrate, searching for organisms which, in addition to possessing the right nutritive properties, grow rapidly and produce the highest yields on the chosen substrate and solving bioengineering problems encountered during industrial scale production. Scientific opinion, including that with a commercial interest, favours hydrocarbon fermentation as that offering the

Enzymes for Transformation

RNA tumour virus particles carry into the cells they infect all the enzymatic machinery necessary for the malignant transformation of their hosts—that is the fascinating conclusion Howard Temin and his colleagues have reached from their latest investigations of the range of enzyme activities present in Rous sarcoma virus particles (see next Wednesday's *Nature New Biology*). The epoch making discovery of reverse transcriptase in RNA tumour viruses, independently reported last June by Temin's group and Baltimore, explained how these viruses can stably transform cells. For reverse transcriptase can use the single stranded RNA genome of these viruses as a template for the synthesis of, first, a complementary DNA strand and then a double helical DNA. And this molecule, containing all the genes of the infecting virus including those responsible for transformation, can then be integrated into the chromosomal DNA of the infected cell and inherited by each daughter cell at mitosis.

The integration of tumour virus DNA into a host cell chromosome could conceivably be brought about by enzymes existing in the cell before it is infected. The enzymes involved in recombination, for example, could, in theory at least, do the job. But it seems, from the experiments of Mizutani, Kodama, Wells and Temin, that in fact the virus carries with it its own integration machinery. They have found that in addition to reverse transcriptase Rous sarcoma virus particles contain a DNA endonuclease activity which can cut long DNA chains into shorter pieces, and a DNA exonuclease activity which can digest DNA by clipping nucleotides one by one from the end of a chain. Furthermore, these viruses contain a DNA ligase activity; that is to say, they have an enzyme which can join together the free ends of two DNA chains.

Although they have yet to prove that all these enzymes are involved in the process of transformation their very presence in the virus particles suggests the following sequence of events. After infection, reverse transcriptase makes a double stranded viral DNA. The two nucleases then cut some part of the DNA of a host chromosome and trim away a gap. The viral DNA is then inserted in the gap and sealed into the host DNA molecule by phosphodiester bonds formed by the DNA ligase.

Most cells transformed by an RNA tumour virus continue to produce progeny virus particles which are budded from the surface of the cell. No doubt the integrated viral DNA molecules act as template for the transcription of viral RNA which can then be wrapped up into progeny particles; but until the advent of reverse transcriptase attempts to detect these progeny RNA molecules in the nucleus of cytoplasm of transformed cells were not crowned with great success. With reverse transcriptase, however, Green and his colleagues have been able to make themselves a highly specific probe for the missing RNA. As they report in Wednesday's *Nature New Biology*, radioactive murine sarcoma virus DNA, made with reverse transcriptase, hybridizes with viral RNA present in transformed cells. They estimate that as much as 5 per cent of the RNA in the nuclei of cells transformed by mouse sarcoma virus is virus specific and that 0.5 to 1.0 per cent of the RNA in the cytoplasm is viral RNA. So another link in the story of RNA tumour virus replication has been found.