that rely on the ingestion of one host by another for the completion of their life cycles can tip the scales in a predator/prey situation in their favour by making the first host more conspicuous to the second. This was clearly shown by Dr J. C. Holmes (University of Alberta) who described how parasitized freshwater shrimps swim to the surface and attach themselves firmly to reeds and floating debris that are more efficiently searched by ducks than the muddy bottom of a pond.

NUCLEIC ACIDS

New Exchange Rates

from our Molecular Biology Correspondent

THE trouble with hydrogen exchange is that although the results are full of information, it has often been unclear what they mean. Several interesting ideas have nevertheless emerged: the relatively slow exchange rates in DNA, for example, compared with mononucleotides, gave substance to the notion of a "breathing" effect in the double helix, involving the transient melting of units of a few base pairs. It was assumed that the reluctant hydrogens in the double helix were only those involved in hydrogen bonds between base pairs, but because of the difficulty in extending the rate plot to very short times the number remained unknown.

That any useful measurements were feasible within the time-scale of exchange in nucleic acids was due to new methods devised by Englander of achieving rapid separation of the nucleic acid from tritiated solvent. By a number of innovations of technique Hanson has effected a diminution in separation time by another order of magnitude, and in a paper in *J. Mol. Biol.* (**58**, 847 ; 1971) he now describes his new results on the tritium exchange kinetics of DNA. Using short columns of 'Sephadex' to separate the DNA from the tritiated water, with forced elution under pressure, the extraneous counts can be separated from the sample in about 6 s. The essential benefit of extending the data to these short times is that the lower limit of the intercept for the number of unexchanged hydrogens at zero time can be raised. With the previous data and with times down to 100 s, the zero-time extrapolation looks to be heading for a value close to the number of protons in Watson–Crick pairs, for example, 2.4 per base pair for calf thymus DNA. Hanson's data show that this extrapolated value is much too low and that a value of 3.8, corresponding to all the N–H protons in the base pair, seems closer to the truth.

An A·T base pair has three exchangeable protons and a G·C pair five, and indeed the higher the G·C content of the DNA, the higher the value at which the rate-plot approaches the zero-time axis. For the alternating polymer, poly d(AT), the value of two protons is again much too low, whereas three looks altogether convincing. Two-stranded poly(dG)·poly(dC) presents difficulties of preparation, but Hanson quotes unpublished data that indicate a value of five hydrogens exchanging at measurable rates. Single stranded polynucleotides, such as poly (A) exchange completely in an immeasurably fast time. It seems then that exchangeable hydrogens in the double helix grooves are protected against exchange. It is probably scarcely profitable to speculate on the mechanism of this retardation—it may or may not involve the structure of water in the hydration shell, the local dielectric constant, or yet other effects. At all events these results provide a new basis for the interpretation of exchange data for nucleic acids in various circumstances. The view still stands that exchange occurs by way of an unpaired state, but that the "breathing" frequency is too great to be rate-limiting. A possible explanation for the spectrum of exchange rates observed in DNAs is that there are two or more "open" or "deformed" states of short duration, offering varying degrees of accessibility to the solvent. Hanson points out the possibilities which rotation rates of amino-groups about the N–C bond within the lifetime of the "open" state offer for determining the equivalence or non-equivalence of the two protons of a hydrogen-bonded amino-group, and he also notes the environmental differences between G·C protons in the wide and in the narrow groove.

An empirical but useful application of the tritium exchange method has been to the study of ribosomes. Here both proteins and RNA have exchangeable protons, some of which are replaced quite slowly. When the subunits are dissociated there is evidently a large conformational disturbance, for rapid exchange at once ensues. Chuang, Silberstein and Simpson (*Arch. Biochem.*, **144**, 78 ; 1971) now report that the exchange rate of 70S *E. coli* ribosomes is detectably modified at the translocation step. The addition of translocation (G) factor and GTP causes a change in the exchange-rate profile, which is not observed when an inactive GTP-analogue is used, or when the translocation inhibitor, fusidic acid, is included. Chuang *et al.* conclude that translocation is accompanied by far-reaching conformational upheavals in the particle, and they permit themselves the fancy that such a distortion of the ribosome cranks the particle along the messenger, while translating the peptidyl-tRNA from the aminoacyl to the peptidyl site.

Superheavy Elements

ONE of the most exciting aspects of nuclear physics in the past few years has been the realization that there might be stable nuclei with a nuclear charge of $Z \approx 112$. The first experimental results that purported to show the existence of such nuclides were obtained by a team based at the Rutherford High Energy Laboratory and published in *Nature* earlier this year (A. Marinov *et al.*, **229**, 464 ; 1971). They claimed that the result of their experiment was not inconsistent with element 112 having been formed when a tungsten target was bombarded with 24 GeV protons. The proposed mechanism for formation of the superheavy element was based on an energetic tungsten nucleus being given enough energy by the proton beam to make it possible for it to react with a stationary tungsten nucleus in the target, and thus lead to a reaction that would form element 112.

This proposed reaction mechanism was soon recognized as the weakest part of the interpretation of Marinov *et al.* and the feeling was that this process would not have a sufficiently large cross-section (that is probability of occurrence) for the reported amount of element 112 to have been formed. This argument is put on a quantitative basis in next Monday's *Nature Physical Science* by P. K. Kabir, himself from the Rutherford Laboratory, and J. S. Trefil of the University of Virginia in work carried out at Virginia while Kabir was on leave. Their calculations give a cross-section for formation of element 112 that is 10^9 times smaller than the value assumed by Marinov *et al.* to explain their results.

This could possibly be the last word and some explanation, other than the production of element 112, would have to be found to explain the effects observed by Marinov *et al.* This does not seem to be the case as Dr Christopher Batty, one of Marinov's colleagues and the coordinator of the work at the Rutherford Laboratory, in a reply published with the article of Kabir and Trefil points out that the calculations are not in agreement with experiment and he cites two recent publications that show the measured cross-sections for the production of fast heavy nuclear fragments to be much greater than calculated. The stage is set for another round of discussion of the work of Marinov *et al.* and the efforts currently under way to confirm the existence of element 112 will continue unabated.