years with pyridoxine, so it may be that there is a relationship between morning sickness, increased oestrogen levels, and the depressions which can occur in early pregnancy.

HERPESVIRUSES

Genetics of HSV 1 and 2

from our Cell Biology Correspondent

THE genetic analysis of animal viruses, be they RNA viruses or DNA viruses, is still very much in its infancy but many animal virologists aspire after the achievements of bacteriophage geneticists and are seriously attempting to isolate suites of mutants that can be used in complementation and recombination tests. Animal virologists, of course, labour under severe disadvantages not shared by bacteriophage geneticists: animal cells grow slowly compared with bacteria, they are far more fastidious and to date nobody has detected suppressible mutants of animal viruses comparable to the amber and ochre mutants of phage. Temperature sensitive mutants of animal viruses, however, can be and have been isolated, and as Brown, Ritchie and Subak-Sharpe (*J. Gen. Virol.*, **18**, 329; 1973) take pains to stress, such mutants offer several distinct advantages which go some way towards compensating for their great disadvantage—their leakiness.

Subak-Sharpe and his colleagues have independently isolated nine 5-bromodeoxyuridine-induced temperature sensitive mutants of herpes simplex type 1 virus, which because of its large genome (about 105×10^6 daltons of double stranded DNA), presents the animal virologist intent upon genetic analysis with a formidable task. These nine *ts* mutants apparently fall into eight complementation groups and, therefore, presumably define eight herpes simplex 1 cistrons. Moreover, because eight of the nine *ts* mutants selected at random fall into different complementation groups, Brown *et al.* estimate that the herpes simplex 1 genome probably contains more than thirty cistrons which specify functions that are indispensable for viral replication at 38° C.

Using these nine *ts* mutants and a plaque morphology marker in three factor recombination tests, Subak-Sharpe's group has also produced a tentative linkage map of the herpes simplex 1 genome. The map is linear, locates nine cistrons—the eight defined by complementation tests and the plaque morphology marker—and spans about twenty-five recombination units. In short, the group has made a useful start to the genetic analysis of this large and complex virus.

With another colleague, Timbury, Subak-Sharpe has also begun to probe the range of genetic interactions between herpes virus type 1 and its relative type 2 (*J. Gen. Virol.*, **18**, 347; 1973). Making the most of their *ts* mutants of type 1 and type 2 viruses they have established not only that herpes simplex viruses types 1 and 2 can complement each other to a considerable extent, but also that the type 1 and type 2 genomes can recombine to produce stable recombinants. Furthermore, the progeny of cells infected with these two viruses include heterozygotes and in some cases viruses with a phenotype distinct from those of both parents. With the possibility that herpes simplex virus type 2 might be involved in the aetiology of human cervical cancer the Glasgow group should find it easy enough to justify extending this analysis.

Herpetologists will no doubt also have noticed Smith and de Harven's recent report (*J. Virol.*, **11**, 325; 1973) of what seems to be a neat method for concentrating stocks of herpesviruses, many of which do not yield high titres when they replicate in cultured cells. Apparently negative pressure ultrafiltration through dialysis tubing does the trick, by converting low titre stocks into high titre concentrates of intact unaggregated virus particles without loss of infectivity.

CELL FREE SYSTEMS

Translation *in vitro*

from our Cell Biology Correspondent

THE person who first manages to isolate strains of cultivated animal cell which harbour suppressor mutations and as a result contain suppressor transfer RNAs capable of translating amber or ochre codons in messenger RNAs will have achieved a triumph. The opportunity to isolate and exploit suppressible nonsense mutants of animal viruses is something animal virologists long after, and until suppressor mutant cells are isolated virologists must content themselves by working with temperture sensitive mutants that are a deal less satisfactory. The isolation of suppressor strains of animal cells is, it scarce needs saying, a formidable task that promises much hard and tedious work with no guarantee of ultimate success and, not surprisingly, nobody has embarked on it seriously. But thanks to the efforts of Schreier, Staehelin, Gesteland and Spahr (*J. Mol. Biol.*, **75**, 575; 1973) there is now at least an *in vitro* assay system that can be used to screen for the suppression of nonsense mutants in eukaryotic cell extracts.

Schreier and Staehelin (*J. Mol. Biol.*, **73**, 329; 1973) have recently devised a highly efficient mammalian cell free system in which, for example, during 40 min at 30° C, each ribosome will translate a globin messenger RNA molecule three or four times. While Gesteland and Spahr during the past several years have made themselves masters of *Escherichia coli* cell free systems which translate efficiently not only the genomic RNAs of RNA bacteriophages such as R17 and $Q\beta$, but also the messenger RNAs of T-even phages. These workers in collaboration have established that the mammalian cell-free systems of Schreier and Staehelin can, with appropriate modifications, be induced to translate faithfully the coat protein cistron and the RNA replicase cistron

Messenger Translation in *Xenopus* Oocytes

A CAUTIONARY tale is told in a short contribution to next Wednesday's *Nature New Biology* (May 16) presented by Lane, Gregory, Iyatzumi and Scherrer. In recent years, evidence for the existence of messenger RNA sequences in high molecular weight RNA (HMW RNA) has been reported, based on experiments in which synthesis of globin or immunoglobin occurred following injection into *Xenopus* oocytes of HMW RNA extracted from the appropriate tissues (erythroblasts or myeloma cells). This made a neat and happy story, but now Lane *et al.* plead caution. The trouble seems to lie in the extreme sensitivity of the oocyte system as a test for mRNA translation. Thus, if as little as 1 per cent of the HMW RNA injected into oocytes is represented by contaminating aggregated cytoplasmic messenger, then synthesis of the appropriate protein would be detected. Even excluding cytoplasmic contamination, it is possible that nuclei, from which the HMW RNA is extracted, may contain functional mRNA.

The control experiment carried out by Williamson *et al.* (*Nature New Biology*, **241**, 66; 1973) to eliminate the possibility of 9S globin mRNA contamination of their HMW mouse erythroblast RNA is inconclusive. Williamson *et al.* demonstrated that no globin was synthesized when brain HMW RNA (extracted from a mixture of brain tissue and reticulocyte lysate) was injected into *Xenopus* oocytes. Lane *et al.* point out, however, that 9S mRNA in the lysate may have been degraded by brain enzymes. They suggest a control experiment to solve the problem. If HMW RNA were extracted from a mixture of duck erythroblast nuclei and rabbit reticulocyte polysomes then, if messenger aggregation does not occur, the HMW RNA should code for duck but not rabbit globin, whereas the 9S fraction from the same preparation should cause the synthesis of both globins.