and was later prosecuted by the Biological Records Centre of the Nature Conservancy. It seems most remarkable that this is the first systematic attempt to map the distribution of freshwater fishes in the British Isles. Earlier statements of their distribution were apparently generalizations, based on reports in literature or museum collections, of presence or absence in river systems. Maitland's work on the mapping of observed occurrences is therefore a welcome addition to basic data.

Records of occurrence are shown by the standard 10 km square grid used by the Biological Records Centre. Like all distribution maps, they are open to the comment always made of such projects—that they show the distribution of recording observers rather than the animals concerned. Although this is true to some extent, it is equally true that this first printing should act as a spur to laggardly recorders, and generate a need for updating and reprinting soon. One hopes that future editions of the maps will be available at a more realistic price than the £1.20 at present charged for the whole publication.

The identification keys are presented in the classical manner with couplets which use several, chiefly meristic, characters at each step. This results in the usual cumbersome arrangement in which no short cuts are permissible, and one mistake can lead to disaster; the student simply has to plough through all the appropriate couplets with the thought that there must be an easier way to identify a fish than counting scales, fin rays, myomenes, gill rakers and so forth. To take an example, to identify a flatfish from a British river, one needs to work through five couplets (out of twenty in the family key) to get to the family (Pleuronectidae) and a page reference, on which one discovers that there is only one species anyway—the flounder.

The example begs the question, why in a key which is presumed to be used in the field or by the beginner in fish taxonomy is it necessary to follow slavishly a systematic order, and to overload each couplet with detail? The flounder, being the only flatfish, could have been dismissed in a single line on the first page to the great benefit of the user and a considerable economy of paper and effort.

The practical result of such a classical method and prolixity will be despair in most cases, and the user forced to look for the "best fit" illustration. Keys intended for use in identification (as opposed to those concocted to show systematic positions, or the ingenuity of the compiler) should be simple and unambiguous, using characters which are, if not trenchant, then easy to assess. The only justification that can be offered for the present style is that a worker totally unfamiliar with the subject could use the key, but even the simplest student is likely to wonder at the choice offered in several couplets, as "Less than 13 rays in the anal fin . . ." *versus* "More than 11 rays in the anal fin . . .". There must be easier ways of identifying fish than this.

TRANSFORMATION

## Genomic Parameters

from our Cell Biology Correspondent

ESTIMATES of the number of genomic equivalents of simian virus 40 DNA in cultured cells transformed by SV40 are markedly dependent upon the methods used to measure the amount of SV40 DNA in a known amount of cellular DNA. Westphal and Dulbecco, who developed a method for transcribing *in vitro* with *Escherichia coli* RNA polymerase SV40 DNA and then hybridized this labelled virus-specific RNA to transformed and untransformed cell DNA stuck to nitrocellulose filters, have estimated that cells of a particular line of SV3T3 transformants contained forty-four genomic equivalents of SV40 DNA. But when Gelb *et al.* estimated this parameter from measurements of the rate of reannealing of SV40 DNA in the presence of DNA from these SV3T3 cells and in the presence of untransformed 3T3 cells they came up with the value of 1.42 SV40 genomes per cell. Even allowing for the different values assumed by these groups for the weight of the 3T3 cell genome there remains a twenty-fold discrepancy.

It is nowadays generally accepted that the estimate of Gelb *et al.* is the more accurate, not least because, as Haas, Vogt and Dulbecco showed recently, DNA hybridized to RNA tends to come free from nitrocellulose filters, and, no doubt for the same reasons, Pettersson and Sambrook's estimate (*J. Mol. Biol.*, **73**, 125; 1973) that rat cells transformed by adenovirus 2 contain about one genomic equivalent of adenovirus 2 DNA per diploid amount of cell DNA is closer to reality than the estimates of fourteen to thirty-seven genomic equivalents of adenovirus 2 DNA per cell genome reported in 1970 by Green and his colleagues, who used the RNA/DNA hybridization technique. The transformed rat cells used by Pettersson and Sambrook were separate stocks, originally derived from the same transformant grown from many cell generations in different laboratories. Clearly the amount of adenovirus DNA in such cells is stable. Furthermore, because the transformed rat cells are aneuploid it is currently difficult to calculate just how many viral genomes there are in each transformed cell genome as opposed to per diploid amount of cell DNA, but the number must be very small.

Like adenovirus 2, adenovirus 12 transforms rodent cells, and according

## Taxonomy of RD114 Virus Particles

RD114 VIRUS is a C-type RNA virus liberated from a line of human tumour cells which was passaged in kittens. Because of the history of these human cells which liberate RD114 virus two possible origins of the virus have to be considered; it might be a feline virus picked up during the passage in kittens or it might be a human virus, related to the RNA tumour viruses of lower mammals, the replication of which was induced when the human cells were passaged in kittens. A variety of serological tests have shown that RD114 virus particles are not antigenically related to known feline C-type viruses, and in *Nature New Biology* next Wednesday (January 31) Huebner's group (Long *et al.*) report experiments which they believe "add to the indication that RD114 is most probably a human virus".

Long *et al.* inoculated partially purified RD114 virus particles into guinea-pigs and obtained from these immunized animals antisera which strongly inhibit the reverse transcriptase activity present in RD114 virions. They then assayed these antisera for their ability to inhibit the reverse transcriptase activities present in primate, feline, murine, avian and viper C-type RNA viruses. It has, of course, been shown repeatedly that the reverse transcriptases present in these different groups of viruses are antigenically distinct and that transcriptase inhibition tests using antivirus antisera indicate taxonomic relationships between these viruses.

Long *et al.* find that antisera to RD114 virions reproducibly and completely inhibit the reverse transcriptase in this virus and also inhibit to a significant extent the transcriptase activities in two primate C-type viruses. The anti-RD114 antisera do not, however, reproducibly inhibit the enzymes in feline, murine, avian and viper viruses. Clearly this result is compatible with the idea that RD114 is a human C-type virus, but it is surprising that Long *et al.* did not carry out the reciprocal tests, challenging RD114 particles with antisera against the two primate viruses; these tests should be done, for they may clinch the case.