

CLASSIFICATION OF TICK-BORNE FLAVIVIRUSES

John R. Stephenson

Division of Biologies, Public Health Laboratory Service, Wiltshire SP4 OJG, England

Received April 4, 1989

In his recent review in *Acta virologica* entitled "Antigenic classification and taxonomy of flaviviruses (Family *Flaviviridae*) emphasising a universal system for the taxonomy of viruses causing Tick-borne Encephalitis" Dr. Calisher draws attention to the apparent confusion surrounding the taxonomy of these viruses. While I wholeheartedly agree that the nomenclature of this group of viruses is unhelpful and would support his suggestion that "Central European TBE" should be employed as a generic term, I think there are a few considerations that should be made before it is decided to adopt a new, internationally agreed nomenclature. Any taxonomic exercise should not only be rational, but be based on a series of parameters which are simple enough to be measured easily and rapidly so that taxonomy is not merely an academic exercise but performs a useful function.

Thus the first decision to be made should be: why do we need to classify our viral isolates? If it is decided that data on the molecular evolution of viruses is the goal to achieve, then only a taxonomic structure based on nucleic acid sequence analysis will achieve that target. Such an approach has resulted in the recent creation of the *Flaviviridae* family and the possible transfer of the pestiviruses from the *Togaviridae* to the *Flaviviridae*. At present these techniques are not available to all scientists and members of the medical profession, and can have only a limited application.

A more useful and practical approach then may be to continue taxonomic studies by analysing antigenic variation. This has several advantages: studies on antigenic variation are important to ensure that current vaccines are sufficiently closely related to recent isolates to maintain good protection. In addition, most research and diagnostic laboratories have facilities to carry out ELISA or IF assays on inactivated antigens, analysis is quick and in the case of ELISA gives an easily quantifiable result. Such analyses have in the past given rise to equivocal results, largely as a result of the use of reagents of varying quality. If such a study is to be undertaken reagents of reproducible quality must be used. Thus monoclonal antibodies only should be employed and they should be produced in tissue culture, preferably in serum free medium. There must also be an agreed method of producing antigen which is simple enough to be carried out in most laboratories: and ideally all laboratories should make their antigen from a common stock. As ELISA assays are the most easily quantifiable, they should be used as the agreed assay system with a common method of expressing titres.

Finally, I think it is probably unwise to exclude the pathogenicity of a viral isolate from a taxonomic system. Given that such parameters are unreliable as they depend upon subjective observation, the immune status of the patient and local environment conditions, they are extremely valuable for public health management. For example the minds of public health officials and the efforts of vaccine manufacturers will be more stimulated by an outbreak of RSSE than they would if they are told an increasing number of school children have antibodies to Langat or Skalka.

If other workers in this area are concerned about the problem of taxonomy, we could be glad to donate our monoclonal antibodies against the E and NS1 proteins to such a study.