BIOCHEMICAL AND SEROLOGICAL CHARACTERIZATION OF DIFFERENT FIELD APHTOVIRUS STRAINS ISOLATED IN SOUTH AMERICA[1]

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SHORT COMMUNICATION

Until recently classical serological techniques were the only ones used to follow the behavior of outbreaks of foot-and-mouth disease (FMD) occurring in South America (*6*). The high mutation rate of the FMD virus (FMDV) genome requires the application of highly sensitive techniques in order to make it feasible to establish the possible source of outbreaks as well as to have a better understanding of the molecular basis of virus variability (*2, 5, 7, 10*) and the epidemiology of FMD which is of critical importance for the eradication of the disease.

In a previous publication (*1*), the application of RNA fingerprinting (RNase T_1 maps in one- and two-dimensional gels) in combination with serological techniques was reported for the characterization of the prototype strains used for vaccine production or as reference strains in South America. The results obtained provide the basis for a data bank containing information about the genomes of strains of aphtovirus prevalent in this continent and can be used as an adjunct to serological and immunological information.

These data are currently being used in South American countries to: (a) complement other tests in the updating of vaccine strains; (b) assess the genetic stability of virus strains during vaccine production; (c) establish possible vaccine origin of occurrence of field outbreaks; (d) identify virus escapes of laboratories which handle FMDV, and (e) monitor the origin, behavior and fate of new virus strains in the field.

In the present communication studies are extended to the analysis of several relevant strains of FMDV serotypes O, A and C isolated at different times in the field in different regions of South America.

Like cardioviruses, FMDV contains a polyribocytidylic acid tract near the 5' end of the genome (*4, 11*). The length of this segment is significantly different for each serotype as well as for each subtype and strain (*3*) and therefore has an additional value for better distinguishing different isolates (*9*). The data clearly show the relevance of applying these biochemical techniques in combination with serological tests for a rapid and precise identification of field isolates. Therefore they provide a basis for defining rapidly the possible source of an FMDV outbreak such as already shown by King *et al.* (*8*).

It is clear that the biochemical analysis, combined with serological identification of strains, is a good approach for the characterization of viruses with techniques which can be rapidly applied to the study of field isolation.

In addition to the characterization of isolated cases we are at present performing more defined epidemiological monitoring including several chronologically related isolates from the same field outbreak.

These studies in which a large number of field isolates are examined within a short period of time will be very relevant to understand in part the epidemiological behavior of viruses and will provide useful basic information to study the biological and biochemical factors of virus variability in the field.

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