The Genotype of Aujeszky’s Disease Viruses Isolated in Argentina

Maria Gabriela ECHEVERRIA, Junzo NORIMINE, Cecilia Monica GALOSI, Graciela Araceli OLIVA, Maria Elisa ETCHEVERRIGARAY*, Edgardo Omar NOSETTO, Yukinobu TOHYA1, and Takeshi MIKAMI2
Area of Virology, Faculty of Veterinary Sciences, National University of La Plata, Argentina and 1Department of Veterinary Microbiology, Faculty of Agriculture, The University of Tokyo, Bunkyo-ku, Tokyo 113, Japan
(Received 16 March 1994/Accepted 28 April 1994)

ABSTRACT. Genomes of four Argentine isolates of Aujeszky’s disease virus (ADV) (Rio Cuarto/79, Mercedes, Chanar Ladeado-7 and Chanar Ladeado-15) from pigs were characterized and compared with four ADV strains obtained from U.S.A. (Indiana-S), Sweden (Sweden 66), France (Alfort) and Japan (Yamagata-S81) by restriction endonuclease (RE) analysis. Although three Argentine isolates were classified into type I of BamHI cleavage pattern, one isolate, Mercedes, belonged to type II, according to the classification by Herrmann et al. [6]. Since this type II virus was first isolated in 1981, no outbreak of ADV infection by this type has so far been reported in Argentina. This may imply that the immediate measures by total slaughter of pigs in the farm led successful eradication of the type II ADV infection in Argentina. This report is the first epidemiological study using RE analysis on ADV strains in this country.—KEY
words: Aujeszky’s disease virus, restriction endonuclease analysis.


Aujeszky’s disease (AD) is a viral infection of swine manifested by various degrees of respiratory distress, nervous and genital disorders, and mortality, according to the age of the host and the virulence of the virus strain involved. Also, after recovery, latent infection is estabilished. Aujeszky’s disease virus (ADV) is classified as Suid Herpesvirus-1, a member of subfamily Alphaherpesviraiae, and has a linear double stranded DNA genome of approximately 90 megadaltons, composed of the long unique and the short unique sequences. The smaller is bracketed by the internal and terminal repeat sequences (IR and TR respectively) [3].

Restriction endonuclease (RE) analysis of ADV genome has been used to differentiate ADV isolates which could not be differentiated by other techniques, such as plaque morphology, heat or trypsin sensitivity and virulence for laboratory animals [6, 7]. Herrmann et al. [6] reported that there are four major genome types among world-wide isolates of ADV in BamHI cleavage pattern, clustering in distinct geographic areas. In general, type I belongs to U.S.A. and Middle Europe (Germany and Belgium). Type II belongs to Middle Europe. Type III is limited to isolates originating from Northern Europe as Denmark and Sweden. Type IV has been isolated only in Thailand [6].

As reported by many others, this classification has much advantage to epidemiological survey of ADV infection. The purpose of the present study is to characterize the genomes of Argentine strains of ADV and compare with other country’s strains using the RE analysis with BamHI.

Argentine strains used are Rio Cuarto/79 (RC/79) [1], Mercedes (Mer) [9], Chanar Ladeado 7 (CL-7) and Chanar Ladeado 15 (CL-15) [4] strains. Reference strains used are Yamagata-S81 (YS-81) [5], Indiana (Ind-S) [7], Alfort (Alf) [6] and Sweden 66 (S-66) [8] strains. All strains were cloned twice using CPK cells. CPK cells were grown in Dulbecco’s modified Eagle’s medium (Nissui,

* Correspondece to: ECHEVERRIGARAY, M. E., Area of Virology, Faculty of Veterinary Sciences, National University of La Plata, 60 y 118-1900 La Plata, Argentina.
strain was similar to YS-81 strain but had slight differences in mobility of fragment 10. Although RC79 strain had almost the same pattern with CL-7 and CL-15 strains, the fragment 10 of RC79 seemed to be shifted to the position of fragment 9. As the variation of fragments 10 and 12 was known even in viruses isolated in the same area, the differences found between CL-7 and CL-15 might be due to those mobilities.

In addition to 3 Argentine isolates being classified as type I, our latest isolates in 1992 also belonged to type I (data not shown). Therefore, since the first outbreak of AD in Argentina occurred in 1979, major outbreaks have been caused by type I. However, Mer strain belonging to type II was isolated from the outbreak occurred in 1980 in a city located in San Luis Province, where the swine production is on a small scale and the farm is isolated from other swine production area in Argentina. The outbreak started among pigs imported from Holland shortly after they arrived in Argentina. The reason why this viral strain seemed to have not spread throughout the country may be that 100% of the piglets died after showing symptoms and the survived adults were totally sacrificed (Fondevila, personal communication). Since specific sequences within ADV genome are expected to be related with biological functions of the virus, we examined the 8 ADV strains if they possess different biological properties (data not shown). However, it was difficult to differentiate those differences clearly. Although these strains showed some degree of antigenic variation when they were analyzed by virus neutralization test using monoclonal antibodies directed against gII (data not shown), it was not sufficient to identify one by one. On the other hand, the several variations were clearly found in their restriction patterns as described above. This indicates the advantage of RE assay in the classification of ADV, because the assay can allow the further differences into groups and is much easier to carry out.

In conclusion, we have had at least 2 genome types of ADV strain in Argentina, types I and II, according to the classification by BamHI cleavage pattern. However, major outbreaks have been caused by type I and the outbreak of type II has occurred so far only once. This may imply that the immediate measures by total slaughter of pigs in the affected farm was successful to prevent the spread of type II ADV. As the present data are not sufficient to know the prevalence of AD in this country, the same effort of these analyses should be continued for surveillance of ADV infection in Argentina.

ACKNOWLEDGEMENTS. The authors are grateful to Dr. K. Sekikawa, Second Research Division, National Institute of Animal Health, Tsukuba, Japan, for providing YS-81 and Ind-S ADV strains; Dr. A. Ambrogi, National University of Rio Cuarto, Dr. N. Fondevila, INTA Castelar, and Dr. C. Pianovi, SENASA, and Dr. J. Moreno-Lopez, SVA Sweden, for providing Argentine strains, and Alf and S-66 ADV strains, respectively; and Miss M. C. Mondragon and Mr. D. D’Andrea for their technical assistance. J. Norimine is supported by Japan International Cooperation Agency (JICA), C. M. Galosi is a member career to Scientific Research Commission, CIC Buenos Aires Province. E. O. Nossetto is a member career to National Research Council CONICET, Argentina. This work was supported in part by JICA.

REFERENCES