Genome Sequences of Rotavirus A Strains Ty-1 and Ty-3, Isolated from Turkeys in Ireland in 1979

Yuji Fujii,a Hiromichi Mitake,b Daigo Yamada,a Makoto Nagai,c Kota Okadera,b Naoto Ito,a,b Kazuma Okada,b Kento Nakagawa,b Tetsuya Mizutani,a Makoto Sugiyamaab

Laboratory of Zoonotic Diseases, Faculty of Applied Biological Sciences, Gifu University, Yanagido, Gifu, Japan; The United Graduate School of Veterinary Sciences, Gifu University, Yanagido, Gifu, Japan; Research and Education Center for Prevention of Global Infectious Disease of Animal, Tokyo University of Agriculture and Technology, Saiwaimachi, Fuchu, Tokyo, Japan;

To obtain complete genome sequences of turkey rotavirus A strains Ty-1 and Ty-3, we sequenced the gene segments that had not been decoded previously. The genotype constellations of the respective strains were determined to be G17-P[38]-I4-R4-C4-M4-A16-N4-T4-E4-H4 and G7-P[35]-I4-R4-C4-M4-A16-N4-T4-E11-H14. Notably, their VP4 and NSP5 genes were classified into novel genotypes.

RotaC (http://rotac.regatools.be) (12) and BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi).

Genotyping by RotaC revealed that all viral genes except for the VP4 gene of Ty-1 and NSP5 gene of Ty-3 were classified into previously established avian RVA genotypes. Meanwhile, the Ty-1 VP4 gene and Ty-3 NSP5 gene were not closely related to the respective genes of any known RVA strains: they showed the highest nucleotide identities of 77.4% with the VP4 gene of velvet scoter RVA strain RK1 (13) and of 83.9% with the NSP5 gene of pigeon RVA strain PO-13, respectively, which are clearly lower than the cut-off values defined by RCWG for genotyping (80% for VP4 gene and 91% for NSP5 gene) (3). RCWG officially confirmed that the Ty-1 VP4 gene and Ty-3 NSP5 gene were classified into new genotypes, P[38] and H14, respectively. Taken together, the genotype constellations of Ty-1 and Ty-3 were determined as G17-P[38]-I4-R4-C4-M4-A16-N4-T4-E4-H4 and G7-P[35]-I4-R4-C4-M4-A16-N4-T4-E11-H14, respectively.

Nucleotide sequence accession numbers. The nucleotide sequences determined in this study have been deposited in GenBank under the accession numbers LC088107 to LC088124.

ACKNOWLEDGMENT

This work was supported by JSPS KAKENHI grant 26292148.

FUNDING INFORMATION

The Japan Society for the Promotion of Science (JSPS) provided funding to Makoto Sugiyama under grant number 26292148.

REFERENCES

1. Estes MK, Greenberg HG. 2013. Rotaviruses, p 1347–1401. In Knipe DM, Howley PM, Cohen JI, Griffin DE, Lamb RA, Martin MA, Racaniello VR,
Roizman B (ed), Fields virology, 6th ed. Walters Kluwer Health/Lippincott Williams & Wilkins, Philadelphia, PA.

2. Matthijnssens J, Ciarelt M, McDonald SM, Attoui H, Bánya K, Brister JR, Buesa J, Esona MD, Estes MK, Gentsch JR, Iturriza-Gómar M, Johne R, Kirkwood CD, Martella V, Mertens PPC, Nakagomi O, Parreiro V, Rahman M, Ruggeri FM, Saif LJ, Santos N, Steyer A, Taniguchi K, Patton JT, Desselberger U, Van Ranst M. 2011. Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). Arch Virol 156:1397–1413. http://dx.doi.org/10.1007/s00705-011-1006-z.

3. Matthijnssens J, Ciarelt M, Rahman M, Attoui H, Bánya K, Estes MK, Gentsch JR, Iturriza-Gómar M, Kirkwood CD, Martella V, Mertens PPC, Nakagomi O, Patton JT, Ruggeri FM, Saif LJ, Santos N, Steyer A, Taniguchi K, Desselberger U, Van Ranst M. 2008. Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. Arch Virol 153:1621–1629. http://dx.doi.org/10.1007/s00705-008-0155-1.

4. Ito H, Sugiyama M, Masubuchi K, Mori Y, Minamoto N. 2001. Complete nucleotide sequence of a group A avian rotavirus genome and a comparison with its counterparts of mammalian rotaviruses. Virus Res 75:123–138. http://dx.doi.org/10.1016/S0168-1702(01)00234-9.

5. Troijnar E, Otto P, Johne R. 2009. The first complete genome sequence of a chicken group A rotavirus indicates independent evolution of mammalian and avian strains. Virology 386:325–333. http://dx.doi.org/10.1016/j.viro.2009.01.034.

6. Troijnar E, Sachsenroder J, Twardziok S, Reetz J, Otto PH, Johne R. 2013. Identification of an avian group A rotavirus containing a novel VP4 gene with a close relationship to those of mammalian rotaviruses. J Gen Virol 94:136–142. http://dx.doi.org/10.1099/vir.0.047381-0.

7. Papp H, Marton S, Farkas SL, Jakab F, Martella V, Malik YS, Palya V, Bánya K. 2014. Classification and characterization of a laboratory chicken rotavirus strain carrying G7P[35] neutralization antigens on the genotype 4 backbone gene configuration. Biologicals 42:299–304. http://dx.doi.org/10.1016/j.biologicals.2014.08.004.

8. McNulty MS, Allan GM, Todd D, McFerran JB, McKillop ER, Collins DS, McCracken RM. 1980. Isolation of rotaviruses from turkeys and chickens: demonstration of distinct serotypes and RNA electropherotypes. Avian Pathol 9:363–375. http://dx.doi.org/10.1080/03079458008418420.

9. Ito H, Minamoto N, Hiraga S, Sugiyama M. 1997. Sequence analysis of the VP6 gene in group A turkey and chicken rotaviruses. Virus Res 47:79–83. http://dx.doi.org/10.1016/S0168-1702(96)01401-3.

10. Patton JT, Salter-Cid L, Kalbach A, Mansell EA, Kattoura M. 1993. Nucleotide and amino acid sequence analysis of the rotavirus nonstructural RNA-binding protein NS35. Virology 192:438–446. http://dx.doi.org/10.1006/viro.1993.1059.

11. Hotop H, Rohwedder A, Ito H, Minamoto N, Nakagomi O, Brüssow H. 1997. Bovine rotavirus 993/83 shows a third subtype of avian VP7 protein. Virus Genes 14:147–151. http://dx.doi.org/10.1023/A:1007921418679.

12. Maes P, Matthijnssens J, Rahman M, Van Ranst M. 2009. RotaC: a web-based tool for the complete genome classification of group A rotaviruses. BMC Microbiol 9:238. http://dx.doi.org/10.1186/1471-2180-9-238.

13. Takehara K, Kiuchi H, Kuwahara M, Yanagisawa F, Mizukami M, Matsuda H, Yoshimura M. 1991. Identification and characterization of a plaque forming avian rotavirus isolated from a wild bird in Japan. J Vet Med Sci 53:479–486. http://dx.doi.org/10.1292/jvms.53.479.