

論文

1. Primadharsini PP, **Nagashima S**, Takahashi M, Kobayashi T, Nishiyama T, Nishizawa T, Yasuda J, Mulyanto, Okamoto H. Multivesicular body sorting and the exosomal pathway are required for the release of rat hepatitis E virus from infected cells. *Virus Res.* 278:197868, 2020. doi: 10.1016/j.virusres.2020.197868.
2. Murata K, Kang JH, **Nagashima S**, Matsui T, Karino Y, Yamamoto Y, Atarashi T, Oohara M, Uebayashi M, Sakata H, Matsubayashi K, Takahashi K, Arai M, Mishiro S, Sugiyama M, Mizokami M, Okamoto H. IFN- λ 3 as a host immune response in acute hepatitis E virus infection. *Cytokine.* 125:154816, 2019. doi: 10.1016/j.cyto.2019.154816.
3. Nishiyama T, Kobayashi T, Jirintai S, **Nagashima S**, Primadharsini PP, Nishizawa T, Okamoto H. Antiviral candidates against the hepatitis E virus (HEV) and their combinations inhibit HEV growth in in vitro. *Antiviral Res.* 170:104570, 2019. doi: 10.1016/j.antiviral.2019.104570.
4. Okano H, Nakano T, Ito R, Tanaka A, Hoshi Y, Matsubayashi K, Asakawa H, Nose K, Tsuruga S, Tochio T, Kumazawa H, Isono Y, Tanaka H, Matsusaki S, Sase T, Saito T, Mukai K, Nishimura A, Kawakami K, **Nagashima S**, Takahashi M, Okamoto H. The spontaneous clearance of hepatitis E virus (HEV) and emergence of HEV antibodies in a transfusion-transmitted chronic hepatitis E case after completion of chemotherapy for acute myeloid leukemia. *Clin J Gastroenterol.* 2019. doi: 10.1007/s12328-019-01024-3.
5. Sato N, Watanabe S, Miura K, Goka R, Morimoto N, Takaoka Y, Nomoto H, Tsukui M, Isoda N, **Nagashima S**, Takahashi M, Okamoto H, Yamamoto H. Acute liver failure caused by the transmission of hepatitis B virus from the spouse after 38 years of marriage. *Intern Med.* 58(20):2963-2968, 2019. doi: 10.2169/internalmedicine.3028-19.
6. Owada Y, Oshiro Y, Inagaki Y, Harada H, Fujiyama N, Kawagishi N, Yagisawa T, Usui J, Akutsu N, Itabashi Y, Saito K, Watarai Y, Ichimaru N, Imamura R, Kyakuno M, Ide K, Shibuya Y, Okabe Y, Ono M, Sasaki K, Shiose A, Yamagishi K, Ohnishi H, **Nagashima S**, Takahashi M, Yuzawa K, Okamoto H, Ohkohchi N. A nationwide survey of hepatitis E virus infection and chronic hepatitis in heart and kidney transplant recipients in Japan. *Transplantation.* 2019. doi: 10.1097/TP.0000000000002801.
7. Primadharsini PP, **Nagashima S**, Okamoto H. Genetic variability and evolution of hepatitis E virus. *Viruses.* 11(5), 2019. doi: 10.3390/v11050456. Review.
8. Nakano T, Okano H, Takahashi M, **Nagashima S**, Shiraki K, Oya Y, Inoue H, Ohmori S, Tsukimoto M, Satoshi I, Fujimoto S, Kobayashi M, Yamawaki M, Kumagai M, Ninomiya J, Maekawa T, Kojima Y, Araki J, Hamaoka S, Horiike S, Yoshimura H, Takeuchi K, Itoh K, Akachi S, Uraki S, Yamamoto N, Ogura S, Sugimoto K, Yoshikawa K, Hasegawa H, Iwasa M, Takei Y, Okamoto H. Changing clinical and molecular characteristics of hepatitis E virus infection in Mie Prefecture, Japan: disappearance of indigenous subtype 3e strains. *Hepatology Res.* 49(9):1003-1014, 2019. doi: 10.1111/hepr.13357.
9. Nishiyama T, Kobayashi T, Jirintai S, Kii I, **Nagashima S**, Primadharsini PP, Nishizawa T, Okamoto H. Screening of novel drugs for inhibiting hepatitis E virus replication. *J Virol Methods.* 270:1-11, 2019. doi: 10.1016/j.jviromet.2019.04.017.

10. Watanabe S, Morimoto N, Miura K, Takaoka Y, Nomoto H, Tsukui M, Isoda N, Ohnishi H, **Nagashima S**, Takahashi M, Okamoto H, Yamamoto H. Full-genome characterization of the RIVM-HAV16-090-like hepatitis A virus strains recovered from Japanese men who have sex with men, with sporadic acute hepatitis A. *Hepatol Res.* 49:521-530, 2019. doi: 10.1111/hepr.13313.
11. Hashimoto K, Miura K, Takaoka Y, Nomoto H, Watanabe S, Tsukui M, Morimoto N, Isoda N, **Nagashima S**, Takahashi M, Okamoto H, Yamamoto H. A 79-year-old woman with acute hepatitis B caused by the infection of subgenotype D1 hepatitis B virus in Japan: A Case Study. *Intern Med.* 57:3099-3104, 2018. doi: 10.2169/internalmedicine.0977-18.
12. Tanggis, Kobayashi T, Takahashi M, Jirintai S, Nishizawa T, **Nagashima S**, Nishiyama T, Kunita S, Hayama E, Tanaka T, Mulyanto, Okamoto H. An analysis of two open reading frames (ORF3 and ORF4) of rat hepatitis E virus genome using its infectious cDNA clones with mutations in ORF3 or ORF4. *Virus Res.* 249:16-30, 2018. doi: 10.1016/j.virusres.2018.02.014.
13. Ishikawa-Sasaki K, **Nagashima S**, Taniguchi K, Sasaki J. A model of OSBP-mediated cholesterol supply to Aichi virus RNA replication sites involving protein-protein interactions among viral proteins, ACBD3, OSBP, VAP-A/B, and SAC1. *J Virol.* 92(8):e01952-17, 2018. doi: 10.1128/JVI.01952-17.
14. Nakano T, Takahashi M, Takahashi K, **Nagashima S**, Suzuki Y, Nishigaki Y, Tomita E, Okano H, Oya Y, Shiraki K, Takase K, Sugimoto K, Koyama J, Mizuo H, Ikezawa K, Aikawa T, Arai M, Okamoto H. Hepatitis E virus subtype 3f strains isolated from Japanese hepatitis patients with no history of travel to endemic areas - The origin analyzed by molecular evolution. *Virology.* 513:146-152, 2017. doi: 10.1016/j.virol.2017.08.008.
15. Nishizawa T, Primadharsini PP, Namikawa M, Yamazaki Y, Uraki S, Okano H, Horiike S, Nakano T, Takaki S, Kawakami M, **Nagashima S**, Takahashi M, Okamoto H. Full-length genomic sequences of new subtype 1g hepatitis E virus strains obtained from four patients with imported or autochthonous acute hepatitis E in Japan. *Infect Genet Evol.* 55:343-349, 2017. doi: 10.1016/j.meegid.2017.10.007.
16. **Nagashima S**, Takahashi M, Kobayashi T, Tanggis, Nishizawa T, Nishiyama T, Primadharsini PP, Okamoto H. Characterization of the quasi-enveloped hepatitis E virus particles released by the cellular exosomal pathway. *J Virol.* 91:e00822-17, 2017. doi: 10.1128/JVI.00822-17.
17. Primadharsini PP, Miyake M, Kunita S, Nishizawa T, Takahashi M, **Nagashima S**, Tanggis, Ohnishi H, Kobayashi T, Nishiyama T, Jirintai S, Okamoto H. Full-length genome of a novel genotype 3 hepatitis E virus strain obtained from domestic pigs in Japan. *Virus Res.* 240:147-153, 2017. doi: 10.1016/j.virusres.2017.08.003.
18. Tsatsralt-Od B, Primadharsini PP, Nishizawa T, Ohnishi H, **Nagashima S**, Takahashi M, Jirintai S, Nyamkhuu D, Okamoto H. Distinct changing profiles of hepatitis A and E virus infection among patients with acute hepatitis in Mongolia: The first report of the full genome sequence of a novel genotype 1 hepatitis E virus strain. *J Med Virol.* 2017. doi: 10.1002/jmv.24907.
19. Yokoyama K, Kumagai H, Takahashi M, **Nagashima S**, Okamoto H, Yamagata T. Occult hepatitis B virus infection in immunized children born to carrier mothers. *Pediatr Int.* 59:1010-1016, 2017. doi: 10.1111/ped.13352.

20. Yamaguchi Y, Takagi H, Suzuki Y, Maruhashi K, Kosone T, Kakizaki S, Sato K, Yamada M, **Nagashima S**, Takahashi M, Okamoto H. Autochthonous sporadic acute hepatitis E caused by two distinct subtype 3b hepatitis E virus strains with only 90% nucleotide identity. *Clin J Gastroenterol*. 10:168-173, 2017. doi: 10.1007/s12328-017-0718-3.
21. Miura M, Inoue J, Tsuruoka M, Nishizawa T, **Nagashima S**, Takahashi M, Shimosegawa T, Okamoto H. Full-length genomic sequence analysis of new subtype 3k hepatitis E virus isolates with 99.97% nucleotide identity obtained from two consecutive acute hepatitis patients in a city in northeast Japan. *J Med Virol*. 89:1116-1120, 2017. doi: 10.1002/jmv.24743.
22. Takahashi M, Kobayashi T, Tanggis, Jirintai S, Mulyanto, **Nagashima S**, Nishizawa T, Kunita S, Okamoto H. Production of monoclonal antibodies against the ORF3 protein of rat hepatitis E virus (HEV) and demonstration of the incorporation of the ORF3 protein into enveloped rat HEV particles. *Arch Virol*. 161:3391-3404, 2016.
23. **Nagashima S**, Kobayashi T, Tanaka T, Tanggis, Jirintai S, Takahashi M, Nishizawa T, Okamoto H. Analysis of adaptive mutations selected during the consecutive passages of hepatitis E virus produced from an infectious cDNA clone. *Virus Res*. 223:170-180, 2016. doi: 10.1016/j.virusres.2016.07.011.
24. Nishizawa T, Hoshino T, Naganuma A, Kobayashi T, **Nagashima S**, Takahashi M, Takagi H, Okamoto H. Enhanced pregenomic RNA levels and lowered precore mRNA transcription efficiency in a genotype A hepatitis B virus genome with C1766T and T1768A mutations obtained from a fulminant hepatitis patient. *J Gen Virol*. 97:2643-2656, 2016. doi: 10.1099/jgv.0.000566.
25. Yamazaki Y, Naganuma A, Arai Y, Takeuchi S, Kobayashi T, Takakusagi S, Hatanaka T, Hoshino T, Namikawa M, Hashizume H, Takizawa D, Ohyama T, Suzuki H, Horiguchi N, Takagi H, Sato K, Kakizaki S, Kusano M, **Nagashima S**, Takahashi M, Okamoto H, Yamada M. Clinical and virological features of acute hepatitis E in Gunma prefecture, Japan between 2004 and 2015. *Hepatol Res*. 47:435-445, 2017. doi: 10.1111/hepr.12765.
26. Kobayashi T, Takahashi M, Tanggis, Mulyanto, Jirintai S, **Nagashima S**, Nishizawa T, Okamoto H. Characterization and epitope mapping of monoclonal antibodies raised against rat hepatitis E virus capsid protein: An evaluation of their neutralizing activity in a cell culture system. *J Virol Methods*. 233:78-88, 2016. doi: 10.1016/j.jviromet.2016.03.004.
27. Inagaki Y, Oshiro Y, Tanaka T, Yoshizumi T, Okajima H, Ishiyama K, Nakanishi C, Hidaka M, Wada H, Hibi T, Takagi K, Honda M, Kuramitsu K, Tanaka H, Tohyama T, Ikegami T, Imura S, Shimamura T, Nakayama Y, Urahashi T, Yamagishi K, Ohnishi H, **Nagashima S**, Takahashi M, Shirabe K, Kokudo N, Okamoto H, Ohkohchi N. A nationwide survey of hepatitis E virus infection and chronic hepatitis E in liver transplant recipients in Japan. *EBioMedicine*. 2:1607-1612, 2015.
28. Tsatsralt-Od B, Baasanjav N, Nyamkhuu D, Ohnishi H, Takahashi M, Kobayashi T, **Nagashima S**, Nishizawa T, Okamoto H. Molecular analysis of hepatitis A virus strains obtained from patients with acute hepatitis A in Mongolia, 2004-2013. *J Med Virol*. 88:622-630, 2015. doi: 10.1002/jmv.24380.
29. Yazaki Y, Sugawara K, Honda M, Ohnishi H, **Nagashima S**, Takahashi M, Okamoto H. Characteristics of 20 Patients with Autochthonous Acute Hepatitis E in Hokkaido, Japan: First Report of Bilateral Facial Palsy

Following the Infection with Genotype 4 Hepatitis E Virus. *Tohoku J Exp Med.* 236:263-271, 2015. doi: 10.1620/tjem.236.263.

30. Kamitsukasa H, Iri M, Tanaka A, **Nagashima S**, Takahashi M, Nishizawa T, Okamoto H. Spontaneous reactivation of hepatitis B virus (HBV) infection in patients with resolved or occult HBV infection. *J Med Virol.* 87:589-600, 2015. doi: 10.1002/jmv.24115.
31. Okamoto D, Nakayama H, Ikeda T, Ikeya S, **Nagashima S**, Takahashi M, Sugai Y, Okamoto H. Molecular analysis of the interspousal transmission of hepatitis B virus in two Japanese patients who acquired fulminant hepatitis B after 50 and 49 years of marriage. *J Med Virol.* 86:1851-1860, 2014. doi: 10.1002/jmv.24040.
32. **Nagashima S**, Jirintai S, Takahashi M, Kobayashi T, Tanggis, Nishizawa T, Kouki T, Yashiro T, Okamoto H. Hepatitis E virus egress depends on the exosomal pathway, with secretory exosomes derived from multivesicular bodies. *J Gen Virol.* 95:2166-2175, 2014. doi: 10.1099/vir.0.066910-0.
33. Jirintai S, Tanggis, Mulyanto, Suparyatmo JB, Takahashi M, Kobayashi T, **Nagashima S**, Nishizawa T, Okamoto H. Rat hepatitis E virus derived from wild rats (*Rattus rattus*) propagates efficiently in human hepatoma cell lines. *Virus Res.* 185:92-102, 2014. doi: 10.1016/j.virusres.2014.03.002.
34. Takahashi M, Nishizawa T, **Nagashima S**, Jirintai S, Kawakami M, Sonoda Y, Suzuki T, Yamamoto S, Shigemoto K, Ashida K, Sato Y, Okamoto H. Molecular characterization of a novel hepatitis E virus (HEV) strain obtained from a wild boar in Japan that is highly divergent from the previously recognized HEV strains. *Virus Res.* 180:59-69, 2014. doi: 10.1016/j.virusres.2013.12.014.
35. Mulyanto, Suparyatmo JB, Andayani IG, Khalid, Takahashi M, Ohnishi H, Jirintai S, **Nagashima S**, Nishizawa T, Okamoto H. Marked genomic heterogeneity of rat hepatitis E virus strains in Indonesia demonstrated on a full-length genome analysis. *Virus Res.* 179:102-112, 2014. doi: 10.1016/j.virusres.2013.10.029.
36. **Nagashima S**, Takahashi M, Jirintai S, Tanggis, Kobayashi T, Nishizawa T, Okamoto H. The membrane on the surface of hepatitis E virus particles is derived from the intracellular membrane and contains trans-Golgi network protein 2. *Arch Virol.* 159:979-991, 2014. doi: 10.1007/s00705-013-1912-3.
37. Okano H, Takahashi M, Isono Y, Tanaka H, Nakano T, Oya Y, Sugimoto K, Ito K, Ohmori S, Maegawa T, Kobayashi M, **Nagashima S**, Nishizawa T, Okamoto H. Characterization of sporadic acute hepatitis E and comparison of hepatitis E virus genomes in acute hepatitis patients and pig liver sold as food in Mie, Japan. *Hepatol Res.* 44(10):E63-E76, 2013. doi: 10.1111/hepr.12216.
38. Okano H, Nakano T, Sugimoto K, Takahashi K, **Nagashima S**, Takahashi M, Arai M, Okamoto H. High genomic similarity between European type hepatitis E virus subgenotype 3e strains isolated from an acute hepatitis patient and a wild boar in Mie, Japan. *Hepatol Res.* 44(6):694-699, 2013. doi: 10.1111/hepr.12155.
39. Jirintai S, Jinshan, Tanggis, Manglai D, Mulyanto, Takahashi M, **Nagashima S**, Kobayashi T, Nishizawa T, Okamoto H. Molecular analysis of hepatitis E virus from farm rabbits in Inner Mongolia, China and its successful propagation in A549 and PLC/PRF/5 cells. *Virus Res.* 170(1-2):126-137, 2012. doi: 10.1016/j.virusres.2012.09.015.
40. Mulyanto, Depamede SN, Sriasih M, Takahashi M, **Nagashima S**, Jirintai S, Nishizawa T, Okamoto H. Frequent detection and characterization of hepatitis E virus variants in wild rats (*Rattus rattus*) in Indonesia.

Arch Virol. 158(1):87-96, 2012. doi: 10.1007/s00705-012-1462-0.

41. Takahashi H, Tanaka T, Jirintai S, **Nagashima S**, Takahashi M, Nishizawa T, Mizuo H, Yazaki Y, Okamoto H. A549 and PLC/PRF/5 cells can support the efficient propagation of swine and wild boar hepatitis E virus (HEV) strains: demonstration of HEV infectivity of porcine liver sold as food. Arch Virol. 157(2):235-246, 2012. doi: 10.1007/s00705-011-1153-2.
42. Mulyanto, Pancawardani P, Depamede SN, Wahyono A, Jirintai S, **Nagashima S**, Takahashi M, Nishizawa T, Okamoto H. Identification of four novel subgenotypes (C13-C16) and two inter-genotypic recombinants (C12/G and C13/B3) of hepatitis B virus in Papua Province, Indonesia. Virus Res. 163(1):129-40, 2012. doi: 10.1016/j.virusres.2011.09.002.
43. **Nagashima S**, Takahashi M, Jirintai S, Tanaka T, Nishizawa T, Yasuda J, Okamoto H. Tumour susceptibility gene 101 and the vacuolar protein sorting pathway are required for the release of hepatitis E virions. J Gen Virol. 92(Pt 12):2838-2848, 2011. doi: 10.1099/vir.0.035378-0.
44. Yokoyama K, Takahashi M, Nishizawa T, **Nagashima S**, Jirintai S, Yotsumoto S, Okamoto H, Momoi MY. Identification and characterization of a natural inter-genotypic (2b/1b) recombinant hepatitis C virus in Japan. Arch Virol. 156(9):1591-1601, 2011. doi: 10.1007/s00705-011-1038-4.
45. Ghosh S, Paul SK, Yamamoto D, **Nagashima S**, Kobayashi N. Full genomic analyses of human rotavirus strains possessing the rare P[8]b VP4 subtype. Infect Genet Evol. 11(6):61481-61486, 2011.
46. Ganesh B, **Nagashima S**, Ghosh S, Nataraju SM, Rajendran K, Manna B, Ramamurthy T, Niyogi SK, Kanungo S, Sur D, Kobayashi N, Krishnan T. Detection and molecular characterization of multiple strains of Picobirnavirus causing mixed infection in a diarrhoeic child: Emergence of prototype Genogroup II-like strain in Kolkata, India. Int J Mol Epidemiol Genet. 2(1):61-72, 2011.
47. Sato Y, Sato H, Naka K, Furuya S, Tsukiji H, Kitagawa K, Sonoda Y, Usui T, Sakamoto H, Yoshino S, Shimizu Y, Takahashi M, **Nagashima S**, Jirintai, Nishizawa T, Okamoto H. A nationwide survey of hepatitis E virus (HEV) infection in wild boars in Japan: identification of boar HEV strains of genotypes 3 and 4 and unrecognized genotypes. Arch Virol. 156(8):1345-1358, 2011. doi: 10.1007/s00705-011-0988-x.
48. Ganesh B, Banyai K, Masachessi G, Mladenova Z, **Nagashima S**, Ghosh S, Nataraju SM, Pativada M, Kumar R, Kobayashi N. Genogroup I picobirnavirus in diarrhoeic foals: Can the horse serve as a natural reservoir for human infection? Vet Res. 42(1):52, 2011. doi: 10.1186/1297-9716-42-52.
49. Ribas Mde L, **Nagashima S**, Calzado A, Acosta G, Tejero Y, Cordero Y, Piedra D, Kobayashi N. Emergence of G9 as a predominant genotype of human rotaviruses in Cuba. J Med Virol. 83(4):738-744, 2011. doi: 10.1002/jmv.22020. doi: 10.1099/vir.0.029470-0.
50. Takahashi M, Nishizawa T, Sato H, Sato Y, Jirintai, **Nagashima S**, Okamoto H. Analysis of the full-length genome of a hepatitis E virus isolate obtained from a wild boar in Japan that is classifiable into a novel genotype. J Gen Virol. 92(Pt 4):902-908, 2011.
51. **Nagashima S**, Takahashi M, Jirintai, Tanaka T, Yamada K, Nishizawa T, Okamoto H. A PSAP motif in the ORF3 protein of hepatitis E virus is necessary for virion release from infected cells. J Gen Virol. 92(Pt 2):269-278, 2011. doi: 10.1099/vir.0.025791-0.

52. Mulyanto, Depamede SN, Wahyono A, Jirintai, **Nagashima S**, Takahashi M, Okamoto H. Analysis of the full-length genomes of novel hepatitis B virus subgenotypes C11 and C12 in Papua, Indonesia. *J Med Virol.* 83(1):54-64, 2011. doi: 10.1002/jmv.21931.
53. Jinshan, Jirintai, Manglai D, Takahashi M, **Nagashima S**, Okamoto H. Molecular and serological survey of hepatitis E virus infection among domestic pigs in Inner Mongolia, China. *Arch Virol.* 155(8):1217-1226, 2010. doi: 10.1007/s00705-010-0706-0.
54. Mulyanto, Depamede SN, Surayah K, Tjahyono AA, Jirintai, **Nagashima S**, Takahashi M, Okamoto H. Identification and characterization of novel hepatitis B virus subgenotype C10 in Nusa Tenggara, Indonesia. *Arch Virol.* 155(5):705-715, 2010. doi: 10.1007/s00705-010-0628-x.
55. Takahashi M, Tanaka T, Takahashi H, Hoshino Y, **Nagashima S**, Jirintai, Mizuo H, Yazaki Y, Takagi T, Azuma M, Kusano E, Isoda N, Sugano K, Okamoto H. Hepatitis E Virus (HEV) strains in serum samples can replicate efficiently in cultured cells despite the coexistence of HEV antibodies: characterization of HEV virions in blood circulation. *J Clin Microbiol.* 48(4):1112-1125, 2010. doi: 10.1128/JCM.02002-09.
56. Takahashi M, Tamura K, Hoshino Y, **Nagashima S**, Yazaki Y, Mizuo H, Iwamoto S, Okayama M, Nakamura Y, Kajii E, Okamoto H. A nationwide survey of hepatitis E virus infection in the general population of Japan. *J Med Virol.* 82(2):271-281, 2010. doi: 10.1002/jmv.21678.
57. **Nagashima S**, Kobayashi N, Paul SK, Ghosh S, Chawla-Sarkar M, Hossain MA, Krishnan T. Identification of P[8]b subtype in OP354-like human rotavirus strains by a modified RT-PCR method. *Jpn J Infect Dis.* 63(3):208-211, 2010.
58. Wang YH, Kobayashi N, **Nagashima S**, Zhou X, Ghosh S, Peng JS, Hu Q, Zhou DJ, Yang ZQ. Full genomic analysis of a porcine-bovine reassortant G4P[6] rotavirus strain R479 isolated from an infant in China. *J Med Virol.* 82(6):1094-1102, 2010. doi: 10.1002/jmv.21760.
59. Llanes R, Soria C, **Nagashima S**, Kobayashi N, Gala A, Guzmán D, Feliciano O, Valdés L, Gutiérrez O, Fernández H, Llop A, Wada A. Phenotypic and genetic characterization of antimicrobial profiles of *Helicobacter pylori* strains in Cuba. *J Health Popul Nutr.* 28(2):124-129, 2010.
60. Ganesh B, Nataraju SM, Rajendran K, Ramamurthy T, Kanungo S, Manna B, **Nagashima S**, Sur D, Kobayashi N, Krishnan T. Detection of closely related Picobirnaviruses among diarrhoeic children in Kolkata: evidence of zoonoses? *Infect Genet Evol.* 10(4):511-516, 2010. doi: 10.1016/j.meegid.2010.02.008.
61. Ghosh S, Kobayashi N, **Nagashima S**, Chawla-Sarkar M, Krishnan T, Ganesh B, Naik TN. Full genomic analysis and possible origin of a porcine G12 rotavirus strain RU172. *Virus Genes.* 40(3):382-388, 2010. doi: 10.1007/s11262-010-0454-y.
62. Ghosh S, Kobayashi N, **Nagashima S**, Chawla-Sarkar M, Krishnan T, Ganesh B, Naik TN. Molecular characterization of the VP1, VP2, VP4, VP6, NSP1 and NSP2 genes of bovine group B rotaviruses: identification of a novel VP4 genotype. *Arch Virol.* 155(2):159-167, 2010. doi: 10.1007/s00705-009-0555-x.
63. Nishimura N, Isoda N, Higashizawa T, Otake T, Tsukui M, **Nagashima S**, Takahashi M, Okamoto H, Sugano K. A case of acute hepatitis C caused by interspousal transmission after 30 years of marriage. *Clin J Gastroenterol.* 3(1):50-56, 2009. doi: 10.1007/s12328-009-0127-3.

64. Ichiyama K, Yamada K, Tanaka T, **Nagashima S**, Jirintai, Takahashi M, Okamoto H. Determination of the 5'-terminal sequence of subgenomic RNA of hepatitis E virus strains in cultured cells. *Arch Virol.* 154(12):1945-1951, 2009. doi: 10.1007/s00705-009-0538-y.
65. Toda T, Mitsui T, Tsukamoto Y, Ebara T, Hirose A, Masuko K, **Nagashima S**, Takahashi M, Okamoto H. Molecular analysis of transmission of hepatitis C virus in a nurse who acquired acute hepatitis C after caring for a viremic patient with epistaxis. *J Med Virol.* 81(8):1363-1370, 2009. doi: 10.1002/jmv.21537.
66. Tanaka T, Takahashi M, Takahashi H, Ichiyama K, Hoshino Y, **Nagashima S**, Mizuo H, Okamoto H. Development and characterization of a genotype 4 hepatitis E virus cell culture system using a HE-JF5/15F strain recovered from a fulminant hepatitis patient. *J Clin Microbiol.* 47(6):1906-1910, 2009. doi: 10.1128/JCM.00629-09.
67. Yamada K, Takahashi M, Hoshino Y, Takahashi H, Ichiyama K, **Nagashima S**, Tanaka T, Okamoto H. ORF3 protein of hepatitis E virus is essential for virion release from infected cells. *J Gen Virol.* 90(Pt 8):1880-1891, 2009. doi: 10.1099/vir.0.010561-0.
68. Quiñones D, Kobayashi N, **Nagashima S**. Molecular epidemiologic analysis of *Enterococcus faecalis* isolates in Cuba by multilocus sequence typing. *Microb Drug Resist.* 15(4):287-293, 2009.
69. Aung TS, Kobayashi N, **Nagashima S**, Ghosh S, Aung MS, Oo KY, Win N. Detection of group B rotavirus in an adult with acute gastroenteritis in Yangon, Myanmar. *J Med Virol.* 81(11):1968-1974, 2009. doi: 10.1002/jmv.21613.
70. Watanabe S, Kobayashi N, Quiñones D, **Nagashima S**, Uehara N, Watanabe N. Genetic diversity of enterococci harboring the high-level gentamicin resistance gene *aac(6)-Ie-aph(2'')-Ia* or *aph(2'')-Ie* in a Japanese hospital. *Microb Drug Resist.* 15(3):185-194, 2009.
71. Dutta D, Bagchi P, Chatterjee A, Nayak MK, Mukherjee A, Chattopadhyay S, **Nagashima S**, Kobayashi N, Komoto S, Taniguchi K, Chawla-Sarkar M. The molecular chaperone heat shock protein-90 positively regulates rotavirus infection. *Virology.* 391(2):325-333, 2009. doi: 10.1016/j.virol.2009.06.044.
72. Ghosh S, Kobayashi N, **Nagashima S**, Naik TN. Molecular characterization of full-length genomic segment 2 of a bovine picobirnavirus (PBV) strain: evidence for high genetic diversity with genogroup I PBVs. *J Gen Virol.* 90(Pt10):2519-2524, 2009. doi: 10.1099/vir.0.013987-0.
73. **Nagashima S**, Kobayashi N, Paul SK, Alam MM, Chawla-Sarkar M, Krishnan T. Characterization of full-length VP4 genes of OP354-like P[8] human rotavirus strains detected in Bangladesh representing a novel P[8] subtype. *Arch Virol.* 54(8):1223-1231, 2009. doi: 10.1007/s00705-009-0436-3.
74. Mukherjee A, Dutta D, Ghosh S, Bagchi P, Chattopadhyay S, **Nagashima S**, Kobayashi N, Dutta P, Krishnan T, Naik TN, Chawla-Sarkar M. Full genomic analysis of a human group A rotavirus G9P[6] strain from Eastern India provides evidence for porcine-to-human interspecies transmission. *Arch Virol.* 154(5):733-746, 2009. doi: 10.1007/s00705-009-0363-3.
75. Watanabe S, Kobayashi N, Quiñones D, Hayakawa S, **Nagashima S**, Uehara N, Watanabe N. Genetic diversity of the low-level vancomycin resistance gene *vanC-2/vanC-3* and identification of a novel *vanC* subtype (*vanC-4*) in *Enterococcus casseliflavus*. *Microb Drug Resist.* 15(1):1-9, 2009.

76. Wang YH, Kobayashi N, Zhou X, **Nagashima S**, Zhu ZR, Peng JS, Liu MQ, Hu Q, Zhou DJ, Watanabe S, Ishino M. Phylogenetic analysis of rotaviruses with predominant G3 and emerging G9 genotypes from adults and children in Wuhan, China. *J Med Virol.* 81(2):382-389, 2009. doi: 10.1002/jmv.21387.
77. Maeno Y, Shinzato M, **Nagashima S**, Rittling SR, Denhardt DT, Uede T, Taniguchi K. Effect of osteopontin on diarrhea duration and innate immunity in suckling mice infected with a murine rotavirus. *Viral Immunol.* 22(2):139-144, 2009. doi: 10.1089/vim.2008.0054.
78. Paul SK, Kobayashi N, **Nagashima S**, Ishino M, Watanabe S, Alam MM, Ahmed MU, Hossain MA, Naik TN. Phylogenetic analysis of rotaviruses with genotypes G1, G2, G9 and G12 in Bangladesh: evidence for a close relationship between rotaviruses from children and adults. *Arch Virol.* 153(11):1999-2012, 2008. doi: 10.1007/s00705-008-0212-9.
79. **Nagashima S**, Kobayashi N, Ishino M, Alam MM, Ahmed MU, Paul SK, Ganesh B, Chawla-Sarkar M, Krishnan T, Naik TN, Wang YH. Whole genomic characterization of a human rotavirus strain B219 belonging to a novel group of the genus Rotavirus. *J Med Virol.* 80(11):2023-2033, 2008. doi: 10.1002/jmv.21286.
80. Afroz S, Kobayashi N, **Nagashima S**, Alam MM, Hossain AB, Rahman MA, Islam MR, Lutfur AB, Muazzam N, Khan MA, Paul SK, Shamsuzzaman AK, Mahmud MC, Musa AK, Hossain MA. Genetic characterization of Staphylococcus aureus isolates carrying Panton-Valentine leukocidin genes in Bangladesh. *Jpn J Infect Dis.* 61(5):393-396, 2008.
81. Kinoshita M, Kobayashi N, **Nagashima S**, Ishino M, Otokozawa S, Mise K, Sumi A, Tsutsumi H, Uehara N, Watanabe N, Endo M. Diversity of staphylocoagulase and identification of novel variants of staphylocoagulase gene in Staphylococcus aureus. *Microbiol Immunol.* 52(7):334-348, 2008.
82. Alam MM, Kobayashi N, Ishino M, **Nagashima S**, Paul SK, Chawla-Sarkar M, Krishnan T, Naik TN. Identical rearrangement of NSP3 genes found in three independently isolated virus clones derived from mixed infection and multiple passages of Rotaviruses. *Arch Virol.* 153(3):555-559, 2008.
83. **Nagashima S**, Sasaki J, Taniguchi K. Interaction between polypeptide 3ABC and the 5'-terminal structural elements of the genome of Aichi virus: implication for negative-strand RNA synthesis. *J Virol.* 82(13):6161-6171, 2008. doi: 10.1128/JVI.02151-07.
84. Maeno Y, Nakazawa S, Yamamoto N, Shinzato M, **Nagashima S**, Tanaka K, Sasaki J, Rittling SR, Denhardt DT, Uede T, Taniguchi K. Osteopontin participates in Th1-mediated host resistance against nonlethal malaria parasite Plasmodium chabaudi chabaudi infection in mice. *Infect Immun.* 74(4):2423-2427, 2006.
85. **Nagashima S**, Sasaki J, Taniguchi K. The 5'-terminal region of the Aichi virus genome encodes cis-acting replication elements required for positive- and negative-strand RNA synthesis. *J Virol.* 79(11):6918-6931, 2005.
86. Shinozaki K, Okada M, **Nagashima S**, Kaiho I, Taniguchi K. Characterization of human rotavirus strains with G12 and P[9] detected in Japan. *J Med Virol.* 73(4):612-616, 2004.
87. Wakuda M, **Nagashima S**, Kobayashi N, Pongsuwanna Y, Taniguchi K. Serologic and genomic characterization of a G12 human rotavirus in Thailand. *J Clin Microbiol.* 41(12):5764-5769, 2003.
88. Sasaki J, **Nagashima S**, Taniguchi K. Aichi virus leader protein is involved in viral RNA replication and encapsidation. *J Virol.* 77(20):10799-10807, 2003.

89. **Nagashima S**, Sasaki J, Taniguchi K. Functional analysis of the stem-loop structures at the 5' end of the Aichi virus genome. *Virology*. 313(1):56-65, 2003.
90. Adah MI, **Nagashima S**, Wakuda M, Taniguchi K. Close relationship between G8-serotype bovine and human rotaviruses isolated in Nigeria. *J Clin Microbiol*. 41(8):3945-3950, 2003.
91. Maeno Y, Nakazawa S, **Nagashima S**, Sasaki J, Higo KM, Taniguchi K. Utility of the dried blood on filter paper as a source of cytokine mRNA for the analysis of immunoreactions in *Plasmodium yoelii* infection. *Acta Trop*. 87(2):295-300, 2003.