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Molecular Evolution of the Capsid Gene in Norovirus Genogroup I.

Kobayashi M[1], Yoshizumi S[2], Kogawa S[3], Takahashi T[4], Ueki Y[5], Shinohara M[6], Mizukoshi F[7], Tsukagoshi H[1], Sasaki Y[1], Suzuki R[8], Shimizu H[9], Iwakiri A[10], Okabe N[9], Shirabe K[11], Shinomiya H[12], Kozawa K[1], Kusunoki H[13], Ryo A[14], Kuroda M[15], Katayama K[16,6], Kimura H[14,17].

[1]Gunma Prefectural Institute of Public Health and Environmental Science, Maebashi-shi, Gunma 371-0052, Japan.
[2]Hokkaido Institute of Public Health, Sapporo-shi, Hokkaido 060-0819, Japan.
[3]Aomori Prefectural Public Health and Environment Center, Aomori-shi, Aomori 030-8566, Japan.
[4]Iwate Prefectural Meat Inspection Center, Shiwa-cho, Iwate 020-3311, Japan.
[5]Miyagi Prefectural Institute of Public Health and Environment, Sendai-shi, Miyagi 983-0836, Japan.
[6]Saitama Institute of Public Health, Yoshimi-machi, Saitama 355-0133, Japan.
[7]Tochigi Prefectural Institute of Public Health and Environmental Science, Utsunomiya-shi, Tochigi 329-1196, Japan.
[8]Kanagawa Prefectural Institute of Public Health, Chigasaki-shi, Kanagawa 253-0087, Japan.
[9]Kawasaki City Institute for Public Health, Kawasaki-shi, Kanagawa 210-0821, Japan.
[10]Miyazaki Prefecture Kobayashi Meat Inspection Center, Kobayashi-shi, Miyazaki 886-0004, Japan.
11Yamaguchi Prefectural Institute of Public Health and Environment, Yamaguchi-shi, Yamaguchi 753-0821, Japan.
[12]Ehime Prefectural Institute of Public Health and Environmental Science, Matsuyama-shi, Ehime 790-0003, Japan.
[13]Department of Safety Research on Blood and Biological Products, Yokohama City University Graduate School of Medicine, Yokohama-shi, Kanagawa 236-0004, Japan.
[14]Department of Molecular Biodefence Research, Yokohama City University Graduate School of Medicine, Yokohama-shi, Kanagawa 236-0004, Japan.
[15]Pathogen Genomics Center, National Institute of Infectious Diseases, Musashimurayama-shi, Tokyo 208-0011, Japan.
[16]Department of Virology II, National Institute of Infectious Diseases,

Musashimurayama-shi, Tokyo 208-0011, Japan.
[17]Infectious Disease Surveillance Center, National Institute of Infectious Diseases, Musashimurayama-shi, Tokyo 208-0011, Japan.

Abstract
We studied the molecular evolution of the capsid gene in all genotypes (genotypes 1-9) of human norovirus (NoV) genogroup I. The evolutionary time scale and rate were estimated by the Bayesian Markov chain Monte Carlo (MCMC) method. We also performed selective pressure analysis and B-cell linear epitope prediction in the deduced NoV GI capsid protein. Furthermore, we analysed the effective population size of the virus using Bayesian skyline plot (BSP) analysis. A phylogenetic tree by MCMC showed that NoV GI diverged from the common ancestor of NoV GII, GIII, and GIV approximately 2,800 years ago with rapid evolution (about 10(-3) substitutions/site/year). Some positive selection sites and over 400 negative selection sites were estimated in the deduced capsid protein. Many epitopes were estimated in the deduced virus capsid proteins. An epitope of GI.1 may be associated with histo-blood group antigen binding sites (Ser377, Pro378, and Ser380). Moreover, BSP suggested that the adaptation of NoV GI strains to humans was affected by natural selection. The results suggested that NoV GI strains evolved rapidly and date back to many years ago. Additionally, the virus may have undergone locally affected natural selection in the host resulting in its adaptation to humans.

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