**Peck and Lauring 2018 - Figure 1 – Mu and K Data References**

\*\*Red text indicates references added after publication of Peck and Lauring 2018

Abram, M. E., A. L. Ferris, W. Shao, W. G. Alvord and S. H. Hughes (2010). "Nature, Position, and Frequency of Mutations Made in a Single Cycle of HIV-1 Replication." Journal of Virology 84(19): 9864-9878.

Almeida, R. P., G. M. Bennett, M. D. Anhalt, C. W. Tsai and P. O'Grady (2009). "Spread of an introduced vector-borne banana virus in Hawaii." Mol Ecol 18(1): 136-146.

Auguste, A. J., O. G. Pybus and C. V. Carrington (2009). "Evolution and dispersal of St. Louis encephalitis virus in the Americas." Infect Genet Evol 9(4): 709-715.

Aulicino, P. C., E. C. Holmes, C. Rocco, A. Mangano and L. Sen (2007). "Extremely rapid spread of human immunodeficiency virus type 1 BF recombinants in Argentina." J Virol 81(1): 427-429.

Babkin, I. V. and I. N. Babkina (2011). "Molecular dating in the evolution of vertebrate poxviruses." Intervirology 54(5): 253-260.

Bai, Z., L. C. Liu, L. Jiang, L. Luo, H. Feng, P. Lin, Q. Jing, X. Xiao, H. Zhou, W. Su, Y. Cao, Y. Li, Q. Cao, W. Chen, B. Di, and Z. Yang. (2018). “Evolutionary and phylodynamic analyses of Dengue virus serotype I in Guangdong Province, China, between 1985 and 2015.” Virus Research. (in press).

Baillie, G. J., S. O. Kolokotronis, E. Waltari, J. G. Maffei, L. D. Kramer and S. L. Perkins (2008). "Phylogenetic and evolutionary analyses of St. Louis encephalitis virus genomes." Mol Phylogenet Evol 47(2): 717-728.

Bello, G., P. C. Aulicino, D. Ruchansky, M. L. Guimaraes, C. Lopez-Galindez, C. Casado, H. Chiparelli, C. Rocco, A. Mangano, L. Sen and M. G. Morgado (2010). "Phylodynamics of HIV-1 circulating recombinant forms 12\_BF and 38\_BF in Argentina and Uruguay." Retrovirology 7: 22.

Bertolotti, L., U. Kitron and T. L. Goldberg (2007). "Diversity and evolution of West Nile virus in Illinois and the United States, 2002-2005." Virology 360(1): 143-149.

Bird, B. H., M. L. Khristova, P. E. Rollin, T. G. Ksiazek and S. T. Nichol (2007). "Complete genome analysis of 33 ecologically and biologically diverse Rift Valley fever virus strains reveals widespread virus movement and low genetic diversity due to recent common ancestry." J Virol 81(6): 2805-2816.

Black, W. C. t., J. B. Doty, M. T. Hughes, B. J. Beaty and C. H. Calisher (2009). "Temporal and geographic evidence for evolution of Sin Nombre virus using molecular analyses of viral RNA from Colorado, New Mexico and Montana." Virol J 6: 102.

Bok, K., E. J. Abente, M. Realpe-Quintero, T. Mitra, S. V. Sosnovtsev, A. Z. Kapikian and K. Y. Green (2009). "Evolutionary dynamics of GII.4 noroviruses over a 34-year period." J Virol 83(22): 11890-11901.

Boon, D., J. E. Mahar, E. J. Abente, C. D. Kirkwood, R. H. Purcell, A. Z. Kapikian, K. Y. Green and K. Bok (2011). "Comparative evolution of GII.3 and GII.4 norovirus over a 31-year period." J Virol 85(17): 8656-8666.

Bradwell, K., M. Combe, P. Domingo-Calap and R. Sanjuán (2013). "Correlation between mutation rate and genome size in riboviruses: mutation rate of bacteriophage Qbeta." Genetics 195(1): 243-251.

Carpi, G., E. C. Holmes and A. Kitchen (2010). "The evolutionary dynamics of bluetongue virus." J Mol Evol 70(6): 583-592.

Carroll, S. A., B. H. Bird, P. E. Rollin and S. T. Nichol (2010). "Ancient common ancestry of Crimean-Congo hemorrhagic fever virus." Molecular Phylogenetics and Evolution 55(3): 1103-1110.

Chen, R. and E. C. Holmes (2006). "Avian influenza virus exhibits rapid evolutionary dynamics." Mol Biol Evol 23(12): 2336-2341.

Chu, P. Y., P. L. Lu, Y. L. Tsai, E. Hsi, C. Y. Yao, Y. H. Chen, L. C. Hsu, S. Y. Wang, H. S. Wu, Y. Y. Lin, H. J. Su and K. H. Lin (2011). "Spatiotemporal phylogenetic analysis and molecular characterization of coxsackievirus A4." Infection Genetics and Evolution 11(6): 1426-1435.

Combe, M. and R. Sanjuán (2014). "Variation in RNA virus mutation rates across host cells." PLoS Pathog 10(1): e1003855.

Cuevas, J. M., M. Combe, M. Torres-Puente, R. Garijo, S. Guix, J. Buesa, J. Rodriguez-Diaz and R. Sanjuán (2016). "Human norovirus hyper-mutation revealed by ultra-deep sequencing." Infect Genet Evol 41: 233-239.

Cuevas, J. M., S. Duffy and R. Sanjuán (2009). "Point Mutation Rate of Bacteriophage Phi X174." Genetics 183(2): 747-749.

Cuevas, J. M., F. Gonzalez-Candelas, A. Moya and R. Sanjuán (2009). "Effect of ribavirin on the mutation rate and spectrum of hepatitis C virus in vivo." J Virol 83(11): 5760-5764.

Dalai, S. C., T. de Oliveira, G. W. Harkins, S. G. Kassaye, J. Lint, J. Manasa, E. Johnston and D. Katzenstein (2009). "Evolution and molecular epidemiology of subtype C HIV-1 in Zimbabwe." AIDS 23(18): 2523-2532.

David, D., G. J. Hughes, B. A. Yakobson, I. Davidson, H. Un, O. Aylan, I. V. Kuzmin and C. E. Rupprecht (2007). "Identification of novel canine rabies virus clades in the Middle East and North Africa." J Gen Virol 88(Pt 3): 967-980.

Davis, P. L., H. Bourhy and E. C. Holmes (2006). "The evolutionary history and dynamics of bat rabies virus." Infect Genet Evol 6(6): 464-473.

Davis, P. L., E. C. Holmes, F. Larrous, W. H. Van der Poel, K. Tjornehoj, W. J. Alonso and H. Bourhy (2005). "Phylogeography, population dynamics, and molecular evolution of European bat lyssaviruses." J Virol 79(16): 10487-10497.

Davis, P. L., A. Rambaut, H. Bourhy and E. C. Holmes (2007). "The evolutionary dynamics of canid and mongoose rabies virus in Southern Africa." Arch Virol 152(7): 1251-1258.

de la Torre, J. C., C. Giachetti, B. L. Semler and J. J. Holland (1992). "High frequency of single-base transitions and extreme frequency of precise multiple-base reversion mutations in poliovirus." Proc Natl Acad Sci U S A 89(7): 2531-2535.

de la Torre, J. C., E. Wimmer and J. J. Holland (1990). "Very high frequency of reversion to guanidine resistance in clonal pools of guanidine-dependent type 1 poliovirus." J Virol 64(2): 664-671.

Dougherty, J. P. and H. M. Temin (1988). "Determination of the Rate of Base-Pair Substitution and Insertion Mutations in Retrovirus Replication." Journal of Virology 62(8): 2817-2822.

Dove, W. F. (1968). "The genetics of the lambdoid phafes." Annu Rev Genet 2: 305-340.

Drake, J. W. (1991). "A Constant Rate of Spontaneous Mutation in DNA-Based Microbes." Proceedings of the National Academy of Sciences of the United States of America 88(16): 7160-7164.

Drake, J. W. (1993). "Rates of spontaneous mutation among RNA viruses." Proc Natl Acad Sci U S A 90(9): 4171-4175.

Drake, J. W., B. Charlesworth, D. Charlesworth and J. F. Crow (1998). "Rates of spontaneous mutation." Genetics 148(4): 1667-1686.

Drake, J. W. and J. J. Holland (1999). "Mutation rates among RNA viruses." Proc Natl Acad Sci U S A 96(24): 13910-13913.

Drake, J. W. and C. B. C. Hwang (2005). "On the mutation rate of herpes simplex virus type 1." Genetics 170(2): 969-970.

Duchêne, S. and E. C. Holmes (2018). “Estimating evolutionary rates in giant viruses using ancient genomes.” Virus Evolution. 4(1): vey006.

Duffy, S. and E. C. Holmes (2008). "Phylogenetic evidence for rapid rates of molecular evolution in the single-stranded DNA begomovirus tomato yellow leaf curl virus." J Virol 82(2): 957-965.

Duffy, S. and E. C. Holmes (2009). "Validation of high rates of nucleotide substitution in geminiviruses: phylogenetic evidence from East African cassava mosaic viruses." J Gen Virol 90(Pt 6): 1539-1547.

Eckerle, L. D., X. Lu, S. M. Sperry, L. Choi and M. R. Denison (2007). "High fidelity of murine hepatitis virus replication is decreased in nsp14 exoribonuclease mutants." J Virol 81(22): 12135-12144.

Fargette, D., A. Pinel, M. Rakotomalala, E. Sangu, O. Traore, D. Sereme, F. Sorho, S. Issaka, E. Hebrad, Y. Sere, Z. Kanyeka and G. Konate (2008). "Rice Yellow Mottle Virus, an RNA plant virus, evolves as rapidly as most RNA animal viruses." Journal of Virology 82(7): 3584-3589.

Faria, N. R., M. de Vries, F. J. van Hemert, K. Benschop and L. van der Hoek (2009). "Rooting human parechovirus evolution in time." Bmc Evolutionary Biology 9.

Firth, C., M. A. Charleston, S. Duffy, B. Shapiro and E. C. Holmes (2009). "Insights into the evolutionary history of an emerging livestock pathogen: porcine circovirus 2." J Virol 83(24): 12813-12821.

Firth, C., A. Kitchen, B. Shapiro, M. A. Suchard, E. C. Holmes and A. Rambaut (2010). "Using time-structured data to estimate evolutionary rates of double-stranded DNA viruses." Mol Biol Evol 27(9): 2038-2051.

Fourment, M., J. T. Wood, A. J. Gibbs and M. J. Gibbs (2010). "Evolutionary dynamics of the N1 neuraminidases of the main lineages of influenza A viruses." Mol Phylogenet Evol 56(2): 526-535.

Furio, V., A. Moya and R. Sanjuán (2005). "The cost of replication fidelity in an RNA virus." Proc Natl Acad Sci U S A 102(29): 10233-10237.

Furuse, Y., A. Suzuki and H. Oshitani (2010). "Origin of measles virus: divergence from rinderpest virus between the 11th and 12th centuries." Virol J 7: 52.

Gao, F., Y. Chen, D. N. Levy, J. A. Conway, T. B. Kepler and H. X. Hui (2004). "Unselected mutations in the human immunodeficiency virus type 1 genome are mostly nonsynonymous and often deleterious." Journal of Virology 78(5): 2426-2433.

Gardy, J. L., M. Naus, A. Amlani, W. Chung, H. Kim, M. Tan, A. Severini, M. Krajden, D. Puddicombe, V. Sahni, A. S. Hayden, R. Gustafson, B. Henry and P. Tang (2015). "Whole-Genome Sequencing of Measles Virus Genotypes H1 and D8 During Outbreaks of Infection Following the 2010 Olympic Winter Games Reveals Viral Transmission Routes." J Infect Dis 212(10): 1574-1578.

Gartner, K., T. Wiktorowicz, J. Park, A. Mergia, A. Rethwilm and C. Scheller (2009). "Accuracy estimation of foamy virus genome copying." Retrovirology 6.

Geller, R., U. Estada, J. B. Peris, I. Andreu, J. V. Bou, R. Garijo, J. M. Cuevas, R. Sabariegos, A. Mas and R. Sanjuán (2016). "Highly heterogeneous mutation rates in the hepatitis C virus genome." Nat Microbiol 1(7): 16045.

Goni, N., A. Fajardo, G. Moratorio, R. Colina and J. Cristina (2009). "Modeling gene sequences over time in 2009 H1N1 influenza A virus populations." Virol J 6: 215.

Gray, R. R., J. Parker, P. Lemey, M. Salemi, A. Katzourakis and O. G. Pybus (2011). "The mode and tempo of hepatitis C virus evolution within and among hosts." BMC Evol Biol 11: 131.

Gullberg, M., C. Tolf, N. Jonsson, M. N. Mulders, C. Savolainen-Kopra, T. Hovi, M. Van Ranst, P. Lemey, S. Hafenstein and A. M. Lindberg (2010). "Characterization of a Putative Ancestor of Coxsackievirus B5." Journal of Virology 84(19): 9695-9708.

Harrison, A., P. Lemey, M. Hurles, C. Moyes, S. Horn, J. Pryor, J. Malani, M. Supuri, A. Masta, B. Teriboriki, T. Toatu, D. Penny, A. Rambaut and B. Shapiro (2011). "Genomic analysis of hepatitis B virus reveals antigen state and genotype as sources of evolutionary rate variation." Viruses 3(2): 83-101.

Heinz, B. A., R. R. Rueckert, D. A. Shepard, F. J. Dutko, M. A. McKinlay, M. Fancher, M. G. Rossmann, J. Badger and T. J. Smith (1989). "Genetic and molecular analyses of spontaneous mutants of human rhinovirus 14 that are resistant to an antiviral compound." J Virol 63(6): 2476-2485.

Hicks, A. L. and S. Duffy (2011). "Genus-specific substitution rate variability among picornaviruses." J Virol 85(15): 7942-7947.

Hoenen, T., D. Safronetz, A. Groseth, K. R. Wollenberg, O. A. Koita, B. Diarra, I. S. Fall, F. C. Haidara, F. Diallo, M. Sanogo, Y. S. Sarro, A. Kone, A. C. Togo, A. Traore, M. Kodio, A. Dosseh, K. Rosenke, E. de Wit, F. Feldmann, H. Ebihara, V. J. Munster, K. C. Zoon, H. Feldmann and S. Sow (2015). "Virology. Mutation rate and genotype variation of Ebola virus from Mali case sequences." Science 348(6230): 117-119.

Holland, J. J., J. C. de la Torre, D. A. Steinhauer, D. Clarke, E. Duarte and E. Domingo (1989). "Virus mutation frequencies can be greatly underestimated by monoclonal antibody neutralization of virions." J Virol 63(12): 5030-5036.

Hon, C. C., T. Y. Lam, A. Drummond, A. Rambaut, Y. F. Lee, C. W. Yip, F. Zeng, P. Y. Lam, P. T. Ng and F. C. Leung (2006). "Phylogenetic analysis reveals a correlation between the expansion of very virulent infectious bursal disease virus and reassortment of its genome segment B." J Virol 80(17): 8503-8509.

Hon, C. C., T. Y. Lam, Z. L. Shi, A. J. Drummond, C. W. Yip, F. Zeng, P. Y. Lam and F. C. Leung (2008). "Evidence of the recombinant origin of a bat severe acute respiratory syndrome (SARS)-like coronavirus and its implications on the direct ancestor of SARS coronavirus." J Virol 82(4): 1819-1826.

Huang, K. J. and D. P. Wooley (2005). "A new cell-based assay for measuring the forward mutation rate of HIV-1." Journal of Virological Methods 124(1-2): 95-104.

Huang, L., F. D. Geng, J. J. Fan, C. Xue, X. Y. Zhang, J.Q. Kang, J. Q. Zhang, and Y. Ren. **(**2018). “Genetic diversity and evolutionary history of four closely related Aquilegia species revealed by 10 nuclear gene fragments.” Journal of Systematics and Evolution 56:129-138.

Hughes, G. J., L. A. Orciari and C. E. Rupprecht (2005). "Evolutionary timescale of rabies virus adaptation to North American bats inferred from the substitution rate of the nucleoprotein gene." J Gen Virol 86(Pt 5): 1467-1474.

Jones, A., K. Lowry, J. Aaskov, E. C. Holmes and A. Kitchen (2010). "Molecular evolutionary dynamics of Ross River virus and implications for vaccine efficacy." Journal of General Virology 91: 182-188.

Jorba, J., R. Campagnoli, L. De and O. Kew (2008). "Calibration of multiple poliovirus molecular clocks covering an extended evolutionary range." J Virol 82(9): 4429-4440.

Kerr, P. J., A. Kitchen and E. C. Holmes (2009). "Origin and phylodynamics of rabbit hemorrhagic disease virus." J Virol 83(23): 12129-12138.

Klungthong, C., C. Zhang, M. P. Mammen, Jr., S. Ubol and E. C. Holmes (2004). "The molecular epidemiology of dengue virus serotype 4 in Bangkok, Thailand." Virology 329(1): 168-179.

Kulkarni, M. A., A. M. Walimbe, S. Cherian and V. A. Arankalle (2009). "Full length genomes of genotype IIIA Hepatitis A Virus strains (1995-2008) from India and estimates of the evolutionary rates and ages." Infection Genetics and Evolution 9(6): 1287-1294.

Kumar, S. R., J. A. Patil, D. Cecilia, S. S. Cherian, P. V. Barde, A. M. Walimbe, P. D. Yadav, P. N. Yergolkar, P. S. Shah, V. S. Padbidri, A. C. Mishra and D. T. Mourya (2010). "Evolution, dispersal and replacement of American genotype dengue type 2 viruses in India (1956-2005): selection pressure and molecular clock analyses." J Gen Virol 91(Pt 3): 707-720.

Kunkel, T. A. (1985). "The Mutational Specificity of DNA Polymerase-Beta during Invitro DNA-Synthesis - Production of Frameshift, Base Substitution, and Deletion Mutations." Journal of Biological Chemistry 260(9): 5787-5796.

Kuroda, M., S. Niwa, T. Sekizuka, H. Tsukagoshi, M. Yokoyama, A. Ryo, H. Sato, N. Kiyota, M. Noda, K. Kozawa, K. Shirabe, T. Kusaka, N. Shimojo, S. Hasegawa, K. Sugai, M. Obuchi, M. Tashiro, K. Oishi, H. Ishii and H. Kimura (2015). "Molecular evolution of the VP1, VP2, and VP3 genes in human rhinovirus species C." Sci Rep 5: 8185.

Lau, S. K., K. S. Li, Y. Huang, C. T. Shek, H. Tse, M. Wang, G. K. Choi, H. Xu, C. S. Lam, R. Guo, K. H. Chan, B. J. Zheng, P. C. Woo and K. Y. Yuen (2010). "Ecoepidemiology and complete genome comparison of different strains of severe acute respiratory syndrome-related Rhinolophus bat coronavirus in China reveal bats as a reservoir for acute, self-limiting infection that allows recombination events." J Virol 84(6): 2808-2819.

Lefeuvre, P., G. W. Harkins, J. M. Lett, R. W. Briddon, M. W. Chase, B. Moury and D. P. Martin (2011). "Evolutionary time-scale of the begomoviruses: evidence from integrated sequences in the Nicotiana genome." PLoS One 6(5): e19193.

Leider, J. M., P. Palese and F. I. Smith (1988). "Determination of the Mutation-Rate of a Retrovirus." Journal of Virology 62(9): 3084-3091.

Leitch, E. C. M., J. Bendig, M. Cabrerizo, J. Cardosa, T. Hyypia, O. E. Ivanova, A. Kelly, A. C. M. Kroes, A. Lukashev, A. MacAdam, P. McMinn, M. Roivainen, G. Trallero, D. J. Evans and P. Simmonds (2009). "Transmission Networks and Population Turnover of Echovirus 30." Journal of Virology 83(5): 2109-2118.

Lemey, P., S. Van Dooren and A. M. Vandamme (2005). "Evolutionary dynamics of human retroviruses investigated through full-genome scanning." Mol Biol Evol 22(4): 942-951.

Lu, J., L. Fang, H. Zheng, J. Lao, F. Yang, L. Sun, J. Xiao, J. Lin, T. Song, J. Raghwani, C. Ke, N. R. Faria, T. A. Bowden, O. G. Pybus and H. Li (2017). "A10 The evolution and molecular epidemiology of epidemic GII.17 noroviruses." Virus Evol 3(Suppl 1).

Lu, Q. S., Y. T. Hwang and C. B. C. Hwang (2002). "Mutation spectra of herpes simplex virus type 1 thymidine kinase mutants." Journal of Virology 76(11): 5822-5828.

Lu, Z., H. Liu, S. Fu, X. Lu, Q. Dong, S. Zhang, S. Tong, M. Li, W. Li, Q. Tang and G. Liang (2011). "Liao ning virus in China." Virol J 8: 282.

Luria, S. E. (1951). "The Frequency Distribution of Spontaneous Bacteriophage Mutants as Evidence for the Exponential Rate of Phage Reproduction." Cold Spring Harbor Symposia on Quantitative Biology 16: 463-470.

Magiorkinis, G., E. Magiorkinis, D. Paraskevis, S. Y. Ho, B. Shapiro, O. G. Pybus, J. P. Allain and A. Hatzakis (2009). "The global spread of hepatitis C virus 1a and 1b: a phylodynamic and phylogeographic analysis." PLoS Med 6(12): e1000198.

Malpica, J. M., A. Fraile, I. Moreno, C. I. Obies, J. W. Drake and F. Garcia-Arenal (2002). "The rate and character of spontaneous mutation in an RNA virus." Genetics 162(4): 1505-1511.

Mansky, L. M. (2000). "In vivo analysis of human T-cell leukemia virus type 1 reverse transcription accuracy." J Virol 74(20): 9525-9531.

Mansky, L. M. and L. C. Bernard (2000). "3 '-azido-3 '-deoxythymidine (AZT) and AZT-resistant reverse transcriptase can increase the in vivo mutation rate of human immunodeficiency virus type 1." Journal of Virology 74(20): 9532-9539.

Mansky, L. M., S. Preveral, L. Selig, R. Benarous and S. Benichou (2000). "The interaction of Vpr with uracil DNA glycosylase modulates the human immunodeficiency virus type 1 in vivo mutation rate." Journal of Virology 74(15): 7039-7047.

Mansky, L. M. and H. M. Temin (1994). "Lower mutation rate of bovine leukemia virus relative to that of spleen necrosis virus." J Virol 68(1): 494-499.

Mansky, L. M. and H. M. Temin (1995). "Lower in-Vivo Mutation-Rate of Human-Immunodeficiency-Virus Type-1 Than That Predicted from the Fidelity of Purified Reverse-Transcriptase." Journal of Virology 69(8): 5087-5094.

Matthijnssens, J., E. Heylen, M. Zeller, M. Rahman, P. Lemey and M. Van Ranst (2010). "Phylodynamic analyses of rotavirus genotypes G9 and G12 underscore their potential for swift global spread." Mol Biol Evol 27(10): 2431-2436.

McKinley, E. T., M. W. Jackwood, D. A. Hilt, J. C. Kissinger, J. S. Robertson, C. Lemke and A. H. Paterson (2011). "Attenuated live vaccine usage affects accurate measures of virus diversity and mutation rates in avian coronavirus infectious bronchitis virus." Virus Res 158(1-2): 225-234.

Mehla, R., S. R. Kumar, P. Yadav, P. V. Barde, P. N. Yergolkar, B. R. Erickson, S. A. Carroll, A. C. Mishra, S. T. Nichol and D. T. Mourya (2009). "Recent ancestry of Kyasanur Forest disease virus." Emerg Infect Dis 15(9): 1431-1437.

Meng, S., G. Xu, X. Wu, Y. Lei, J. Yan, S. A. Nadin-Davis, H. Liu, J. Wu, D. Wang, G. Dong, X. Yang and C. E. Rupprecht (2010). "Transmission dynamics of rabies in China over the last 40 years: 1969-2009." J Clin Virol 49(1): 47-52.

Ming, P., J. Yan, S. Rayner, S. Meng, G. Xu, Q. Tang, J. Wu, J. Luo and X. Yang (2010). "A history estimate and evolutionary analysis of rabies virus variants in China." J Gen Virol 91(Pt 3): 759-764.

Mirand, A., I. Schuffenecker, C. Henquell, G. Billaud, G. Jugie, D. Falcon, A. Mahul, C. Archimbaud, E. Terletskaia-Ladwig, S. Diedrich, H. P. Huemer, M. Enders, B. Lina, H. Peigue-Lafeuille and J. L. Bailly (2010). "Phylogenetic evidence for a recent spread of two populations of human enterovirus 71 in European countries." Journal of General Virology 91: 2263-2277.

Mohammed, M. A., S. E. Galbraith, A. D. Radford, W. Dove, T. Takasaki, I. Kurane and T. Solomon (2011). "Molecular phylogenetic and evolutionary analyses of Muar strain of Japanese encephalitis virus reveal it is the missing fifth genotype." Infect Genet Evol 11(5): 855-862.

Monk, R. J., F. G. Malik, D. Stokesberry and L. H. Evans (1992). "Direct Determination of the Point Mutation-Rate of a Murine Retrovirus." Journal of Virology 66(6): 3683-3689.

Moratorio, G., M. Costa-Mattioli, R. Piovani, H. Romero, H. Musto and J. Cristina (2007). "Bayesian coalescent inference of hepatitis A virus populations: evolutionary rates and patterns." Journal of General Virology 88: 3039-3042.

Nobusawa, E. and K. Sato (2006). "Comparison of the mutation rates of human influenza A and B viruses." J Virol 80(7): 3675-3678.

Padhi, A., A. T. Moore, M. B. Brown, J. E. Foster, M. Pfeffer, K. P. Gaines, V. A. O'Brien, S. A. Strickler, A. E. Johnson and C. R. Brown (2008). "Phylogeographical structure and evolutionary history of two Buggy Creek virus lineages in the western Great Plains of North America." Journal of General Virology 89: 2122-2131.

Padhi, A. and M. Poss (2009). "Population dynamics and rates of molecular evolution of a recently emerged paramyxovirus, avian metapneumovirus subtype C." J Virol 83(4): 2015-2019.

Pagan, I., C. Firth and E. C. Holmes (2010). "Phylogenetic analysis reveals rapid evolutionary dynamics in the plant RNA virus genus tobamovirus." J Mol Evol 71(4): 298-307.

Pagan, I. and E. C. Holmes (2010). "Long-Term Evolution of the Luteoviridae: Time Scale and Mode of Virus Speciation." Journal of Virology 84(12): 6177-6187.

Parsyan, A., C. Szmaragd, J. P. Allain and D. Candotti (2007). "Identification and genetic diversity of two human parvovirus B19 genotype 3 subtypes." J Gen Virol 88(Pt 2): 428-431.

Parthasarathi, S., A. Varelaechavarria, Y. Ron, B. D. Preston and J. P. Dougherty (1995). "Genetic Rearrangements Occurring during a Single-Cycle of Murine Leukemia-Virus Vector Replication - Characterization and Implications." Journal of Virology 69(12): 7991-8000.

Parvin, J. D., A. Moscona, W. T. Pan, J. M. Leider and P. Palese (1986). "Measurement of the mutation rates of animal viruses: influenza A virus and poliovirus type 1." J Virol 59(2): 377-383.

Pathak, V. K. and H. M. Temin (1990). "Broad-Spectrum of Invivo Forward Mutations, Hypermutations, and Mutational Hotspots in a Retroviral Shuttle Vector after a Single Replication Cycle - Deletions and Deletions with Insertions." Proceedings of the National Academy of Sciences of the United States of America 87(16): 6024-6028.

Patil, J. A., S. Cherian, A. M. Walimbe, B. R. Patil, P. S. Sathe, P. S. Shah and D. Cecilia (2011). "Evolutionary dynamics of the American African genotype of dengue type 1 virus in India (1962-2005)." Infect Genet Evol 11(6): 1443-1448.

Petterson, J. H. O., V. Eldholm, S. J. Seligman, A. Lundkvist, A. K. Falconar, M. W. Gaunt, D. Musso, A. Nougairede, R. Charrel, E. A. Gould, X. de Lamballerie. (2016). “How did Zika virus emerge in the Pacific Islands and Latin America?” mBio 7(5):e01239-16.

Petterson, J. H. O., J. Bohlin, M. Dupont-Rouzeyrol, O. B. Brynildsrud, K. Alfsnes, V. Cao-Lormeau, M. W. Gaunt, A. K. Falconar, X. de Lamballerie, V. Eldholm, D. Musso, E. A. Gould. (2018). “Re-visiting the evolution, dispersal, and epidemiology of Zika virus in Asia.” Emerging Microbes and Infections 7(79).

Pomeroy, L. W., O. N. Bjornstad and E. C. Holmes (2008). "The evolutionary and epidemiological dynamics of the paramyxoviridae." J Mol Evol 66(2): 98-106.

Pult, I., N. Abbott, Y. Y. Zhang and J. Summers (2001). "Frequency of spontaneous mutations in an avian hepadnavirus infection." Journal of Virology 75(20): 9623-9632.

Pyrc, K., R. Dijkman, L. Deng, M. F. Jebbink, H. A. Ross, B. Berkhout and L. van der Hoek (2006). "Mosaic structure of human coronavirus NL63, one thousand years of evolution." J Mol Biol 364(5): 964-973.

Ramirez, A., A. Fajardo, Z. Moros, M. Gerder, G. Caraballo, D. Camacho, G. Comach, V. Alarcon, J. Zambrano, R. Hernandez, G. Moratorio, J. Cristina and F. Liprandi (2010). "Evolution of dengue virus type 3 genotype III in Venezuela: diversification, rates and population dynamics." Virol J 7: 329.

Ramsden, C., E. C. Holmes and M. A. Charleston (2009). "Hantavirus evolution in relation to its rodent and insectivore hosts: no evidence for codivergence." Mol Biol Evol 26(1): 143-153.

Raney, J. L., R. R. Delongchamp and C. R. Valentine (2004). "Spontaneous mutant frequency and mutation spectrum for gene A of Phi X174 grown in E-coli." Environmental and Molecular Mutagenesis 44(2): 119-127.

Renzette, N., C. Pokalyuk, L. Gibson, B. Bhattacharjee, M. R. Schleiss, K. Hamprecht, A. Y. Yamamoto, M. M. Mussi-Pinhata, W. J. Britt, J. D. Jensen and T. F. Kowalik (2015). "Limits and patterns of cytomegalovirus genomic diversity in humans." Proceedings of the National Academy of Sciences of the United States of America 112(30): E4120-E4128.

Ribeiro, R. M., H. Li, S. Wang, M. B. Stoddard, G. H. Learn, B. T. Korber, T. Bhattacharya, J. Guedj, E. H. Parrish, B. H. Hahn, G. M. Shaw and A. S. Perelson (2012). "Quantifying the diversification of hepatitis C virus (HCV) during primary infection: estimates of the in vivo mutation rate." PLoS Pathog 8(8): e1002881.

Risso-Ballester, J., J. M. Cuevas and R. Sanjuán (2016). "Genome-Wide Estimation of the Spontaneous Mutation Rate of Human Adenovirus 5 by High-Fidelity Deep Sequencing." PLoS Pathog 12(11): e1006013.

Robles-Sikisaka, R., A. J. Bohonak, L. R. McClenaghan, Jr. and A. K. Dhar (2010). "Genetic signature of rapid IHHNV (infectious hypodermal and hematopoietic necrosis virus) expansion in wild Penaeus shrimp populations." PLoS One 5(7): e11799.

Romano, C. M., P. M. Zanotto and E. C. Holmes (2008). "Bayesian coalescent analysis reveals a high rate of molecular evolution in GB virus C." J Mol Evol 66(3): 292-297.

Sanjuán, R., P. Agudelo-Romero and S. F. Elena (2009). "Upper-limit mutation rate estimation for a plant RNA virus." Biol Lett 5(3): 394-396.

Shackelton, L. A. and E. C. Holmes (2006). "Phylogenetic evidence for the rapid evolution of human B19 erythrovirus." J Virol 80(7): 3666-3669.

Shackelton, L. A., C. R. Parrish, U. Truyen and E. C. Holmes (2005). "High rate of viral evolution associated with the emergence of carnivore parvovirus." Proc Natl Acad Sci U S A 102(2): 379-384.

Shackelton, L. A., A. Rambaut, O. G. Pybus and E. C. Holmes (2006). "JC virus evolution and its association with human populations." J Virol 80(20): 9928-9933.

Simmons, H. E., E. C. Holmes and A. G. Stephenson (2008). "Rapid evolutionary dynamics of zucchini yellow mosaic virus." Journal of General Virology 89: 1081-1085.

Stech, J., X. Xiong, C. Scholtissek and R. G. Webster (1999). "Independence of evolutionary and mutational rates after transmission of avian influenza viruses to swine." J Virol 73(3): 1878-1884.

Stenger, D. C., M. S. Sisterson and R. French (2010). "Population genetics of Homalodisca vitripennis reovirus validates timing and limited introduction to California of its invasive insect host, the glassy-winged sharpshooter." Virology 407(1): 53-59.

Streck, A. F., S. L. Bonatto, T. Homeier, C. K. Souza, K. R. Goncalves, D. Gava, C. W. Canal and U. Truyen (2011). "High rate of viral evolution in the capsid protein of porcine parvovirus." J Gen Virol 92(Pt 11): 2628-2636.

Tromas, N. and S. F. Elena (2010). "The rate and spectrum of spontaneous mutations in a plant RNA virus." Genetics 185(3): 983-989.

van Niekerk, S. and M. Venter (2011). "Replacement of previously circulating respiratory syncytial virus subtype B strains with the BA genotype in South Africa." J Virol 85(17): 8789-8797.

Varelaechavarria, A., N. Garvey, B. D. Preston and J. P. Dougherty (1992). "Comparison of Moloney Murine Leukemia-Virus Mutation-Rate with the Fidelity of Its Reverse-Transcriptase Invitro." Journal of Biological Chemistry 267(34): 24681-24688.

Vignuzzi, M., J. K. Stone, J. J. Arnold, C. E. Cameron and R. Andino (2006). "Quasispecies diversity determines pathogenesis through cooperative interactions in a viral population." Nature 439(7074): 344-348.

Vijgen, L., E. Keyaerts, E. Moes, I. Thoelen, E. Wollants, P. Lemey, A. M. Vandamme and M. Van Ranst (2005). "Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event." J Virol 79(3): 1595-1604.

Volk, S. M., R. Chen, K. A. Tsetsarkin, A. P. Adams, T. I. Garcia, A. A. Sall, F. Nasar, A. J. Schuh, E. C. Holmes, S. Higgs, P. D. Maharaj, A. C. Brault and S. C. Weaver (2010). "Genome-scale phylogenetic analyses of chikungunya virus reveal independent emergences of recent epidemics and various evolutionary rates." J Virol 84(13): 6497-6504.

Wang, W., W. M. Lee, A. G. Mosser and R. R. Rueckert (1998). "WIN 52035-dependent human rhinovirus 16: assembly deficiency caused by mutations near the canyon surface." J Virol 72(2): 1210-1218.

Wertheim, J. O., K. F. Tang, S. A. Navarro and D. V. Lightner (2009). "A quick fuse and the emergence of Taura syndrome virus." Virology 390(2): 324-329.

Wong, K. K., R. A. Bull, S. Rockman, G. Scott, S. Stelzer-Braid and W. Rawlinson (2011). "Correlation of polymerase replication fidelity with genetic evolution of influenza A/Fujian/411/02(H3N2) viruses." J Med Virol 83(3): 510-516.

Wu, B. L., A. Blanchard-Letort, Y. Liu, G. H. Zhou, X. F. Wang and S. F. Elena (2011). "Dynamics of Molecular Evolution and Phylogeography of Barley yellow dwarf virus-PAV." Plos One 6(2).

Xu, J., M. C. Christman, R. O. Donis and G. Lu (2011). "Evolutionary dynamics of influenza A nucleoprotein (NP) lineages revealed by large-scale sequence analyses." Infect Genet Evol 11(8): 2125-2132.

Yang, C. F., C. K. Wang, S. J. Tollefson, R. Piyaratna, L. D. Lintao, M. Chu, A. Liem, M. Mark, R. R. Spaete, J. E. Crowe, Jr. and J. V. Williams (2009). "Genetic diversity and evolution of human metapneumovirus fusion protein over twenty years." Virol J 6: 138.

Yoon, S. H., W. Park, D. P. King and H. Kim (2011). "Phylogenomics and molecular evolution of foot-and-mouth disease virus." Molecules and Cells 31(5): 413-421.

Zhou, Y. and E. C. Holmes (2007). "Bayesian estimates of the evolutionary rate and age of hepatitis B virus." J Mol Evol 65(2): 197-205.