

## S2 | Methods used to analyse articles

**Supporting Information****Methods**

In order to assess the research emphasis and approaches used for studying viral host jumps, we focused on four specific viruses: Influenza A (IAV), Severe acute respiratory syndrome coronavirus (SARS-CoV), canine parvovirus (CPV) and Venezuelan equine encephalitis virus (VEEV) because these viruses have been: 1) among the most researched on the topic of host jumps, or 2) studied using approaches that we deemed to be extremely fruitful for understanding evolutionary mechanisms of host jumps. We acknowledge that other viruses (e.g., HIV) fall into these categories, and thus emphasize that our goal is not to be comprehensive but to use a few strong examples to point out methodological strengths and weaknesses, data gaps and biases and effective future directions.

**Search methodology.** We used the Web of Science (WofS) to search for studies that addressed host jumps or changes in host range for each of the four viruses. All searches were conducted on Jan. 20th, 2010 meaning that publications after this date were excluded. Our search query (see below) contained a set of terms that are commonly used in addressing host jumps as well as the name of the specific virus (and variants of this name where necessary). We required that the host jump terms and virus name be in the WofS "Topic" category which includes titles, abstracts and keywords. We refined each search by only selecting journal articles. We emphasize that our search results are not meant to be absolutely quantitative but should be regarded as a sample of the studies that address host jumps. This approach allows us to draw conclusions about the relative effort dedicated towards collecting different types of data and addressing evolutionary hypotheses, which are our goals. Our search query was: (TS=("host jump\*" OR "host switch\*" OR ("host species" SAME (different OR novel OR new OR alternat\* )) OR ("host range" SAME (expan\* OR decreas\* OR increas\* OR change\* OR shift)) OR "host specialization" OR "host specificity" OR "cross-species" OR "host transfer" OR "cross-host" OR "species barriers" OR "species tropism" OR "animal-to-human" OR "interspecies trans\*" OR "inter-species trans\*" OR "zoonotic transm\*" OR "host radiation" OR spillover OR "spill over" OR xenotrop\*) AND TS=(virus name)).

**Criteria for paper selection.** We screened the final set of host jump papers for each virus to eliminate inappropriate hits and to subdivide the relevant papers into 3 categories for further analysis. The following papers were eliminated: review articles, book chapters, papers that did not address host range change or host jumps, papers that did not address the specified virus or papers that were in languages other than English, French or German (languages in which the authors are competent). Papers in the final set were scored as (see column Supp. Table 1, column 3): 1) 0 for papers that address host range change or host jumps but do not collect data that would be relevant for testing evolutionary hypotheses, 2) 1 for papers that collect relevant data for addressing evolutionary hypotheses but they do not explicitly test an evolutionary hypothesis nor mention evolutionary processes in the abstract, and 3) 2 for papers that collect data that address evolutionary mechanisms of host range change or host jumps. We classified data as being relevant to addressing evolutionary hypotheses if the study included genetic or phenotypic viral data.

**Paper review.** Papers in the 0 category were not analyzed further except for being tallied as part of the denominator representing the total set of papers addressing host range change or host jumps. For 1 papers, only the virus type, broad scope of the sampling, type of data and approach were recorded (first 4 sections of Supp. Table 1) abstracts were recorded from information in the abstracts. For 2 papers, the entire paper was used to fill out the data in all of Supp. Table 1. By tallying the number of papers in each category, we calculated the effort on addressing evolutionary hypotheses relative to total effort on host

jumps (2 / 0 + 1 + 2), the effort on addressing evolutionary hypotheses out of total data that are relevant to evolutionary hypotheses (2 / 1 + 2), and the effort on collecting evolutionary-type data relative to total host jump data (2 + 1 / 0 + 1 + 2).

## References

**Influenza**<sup>1-49,50-72,2, 44, 63, 73-152</sup>; **SARS-coV**<sup>66, 87, 153-188</sup>; **CPV**<sup>189-213</sup>; **VEEV**<sup>214-228</sup>

1. Aamir, U.B., Wernery, U., Ilyushina, N. & Webster, R.G. Characterization of avian H9N2 influenza viruses from United Arab Emirates 2000 to 2003. *Virology* 361, 45-55 (2007).
2. Allen, J.E., Gardner, S.N., Vitalis, E.A. & Slezak, T.R. Conserved amino acid markers from past influenza pandemic strains. *Bmc Microbiology* 9 (2009).
3. Banks, J. et al. Changes in the haemagglutinin and the neuraminidase genes prior to the emergence of highly pathogenic H7N1 avian influenza viruses in Italy. *Archives of Virology* 146, 963-973 (2001).
4. Brower-Sinning, R. et al. The role of RNA folding free energy in the evolution of the polymerase genes of the influenza A virus. *Genome Biology* 10 (2009).
5. Campitelli, L. et al. Molecular analysis of avian H7 influenza viruses circulating in Eurasia in 1999-2005: detection of multiple reassortant virus genotypes. *Journal of General Virology* 89, 48-59 (2008).
6. Campitelli, L. et al. Interspecies transmission of an H7N3 influenza virus from wild birds to intensively reared domestic poultry in Italy. *Virology* 323, 24-36 (2004).
7. Chen, R. & Holmes, E.C. Frequent inter-species transmission and geographic subdivision in avian influenza viruses from wild birds. *Virology* 383, 156-161 (2009).
8. Choi, Y.K. et al. H3N2 influenza virus transmission from swine to turkeys, United States. *Emerging Infectious Diseases* 10, 2156-2160 (2004).
9. Choi, Y.K. et al. Continuing evolution of H9N2 influenza viruses in Southeastern China. *Journal of Virology* 78, 8609-8614 (2004).
10. Cong, Y.L. et al. Antigenic and genetic characterization of H9N2 swine influenza viruses in China. *Journal of General Virology* 88, 2035-2041 (2007).
11. Dugan, V.G. et al. The evolutionary genetics and emergence of avian influenza viruses in wild birds. *Plos Pathogens* 4 (2008).
12. Dunham, E.J. et al. Different Evolutionary Trajectories of European Avian-Like and Classical Swine H1N1 Influenza A Viruses. *Journal of Virology* 83, 5485-5494 (2009).
13. Forsberg, R. & Christiansen, F.B. A codon-based model of host-specific selection in parasites, with an application to the influenza A virus. *Molecular Biology and Evolution* 20, 1252-1259 (2003).
14. Gabriel, G. et al. Differential polymerase activity in avian and mammalian cells determines host range of influenza virus. *Journal of Virology* 81, 9601-9604 (2007).
15. Gabriel, G., Herwig, A. & Klenk, H.D. Interaction of polymerase subunit PB2 and NP with importin alpha 1 is a determinant of host range of influenza a virus. *Plos Pathogens* 4 (2008).
16. Gambaryan, A.S. et al. 6-sulfo sialyl Lewis X is the common receptor determinant recognized by H5, H6, H7 and H9 influenza viruses of terrestrial poultry. *Virology Journal* 5 (2008).
17. Matrosovich, M.N., Krauss, S. & Webster, R.G. H9N2 influenza a viruses from poultry in Asia have human virus-like receptor specificity. *Virology* 281, 156-162 (2001).
18. Mehle, A. & Doudna, J.A. An inhibitory activity in human cells restricts the function of an avian-like influenza virus polymerase. *Cell Host & Microbe* 4, 111-122 (2008).
19. Narasaraju, T. et al. Adaptation of human influenza H3N2 virus in a mouse pneumonitis model: insights into viral virulence, tissue tropism and host pathogenesis. *Microbes and Infection* 11, 2-11 (2009).

20. Pan, C.E., Wang, G.P., Liao, M., Zhang, G.H. & Jiang, S.B. High genetic and antigenic similarity between a swine H3N2 influenza A virus and a prior human influenza vaccine virus: A possible immune pressure-driven cross-species transmission. *Biochemical and Biophysical Research Communications* 385, 402-407 (2009).
21. Peiris, J.S.M. et al. Cocirculation of avian H9N2 and contemporary "human" H3N2 influenza A viruses in pigs in southeastern China: Potential for genetic reassortment? *Journal of Virology* 75, 9679-9686 (2001).
22. Pekosz, A., Newby, C., Bose, P.S. & Lutz, A. Sialic acid recognition is a key determinant of influenza A virus tropism in murine trachea epithelial cell cultures. *Virology* 386, 61-67 (2009).
23. Perez, D.R. et al. Role of quail in the interspecies transmission of H9 influenza A viruses: Molecular changes on HA that correspond to adaptation from ducks to chickens. *Journal of Virology* 77, 3148-3156 (2003).
24. Qi, L. et al. Role of Sialic Acid Binding Specificity of the 1918 Influenza Virus Hemagglutinin Protein in Virulence and Pathogenesis for Mice. *Journal of Virology* 83, 3754-3761 (2009).
25. Reid, A.H., Fanning, T.G., Janczewski, T.A., Lourens, R.M. & Taubenberger, J.K. Novel origin of the 1918 pandemic influenza virus nucleoprotein gene. *Journal of Virology* 78, 12462-12470 (2004).
26. Reid, A.H., Fanning, T.G., Janczewski, T.A. & Taubenberger, J.K. Characterization of the 1918 "Spanish" influenza virus neuraminidase gene. *Proceedings of the National Academy of Sciences of the United States of America* 97, 6785-6790 (2000).
27. Scholtissek, C., Burger, H., Kistner, O. & Shortridge, K.F. THE NUCLEOPROTEIN AS A POSSIBLE MAJOR FACTOR IN DETERMINING HOST SPECIFICITY OF INFLUENZA H3N2 VIRUSES. *Virology* 147, 287-294 (1985).
28. Scull, M.A. et al. Avian Influenza Virus Glycoproteins Restrict Virus Replication and Spread through Human Airway Epithelium at Temperatures of the Proximal Airways. *Plos Pathogens* 5 (2009).
29. Shu, L.L., Bean, W.J. & Webster, R.G. ANALYSIS OF THE EVOLUTION AND VARIATION OF THE HUMAN INFLUENZA-A VIRUS NUCLEOPROTEIN GENE FROM 1933 TO 1990. *Journal of Virology* 67, 2723-2729 (1993).
30. Smirnov, Y.A. et al. Characterization of adaptation of an avian influenza a (H5N2) virus to a mammalian host. *Acta Virologica* 44, 1-8 (2000).
31. Smith, G.J.D. et al. Evolution and adaptation of H5N1 influenza virus in avian and human hosts in Indonesia and Vietnam. *Virology* 350, 258-268 (2006).
32. Song, D. et al. Transmission of avian influenza virus (H3N2) to dogs. *Emerging Infectious Diseases* 14, 741-746 (2008).
33. Sorrell, E.M., Wan, H.Q., Araya, Y., Song, H.C. & Perez, D.R. Minimal molecular constraints for respiratory droplet transmission of an avian-human H9N2 influenza A virus. *Proceedings of the National Academy of Sciences of the United States of America* 106, 7565-7570 (2009).
34. Swayne, D.E., Beck, J.R., Perdue, M.L., Brugh, M. & Slemons, R.D. Assessment of the ability of ratite-origin influenza viruses to infect and produce disease in rheas and chickens. *Avian Diseases* 40, 438-447 (1996).
35. Swayne, D.E. & Slemons, R.D. Using Mean Infectious Dose of High- and Low-Pathogenicity Avian Influenza Viruses Originating from Wild Duck and Poultry as One Measure of Infectivity and Adaptation to Poultry. *Avian Diseases* 52, 455-460 (2008).
36. Tarendeau, F. et al. Host determinant residue lysine 627 lies on the surface of a discrete, folded domain of influenza virus polymerase PB2 subunit. *Plos Pathogens* 4 (2008).
37. Taubenberger, J.K. et al. Characterization of the 1918 influenza virus polymerase genes. *Nature* 437, 889-893 (2005).
38. Tu, J.G. et al. Isolation and molecular characterization of equine H3N8 influenza viruses from pigs in China. *Archives of Virology* 154, 887-890 (2009).

39. Vijaykrishna, D. *et al.* Evolutionary dynamics and emergence of panzootic H5N1 influenza viruses. *Plos Pathogens* 4 (2008).
40. Wan, H.Q. & Perez, D.R. Quail carry sialic acid receptors compatible with binding of avian and human influenza viruses. *Virology* 346, 278-286 (2006).
41. Webby, R.J., Woolcock, P.R., Krauss, S.L. & Webster, R.G. Reassortment and interspecies transmission of North American H6N2 influenza viruses. *Virology* 295, 44-53 (2002).
42. Wright, S.M., Kawaoka, Y., Sharp, G.B., Senne, D.A. & Webster, R.G. INTERSPECIES TRANSMISSION AND REASSORTMENT OF INFLUENZA-A VIRUSES IN PIGS AND TURKEYS IN THE UNITED-STATES. *American Journal of Epidemiology* 136, 488-497 (1992).
43. Wu, G. & Yan, S.M. Fate of 130 hemagglutinins from different influenza A viruses. *Biochemical and Biophysical Research Communications* 317, 917-924 (2004).
44. Wu, R. *et al.* Multiple amino acid substitutions are involved in the adaptation of H9N2 avian influenza virus to mice. *Veterinary Microbiology* 138, 85-91 (2009).
45. Xu, K.M. *et al.* The genesis and evolution of H9N2 influenza viruses in poultry from southern china, 2000 to 2005. *Journal of Virology* 81, 10389-10401 (2007).
46. Yassine, H.M., Al-Natour, M.Q., Lee, C.W. & Saif, Y.M. Interspecies and intraspecies transmission of triple reassortant H3N2 influenza A viruses. *Virology Journal* 4 (2007).
47. Yu, H. *et al.* Isolation and genetic characterization of avian origin H9N2 influenza viruses from pigs in China. *Veterinary Microbiology* 131, 82-92 (2008).
48. Zhou, N.N. *et al.* Genetic reassortment of avian, swine, and human influenza A viruses in American pigs. *Journal of Virology* 73, 8851-8856 (1999).
49. Zhou, N.N., Shortridge, K.F., Claas, E.C.J., Krauss, S.L. & Webster, R.G. Rapid evolution of H5N1 influenza viruses in chickens in Hong Kong. *Journal of Virology* 73, 3366-3374 (1999).
50. Gambaryan, A.S. *et al.* Specification of receptor-binding phenotypes of influenza virus isolates from different hosts using synthetic sialylglycopolymers: Non-egg-adapted human H1 and H3 influenza A and influenza B viruses share a common high binding affinity for 6'-sialyl(N-acetyl)lactosamine. *Virology* 232, 345-350 (1997).
51. Giannecchini, S. *et al.* Comparison of in vitro replication features of H7N3 influenza viruses from wild ducks and turkeys: potential implications for interspecies transmission. *Journal of General Virology* 87, 171-175 (2006).
52. Gibbs, M.J. *et al.* The variable codons of H3 influenza A virus haemagglutinin genes. *Archives of Virology* 152, 11-24 (2007).
53. Giese, M. *et al.* Experimental infection and natural contact exposure of dogs with avian influenza virus (H5N1). *Emerging Infectious Diseases* 14, 308-310 (2008).
54. Gillim-Ross, L. *et al.* Avian Influenza H6 Viruses Productively Infect and Cause Illness in Mice and Ferrets. *Journal of Virology* 82, 10854-10863 (2008).
55. Gorman, O.T. *et al.* EVOLUTION OF INFLUENZA-A VIRUS NUCLEOPROTEIN GENES - IMPLICATIONS FOR THE ORIGINS OF H1N1 HUMAN AND CLASSICAL SWINE VIRUSES. *Journal of Virology* 65, 3704-3714 (1991).
56. Guan, Y. *et al.* H5N1 influenza viruses isolated from Geese in southeastern China: Evidence for genetic reassortment and interspecies transmission to ducks. *Virology* 292, 16-23 (2002).
57. Hughes, M.T., McGregor, M., Suzuki, T., Suzuki, Y. & Kawaoka, Y. Adaptation of influenza A viruses to cells expressing low levels of sialic acid leads to loss of neuraminidase activity. *Journal of Virology* 75, 3766-3770 (2001).
58. Keleta, L., Ibricevic, A., Bovin, N.V., Brody, S.L. & Brown, E.G. Experimental Evolution of Human Influenza Virus H3 Hemagglutinin in the Mouse Lung Identifies Adaptive Regions in HA1 and HA2. *Journal of Virology* 82, 11599-11608 (2008).

59. Kongchanagul, A. *et al.* Positive selection at the receptor-binding site of haemagglutinin H5 in viral sequences derived from human tissues. *Journal of General Virology* 89, 1805-1810 (2008).
60. Kou, Z., Fumin, L.M., Wang, S.Y., Zhou, Y.H. & Li, T.X. Molecular patterns of avian influenza A viruses. *Chinese Science Bulletin* 53, 2002-2007 (2008).
61. Kryazhimskiy, S., Bazykin, G.A. & Dushoff, J. Natural selection for nucleotide usage at synonymous and nonsynonymous sites in influenza A virus genes. *Journal of Virology* 82, 4938-4945 (2008).
62. Lee, M.S. *et al.* Genetic and pathogenic characterization of H6N1 avian influenza viruses isolated in Taiwan between 1972 and 2005. *Avian Diseases* 50, 561-571 (2006).
63. Lee, Y.J. *et al.* Continuing evolution of H9 influenza viruses in Korean poultry. *Virology* 359, 313-323 (2007).
64. Leneva, I.A., Goloubeva, O., Fenton, R.J., Tisdale, M. & Webster, R.G. Efficacy of zanamivir against avian influenza A viruses that possess genes encoding H5N1 internal proteins and are pathogenic in mammals. *Antimicrobial Agents and Chemotherapy* 45, 1216-1224 (2001).
65. Li, G.L., Tao, S.H. & Wang, X.J. Sequence and epitope analysis of surface proteins of avian influenza H5N1 viruses from Asian patients. *Chinese Science Bulletin* 51, 2472-2481 (2006).
66. Song, H.D. *et al.* Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human. *Proceedings of the National Academy of Sciences of the United States of America* 102, 2430-2435 (2005).
67. Ma, W. *et al.* Identification of H2N3 influenza A viruses from swine in the United States. *Proceedings of the National Academy of Sciences of the United States of America* 104, 20949-20954 (2007).
68. Macken, C.A., Webby, R.J. & Bruno, W.J. Genotype turnover by reassortment of replication complex genes from avian Influenza A virus. *Journal of General Virology* 87, 2803-2815 (2006).
69. Makarova, N.V., Ozaki, H., Kida, H., Webster, R.G. & Perez, D.R. Replication and transmission of influenza viruses in Japanese quail. *Virology* 310, 8-15 (2003).
70. Matrosovich, M., Gao, P. & Kawaoka, Y. Molecular mechanisms of serum resistance of human influenza H3N2 virus and their involvement in virus adaptation in a new host. *Journal of Virology* 72, 6373-6380 (1998).
71. Matrosovich, M. *et al.* Early alterations of the receptor-binding properties of H1, H2, and H3 avian influenza virus hemagglutinins after their introduction into mammals. *Journal of Virology* 74, 8502-8512 (2000).
72. Matrosovich, M., Zhou, N., Kawaoka, Y. & Webster, R. The surface glycoproteins of H5 influenza viruses isolated from humans, chickens, and wild aquatic birds have distinguishable properties. *Journal of Virology* 73, 1146-1155 (1999).
73. Alvarez, A.C. *et al.* A broad spectrum, one-step reverse-transcription PCR amplification of the neuraminidase gene from multiple subtypes of influenza A virus. *Virology Journal* 5 (2008).
74. Banet-Noach, C. *et al.* Genetic analysis of nonstructural genes (NS1 and NS2) of H9N2 and H5N1 viruses recently isolated in Israel. *Virus Genes* 34, 157-168 (2007).
75. Belser, J.A. *et al.* Pathogenesis of avian influenza (H7) virus infection in mice and ferrets: Enhanced virulence of Eurasian H7N7 viruses isolated from humans. *Journal of Virology* 81, 11139-11147 (2007).
76. Bikour, M.H., Frost, E.H., Deslandes, S., Talbot, B. & Elazhary, Y. PERSISTENCE OF A 1930 SWINE INFLUENZA-A (H1N1) VIRUS IN QUEBEC. *Journal of General Virology* 76, 2539-2547 (1995).
77. Brown, J.D., Stallknecht, D.E., Valeika, S. & Swayne, D.E. Susceptibility of wood ducks to H5N1 highly pathogenic avian influenza virus. *Journal of Wildlife Diseases* 43, 660-667 (2007).
78. Butt, K.M. *et al.* Human infection with an avian H9N2 influenza A virus in Hong Kong in 2003. *Journal of Clinical Microbiology* 43, 5760-5767 (2005).



79. Chen, M.W. *et al.* A consensus-hemagglutinin-based DNA vaccine that protects mice against divergent H5N1 influenza viruses. *Proceedings of the National Academy of Sciences of the United States of America* 105, 13538-13543 (2008).
80. Cong, Y.L. *et al.* Swine infection with H9N2 influenza viruses in China in 2004. *Virus Genes* 36, 461-469 (2008).
81. Das, A. & Suarez, D.L. Development and bench validation of real-time reverse transcription polymerase chain reaction protocols for rapid detection of the subtypes H6, H9, and H11 of avian influenza viruses in experimental samples. *Journal of Veterinary Diagnostic Investigation* 19, 625-634 (2007).
82. Day, T., Andre, J.B. & Park, A. The evolutionary emergence of pandemic influenza. *Proceedings of the Royal Society B-Biological Sciences* 273, 2945-2953 (2006).
83. de Jong, M.C.M., Stegeman, A., van der Goot, J. & Koch, G. Intra- and interspecies transmission of H7N7 highly pathogenic avian influenza virus during the avian influenza epidemic in the Netherlands in 2003. *Revue Scientifique Et Technique-Office International Des Epizooties* 28, 333-340 (2009).
84. Di Trani, L. *et al.* A sensitive one-step real-time PCR for detection of avian influenza viruses using a MGB probe and an internal positive control. *Bmc Infectious Diseases* 6 (2006).
85. Donatelli, I. *et al.* DETECTION OF 2 ANTIGENIC SUBPOPULATIONS OF A(H1N1) INFLUENZA-VIRUSES FROM PIGS - ANTIGENIC DRIFT OR INTERSPECIES TRANSMISSION. *Journal of Medical Virology* 34, 248-257 (1991).
86. Douglas, K.O., Lavoie, M.C., Kim, L.M., Afonso, C.L. & Suarez, D.L. Isolation and Genetic Characterization of Avian Influenza Viruses and a Newcastle Disease Virus from Wild Birds in Barbados: 2003-2004. *Avian Diseases* 51, 781-787 (2007).
87. Roberts, A. *et al.* A mouse-adapted SARS-coronavirus causes disease and mortality in BALB/c mice. *Plos Pathogens* 3, 23-37 (2007).
88. Hatchette, T.F. *et al.* Influenza A viruses in feral Canadian ducks: extensive reassortment in nature. *Journal of General Virology* 85, 2327-2337 (2004).
89. Heard, D.J. *et al.* A blood survey of elements, viral antibodies, and hemoparasites in wintering Harlequin Ducks (*Histrionicus histrionicus*) and Barrow's Goldeneyes (*Bucephala islandica*). *Journal of Wildlife Diseases* 44, 486-493 (2008).
90. Hidari, K. *et al.* Chemoenzymatic synthesis, characterization, and application of glycopolymers carrying lactosamine repeats as entry inhibitors against influenza virus infection. *Glycobiology* 18, 779-788 (2008).
91. Hidari, K., Shimada, S., Suzuki, Y. & Suzuki, T. Binding kinetics of influenza viruses to sialic acid-containing carbohydrates. *Glycoconjugate Journal* 24, 583-590 (2007).
92. Hlinak, A. *et al.* A virological survey in migrating waders and other waterfowl in one of the most important resting sites of Germany. *Journal of Veterinary Medicine Series B-Infectious Diseases and Veterinary Public Health* 53, 105-110 (2006).
93. Humberd, J., Guan, Y. & Webster, R.G. Comparison of the replication of influenza A viruses in Chinese ring-necked pheasants and chukar partridges. *Journal of Virology* 80, 2151-2161 (2006).
94. Ito, T. *et al.* Recognition of N-glycolylneuraminic acid linked to galactose by the alpha 2,3 linkage is associated with intestinal replication of influenza A virus in ducks. *Journal of Virology* 74, 9300-9305 (2000).
95. Jahangir, A. *et al.* Avian influenza and Newcastle disease viruses from northern pintail in Japan: Isolation, characterization and inter-annual comparisons during 2006-2008. *Virus Research* 143, 44-52 (2009).
96. Karasin, A.I., Brown, I.H., Carman, S. & Olsen, C.W. Isolation and characterization of H4N6 avian influenza viruses from pigs with pneumonia in Canada. *Journal of Virology* 74, 9322-9327 (2000).

97. Karasin, A.I., West, K., Carman, S. & Olsen, C.W. Characterization of avian H3N3 and H1N1 influenza A viruses isolated from pigs in Canada. *Journal of Clinical Microbiology* 42, 4349-4354 (2004).
98. Kash, J.C. et al. Global host immune response: Pathogenesis and transcriptional profiling of type A influenza viruses expressing the hemagglutinin and neuraminidase genes from the 1918 pandemic virus. *Journal of Virology* 78, 9499-9511 (2004).
99. Klopfleisch, R. et al. Encephalitis in a stone marten (*Martes foina*) after natural infection with highly pathogenic avian influenza virus subtype H5N1. *Journal of Comparative Pathology* 137, 155-159 (2007).
100. Kodihalli, S., Kobasa, D.L. & Webster, R.G. Strategies for inducing protection against avian influenza A virus subtypes with DNA vaccines. *Vaccine* 18, 2592-2599 (2000).
101. Krauss, S. et al. Influenza A viruses of migrating wild aquatic birds in North America. *Vector-Borne and Zoonotic Diseases* 4, 177-189 (2004).
102. Lang, C. et al. Investigation on the occurrence of the porcine influenza virus A-subtype H1N2 in Austria. *Wiener Tierärztliche Monatsschrift* 91, 297-308 (2004).
103. Lekcharoensuk, P. et al. Novel swine influenza virus subtype H3N1, United States. *Emerging Infectious Diseases* 12, 787-794 (2006).
104. Lipatov, A.S. et al. Neurovirulence in mice of H5N1 influenza virus genotypes isolated from Hong Kong poultry in 2001. *Journal of Virology* 77, 3816-3823 (2003).
105. Liu, M. et al. The influenza virus gene pool in a poultry market in South Central China. *Virology* 305, 267-275 (2003).
106. Myers, K.P. et al. Are swine workers in the United States at increased risk of infection with zoonotic influenza virus? *Clinical Infectious Diseases* 42, 14-20 (2006).
107. Newby, C.M., Rowe, R.K. & Pekosz, A. Influenza A virus infection of primary differentiated airway epithelial cell cultures derived from Syrian golden hamsters. *Virology* 354, 80-90 (2006).
108. Nguyen, D.C. et al. Isolation and characterization of avian influenza viruses, including highly pathogenic H5N1, from poultry in live bird markets in Hanoi, Vietnam, in 2001. *Journal of Virology* 79, 4201-4212 (2005).
109. Obayashi, E. et al. The structural basis for an essential subunit interaction in influenza virus RNA polymerase. *Nature* 454, 1127-U57 (2008).
110. Olson, S.R. & Gray, G.C. The Trojan chicken study, Minnesota. *Emerging Infectious Diseases* 12, 795-799 (2006).
111. Rigoni, M. et al. Pneumo- and neurotropism of avian origin Italian highly pathogenic avian influenza H7N1 isolates in experimentally infected mice. *Virology* 364, 28-35 (2007).
112. Saito, T. et al. Pathogenicity of highly pathogenic avian influenza viruses of H5N1 subtype isolated in Thailand for different poultry species. *Veterinary Microbiology* 133, 65-74 (2009).
113. Shaw, M. et al. Molecular changes associated with the transmission of avian influenza A H5N1 and H9N2 viruses to humans. *Journal of Medical Virology* 66, 107-114 (2002).
114. Shu, L.L., Lin, Y.P., Wright, S.M., Shortridge, K.F. & Webster, R.G. EVIDENCE FOR INTERSPECIES TRANSMISSION AND REASSORTMENT OF INFLUENZA-A VIRUSES IN PIGS IN SOUTHERN CHINA. *Virology* 202, 825-833 (1994).
115. Shu, L.L. et al. An epidemiological study of influenza viruses among Chinese farm families with household ducks and pigs. *Epidemiology and Infection* 117, 179-188 (1996).
116. Shu, L.P. et al. Genetic reassortment in pandemic and interpandemic influenza viruses - A study of 122 viruses infecting humans. *European Journal of Epidemiology* 12, 63-70 (1996).
117. Song, M.S. et al. Ecology of H3 avian influenza viruses in Korea and assessment of their pathogenic potentials. *Journal of General Virology* 89, 949-957 (2008).

118. Stoloff, G.A. & Caparros-Wanderley, W. Synthetic multi-epitope peptides identified in silico induce protective immunity against multiple influenza serotypes. *European Journal of Immunology* 37, 2441-2449 (2007).
119. Suarez, D.L., Woolcock, P.R., Bermudez, A.J. & Senne, D.A. Isolation from turkey breeder hens of a reassortant H1N2 influenza virus with swine, human, and avian lineage genes. *Avian Diseases* 46, 111-121 (2002).
120. Szretter, K.J. et al. Early Control of H5N1 Influenza Virus Replication by the Type I Interferon Response in Mice. *Journal of Virology* 83, 5825-5834 (2009).
121. Szretter, K.J. et al. Role of host cytokine responses in the pathogenesis of avian H5N1 influenza viruses in mice. *Journal of Virology* 81, 2736-2744 (2007).
122. Tang, Y. et al. Isolation and characterization of H3N2 influenza A virus from turkeys. *Avian Diseases* 49, 207-213 (2005).
123. Tumpey, T.M. et al. Characterization of a highly pathogenic H5N1 avian influenza a virus isolated from duck meat. *Journal of Virology* 76, 6344-6355 (2002).
124. Wahlgren, J. et al. Gene Segment Reassortment Between American and Asian Lineages of Avian Influenza Virus from Waterfowl in the Beringia Area. *Vector-Borne and Zoonotic Diseases* 8, 783-790 (2008).
125. Webster, R.G. et al. The spread of the H5N1 bird flu epidemic in Asia in 2004. *Archives of Virology*, 117-129 (2005).
126. Wentworth, D.E. et al. AN INFLUENZA-A (H1N1) VIRUS, CLOSELY-RELATED TO SWINE INFLUENZA-VIRUS, RESPONSIBLE FOR A FATAL CASE OF HUMAN INFLUENZA. *Journal of Virology* 68, 2051-2058 (1994).
127. Widjaja, L., Krauss, S.L., Webby, R.J., Xie, T. & Webster, R.G. Matrix gene of influenza a viruses isolated from wild aquatic birds: Ecology and emergence of influenza A viruses. *Journal of Virology* 78, 8771-8779 (2004).
128. Yassine, H.M., Lee, C.W., Suarez, D.L. & Saif, Y.M. Genetic and antigenic relatedness of H3 subtype influenza A viruses isolated from avian and mammalian species. *Vaccine* 26, 966-977 (2008).
129. Yeung, J.W.K. A hypothesis: Sunspot cycles may detect pandemic influenza A in 1700-2000 AD. *Medical Hypotheses* 67, 1016-1022 (2006).
130. Yu, H. et al. Genetic evolution of swine influenza A (H3N2) viruses in China from 1970 to 2006. *Journal of Clinical Microbiology* 46, 1067-1075 (2008).
131. Yu, H. et al. Isolation and genetic analysis of human origin H1N1 and H3N2 influenza viruses from pigs in China. *Biochemical and Biophysical Research Communications* 356, 91-96 (2007).
132. Zhilinskaya, I.N. et al. Contribution of influenza virus hemagglutinin to anticoagulation processes. *Voprosy Virusologii* 41, 179-183 (1996).
133. Zhou, N. et al. Influenza infection in humans and pigs in southeastern China. *Archives of Virology* 141, 649-661 (1996).
134. Aamir, U.B. et al. Zoonotic potential of highly pathogenic avian H7N3 influenza viruses from Pakistan. *Virology* 390, 212-220 (2009).
135. Babakir-Mina, M. et al. Phylogenetic analysis of the surface proteins of influenza A (H5N1) viruses isolated in asian and african populations. *New Microbiologica* 32, 397-403 (2009).
136. Clifford, M., Twigg, J. & Upton, C. Evidence for a novel gene associated with human influenza A viruses. *Virology Journal* 6 (2009).
137. Crowley, T.M., Haring, V.R., Burggraaf, S. & Moore, R.J. Application of chicken microarrays for gene expression analysis in other avian species. *BMC Genomics* 10, Article No.: S3 (2009).
138. Hossain, M.J., Hickman, D. & Perez, D.R. Evidence of Expanded Host Range and Mammalian-Associated Genetic Changes in a Duck H9N2 Influenza Virus Following Adaptation in Quail and Chickens. *Plos One* 3 (2008).



139. Howden, K.J. et al. An investigation into human pandemic influenza virus (H1N1) 2009 on an Alberta swine farm. *Canadian Veterinary Journal-Revue Veterinaire Canadienne* 50, 1153-1161 (2009).
140. Holler, O., Staeheli, P. & Kochs, G. Protective role of interferon-induced Mx GTPases against influenza viruses. *Revue Scientifique Et Technique-Office International Des Epizooties* 28, 219-231 (2009).
141. Mehle, A. & Doudna, J.A. Adaptive strategies of the influenza virus polymerase for replication in humans. *Proceedings Of The National Academy Of Sciences Of The United States Of America* 106, 21312-21316 (2009).
142. Munier, S. et al. A Genetically Engineered Waterfowl Influenza Virus with a Deletion in the Stalk of the Neuraminidase Has Increased Virulence for Chickens. *Journal Of Virology* 84, 940-952 (2010).
143. Qi, X. et al. Molecular Characterization of Highly Pathogenic H5N1 Avian Influenza A Viruses Isolated from Raccoon Dogs in China. *Plos One* 4 (2009).
144. Ramakrishnan, M.A., Gramer, M.R., Goyal, S.M. & Sreevatsan, S. A Serine12Stop mutation in PB1-F2 of the 2009 pandemic (H1N1) influenza A: a possible reason for its enhanced transmission and pathogenicity to humans. *Journal Of Veterinary Science* 10, 349-351 (2009).
145. Song, H.C., Wan, H.Q., Araya, Y. & Perez, D.R. Partial direct contact transmission in ferrets of a mallard H7N3 influenza virus with typical avian-like receptor specificity. *Virology Journal* 6 (2009).
146. Song, M.S. et al. The Polymerase Acidic Protein Gene of Influenza A Virus Contributes to Pathogenicity in a Mouse Model. *Journal Of Virology* 83, 12325-12335 (2009).
147. Spackman, E. et al. Characterization of low pathogenicity avian influenza viruses isolated from wild birds in Mongolia 2005 through 2007. *Virology Journal* 6 (2009).
148. Yamanaka, T., Nemoto, M., Tsujimura, K., Kondo, T. & Matsumura, T. Interspecies transmission of equine influenza virus (H3N8) to dogs by close contact with experimentally infected horses. *Veterinary Microbiology* 139, 351-355 (2009).
149. Zhirnov, O.P. & Klenk, H.-D. Alterations in caspase cleavage motifs of NP and M2 proteins attenuate virulence of a highly pathogenic avian influenza virus. *Virology* 394, 57-63 (2009).
150. Furuse, Y., Suzuki, A., Kamigaki, T. & Oshitani, H. Evolution of the M gene of the influenza A virus in different host species: large-scale sequence analysis. *Viral J* 6, 67 (2009).
151. McLeod, A., Kobayashi, M., Gilman, J., Siagian, A. & Young, M. The use of poultry value chain mapping in developing HPAI control programmes. *World's Poultry Science Journal* 65, 217-224 (2009).
152. Nava, G.M., Attene-Ramos, M.S., Ang, J.K. & Escorcia, M. Origins of the new influenza A(H1N1) virus: time to take action. *Euro Surveill* 14 (2009).
153. Fukushi, S. et al. Amino acid substitutions in the S2 region enhance severe acute respiratory syndrome coronavirus infectivity in rat angiotensin-converting enzyme 2-expressing Cells. *Journal of Virology* 81, 10831-10834 (2007).
154. Li, F. Structural analysis of major species barriers between humans and palm civets for severe acute respiratory syndrome coronavirus infections. *Journal of Virology* 82, 6984-6991 (2008).
155. Li, F., Li, W.H., Farzan, M. & Harrison, S.C. Structure of SARS coronavirus spike receptor-binding domain complexed with receptor. *Science* 309, 1864-1868 (2005).
156. Li, W.H. et al. Receptor and viral determinants of SARS-coronavirus adaptation to human ACE2. *Embo Journal* 24, 1634-1643 (2005).
157. Qu, X.X. et al. Identification of two critical amino acid residues of the severe acute respiratory syndrome coronavirus spike protein for its variation in zoonotic tropism transition via a double substitution strategy. *Journal of Biological Chemistry* 280, 29588-29595 (2005).
158. Ren, W. et al. Difference in receptor usage between severe acute respiratory syndrome (SARS) coronavirus and SARS-like coronavirus of bat origin. *Journal of Virology* 82, 1899-1907 (2008).
159. Sheahan, T., Rockx, B., Donaldson, E., Corti, D. & Baric, R. Pathways of cross-species transmission of synthetically reconstructed zoonotic severe acute respiratory syndrome coronavirus. *Journal of Virology* 82, 8721-8732 (2008).

160. Sheahan, T. et al. Mechanisms of zoonotic severe acute respiratory syndrome coronavirus host range expansion in human airway epithelium. *Journal of Virology* 82, 2274-2285 (2008).
161. Vega, V.B. et al. Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003. *Bmc Infectious Diseases* 4 (2004).
162. Zhang, C.Y., Wei, J.F. & He, S.H. Adaptive evolution of the spike gene of SARS coronavirus: changes in positively selected sites in different epidemic groups. *Bmc Microbiology* 6 (2006).
163. Zhang, Y. et al. Computational simulation of interactions between SARS coronavirus spike mutants and host species-specific receptors. *Computational Biology and Chemistry* 31, 134-137 (2007).
164. Liu, L. et al. Natural mutations in the receptor binding domain of spike glycoprotein determine the reactivity of cross-neutralization between palm civet coronavirus and severe acute respiratory syndrome coronavirus. *Journal of Virology* 81, 4694-4700 (2007).
165. Becker, M.M. et al. Synthetic recombinant bat SARS-like coronavirus is infectious in cultured cells and in mice. *Proceedings of the National Academy of Sciences of the United States of America* 105, 19944-19949 (2008).
166. Che, X.Y. et al. A patient with asymptomatic severe acute respiratory syndrome (SARS) and antigenemia from the 2003-2004 community outbreak of SARS in Guangzhou, China. *Clinical Infectious Diseases* 43, E1-E5 (2006).
167. Day, C.W. et al. A new mouse-adapted strain of SARS-CoV as a lethal model for evaluating antiviral agents in vitro and in vivo. *Virology* 395, 210-222 (2009).
168. Guan, Y. et al. Isolation and characterization of viruses related to the SARS coronavirus from animals in Southern China. *Science* 302, 276-278 (2003).
169. Han, D.P., Lohani, M. & Cho, M.W. Specific asparagine-linked glycosylation sites are critical for DC-SIGN- and L-SIGN-Mediated severe acute respiratory syndrome coronavirus entry. *Journal of Virology* 81, 12029-12039 (2007).
170. He, J.F. et al. Molecular evolution of the SARS coronavirus during the course of the SARS epidemic in China. *Science* 303, 1666-1669 (2004).
171. Lau, S.K.P. et al. Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. *Proceedings of the National Academy of Sciences of the United States of America* 102, 14040-14045 (2005).
172. Liu, W. et al. Molecular epidemiology of SARS-associated coronavirus, Beijing. *Emerging Infectious Diseases* 11, 1420-1424 (2005).
173. Nagata, N. et al. Participation of both host and virus factors in induction of severe acute respiratory syndrome (SARS) in F344 rats infected with SARS coronavirus. *Journal of Virology* 81, 1848-1857 (2007).
174. Poon, L.L.M. et al. Identification of a novel coronavirus in bats. *Journal of Virology* 79, 2001-2009 (2005).
175. Poon, L.L.M. et al. Recurrent mutations associated with isolation and passage of SARS coronavirus in cells from non-human primates. *Journal of Medical Virology* 76, 435-440 (2005).
176. Tang, X.C. et al. Differential stepwise evolution of SARS coronavirus functional proteins in different host species. *Bmc Evolutionary Biology* 9 (2009).
177. Vijaykrishna, D. et al. Evolutionary insights into the ecology of coronaviruses. *Journal of Virology* 81, 4012-4020 (2007).
178. Wang, M. et al. SARS-CoV infection in a restaurant from palm civet. *Emerging Infectious Diseases* 11, 1860-1865 (2005).
179. Yeh, S.H. et al. Characterization of severe acute respiratory syndrome coronavirus genomes in Taiwan: Molecular epidemiology and genome evolution. *Proceedings of the National Academy of Sciences of the United States of America* 101, 2542-2547 (2004).

180. Zhang, Y., Zheng, N., Hao, P. & Zhong, Y. Reconstruction of the most recent common ancestor sequences of SARS-Cov S gene and detection of adaptive evolution in the spike protein. *Chinese Science Bulletin* 49, 1311-1313 (2004).
181. Beniac, D.R., Andonov, A., Grudeski, E. & Booth, T.F. Architecture of the SARS coronavirus prefusion spike. *Nature Structural & Molecular Biology* 13, 751-752 (2006).
182. He, Y.X. et al. Cross-neutralization of human and palm civet severe acute respiratory syndrome coronaviruses by antibodies targeting the receptor-binding domain of spike protein. *Journal of Immunology* 176, 6085-6092 (2006).
183. Hon, C.C. et al. 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. *Journal of Virology* 82, 1819-1826 (2008).
184. Oostra, M., de Haan, C.A.M. & Rottier, P.J.M. The 29-nucleotide deletion present in human but not in animal severe acute respiratory syndrome coronaviruses disrupts the functional expression of open reading frame 8. *Journal of Virology* 81, 13876-13888 (2007).
185. Sui, J.H. et al. Broadening of Neutralization Activity to Directly Block a Dominant Antibody-Driven SARS-Coronavirus Evolution Pathway. *Plos Pathogens* 4 (2008).
186. Tang, X.C. et al. Prevalence and genetic diversity of coronaviruses in bats from China. *Journal of Virology* 80, 7481-7490 (2006).
187. Yu, M. et al. Determination and application of immunodominant regions of SARS coronavirus spike and nucleocapsid proteins recognized by sera from different animal species. *Journal of Immunological Methods* 331, 1-12 (2008).
188. Zhu, Z.Y. et al. Potent cross-reactive neutralization of SARS coronavirus isolates by human monoclonal antibodies. *Proceedings of the National Academy of Sciences of the United States of America* 104, 12123-12128 (2007).
189. Chang, S.F., Sgro, J.Y. & Parrish, C.R. MULTIPLE AMINO-ACIDS IN THE CAPSID STRUCTURE OF CANINE PARVOVIRUS COORDINATELY DETERMINE THE CANINE HOST RANGE AND SPECIFIC ANTIGENIC AND HEMAGGLUTINATION PROPERTIES. *Journal of Virology* 66, 6858-6867 (1992).
190. Courtenay, O., Quinnell, R.J. & Chalmers, W.S.K. Contact rates between wild and domestic canids: no evidence of parvovirus or canine distemper virus in crab-eating foxes. *Veterinary Microbiology* 81, 9-19 (2001).
191. Decaro, N. et al. Genetic analysis of feline panleukopenia viruses from cats with gastroenteritis. *Journal of General Virology* 89, 2290-2298 (2008).
192. Hoelzer, K., Shackelton, L.A., Holmes, E.C. & Parrish, C.R. Within-Host Genetic Diversity of Endemic and Emerging Parvoviruses of Dogs and Cats. *Journal of Virology* 82, 11096-11105 (2008).
193. Hoelzer, K., Shackelton, L.A., Parrish, C.R. & Holmes, E.C. Phylogenetic analysis reveals the emergence, evolution and dispersal of carnivore parvoviruses. *Journal of General Virology* 89, 2280-2289 (2008).
194. Horiuchi, M. et al. Differences in the evolutionary pattern of feline panleukopenia virus and canine parvovirus. *Virology* 249, 440-452 (1998).
195. Hueffer, K. et al. The natural host range shift and subsequent evolution of canine parvovirus resulted from virus-specific binding to the canine transferrin receptor. *Journal of Virology* 77, 1718-1726 (2003).
196. LlimasSaiz, A.L. et al. Structural analysis of a mutation in canine parvovirus which controls antigenicity and host range. *Virology* 225, 65-71 (1996).
197. Mochizuki, M. et al. Isolation of canine parvovirus from a cat manifesting clinical signs of feline panleukopenia. *Journal of Clinical Microbiology* 34, 2101-2105 (1996).
198. Ohshima, T. & Mochizuki, M. Evidence for Recombination Between Feline Panleukopenia Virus and Canine Parvovirus Type 2. *Journal of Veterinary Medical Science* 71, 403-408 (2009).

199. Parker, J.S.L. & Parrish, C.R. Cellular uptake and infection by canine parvovirus involves rapid dynamin-regulated clathrin-mediated endocytosis, followed by slower intracellular trafficking. *Journal of Virology* 74, 1919-1930 (2000).
200. Shackelton, L.A., Parrish, C.R., Truyen, U. & Holmes, E.C. High rate of viral evolution associated with the emergence of carnivore parvovirus. *Proceedings of the National Academy of Sciences of the United States of America* 102, 379-384 (2005).
201. Steinel, A., Munson, L., van Vuuren, M. & Truyen, U. Genetic characterization of feline parvovirus sequences from various carnivores. *Journal of General Virology* 81, 345-350 (2000).
202. Steinel, A., Venter, E.H., Van Vuuren, M., Parrish, C.R. & Truyen, U. Antigenic and genetic analysis of canine parvoviruses in southern Africa. *Onderstepoort Journal of Veterinary Research* 65, 239-242 (1998).
203. Truyen, U., Agbandje, M. & Parrish, C.R. CHARACTERIZATION OF THE FELINE HOST-RANGE AND A SPECIFIC EPITOPE OF FELINE PANLEUKOPENIA VIRUS. *Virology* 200, 494-503 (1994).
204. Truyen, U., Evermann, J.F., Vieler, E. & Parrish, C.R. Evolution of canine parvovirus involved loss and gain of feline host range. *Virology* 215, 186-189 (1996).
205. Truyen, U., Muller, T., Heidrich, R., Tackmann, K. & Carmichael, L.E. Survey on viral pathogens in wild red foxes (*Vulpes vulpes*) in Germany with emphasis on parvoviruses and analysis of a DNA sequence from a red fox parvovirus. *Epidemiology and Infection* 121, 433-440 (1998).
206. Bronson, E., Emmons, L.H., Murray, S., Dubovi, E.J. & Deem, S.L. Serosurvey of pathogens in domestic dogs on the border of Noel Kempff Mercado National Park, Bolivia. *Journal of Zoo and Wildlife Medicine* 39, 28-36 (2008).
207. Fiorello, C.V., Deem, S.L., Gompper, M.E. & Dubovi, E.J. Seroprevalence of pathogens in domestic carnivores on the border of Madidi National Park, Bolivia. *Animal Conservation* 7, 45-54 (2004).
208. Franklin, S.P. et al. Ocelots on Barro Colorado Island are infected with feline immunodeficiency virus but not other common feline and canine viruses. *Journal of Wildlife Diseases* 44, 760-765 (2008).
209. Gaydos, J.K., Conrad, P.A., Gilardi, K.V.K., Blundell, G.M. & Ben-David, M. Does human proximity affect antibody prevalence in marine-foraging river otters (*Lontra canadensis*)? *Journal of Wildlife Diseases* 43, 116-123 (2007).
210. Junge, R.E., Bauman, K., King, M. & Gompper, M.E. A serologic assessment of exposure to viral pathogens and *Leptospira* in an urban raccoon (*Procyon lotor*) population inhabiting a large zoological park. *Journal of Zoo and Wildlife Medicine* 38, 18-26 (2007).
211. McFadden, K.W., Wade, S.E., Dubovi, E.J. & Gompper, M.E. A serological and fecal parasitologic survey of the critically endangered pygmy raccoon (*Procyon pygmaeus*). *Journal of Wildlife Diseases* 41, 615-617 (2005).
212. Millan, J. et al. Disease threats to the endangered Iberian lynx (*Lynx pardinus*). *Veterinary Journal* 182, 114-124 (2009).
213. Mochizuki, M. Growth characteristics of canine pathogenic viruses in MDCK cells cultured in RPMI 1640 medium without animal protein. *Vaccine* 24, 1744-1748 (2006).
214. Anishchenko, M. et al. Venezuelan encephalitis emergence mediated by a phylogenetically predicted viral mutation. *Proceedings of the National Academy of Sciences of the United States of America* 103, 4994-4999 (2006).
215. Bernard, K.A., Klimstra, W.B. & Johnston, R.E. Mutations in the E2 glycoprotein of Venezuelan equine encephalitis virus confer heparan sulfate interaction, low morbidity, and rapid clearance from blood of mice. *Virology* 276, 93-103 (2000).
216. Brault, A.C., Powers, A.M., Holmes, E.C., Woelk, C.H. & Weaver, S.C. Positively charged amino acid substitutions in the E2 envelope glycoprotein are associated with the emergence of Venezuelan equine encephalitis virus. *Journal of Virology* 76, 1718-1730 (2002).

217. Brault, A.C. et al. Venezuelan equine encephalitis emergence: Enhanced vector infection from a single amino acid substitution in the envelope glycoprotein. *Proceedings of the National Academy of Sciences of the United States of America* 101, 11344-11349 (2004).
218. Carrara, A.S. et al. Venezuelan equine encephalitis virus infection of spiny rats. *Emerging Infectious Diseases* 11, 663-669 (2005).
219. Coffey, L.L. et al. Arbovirus evolution in vivo is constrained by host alternation. *Proceedings of the National Academy of Sciences of the United States of America* 105, 6970-6975 (2008).
220. Greene, I.P. et al. Envelope glycoprotein mutations mediate equine amplification and virulence of epizootic Venezuelan equine encephalitis virus. *Journal of Virology* 79, 9128-9133 (2005).
221. Michel, G., Petrakova, O., Atasheva, S. & Frolov, I. Adaptation of Venezuelan equine encephalitis virus lacking 51-nt conserved sequence element to replication in mammalian and mosquito cells. *Virology* 362, 475-487 (2007).
222. Oberste, M.S., Parker, M.D. & Smith, J.F. Complete sequence of venezuelan equine encephalitis virus subtype IE reveals conserved and hypervariable domains within the C terminus of nsP3. *Virology* 219, 314-320 (1996).
223. Ortiz, D.I., Anishchenko, M. & Weaver, S.C. Susceptibility of *Psorophora confinnis* (Diptera : Culicidae) to infection with epizootic (subtype IC) and enzootic (subtype ID) Venezuelan equine encephalitis viruses. *Journal of Medical Entomology* 42, 857-863 (2005).
224. Ortiz, D.I., Kang, W.L. & Weaver, S.C. Susceptibility of *Ae. aegypti* (Diptera: Culicidae) to Infection with Epidemic (Subtype IC) and Enzootic (Subtypes ID, IIIC, IIID) Venezuelan Equine Encephalitis Complex Alphaviruses. *Journal of Medical Entomology* 45, 1117-1125 (2008).
225. Ortiz, D.I. & Weaver, S.C. Susceptibility of *Ochlerotatus taeniorhynchus* (Diptera : Culicidae) to infection with epizootic (subtype IC) and enzootic (subtype ID) Venezuelan equine encephalitis viruses: Evidence for epizootic strain adaptation. *Journal of Medical Entomology* 41, 987-993 (2004).
226. Paessler, S. et al. Recombinant Sindbis/Venezuelan equine encephalitis virus is highly attenuated and immunogenic. *Journal of Virology* 77, 9278-9286 (2003).
227. Smith, D.R., Arrigo, N.C., Leal, G., Muehlberger, L.E. & Weaver, S.C. Infection and dissemination of Venezuelan equine encephalitis virus in the epidemic mosquito vector, *Aedes taeniorhynchus*. *American Journal of Tropical Medicine and Hygiene* 77, 176-187 (2007).
228. Volkova, E. et al. IRES-dependent replication of Venezuelan equine encephalitis virus makes it highly attenuated and incapable of replicating in mosquito cells. *Virology* 377, 160-169 (2008).