



# BIBLIOGRAPHY

## BIBLIOGRAPHY

- Ahn, I. and Son, H.S., 2010. Comparative study of the nucleotide bias between the novel H1N1 and H5N1 subtypes of influenza A viruses using bioinformatics techniques. *J Microbiol Biotechnol* 20, 63-70.
- Akashi, H., 1994. Synonymous codon usage in *Drosophila melanogaster*: natural selection and translational accuracy. *Genetics* 136, 927-35.
- Akashi, H. and Eyre-Walker, A., 1998. Translational selection and molecular evolution. *Curr Opin Genet Dev* 8, 688-693.
- Akashi, H., Kliman, R.M. and Eyre-Walker, A., 1998. Mutation pressure, natural selection, and the evolution of base composition in *Drosophila*. *Genetica* 102-103, 49-60.
- Andersson, S. and Kurland, C., 1990. Codon preferences in free-living microorganisms. *Microbiological reviews* 54, 198-210.
- Aota, S.-i. and Ikemura, T., 1986. Diversity in G+ C content at the third position of codons in vertebrate genes and its cause. *Nucleic Acids Res* 14, 6345-6355.
- Behura, S.K. and Severson, D.W., 2013. Codon usage bias: causative factors, quantification methods and genome-wide patterns: with emphasis on insect genomes. *Biol Rev Camb Philos Soc* 88, 49-61.
- Belalov, I.S. and Lukashev, A.N., 2013. Causes and implications of codon usage bias in RNA viruses. *PLoS One* 8, e56642.

- Bernardi, G. and Bernardi, G., 1986. Compositional constraints and genome evolution. *J Mol Evol* 24, 1-11.
- Bodilis, J. and Baray, S., 2006. Molecular evolution of the major outer-membrane protein gene (*oprF*) of *Pseudomonas*. *Microbiology* 152, 1075-88.
- Boycheva, S., Chkodrov, G. and Ivanov, I., 2003. Codon pairs in the genome of *Escherichia coli*. *Bioinformatics* 19, 987-98.
- Bulmer, M., 1987. Coevolution of codon usage and transfer RNA abundance. *Nature* 325, 728-30.
- Butt, A.M., Nasrullah, I., Qamar, R. and Tong, Y., 2016. Evolution of codon usage in Zika virus genomes is host and vector specific. *Emerg Microbes Infect* 5, e107.
- Butt, A.M., Nasrullah, I. and Tong, Y., 2014. Genome-wide analysis of codon usage and influencing factors in chikungunya viruses. *PLoS One* 9, e90905.
- Carbone, A., Zinovyev, A. and Kepes, F., 2003. Codon adaptation index as a measure of dominating codon bias. *Bioinformatics* 19, 2005-15.
- Chen, H., Sun, S., Norenburg, J.L. and Sundberg, P., 2014. Mutation and selection cause codon usage and bias in mitochondrial genomes of ribbon worms (*Nemertea*). *PLoS One* 9, e85631.
- Chen, Q., Wang, H., Zhao, L., Ma, L., Wang, R., Lei, Y., Li, Y., Yang, G., Chen, J., Chen, G., Li, L., Jin, T., Li, J., Liu, X., Xu, X., Wong, G., Liu, L., Liu, Y., Shi, W., Bi, Y. and Gao, G.F., 2016. First documented case of avian influenza (H5N1) virus infection in a lion. *Emerg Microbes Infect* 5, e125.

Chen, Y., 2013. A comparison of synonymous codon usage bias patterns in DNA and RNA virus genomes: quantifying the relative importance of mutational pressure and natural selection. *Biomed Res Int* 2013, 406342.

Cheng, X., Virk, N., Chen, W., Ji, S., Sun, Y. and Wu, X., 2013. CpG usage in RNA viruses: data and hypotheses. *PLoS ONE* 8, e74109.

Chevallier, A. and Garel, J.-P., 1979. Studies on tRNA adaptation, tRNA turnover, precursor tRNA and tRNA gene distribution in *Bombyx mori* by using two-dimensional polyacrylamide gel electrophoresis. *Biochimie* 61, 245-262.

Chiapello, H., Lisacek, F., Caboche, M. and Henaut, A., 1998. Codon usage and gene function are related in sequences of *Arabidopsis thaliana*. *Gene* 209, GC1-GC38.

Chiusano, M.L., D'Onofrio, G., Alvarez-Valin, F., Jabbari, K., Colonna, G. and Bernardi, G., 1999. Correlations of nucleotide substitution rates and base composition of mammalian coding sequences with protein structure. *Gene* 238, 23-31.

Clarke, B., 1970. Darwinian evolution of proteins. *Science* 168, 1009-11.

Coleman, J.R., Papamichail, D., Skiena, S., Futcher, B., Wimmer, E. and Mueller, S., 2008a. Virus attenuation by genome-scale changes in codon pair bias. *Science* 320, 1784-7.

Coleman, J.R., Papamichail, D., Skiena, S., Futcher, B., Wimmer, E. and Mueller, S., 2008b. Virus attenuation by genome-scale changes in codon pair bias. *Science* 320, 1784-1787.

Comeron, J.M. and Aguade, M., 1998. An evaluation of measures of synonymous codon usage bias. *J Mol Evol* 47, 268-74.

Compans, R.W., Klenk, H.-D., Caliguri, L.A. and Choppin, P.W., 1970. Influenza virus proteins: I. Analysis of polypeptides of the virion and identification of spike glycoproteins. *Virology* 42, 880-889.

Cortez, D.Q., Lazcano, A. and Becerra, A., 2005. Comparative analysis of methodologies for the detection of horizontally transferred genes: a reassessment of first-order Markov models. *In Silico Biol* 5, 581-92.

Cox, N.J. and Subbarao, K., 2000. Global epidemiology of influenza: past and present. *Annu Rev Med* 51, 407-21.

Cristina, J., Fajardo, A., Sonora, M., Moratorio, G. and Musto, H., 2016. A detailed comparative analysis of codon usage bias in Zika virus. *Virus Res* 223, 147-52.

D'Onofrio, G., Ghosh, T.C. and Bernardi, G., 2002. The base composition of the genes is correlated with the secondary structures of the encoded proteins. *Gene* 300, 179-87.

Daidone, V., Gallinaro, L., Cattini, M.G., Pontara, E., Bertomoro, A., Pagnan, A. and Casonato, A., 2011. An apparently silent nucleotide substitution (c. 7056C>T) in the von Willebrand factor gene is responsible for type 1 von Willebrand disease. *haematologica* 96, 881-887.

Dawood, F.S., Iuliano, A.D., Reed, C., Meltzer, M.I., Shay, D.K., Cheng, P.-Y., Bandaranayake, D., Breiman, R.F., Brooks, W.A. and Buchy, P., 2012.

Estimated global mortality associated with the first 12 months of 2009 pandemic influenza A H1N1 virus circulation: a modelling study. The Lancet infectious diseases 12, 687-695.

Dawood, F.S., Jain, S., Finelli, L., Shaw, M.W., Lindstrom, S., Garten, R.J., Gubareva, L.V., Xu, X., Bridges, C.B. and Uyeki, T.M., 2009. Emergence of a novel swine-origin influenza A (H1N1) virus in humans. N Engl J Med 360, 2605-15.

De Amicis, F. and Marchetti, S., 2000. Intercodon dinucleotides affect codon choice in plant genes. Nucleic Acids Res 28, 3339-45.

Drake, J.W. and Holland, J.J., 1999. Mutation rates among RNA viruses. Proceedings of the National Academy of Sciences 96, 13910-13913.

Drummond, D.A. and Wilke, C.O., 2008. Mistranslation-induced protein misfolding as a dominant constraint on coding-sequence evolution. Cell 134, 341-352.

Duret, L., 2002. Evolution of synonymous codon usage in metazoans. Curr Opin Genet Dev 12, 640-9.

Duret, L. and Mouchiroud, D., 1999. Expression pattern and, surprisingly, gene length shape codon usage in *Caenorhabditis*, *Drosophila*, and *Arabidopsis*. Proceedings of the National Academy of Sciences 96, 4482-4487.

Ehrhardt, C., Seyer, R., Hrincius, E.R., Eierhoff, T., Wolff, T. and Ludwig, S., 2010. Interplay between influenza A virus and the innate immune signaling. Microbes Infect 12, 81-7.

Epstein, R.J., Lin, K. and Tan, T.W., 2000. A functional significance for codon third bases. *Gene* 245, 291-8.

Faa, V., Coiana, A., Incani, F., Costantino, L., Cao, A. and Rosatelli, M.C., 2010. A synonymous mutation in the CFTR gene causes aberrant splicing in an italian patient affected by a mild form of cystic fibrosis. *The Journal of Molecular Diagnostics* 12, 380-383.

Ferguson, N.M., Galvani, A.P. and Bush, R.M., 2003. Ecological and immunological determinants of influenza evolution. *Nature* 422, 428-33.

Filipski, J., 1987. Correlation between molecular clock ticking, codon usage, fidelity of DNA repair, chromosome banding and chromatin compactness in germline cells. *FEBS letters* 217, 184-186.

Finkelman, B.S., Viboud, C., Koelle, K., Ferrari, M.J., Bharti, N. and Grenfell, B.T., 2007. Global patterns in seasonal activity of influenza A/H3N2, A/H1N1, and B from 1997 to 2005: viral coexistence and latitudinal gradients. *PLoS One* 2, e1296.

Fletcher, S.P., Muto, M. and Mayfield, S.P., 2007. Optimization of recombinant protein expression in the chloroplasts of green algae. *Adv Exp Med Biol* 616, 90-8.

Francino, M.P. and Ochman, H., 1999. Isochores result from mutation not selection. *Nature* 400, 30-31.

Freire-Picos, M.A., Gonzalez-Siso, M.I., Rodríguez-Belmonte, E., Rodríguez-Torres, A.M., Ramil, E. and Cerdan, M.E., 1994. Codon usage in *Kluyveromyces lactis* and in yeast cytochrome c-encoding genes. *Gene* 139, 43-49.

Fu, M., 2010. Codon usage bias in herpesvirus. *Arch Virol* 155, 391-6.

Garel, J.-P., 1982. The silkworm, a model for molecular and cellular biologists. *Trends Biochem Sci* 7, 105-108.

Garten, R.J., Davis, C.T., Russell, C.A., Shu, B., Lindstrom, S., Balish, A., Sessions, W.M., Xu, X., Skepner, E., Deyde, V., Okomo-Adhiambo, M., Gubareva, L., Barnes, J., Smith, C.B., Emery, S.L., Hillman, M.J., Rivailleur, P., Smagala, J., de Graaf, M., Burke, D.F., Fouchier, R.A., Pappas, C., Alpuche-Aranda, C.M., Lopez-Gatell, H., Olivera, H., Lopez, I., Myers, C.A., Faix, D., Blair, P.J., Yu, C., Keene, K.M., Dotson, P.D., Jr., Boxrud, D., Sambol, A.R., Abid, S.H., St George, K., Bannerman, T., Moore, A.L., Stringer, D.J., Blevins, P., Demmler-Harrison, G.J., Ginsberg, M., Kriner, P., Waterman, S., Smole, S., Guevara, H.F., Belongia, E.A., Clark, P.A., Beatrice, S.T., Donis, R., Katz, J., Finelli, L., Bridges, C.B., Shaw, M., Jernigan, D.B., Uyeki, T.M., Smith, D.J., Klimov, A.I. and Cox, N.J., 2009. Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. *Science* 325, 197-201.

Gaydos, J.C., Top Jr, F.H., Hodder, R.A. and Russell, P.K., 2006. Swine influenza a outbreak, Fort Dix, New Jersey, 1976. DTIC Document.

Gething, M.J., Bye, J., Skehel, J. and Waterfield, M., 1980. Cloning and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3

strains elucidates antigenic shift and drift in human influenza virus. *Nature* 287, 301-6.

Goni, N., Iriarte, A., Comas, V., Sonora, M., Moreno, P., Moratorio, G., Musto, H. and Cristina, J., 2012. Pandemic influenza A virus codon usage revisited: biases, adaptation and implications for vaccine strain development. *Virol J* 9, 263.

Gouy, M. and Gautier, C., 1982. Codon usage in bacteria: correlation with gene expressivity. *Nucleic Acids Res* 10, 7055-74.

Grantham, R., Gautier, C. and Gouy, M., 1980a. Codon frequencies in 119 individual genes confirm consistent choices of degenerate bases according to genome type. *Nucleic Acids Res* 8, 1893-912.

Grantham, R., Gautier, C., Gouy, M., Mercier, R. and Pave, A., 1980b. Codon catalog usage and the genome hypothesis. *Nucleic Acids Res* 8, r49-r62.

Greenacre, M. and Hastie, T., 1987. The geometric interpretation of correspondence analysis. *Journal of the American statistical association* 82, 437-447.

Greenbaum, B.D., Levine, A.J., Bhanot, G. and Rabadan, R., 2008. Patterns of evolution and host gene mimicry in influenza and other RNA viruses. *PLoS Pathog* 4, e1000079.

Gribskov, M., Devereux, J. and Burgess, R.R., 1984. The codon preference plot: graphic analysis of protein coding sequences and prediction of gene expression. *Nucleic Acids Res* 12, 539-49.

Grosjean, H. and Fiers, W., 1982. Preferential codon usage in prokaryotic genes: the optimal codon-anticodon interaction energy and the selective codon usage in efficiently expressed genes. *Gene* 18, 199-209.

Gu, W., Zhou, T., Ma, J., Sun, X. and Lu, Z., 2004a. Analysis of synonymous codon usage in SARS Coronavirus and other viruses in the Nidovirales. *Virus Res* 101, 155-161.

Gu, W., Zhou, T., Ma, J., Sun, X. and Lu, Z., 2004b. The relationship between synonymous codon usage and protein structure in *Escherichia coli* and *Homo sapiens*. *Biosystems* 73, 89-97.

Guan, Y., Shortridge, K., Krauss, S., Chin, P., Dyrting, K., Ellis, T., Webster, R. and Peiris, M., 2000. H9N2 influenza viruses possessing H5N1-like internal genomes continue to circulate in poultry in southeastern China. *J Virol* 74, 9372-9380.

Guo, Y., Xu, X. and Cox, N.J., 1992. Human influenza A (H1N2) viruses isolated from China. *Journal of general virology* 73, 383-387.

Gupta, S.K., Majumdar, S., Bhattacharya, T.K. and Ghosh, T.C., 2000. Studies on the relationships between the synonymous codon usage and protein secondary structural units. *Biochem Biophys Res Commun* 269, 692-6.

Haas, J., Park, E.-C. and Seed, B., 1996. Codon usage limitation in the expression of HIV-1 envelope glycoprotein. *Current Biology* 6, 315-324.

Han, J.S., Szak, S.T. and Boeke, J.D., 2004. Transcriptional disruption by the L1 retrotransposon and implications for mammalian transcriptomes. *Nature* 429, 268-74.

Hartl, D.L., Moriyama, E.N. and Sawyer, S.A., 1994. Selection intensity for codon bias. *Genetics* 138, 227-34.

Hilleman, M.R., 2002. Realities and enigmas of human viral influenza: pathogenesis, epidemiology and control. *Vaccine* 20, 3068-87.

Ikemura, T., 1981. Correlation between the abundance of *Escherichia coli* transfer RNAs and the occurrence of the respective codons in its protein genes. *J Mol Biol* 146, 1-21.

Ikemura, T., 1982. Correlation between the abundance of yeast transfer RNAs and the occurrence of the respective codons in protein genes. Differences in synonymous codon choice patterns of yeast and *Escherichia coli* with reference to the abundance of isoaccepting transfer RNAs. *J Mol Biol* 158, 573-97.

Ikemura, T., 1985. Codon usage and tRNA content in unicellular and multicellular organisms. *Mol Biol Evol* 2, 13-34.

Jenkins, G.M. and Holmes, E.C., 2003. The extent of codon usage bias in human RNA viruses and its evolutionary origin. *Virus Res* 92, 1-7.

Jenkins, G.M., Pagel, M., Gould, E.A., Paolo, M.d.A. and Holmes, E.C., 2001. Evolution of base composition and codon usage bias in the genus Flavivirus. *J Mol Evol* 52, 383-390.

Jiang, Y., Yu, K., Zhang, H., Zhang, P., Li, C., Tian, G., Li, Y., Wang, X., Ge, J. and Bu, Z., 2007. Enhanced protective efficacy of H5 subtype avian influenza DNA vaccine with codon optimized HA gene in a pCAGGS plasmid vector. *Antiviral research* 75, 234-241.

Kamps, B.S., Hoffmann, C. and Preiser, W., 2006. Influenza report 2006.

Karlin, S. and Burge, C., 1995. Dinucleotide relative abundance extremes: a genomic signature. *Trends Genet* 11, 283-90.

Karlin, S., Doerfler, W. and Cardon, L.R., 1994. Why is CpG suppressed in the genomes of virtually all small eukaryotic viruses but not in those of large eukaryotic viruses? *J Virol* 68, 2889-97.

Kawaoka, Y., Krauss, S. and Webster, R.G., 1989. Avian-to-human transmission of the PB1 gene of influenza A viruses in the 1957 and 1968 pandemics. *J Virol* 63, 4603-8.

Kimura, M., 1968. Evolutionary rate at the molecular level. *Nature* 217, 624-626.

Knight, R.D., Freeland, S.J. and Landweber, L.F., 2001. A simple model based on mutation and selection explains trends in codon and amino-acid usage and GC composition within and across genomes. *Genome Biol* 2, RESEARCH0010.

Kobasa, D., Takada, A., Shinya, K., Hatta, M., Halfmann, P., Theriault, S., Suzuki, H., Nishimura, H., Mitamura, K., Sugaya, N., Usui, T., Murata, T., Maeda, Y., Watanabe, S., Suresh, M., Suzuki, T., Suzuki, Y., Feldmann, H. and Kawaoka, Y., 2004. Enhanced virulence of influenza A viruses with the haemagglutinin of the 1918 pandemic virus. *Nature* 431, 703-7.

Korteweg, C. and Gu, J., 2008. Pathology, molecular biology, and pathogenesis of avian influenza A (H5N1) infection in humans. *Am J Pathol* 172, 1155-70.

Kudla, G., Lipinski, L., Caffin, F., Helwak, A. and Zylicz, M., 2006. High guanine and cytosine content increases mRNA levels in mammalian cells. *PLoS Biol* 4, e180.

Kudla, G., Murray, A.W., Tollervey, D. and Plotkin, J.B., 2009. Coding-sequence determinants of gene expression in *Escherichia coli*. *Science* 324, 255-258.

Kurland, C. and Ehrenberg, M., 1984. Optimization of translation accuracy. *Progress in nucleic acid research and molecular biology* 31, 191-219.

Lavner, Y. and Kotlar, D., 2005. Codon bias as a factor in regulating expression via translation rate in the human genome. *Gene* 345, 127-38.

Levin, D.B. and Whittome, B., 2000. Codon usage in nucleopolyhedroviruses. *Journal of general virology* 81, 2313-2325.

Li, Z.P., Ying, D.Q., Li, P., Li, F., Bo, X.C. and Wang, S.Q., 2010. Analysis of synonymous codon usage bias in 09H1N1. *Virol Sin* 25, 329-40.

Lindstrom, S.E., Cox, N.J. and Klimov, A., 2004. Genetic analysis of human H2N2 and early H3N2 influenza viruses, 1957-1972: evidence for genetic divergence and multiple reassortment events. *Virology* 328, 101-19.

Lithwick, G. and Margalit, H., 2005. Relative predicted protein levels of functionally associated proteins are conserved across organisms. *Nucleic Acids Res* 33, 1051-1057.

Lobry, J.R. and Gautier, C., 1994. Hydrophobicity, expressivity and aromaticity are the major trends of amino-acid usage in 999 *Escherichia coli* chromosome-encoded genes. Nucleic Acids Res 22, 3174-80.

Ma, J., Zhou, T., Gu, W., Sun, X. and Lu, Z., 2002. Cluster analysis of the codon use frequency of MHC genes from different species. Biosystems 65, 199-207.

Machado, H.E., Lawrie, D.S. and Petrov, D.A., 2017. Strong purifying selection on codon usage bias. bioRxiv, 106476.

Makarova, N.V., Kaverin, N.V., Krauss, S., Senne, D. and Webster, R.G., 1999. Transmission of Eurasian avian H2 influenza virus to shorebirds in North America. J Gen Virol 80 ( Pt 12), 3167-71.

McArthur, G.H.t. and Fong, S.S., 2010. Toward engineering synthetic microbial metabolism. J Biomed Biotechnol 2010, 459760.

Moriyama, E.N. and Powell, J.R., 1998. Gene length and codon usage bias in *Drosophila melanogaster*, *Saccharomyces cerevisiae* and *Escherichia coli*. Nucleic Acids Res 26, 3188-93.

Morton, B.R., 1993. Chloroplast DNA codon use: evidence for selection at the psb A locus based on tRNA availability. J Mol Evol 37, 273-280.

Moura, G., Pinheiro, M., Arrais, J., Gomes, A.C., Carreto, L., Freitas, A., Oliveira, J.L. and Santos, M.A., 2007. Large scale comparative codon-pair context analysis unveils general rules that fine-tune evolution of mRNA primary structure. PLoS One 2, e847.

- Moura, G., Pinheiro, M., Silva, R., Miranda, I., Afreixo, V., Dias, G., Freitas, A., Oliveira, J.L. and Santos, M.A., 2005. Comparative context analysis of codon pairs on an ORFeome scale. *Genome Biol* 6, R28.
- Mueller, S., Papamichail, D., Coleman, J.R., Skiena, S. and Wimmer, E., 2006. Reduction of the rate of poliovirus protein synthesis through large-scale codon deoptimization causes attenuation of viral virulence by lowering specific infectivity. *J Virol* 80, 9687-96.
- Nackley, A.G., Shabalina, S.A., Tchivileva, I.E., Satterfield, K., Korchynskyi, O., Makarov, S.S., Maixner, W. and Diatchenko, L., 2006. Human catechol-O-methyltransferase haplotypes modulate protein expression by altering mRNA secondary structure. *Science* 314, 1930-3.
- Nelson, M.I. and Holmes, E.C., 2007. The evolution of epidemic influenza. *Nature Reviews Genetics* 8, 196-205.
- Neumann, G., Shinya, K. and Kawaoka, Y., 2007. Molecular pathogenesis of H5N1 influenza virus infections. *Antivir Ther* 12, 617-26.
- Novembre, J.A., 2002. Accounting for background nucleotide composition when measuring codon usage bias. *Mol Biol Evol* 19, 1390-4.
- Ogle, J.M. and Ramakrishnan, V., 2005. Structural insights into translational fidelity. *Annu Rev Biochem* 74, 129-77.
- Osawa, S., Ohama, T., Yamao, F., Muto, A., Jukes, T.H., Ozeki, H. and Umesono, K., 1988. Directional mutation pressure and transfer RNA in choice of the third

- nucleotide of synonymous two-codon sets. Proc Natl Acad Sci U S A 85, 1124-8.
- Palese, P., 2004. Influenza: old and new threats. Nature medicine 10, S82-S87.
- Palese, P. and Shaw, M., 2007. Orthomyxoviridae: the viruses and their replication In: Knipe DM, Howley PM, eds. Fields' Virology [monograph on the internet]. Philadelphia: Lippincott, Williams, & Wilkins.
- Parker, J., Johnston, T.C., Borgia, P.T., Holtz, G., Remaut, E. and Fiers, W., 1983. Codon usage and mistranslation. *In vivo* basal level misreading of the MS2 coat protein message. J Biol Chem 258, 10007-12.
- Parker, J., Precup, J. and Fu, C., 1992. Misreading of the argI message in *Escherichia coli*. FEMS Microbiol Lett 100, 141-5.
- Pavesi, A., Magiorkinis, G. and Karlin, D.G., 2013. Viral proteins originated de novo by overprinting can be identified by codon usage: application to the “gene nursery” of Deltaretroviruses. PLoS Comput Biol 9, e1003162.
- Plotkin, J.B. and Kudla, G., 2011. Synonymous but not the same: the causes and consequences of codon bias. Nat Rev Genet 12, 32-42.
- Rabadan, R., Levine, A.J. and Robins, H., 2006. Comparison of avian and human influenza A viruses reveals a mutational bias on the viral genomes. J Virol 80, 11887-91.
- Rima, B.K. and McFerran, N.V., 1997. Dinucleotide and stop codon frequencies in single-stranded RNA viruses. Journal of general virology 78, 2859-2870.

Rocha, E.P., 2004. Codon usage bias from tRNA's point of view: redundancy, specialization, and efficient decoding for translation optimization. *Genome Res* 14, 2279-86.

Romero, H., Zavala, A. and Musto, H., 2000. Codon usage in *Chlamydia trachomatis* is the result of strand-specific mutational biases and a complex pattern of selective forces. *Nucleic Acids Res* 28, 2084-90.

Roth, A., Anisimova, M. and Cannarozzi, G.M., 2012. Measuring codon usage bias. Codon evolution: mechanisms and models. New York: Oxford University Press Inc, 189-217.

Ruiz, L.M., Armengol, G., Habeych, E. and Orduz, S., 2006. A theoretical analysis of codon adaptation index of the *Boophilus microplus* bm86 gene directed to the optimization of a DNA vaccine. *J Theor Biol* 239, 445-449.

Sauna, Z.E. and Kimchi-Sarfaty, C., 2011. Understanding the contribution of synonymous mutations to human disease. *Nature Reviews Genetics* 12, 683-691.

Schulze, I.T., 1970. The structure of influenza virus: I. The polypeptides of the virion. *Virology* 42, 890-904.

Shackelton, L.A., Parrish, C.R. and Holmes, E.C., 2006. Evolutionary basis of codon usage and nucleotide composition bias in vertebrate DNA viruses. *J Mol Evol* 62, 551-63.

Sharp, P.M., Emery, L.R. and Zeng, K., 2010. Forces that influence the evolution of codon bias. *Philos Trans R Soc Lond B Biol Sci* 365, 1203-12.

Sharp, P.M. and Li, W.H., 1986. Codon usage in regulatory genes in *Escherichia coli* does not reflect selection for 'rare' codons. Nucleic Acids Res 14, 7737-49.

Sharp, P.M. and Li, W.H., 1987. The codon Adaptation Index--a measure of directional synonymous codon usage bias, and its potential applications. Nucleic Acids Res 15, 1281-95.

Sharp, P.M. and Matassi, G., 1994. Codon usage and genome evolution. Curr Opin Genet Dev 4, 851-60.

Sharp, P.M., Stenico, M., Peden, J.F. and Lloyd, A.T., 1993. Codon usage: mutational bias, translational selection, or both? Biochem Soc Trans 21, 835-41.

Shields, D.C., Sharp, P.M., Higgins, D.G. and Wright, F., 1988. " Silent" sites in *Drosophila* genes are not neutral: evidence of selection among synonymous codons. Mol Biol Evol 5, 704-716.

Skehel, J.J. and Schild, G., 1971. The polypeptide composition of influenza A viruses. Virology 44, 396-408.

Skeik, N. and Jabr, F.I., 2008. Influenza viruses and the evolution of avian influenza virus H5N1. Int J Infect Dis 12, 233-8.

Sørensen, M.A. and Pedersen, S., 1991. Absolute in vivo translation rates of individual codons in *Escherichia coli*: The two glutamic acid codons GAA and GAG are translated with a threefold difference in rate. J Mol Biol 222, 265-280.

Stoletzki, N. and Eyre-Walker, A., 2007. Synonymous codon usage in *Escherichia coli*: selection for translational accuracy. Mol Biol Evol 24, 374-381.

- Sueoka, N., 1988. Directional mutation pressure and neutral molecular evolution. Proc Natl Acad Sci U S A 85, 2653-7.
- Sueoka, N., 1995. Intrastrand parity rules of DNA base composition and usage biases of synonymous codons. J Mol Evol 40, 318-25.
- Sueoka, N., 2002. Wide intra-genomic G+C heterogeneity in human and chicken is mainly due to strand-symmetric directional mutation pressures: dGTP-oxidation and symmetric cytosine-deamination hypotheses. Gene 300, 141-54.
- Sun, L., Petrounia, I.P., Yagasaki, M., Bandara, G. and Arnold, F.H., 2001. Expression and stabilization of galactose oxidase in *Escherichia coli* by directed evolution. Protein engineering 14, 699-704.
- Supek, F. and Vlahovicek, K., 2005. Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity. BMC Bioinformatics 6, 182.
- Tao, P., Dai, L., Luo, M., Tang, F., Tien, P. and Pan, Z., 2009. Analysis of synonymous codon usage in classical swine fever virus. Virus Genes 38, 104-12.
- Tsuchiya, E., Sugawara, K., Hongo, S., Matsuzaki, Y., Muraki, Y., Li, Z.N. and Nakamura, K., 2001. Antigenic structure of the haemagglutinin of human influenza A/H2N2 virus. J Gen Virol 82, 2475-84.
- Tumpey, T.M., Basler, C.F., Aguilar, P.V., Zeng, H., Solorzano, A., Swayne, D.E., Cox, N.J., Katz, J.M., Taubenberger, J.K., Palese, P. and Garcia-Sastre, A.,

2005. Characterization of the reconstructed 1918 Spanish influenza pandemic virus. *Science* 310, 77-80.

Ungchusak, K., Auewarakul, P., Dowell, S.F., Kitphati, R., Auwanit, W., Puthavathana, P., Uiprasertkul, M., Boonnak, K., Pittayawonganon, C., Cox, N.J., Zaki, S.R., Thawatsupha, P., Chittaganpitch, M., Khontong, R., Simmerman, J.M. and Chunsutthiwat, S., 2005. Probable person-to-person transmission of avian influenza A (H5N1). *N Engl J Med* 352, 333-40.

Viboud, C., Simonsen, L., Fuentes, R., Flores, J., Miller, M.A. and Chowell, G., 2016. Global Mortality Impact of the 1957-1959 Influenza Pandemic. *J Infect Dis* 213, 738-45.

Vicario, S., Moriyama, E.N. and Powell, J.R., 2007. Codon usage in twelve species of *Drosophila*. *BMC Evol Biol* 7, 226.

Wan, X.F., Xu, D., Kleinhofs, A. and Zhou, J., 2004. Quantitative relationship between synonymous codon usage bias and GC composition across unicellular genomes. *BMC Evol Biol* 4, 19.

Wang, S.-F., Su, M.-W., Tseng, S.-P., Li, M.-C., Tsao, C.-H., Huang, S.-W., Chu, W.-C., Liu, W.-T., Chen, Y.-M.A. and Huang, J.C., 2014. Analysis of codon usage preference in hemagglutinin genes of the swine-origin influenza A (H1N1) virus. *Journal of Microbiology, Immunology and Infection* 20, 1e10.

Watanabe, Y., Ibrahim, M.S., Suzuki, Y. and Ikuta, K., 2012. The changing nature of avian influenza A virus (H5N1). *Trends in microbiology* 20, 11-20.

Webby, R.J. and Webster, R.G., 2003. Are we ready for pandemic influenza? *Science* 302, 1519-22.

Webster, R.G., Bean, W.J., Gorman, O.T., Chambers, T.M. and Kawaoka, Y., 1992. Evolution and ecology of influenza A viruses. *Microbiol Rev* 56, 152-79.

Webster, R.G., Laver, W.G., Air, G.M. and Schild, G.C., 1982. Molecular mechanisms of variation in influenza viruses. *Nature* 296, 115-21.

Wei, W. and Guo, F.B., 2010. Strong Strand Composition Bias in the Genome of *Ehrlichia canis* Revealed by Multiple Methods. *Open Microbiol J* 4, 98-102.

Wolfe, K.H., Sharp, P.M. and Li, W.-H., 1989. Mutation rates differ among regions of the mammalian genome. *Nature* 337, 283-285.

Wong, E.H., Smith, D.K., Rabadan, R., Peiris, M. and Poon, L.L., 2010. Codon usage bias and the evolution of influenza A viruses. *Codon Usage Biases of Influenza Virus*. *BMC Evol Biol* 10, 253.

Wright, F., 1990. The 'effective number of codons' used in a gene. *Gene* 87, 23-9.

Xia, X., 1996. Maximizing transcription efficiency causes codon usage bias. *Genetics* 144, 1309-20.

Xiang, H., Zhang, R., Butler, R.R., 3rd, Liu, T., Zhang, L., Pombert, J.F. and Zhou, Z., 2015. Comparative Analysis of Codon Usage Bias Patterns in Microsporidian Genomes. *PLoS One* 10, e0129223.

Xu, X., Smith, C.B., Mungall, B.A., Lindstrom, S.E., Hall, H.E., Subbarao, K., Cox, N.J. and Klimov, A., 2002. Intercontinental circulation of human influenza

A(H1N2) reassortant viruses during the 2001-2002 influenza season. J Infect Dis 186, 1490-3.

Yang, X., Luo, X. and Cai, X., 2014. Analysis of codon usage pattern in *Taenia saginata* based on a transcriptome dataset. Parasit Vectors 7, 527.

Zalucki, Y.M., Beacham, I.R. and Jennings, M.P., 2009. Biased codon usage in signal peptides: a role in protein export. Trends in microbiology 17, 146-150.

Zhao, Y., Zheng, H., Xu, A., Yan, D., Jiang, Z., Qi, Q. and Sun, J., 2016. Analysis of codon usage bias of envelope glycoprotein genes in nuclear polyhedrosis virus (NPV) and its relation to evolution. BMC Genomics 17, 677.

Zhong, J., Li, Y., Zhao, S., Liu, S. and Zhang, Z., 2007. Mutation pressure shapes codon usage in the GC-Rich genome of foot-and-mouth disease virus. Virus Genes 35, 767-76.

Zhou, J., Liu, W.J., Peng, S.W., Sun, X.Y. and Frazer, I., 1999. Papillomavirus capsid protein expression level depends on the match between codon usage and tRNA availability. J Virol 73, 4972-4982.

Zhou, T., Gu, W., Ma, J., Sun, X. and Lu, Z., 2005. Analysis of synonymous codon usage in H5N1 virus and other influenza A viruses. Biosystems 81, 77-86.