

Olga K. Kamneva

Postdoctoral Fellow

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Research Interest

Statistical phylogenetics, molecular evolution, adaptation, horizontal processes, microbial evolutionary genomics and ecology

Education

2013 Doctor of Philosophy in Molecular Biology, minor in Statistics

Molecular and Cellular Life Sciences PhD program, University of Wyoming, Laramie, WY, USA

2007 Diploma Degree in Bioinformatics with High Honors

equivalent of combined Bachelors and Master of Science

Department of Natural Sciences, Novosibirsk State University, Novosibirsk, Russia

Research Experience

2013 - present Postdoctoral Fellow

Stanford University, Department of Biology, Stanford, CA

2008 - 2013 PhD student

Department of Molecular Biology, University of Wyoming, Laramie, WY, USA

2011 Summer Intern

J Craig Venter Institute, Rockville, MD, USA

2007 - 2008 Rotation Student

Molecular and Cellular Life Sciences PhD Program, University of Wyoming, Laramie, WY, USA

2006 - 2007 Diploma Student

Theoretical Genetics Group, Institute of Cell Biology and Genetics, Novosibirsk, Russia

2004 - 2005 Research Assistant

Developmental Epigenetics Group, Institute of Cell Biology and Genetics, Novosibirsk, Russia

Selected Honors and Fellowships

2013-2014 Postdoctoral Fellowship

Center for Computational Evolutionary and Human Genomics, Stanford University

2009 Best Graduate Student Poster Award

SMBE satellite meeting on Mechanisms of Protein Evolution, 2013. Denver, USA

2010-2013 Mary Mead Memorial Scholarship for Women in Agriculture

College of Agriculture, University of Wyoming

2010-2012 International Student Scholarship

University of Wyoming

2009 Invited Talk and Student Travel Scholarship

Molecular Biology and Evolution (SMBE) annual meeting. Iowa City, USA

Peer Review

Biology Direct, PLoS ONE, BMC Evolutionary Biology, Trends in Evolutionary Biology, Journal of Bioinformatics and Computational Biology, Journal of Molecular Evolution

Professional Memberships

Postdoc Member of the Society for Molecular Biology and Evolution (SMBE)

Postdoc Member of the American Society for Microbiology (ASM)

Peer-Reviewed Publications

1. **OK Kamneva**, S Poudel, NL Ward (2015). Proteins related to the type I secretion system are associated with secondary SecA_DEAD domain proteins in some species of *Planctomycetes*, *Verrucomicrobia*, *Proteobacteria*, *Nitrospirae* and *Chlorobi*. PLoS ONE. 10(6):e0129066.
2. **OK Kamneva**, NL Ward (2014). Reconciliation approaches to determining HGT, duplications and losses in gene trees. Chapter in “Methods in Microbiology”, 41. 183-199.
3. **OK Kamneva**, DH Haft, SJ Knight, DA Liberles, NL Ward (2013). Genomics and bioinformatics of the PVC superphylum. Chapter in “New Models for Cell Structure, Origins and Biology: Planctomycetes”. 165-193. Springer.
4. **OK Kamneva**, SJ Knight, DA Liberles, NL Ward (2012). Analysis of genome content evolution in PVC super-phylum: assessment of candidate genes associated with cellular compartmentalization and host-dependent life-style in bacteria. Genome Biology and Evolution. 4(12): 375-390.
5. M Sait, **OK Kamneva**, DS Fay, NV Kirienko, J Polek, MM Shirasu-Hiza, NL Ward(2011). Genomic and experimental evidence suggests that *Verrucomicrobium spinosum* interacts with eukaryotes. Frontiers in Microbiology. 2: 211.
6. CT Hensley, **OK Kamneva**, KM Levy, SK Labahn, LA Africa, HJ Wing (2011). Two promoters and two translation start sites control the expression of the *Shigella flexneri* outer membrane protease IcsP. Archives of Microbiology. 193(4): 263-274.
7. **OK Kamneva**, DA Liberles, NL Ward (2010). Genome-wide influence of indel substitutions on evolution of bacteria of the PVC super-phylum, revealed using a novel computational method. Genome Biology and Evolution. 2: 870-886.
8. A Volkov, A Liavonchanka, **OK Kamneva**, T Fiedler, C Goebel, B Kreikemeyer, I Feussner (2010). Myosin cross-reactive antigen of Streptococcus pyogenes M49 encodes a fatty acid double bond hydratase that plays a role in oleic acid detoxification and bacterial virulence. Journal of Biological Chemistry. 285(14): 10353-10361.
9. AV Katokhin, VM Ephimov, MSh Badratinov, **OK Kamneva**, VA Mordvinov (2006). Multidimensional analysis and functional assignment of DNA-microarray transcription profiles of genes involved in adipogenesis. Biophysics. 51(1): 100-109.

Conference Abstracts

1. **OK Kamneva**. Inferring Microbe-Microbe Interactions Using Genome Content. General Meeting, American Society For Microbiology, 2015. New Orleans, USA.
2. **OK Kamneva**, NL Ward. Evolution of Sec pathway proteins in PVC bacteria. Society for Molecular Biology and Evolution (SMBE) annual meeting, 2013. Chicago, USA.
3. **OK Kamneva**, DA Liberles, NL Ward. Evolution of Sec pathway proteins in PVC bacteria. SMBE satellite meeting on Mechanisms of Protein Evolution, 2013. Denver, USA.
4. **OK Kamneva**, SJ Knight, DA Liberles, NL Ward. Whole genome evolutionary analysis of *Desulfovibrio* species. RECOMB Satellite Workshop on Comparative Genomics, 2010. Ottawa, Canada.
5. **OK Kamneva**, NL Ward. An evolutionary approach to characterizing predicted type III secretion systems in free-living bacteria. Wind River Conference on Prokaryotic Biology, 2010. Estes Park, USA.
6. **OK Kamneva**, DA Liberles, NL Ward. Genome-wide influence of indel substitutions on evolution of bacteria of the PVC super-phylum, revealed using a novel computational framework. Intelligent Systems for Molecular Biology (ISMB), 2010. Boston, USA.
7. **OK Kamneva**, DA Liberles, NL Ward. Inferring cases of lineage-specific adaptive evolution in genomes of planctomycete bacteria. Society for Molecular Biology and Evolution (SMBE) annual meeting. Darwin to the Next Generation, 2009. Iowa City, USA.
8. M Sait, B Steven, **OK Kamneva**, S McCann, D Domman, G Lawlis, NL Ward. Exploring the cosmopolitan phyla: genome-enabled investigations of the verrucomicrobia and planctomycetes. Wind River Conference on Prokaryotic Biology, 2009. Estes Park, USA.
9. **OK Kamneva**. Analysis of microarray data from adipocyte differentiation. Students and Technical Progress, 2007. Novosibirsk, Russia.