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Lomonosov Moscow State University
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GEORGII A. BAZYKIN

Research interests and experience

I am interested in biological evolution on different levels. I mainly focus on disentangling the relative roles of natural selection and non-selective processes in evolution of nucleotide and amino acid sequences. I use comparative genomics and bioinformatics to investigate different aspects of evolution of coding and regulatory sequences on genome level, and theoretical analysis to interpret the observed patterns. Recently, I've also become interested in applications of evolutionary reasoning to medical genetics.

Academic position

Head of sector, Institute for Information Transmission Problems, Moscow, Russia, 2007–present

Leading researcher, Lomonosov Moscow State University, Moscow, Russia, 2011–present

Senior lecturer, Lomonosov Moscow State University, Moscow, Russia, 2008–present

Education

2002–2007 **Princeton University**, Princeton, New Jersey, USA
PhD in Ecology and Evolution
Advisors: Dr. Simon A. Levin, Dr. Alexey S. Kondrashov
Dissertation: Natural selection in sequence evolution:
genome-scale, parsimony-based approach

1996–2001 **Moscow State University**, Moscow, Russia
Diploma (B.S.) in Biology (subfield: vertebrate zoology)
Honours Thesis: The spatial structure of rodent community
in North-Eastern Cis-Caspian Region

Born May 8, 1979 in Moscow, Russia.

Teaching experience

2012–2013	Developed curriculum and teaching (jointly with A. Markov) a graduate course: Evolutionary Biology (Yandex School of Data Analysis)
2011–2013	Developed curriculum and teaching (jointly with A. Kondrashov) an undergraduate course: Evolutionary Biology (Faculty of Bioengineering and Bioinformatics, Moscow State University)
2007–2013	Multiple invited public lectures throughout Russia
2010–2013	Developed curriculum and teaching an undergraduate course: Evolutionary Genomics (Faculty of Bioengineering and Bioinformatics, Moscow State University)
2007–2010	Developed curriculum and teaching (jointly with V. Ramensky) an undergraduate course: Evolutionary and Medical Genomics (Faculty of Bioengineering and Bioinformatics, Moscow State University)
2007	Guest lecturer: EEB 320/MOL 330: <i>Molecular Evolutionary Genetics</i> , Princeton undergraduate course
2006	Teaching assistant and guest lecturer, EEB 320/MOL 330: <i>Molecular Evolutionary Genetics</i> , Princeton undergraduate course
2003	Teaching assistant, EEB/MOL 211: <i>The Biology of Organisms</i> , Princeton undergraduate course
1998	Guest lecturer in Children's Summer Ecological School, Moscow, Russia

Additional research experience

1999–2002	Field researcher on behaviour and social demography (1999-2002) and community ecology (2001-2002) of rodent species in the Kalmykia semidesert, Russia
1995–2001	Field research assistant in multiple research projects.

Peer-reviewed publications

1. Tchabovsky A, **Bazykin G**. Females delay dispersal and breeding in a solitary gerbil *Meriones tamariscinus*. *Journal of Mammalogy* 85(1):105–112, 2004.
2. **Bazykin G**, Kondrashov F, Ogurtsov A, Sunyaev S, Kondrashov A. Positive selection at sites of multiple amino acid replacements since rat–mouse divergence. *Nature* 429: 558–562, 2004.
3. **Bazykin G**, Ogurtsov A, Kondrashov A. Change in CpG context is a leading cause of correlation between rates of non-synonymous and synonymous substitutions in rodents. *In: Bioinformatics of Genome Regulation and Structure II*, eds. N Kolchanov et al., Springer, 2006.
4. **Bazykin G**, Kondrashov A. Rate of promoter class turn-over in yeast evolution. *BMC Evolutionary Biology*, 10;6(1):14, 2006.
5. Kovaleva G, **Bazykin G**, Brudno M, Gelfand M. Comparative genomics of transcriptional regulation in yeasts and its application to identification of a candidate alpha-isopropylmalate transporter. *Journal of Bioinformatics and Computational Biology* 4(5):981–998, 2006.
6. **Bazykin G**, Dushoff J, Levin S, Kondrashov A. Bursts of nonsynonymous substitutions in HIV-1 evolution reveal instances of positive selection at conservative protein sites. *Proceedings of the National Academy of Sciences of the United States of America* 103:19396–19401, 2006.

7. **Bazykin G**, Kondrashov F, Brudno M, Poliakov A, Dubchak I, Kondrashov A. Extensive parallelism in protein evolution. *Biology Direct* 2:20, 2007.
8. Kryazhimskiy S, **Bazykin G**, Dushoff J. Natural selection for nucleotide usage at synonymous and non-synonymous sites in the influenza A genes. *Journal of Virology* 82(10): 4938–4945, 2008.
9. Kryazhimskiy S, **Bazykin G**, Plotkin J, Dushoff J. Directionality in the evolution of influenza A hemagglutinin. *Proceedings of the Royal Society B (Biological Sciences)* 275(1650): 2455–2464, 2008.
10. Donmez N, **Bazykin G**, Brudno M, Kondrashov A. Polymorphism due to multiple amino acid substitutions at a codon site within *Ciona savignyi*. *Genetics* 181: 685–690, 2009.
11. Popadin K, **Bazykin G**. Nucleotide repeats in mitochondrial genome determine human lifespan. *Nature Precedings* hdl:10101/npre.2008.2399.1, 2008.
12. **Bazykin G**, Kochetov A. Alternative translation start sites are conserved in eukaryotic genomes. *Nucleic Acids Research*, 2011 Jan;39(2):567-77. Epub 2010 Sep 22.
13. Vishnoi A, Kryazhimskiy S, **Bazykin G**, Hannenhalli S, Plotkin J. Young proteins experience more variable selection pressures than old proteins. *Genome Research*, 2010 Nov;20(11):1574-81. Epub 2010 Oct 4.
14. Kryazhimskiy S, Dushoff J, **Bazykin G**, Plotkin J. Prevalence of epistasis in the evolution of influenza A surface proteins. *PLoS Genetics*, 2011 Feb;7(2):e1001301. Epub 2011 Feb 17.
15. Vakhrusheva AA, Kazanov MD, Mironov AA, **Bazykin GA**. Evolution of prokaryotic genes by shift of stop codons. *Journal of Molecular Evolution*, 2011 Feb;72(2):138-46. Epub 2010 Nov 17.
16. **Bazykin GA**, Kondrashov AS. Detecting past positive selection through ongoing negative selection. *Genome Biology and Evolution* 2011;3:1006-13. Epub 2011 Aug 22.
17. Seplyarskiy VB, Kharchenko P, Kondrashov AS, **Bazykin GA**. Heterogeneity of the Transition/Transversion Ratio in *Drosophila* and Hominidae Genomes. *Molecular Biology and Evolution*. 2012 Aug;29(8):1943-55. Epub 2012 Feb 15.
18. Leushkin EV, **Bazykin GA**, Kondrashov AS. Insertions and deletions trigger adaptive walks in *Drosophila* proteins. *Proceedings of the Royal Society B (Biological Sciences)*. 2012;279(1740):3075-82. Epub 2012 Mar 28.
19. Naumenko SA, Kondrashov AS, **Bazykin GA**. Fitness conferred by replaced amino acids declines with time. *Biology Letters*. 2012 Oct 23;8(5):825-8. [Epub ahead of print]
20. **Bazykin GA**, Kondrashov AS. Major role of positive selection in the evolution of conservative segments of *Drosophila* proteins. *Proceedings of the Royal Society B (Biological Sciences)*. 2012 Sep 7;279(1742):3409-17. Epub 2012 Jun 6.
21. Leushkin EV, **Bazykin GA**, Kondrashov AS. Strong Mutational Bias Toward Deletions in the *Drosophila melanogaster* Genome Is Compensated by Selection. *Genome Biology and Evolution*. 2013 Jan;5(3):514-24.
22. Vakhrusheva OA, **Bazykin GA**, Kondrashov AS. Genome-Level Analysis of Selective Constraint without Apparent Sequence Conservation. *Genome Biology and Evolution*. 2013 Jan;5(3):532-41.
23. Terekhanova NV, **Bazykin GA**, Neverov A, Kondrashov AS, Seplyarskiy VB. Prevalence of multinucleotide replacements in evolution of primates and *Drosophila*. *Molecular Biology and Evolution*. 2013 Jun;30(6):1315-25.
24. Leushkin EV, **Bazykin GA**. Short indels are subject to insertion-biased gene conversion. *Evolution*. 2013 Sep;67(9):2604-13.

25. Kurmangaliyev YZ, Sutormin RA, Naumenko SA, **Bazykin GA**, Gelfand MS. Functional implications of splicing polymorphisms in the human genome. *Human Molecular Genetics*. 2013 Sep 1;22(17):3449-59.
26. Flot JF, ..., **Bazykin GA**, ..., et al. (39 co-authors). Genomic evidence for ameiotic evolution in the bdelloid rotifer *Adineta vaga*. *Nature*. 2013 Aug 22;500(7463):453-7.
27. Neverov AD, Lezhnina KV, Kondrashov AS, **Bazykin GA**. Intratype reassortments cause adaptive amino acid replacements in H3N2 influenza genes. *PLOS Genetics*. 2014 Jan;10(1):e1004037.

Awards and grants

2012–2013*	Russian Foundation for Basic Research Project 13-04-02098-a (\$13,000 per annum)
2012*	Young scientist award of the Russian Club of the European Academy
2012–2013*	Russian Federal Agency for Science and Innovations grant (\$95,000 over two years)
2012–2013*	Russian Foundation for Basic Research Project 12-04-33202_mol-a-ved (\$95,000 per annum)
2010–2012	Russian Ministry of Science and Education grant (\$5,000,000 over three years)
2010–2012*	Russian Academy of Sciences (Molecular and Cellular Biology Program) grant (\$23,000 per annum)
2009–2011*	Russian Federal Agency for Science and Innovations grant (\$21,500 per annum)
2008*	SMBE-2008 PostDoctoral researcher Travel Award
2008–2010*	Russian Foundation for Basic Research Project 08-04-01394-a (\$10,000 per annum)
2008–2009*	Outstanding scientist of the Russian Academy of Sciences Award, Russian Science Support Foundation.
2007*	Best Talk in Bioinformatics Section Award, Information Technologies and Systems (ITaS) conference, Zvenigorod, Russia
2007–2009*	Russian Academy of Sciences (Molecular and Cellular Biology Program) grant (\$38,000 per annum)
2003–2007	Burroughs Wellcome Program in Biological Dynamics Training Grant (\$105,000)
2002–2005	Pew Charitable Trust Program in Biocomplexity Training Grant (\$48,000 per annum)
2001*	Honours Diploma, Moscow State University
1996–2001*	Moscow State University Honours Scholarship

* PI: Georgii Bazykin.

Referee activities

Journals: *Trends in Genetics*, *Journal of Molecular Evolution*, *Gene*, *Molecular Biology and Evolution*, *Genome Biology and Evolution*, *Biology Direct*, *In Silico Biology*, *Journal of Bioinformatics and Computational Biology*, *Journal of Computational Biology*, *PLOS Computational Biology*, *PLOS One*, *BMC Genomics*, *Biofizika*, *Molekulyarnaya Biologiya*, *Doklady Akademii Nauk*

Foundations: Russian Foundation for Basic Research, Russian Scientific Foundation

Professional memberships

Editorial board member, *Biology Letters*

Faculty member (Evolutionary / Comparative Genetics), *F1000 Prime*
New York Academy of Sciences (NYAS)
Society for Industrial and Applied Mathematics (SIAM)
Society for the Study of Evolution (SSE)
Society for Molecular Biology and Evolution (SMBE)