

Biographical Sketch

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| Name: Igor Sharakhov | Title: Associate Professor |
| Email: igor@vt.edu | Department: Entomology |

Education/Training:

| Institution/Location | Degree/Postdoc | Year(s) | Field of Study |
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| University of Notre Dame, Notre Dame, IN, USA | Postdoc | 2001-2004 | Genomics |
| State University of New York at Buffalo, Buffalo, NY, USA | Postdoc | 1999-2001 | Genetics |
| Institute of Cytology and Genetics, Novosibirsk, Russia | Ph.D. | 1996 | Genetics |
| Tomsk State University, Tomsk, Russia | B.S. | 1989 | Biology |

Personal Statement:

I am broadly interested in understanding of how a eukaryotic genome is organized and how it changes over time. More specifically I am looking at if and how the linear and three-dimensional organization of chromosomes affect the function and evolution of insect genomes. We use light microscopy, molecular techniques, and bioinformatics to delve into the genome at three different levels: the 3D structure of the cell nucleus, epigenetic modifications of chromosomes, and organization of DNA sequence. We investigate the effect of chromosomal attachments to the nuclear envelope on chromosome territories, gene-gene contacts, and genome rearrangements. We found that computational models of a fruit fly nucleus with more numerous attachments form more distinct chromosome territories, the frequency of intra-chromosomal gene-gene contacts increases, but the frequency of inter-chromosomal contacts decreases. By analyzing mapped genome assemblies of *Anopheles gambiae*, *An. stephensi*, *An. funestus*, *An. atroparvus*, and *An. albimanus*, we found that rearrangements of the X chromosome occur 3 times faster than autosomal rearrangements pointing to a special role of sex chromosomes in evolution of malaria mosquitoes. We characterized a major epigenetic component of the *An. gambiae* germ-line – small non-coding Piwi-interacting RNA (piRNA) sequences and their euchromatic and heterochromatic clusters. We also identified a subset of the piRNA-enriched genes that have functions related to reproduction and embryonic development. Overall, my research helps to understand the mechanisms of mosquito evolution, adaptation, and reproduction. This knowledge can facilitate the development of innovative genome-based approaches for mosquito-borne disease control.

Selected Publications:

- Hall, A.B., Papathanos, P., Sharma, A., Cheng, C., Akbari, O.S., Assour, L., Bergman, N.H., Cagnetti, A., Crisanti, A., Dottorini, T., Fiorentini, E., Galizi, R., Hnath, H., Jiang, X., Koren, S., Nolan, T., Radune, R., Sharakhova, M.V., Steele, A., Timoshevskiy, V.A., Windbichler, N., Zhang, S.V., Hahn, M.W., Phillippy, A.M., Emrich, S.J., **Sharakhov, I.V.**, Tu, Z., and Besansky, N.J. 2016. Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. *Proc Natl Acad Sci USA* 113(15):E2114–E2123.
<http://www.pnas.org/content/113/15/E2114.long>
- George, P., Jensen, S., Pogorelcnik, R., Lee, J., Xing, Y., Brasslet, E., Vaury, C., and **Sharakhov, I.V.** 2015. Increased production of piRNAs from euchromatic clusters and genes in *Anopheles gambiae* compared with *Drosophila melanogaster*. *Epigenetics Chromatin* 8:50.
<http://epigeneticsandchromatin.biomedcentral.com/articles/10.1186/s13072-015-0041-5>

3. **Sharakhov, I.V.**, and Sharakhova, M.V. 2015. Heterochromatin, histone modifications, and nuclear architecture in disease vectors. *Curr Opin Insect Sci* 10:110-117.
<http://www.sciencedirect.com/science/article/pii/S2214574515000814>
4. Kinney, N.A., Onufriev, A.V., and **Sharakhov, I.V.** 2015. Quantified effects of chromosome-nuclear envelope attachments on 3D organization of chromosomes. *Nucleus* 6(3):212-24
<http://www.tandfonline.com/doi/full/10.1080/19491034.2015.1056441>
5. Neafsey, D.E., Waterhouse, R.M., Abai, M.R., Aganezov, S.S., Alekseyev, M.A., Allen, J.E., Amon, J., Arcà, B., Arensburger, P., Artemov, G., Assour, L.A., Basseri, H., Berlin, A., Birren, B.W., Blandin, S.A., Brockman, A.I., Burkot, T.R., Burt, A., Chan, C.S., Chauve, C., Chiu, J.C., Christensen, M., Costantini, C., Davidson, V.L., Deligianni, E., Dottorini, T., Dritsou, V., Gabriel, S.B., Guelbeogo, W.M., Hall, A.B., Han, M.V., Hlaing, T., Hughes, D.S., Jenkins, A.M., Jiang, X., Jungreis, I., Kakani, E.G., Kamali, M., Kemppainen, P., Kennedy, R.C., Kirmizoglou, I.K., Koekemoer, L.L., Laban, N., Langridge, N., Lawniczak, M.K., Lirakis, M., Lobo, N.F., Lowy, E., MacCallum, R.M., Mao, C., Maslen, G., Mbogo, C., McCarthy, J., Michel, K., Mitchell, S.N., Moore, W., Murphy, K.A., Naumenko, A.N., Nolan, T., Novoa, E.M., O'Loughlin, S., Oringanje, C., Oshaghi, M.A., Pakpour, N., Papathanos, P.A., Peery, A.N., Povelones, M., Prakash, A., Price, D.P., Rajaraman, A., Reimer, L.J., Rinker, D.C., Rokas, A., Russell, T.L., Sagnon, N., Sharakhova, M.V., Shea, T., Simão, F.A., Simard, F., Slotman, M.A., Somboon, P., Stegniy, V., Struchiner, C.J., Thomas, G.W., Tojo, M., Topalis, P., Tubio, J.M., Unger, M.F., Vontas, J., Walton, C., Wilding, C.S., Willis, J.H., Wu, Y.C., Yan, G., Zdobnov, E.M., Zhou, X., Catteruccia, F., Christophides, G.K., Collins, F.H., Cornman, R.S., Crisanti, A., Donnelly, M.J., Emrich, S.J., Fontaine, M.C., Gelbart, W., Hahn, M.W., Hansen, I.A., Howell, P.I., Kafatos, F.C., Kellis, M., Lawson, D., Louis, C., Luckhart, S., Muskavitch, M.A., Ribeiro, J.M., Riehle, M.A., **Sharakhov, I.V.**, Tu, Z., Zwiebel, L.J., and Besansky, N.J. 2015. Highly evolvable malaria vectors: the genomes of 16 *Anopheles* mosquitoes. *Science* 347(6217):1258522.
<http://science.sciencemag.org/content/347/6217/1258522.long>
6. Kinney, N.A., **Sharakhov, I.V.**, and Onufriev, A.V. 2014. Investigation of the chromosome regions with significant affinity for the nuclear envelope in fruit fly—a model based approach. *PLoS One* 9(3):e91943.
<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0091943>
7. Jiang, X., Peery, A., Hall, A.B., Sharma, A., Chen, X.G., Waterhouse, R.M., Komissarov, A., Riehle, M.M., Shouche, Y., Sharakhova, M.V., Lawson, D., Pakpour, N., Arensburger, P., Davidson, V.L., Eglmeier, K., Emrich, S., George, P., Kennedy, R.C., Mane, S.P., Maslen, G., Oringanje, C., Qi, Y., Settlege, R., Tojo, M., Tubio, J.M., Unger, M.F., Wang, B., Vernick, K.D., Ribeiro, J.M., James, A.A., Michel, K., Riehle, M.A., Luckhart, S., **Sharakhov, I.V.**, and Tu, Z. 2014. Genome analysis of a major urban malaria vector mosquito, *Anopheles stephensi*. *Genome Biol* 15(9):459. <http://genomebiology.biomedcentral.com/articles/10.1186/s13059-014-0459-2>

Current and/or Recently Completed Research Grants: (as applicable)

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| NIH/NIAID | 1R21AI099528-01A1 | PI: Sharakhov | 01/15/2014 – 12/31/2016 |
| Title: Comparative genome mapping of the <i>Anopheles</i> species cluster | | | |
| The major goal of this R21 project is to develop chromosome-based reference genome assemblies for three major malaria vectors: <i>An. arabiensis</i> , <i>An. stephensi</i> , and <i>An. albimanus</i> . The project will determine the pattern and mechanisms of chromosome evolution in genus <i>Anopheles</i> . | | | |
| Russian Science Foundation | 15-14-20011 | PI: Sharakhov | 07/08/2015 – 12/31/2017 |
| Title: Phylogeny reconstruction in the <i>Maculipennis</i> group of malaria mosquitoes | | | |
| This project aims to better understanding of the phylogenetic relationship in the <i>An. maculipennis</i> group of malaria mosquitoes. The phylogenetic relationships among North American and Eurasian species of the <i>Maculipennis</i> group will be reconstructed using the whole-genome molecular and gene-order based approaches. | | | |
| NIH/NIAID | 1R21AI121853-01 | PI: Sharakhova | 01/03/2016 – 01/02/2018 |
| Title: Improving the reference genome assembly for the dengue fever vector <i>Aedes aegypti</i> | | | |

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| The major thrust of this grant is to improve the reference genome assembly for the dengue and Zika fever vector <i>Aedes aegypti</i> . The new genome assembly based on PacBio sequencing will be used to detect inversions in two subspecies of <i>Ae. aegypti</i> and in a sister taxon, <i>Ae. mascarensis</i> . | | | |
| NIH/NIAID | 1R21AI112734-01 | PI: Besansky | 06/01/2014 – 05/31/2017 |
| Title: Anchoring and uniting the <i>An. funestus</i> assembly for improved vector analysis | | | |
| The central goal of this R21 is to upgrade the draft <i>An. funestus</i> reference to a chromosome-based assembly in which the unanchored scaffolds are united, ordered and oriented on chromosome arms, enabling a preliminary assessment of genomic divergence between the cytotypes. | | | |
| NIH/NIAID | 5R21AI113643-02 | PI: Tu | 06/01/2014 – 05/31/2017 |
| Title: Function of a novel male-specific gene in <i>Aedes aegypti</i> | | | |
| This exploratory R21 project, will determine the effect of ectopic expression and knockout of a novel male-specific gene <i>nix</i> in <i>Aedes aegypti</i> . It will test the hypothesis that <i>nix</i> plays an important role in sexual differentiation in <i>Ae. aegypti</i> . | | | |