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Academic appointments and name of projects

CENTRAL RESEARCH INSTITUTE FOR EPIDEMIOLOGY, *Moscow, Russia*
Postdoctoral associate March 2012 - present

- Study of genome instability of strains *Mycobacterium tuberculosis* complex by NGS
- Study of interaction effect (complementary and epistasis effects) between genes, associated with phenomena of drug resistance
- Study of genetic architecture and immunological repertoire in series of passages vaccine strains *Mycobacterium bovis* BCG in Russia from 1948-2014 collection
- Study of host-pathogen interaction between virulent MTC strains and Russian cohort of patients

UNIVERSITY OF FREIBURG, *Freiburg im Breisgau, Baden-Württemberg, Germany*
Postdoctoral short fellowship EMBO September - December 2010

- Study of ribosomal genes associated with Diamond's blackfan anaemia in children from Europe
- Comparative analysis of conformation changes in ribosomal proteins, as response on genetic replacements

INSTITUTE OF GENE BIOLOGY RAS, *Moscow, Russia*
Postdoctoral fellowship February 2010 - March 2012

- Study of mitochondrial genome organization and genetic diversity in subspecies *Cyprinus carpio carpio* L. and *Cyprinus Carpio haematopterus* S&H

INSTITUTE OF GENE BIOLOGY RAS, *Moscow, Russia*
Diploma and Ph.D. project October 2002 - March 2008

- Study of genetic evolution processes and events in natural and domestic population of fishes from cyprinidae family
- Study of domain organisation of non-coding and coding region especially in cytochrome oxidase genes mtDNA
- Study of hot spot points of genetic recombination in r-DNA cistron genes on laboratory population of interspecies F1 hybrids between *Rutilus rutilus* L. and *Abramis brama* L.
- Study of genetic alterations in Lph gene in morphotype complex of Ethiopian *Barbus barbus* from natural population, located in Tana lake

Education

INSTITUTE OF GENE BIOLOGY RAS, *Moscow, Russia*
Ph.D. in molecular genetics December, 2008

MOSCOW STATE PEDAGOGICAL UNIVERSITY, *Moscow, Russia*
Ms.c. in biology and chemistry August, 2003

COLLEGE OF HUMANITIES AND ECOLOGY, *Moscow, Russia*
Bs.c. in ecology August, 1998

Awards, honors and professional recognition

ASTF 312-2010 EMBO Study of ribosomal genes associated with Diamond Blackfan anemia (DBA) Department of Oncology and Hematology, University of Freiburg
December, 2010

RFBR 08-06-00669 Mitogenomic of *Cyprinidae* fishes, Institute of Gene Biology RAS
April 2009 - August 2010

SPECIAL AWARD OF RUSSIAN GOVERNMENT FOR YOUNG SCIENTIST, Institute of Gene Biology RAS
January 2007-December 2008

RFBR 08-04-13734 The molecular genetic basis of differentiation of fish from Cyprinidae family, Institute of Gene Biology RAS
October 2007 – December 2008

Advising of diploma students
September 2007- June 2008

The special award for the best report about infection disease. The comparative genomic of vaccine strain M. Bovis BCG-1 Russia by whole genome sequencing.

June, 2013

Professional experience

The Molecular genetic techniques:

- DNA/RNA analysis: extraction, purification, restriction, elution, cloning, electrophoresis (agarose and acrylamide), northern and Southern blotting, sequencing;
- PCR, RT-PCR, RAPD-PCR, Real Time PCR, MICROSATELLITE ANALYSIS; - NEXT-GENERATION SEQUENCING technologies (Roche 454, Illumina (MiSeq), Nextera library preparation kit), SNP arrays;
- PROTEIN analysis: PAAG electrophoresis, 2-D electrophoresis, Western-blot analysis;
- Microbiological technique in progress (cell culture, BACTEC, drug-susceptibility testing)

The bioinformatics techniques:

- General: Windows, partially Linux (Ubuntu plus Biolinux);
- Genetic data:
Vector NTI, TRF, AltAnalyser, Microsat, TCS, Alamut; Genome studio data analysis software;
Software for quality control of DNA in LAMP sequencing;
ERGO and MetaMerge (metabolic network),
WGA Viewer, Artemis;
- Phylogenetic data:
Arlequin, Paup, Mr. Bayes, Epos, Splitstree;
- Biophysical data:
3D structure molecular analysis: Swiss-PDBViewer, VMD;
- Statistical data:
Statistica, Gelstat, GDA, R-Statistik
- Predicted analysis of active and regulatory sites, structure and work with different database: NCBI, EMBL, Expasy, Pfam, Swiss model., BioCYC (metabolomics), BIGG

- Whole genome sequencing:
Amos, Mira and Geneious for assembling de novo or mapping;
SOAP, GATK for validation;
Blast2go for blasting and automatic annotation,
Mauve and GeneWiz for comparative analysis,
ERGO for metabolic network.
GWAS e t c
- Visualisation of genetic data:
CIRCOS, Artemis, AIspace

Publications and Patent

R. Ludannyy, M. Alvarez Figueroa, A. Prokopenko The study of interaction's effect between genes associated to drug resistance in Mycobacterium tuberculosis complex. FEBS Journal 281(S1). 672 (2014)

M. Alvarez, D. Levi, R. Ludannyy, E. Elbert, N. Aleksandrova Quality control of BCG vaccine seed lots by molecular methods The International Journal of Tuberculosis and Lung Disease, 17(12), vol. 2, 526 (2013).

Ludannyy, R.I., Khrisanfova, G.G., Prizenko, V.K., Bogeruk, A.K. And Semenova, S.K., "Polymorphism of microsatellite markers at the breeds of domestic carp (*Cyprinus Carpio L.*) Russian selection" Rus. J. Genet., **46**, 572-577, (2010).

Ludannyy, R.I. "The identification and differentiation Cyprinid fishes (*Cyprinidae*)", Author's abstract of dissertation, IGB RAS, Moscow, Russia, 1-141 (2008), In Russian.

Ludannyy, R. I., Khrisanfova, G. G., Vasilyev, V. A., Prizenko, V. K., Bogeruk, A. K., Ryskov, A. P. and Semyenova, S. K., "Genetic diversity and differentiation of Russian common carp (*Cyprinus Carpio L.*) breeds inferred from the RAPD markers", Rus. J. Genet., **42**, 1121- 1129, (2006).

Khrisanfova, G. G., Ludannyy, R. I., Slynko, Yu. V.,Yakovlev, V. N. and Semyenova, S. K., "RAPD Fingerprinting of Common Bream (*Abramis Brama L.*), Roach (*Rutilus rutilus L.*), and cross F1 hybrids (*A. Brama x R. Rutilus* and *R. Rutilus x A. Brama*)", Rus. J. Genet., **40** , 1432-1436, (2004).

Khrisanfova, G.G., Ludannyy, R.I., Vasiliev V.A., Filipova, E.K., Prizenko,V.K. and Semenova, S.K. (2004): Genetic certification breeds of wild and domestic Carps from Russia. Cytology and genetic 46, 852-853

Presentations

Ludannyy, R., Torgynakova, O., Chrisanfova, G. and Semenova S., "The molecular phylogeny of Cyprinid fishes, based on coding and non-coding region of mitochondrial DNA", 11-th conference for junior scientist, "Biology – XXI", Pushino, Moscow region, Russia.

November 2008

Ludannyy, R., Chrisanfova, G., Stolbunova, V., Slynko, Y. and Semyenova, S., "The comparative mitogenomic study of *Cyprinidae* species (common carp, bream and roach)", XII European Congress of Ichthyology, Cavtat (Dubrovnik), Croatia.

September 2007

Ludannyy, R.I., Chrisanfova, G.G., Stolbunova, V.V., Slynko, Y.V., Ryskov, A.P. and Semyenova, S.K., "The mitogenomic study of freshwater Cyprinids fishes. General meeting "Barcode Fish in Russia", Vladivostok, Primorskiy region, Russia.

June 2007

Semyenova, S. K., Ludanny, R.I., Chrisanfova, G., G., Slynko, Y. V., Yakovlev, V. N. and Ryskov, A. P., "The genome variability of common bream (*Abramis Brama L.*), roach (*Rutilus Rutilus L.*) and their F1 hybrids. Symposium on hybridization in animals – extent, processes and evolutionary impact", Frankfurt, Germany.

October 2006

Bogueruk, A.K., Semyenova, S.K., Chrisanfova, G.G., Ludanny, R.I., Vasilyev, V.A., Filipova, E.K., Prizenko, V.K. and Ryskov, A.P., "The genetic variability and pasportization of wild carp and Russian common carp breeds (*Cyprinus Carpio*)", World aquaculture 2005, Bali, Indonesia.

May 2005,

Ludanny, R., "The genome variability of common carp (*Cyprinus Carpio*) and evolution of Cyprinid fishes. 9th Conference for junior scientist "Biology – XXI", Pushino, Moscow region, Russia.

April 2005

Bogueruk, A.K., Chrisanfova, G.G., Ludanny, R.I., Vasilyev, V.A., Phylipova, E.K., Prizenko, V.K. and Semyenova, S.K., "The Genetic pasportization of wild and domestic carps (*Cyprinus Carpio*) from Russian river system", Conservation of genetic resources, Sankt-Petersburg, Russia.

October 2004

Vasilyev, V.A., Phylipova, E.K., Ludanny, R.I., Prizenko, V.K., Bogeruk, A.K. and Chrisanfova, G.G., "RAPD-fingerprinting and genetic pasportization of wild and domestic carps (*Cyprinus Carpio*) from Russia. Genetic XXI - prospects of development, , Moscow, Russia.

June 2004.

Mihaela Pali, Jessica Moetter, Ruslan Ludanny, Joerg Meerpohl, Mutlu Kartal, Alexandra Fischer, Sandra Urbaniak, Peter Noellke, Manfred Fliegau, Lydie M. Da Costa, Charlotte M Niemeyer, and Marcin W. Wlodarski., "Identification of Novel Mutations In Ribosomal Genes In Patients with Diamond Blackfan Anemia (DBA) in Germany and Genotype-Phenotype Correlation Analysis, The 52-nd American Society of Hematology, Annual Meeting and Exposition, Orlando, USA.

December, 2010

Alvaers Figueroa M., Ludanny R., Dolgova E., Braslavskaya S. and Lobashova G.P. The study of resistance MTB by molecular and cultural methods. The 5th Congress of infection diseases, Moscow, Russia

19-21 March, 2013

Ludanny R. The comparative genomic of vaccine strain *M. Bovis BCG-1* Russia by whole genome sequencing. The molecular epidemiology of topical infection. The 90th anniversary of the Institute of epidemiology and microbiology of the Pasteur. Sankt-Petersburg, Russia.

21-23 June, 2013

Ludanny R., Alvares Figueroa M and Prokopenko M. The correlation between phenotypical and genetic resistance to Ethambutol in patients from Moscow region. The 34-th congress of European society of Mycobateriology, Florence, Toskana, Itally.

29 June- 3 July, 2013

Lavrova O., Alvarez Figueroa M., Ludanny R. The study of genetic arhitecture *InhA* gene and their promoter region in clinical isolates of *Mycobacterium tuberculosis* complex (Moscow region). Congress of molecular diagnostics, Moscow, Russia.

18-20 March 2014

Ludanny R., Alvarez Figueroa M., Levi D., Dedkov V., Markelov M. Shipulin G. Molecular genetics of vaccine Russian strain *M. Bovis BCG-1*. Congress of molecular diagnostics, Moscow, Russia.

18-20 March 2014

Ludanny R., Alvarez Figueroa M., Prokopenko A., Dolgova E., Lobashova G., Domotenko L. The phenomenon of cross-resistance to Streptomycin and injection second-line drugs for *Mycobacterium tuberculosis* complex. Congress of molecular diagnostics, Moscow, Russia.

18-20 March 2014

Ludannyy, R. The study of phenomenon of drug-resistance for *mycobacterium tuberculosis* complex. International bioforum 2014, Russian-German session. Pushino, Moscow region.
23 April 2014

R. Ludannyy, A. Prokopenko, M. Alvarez Figueroa The interaction between genetic replacements in genes, associated with antituberculosis drugs resistance. The 35-th congress of European society of Mycobacteriology, Vienna, Austria.
29 June- 3 July, 2013

A. Prokopenko, R. Ludannyy, G. Lobashova, L. Domotenko, M. Alvarez Figueroa The study of molecular genetic determinants for phenomenon of cross-resistance between streptomycin and injectable second-line drugs The 35-th congress of European society of Mycobacteriology, Vienna, Austria.
29 June- 3 July, 2013

Ludannyy R., Alvarez Figueroa M., Prokopenko A., Domotenko L. The study of interaction effect between genes associated to drug resistance in *Mycobacterium tuberculosis* complex. 2-nd Ecoforum, . Sankt-Petersburg, Russia.
23 September, 2014

The articles under print:

R.I. Ludannyy, M.V. Alvarez Figueroa, A.V. Prokopenko, A.V. Valdokhina, G.A. Shipulin
The study of interaction's effect between genes, associated with phenomenon of drug resistance in *mycobacterium tuberculosis* complex. J. of Molecular medicine (Russian) in October.

The articles under review:

The whole genome sequencing of Russian vaccine strain BCG-1. J. of Microbiology

Membership

FEBS (Federation of European Biochemical Societies) since 2006
ESM (European Society of Mycobacteriology) since 2014

Referees

Alexey P. Ryskov, Professor, Head of the laboratory of genome organization, Institute of Gene Biology RAS, Moscow, Russia
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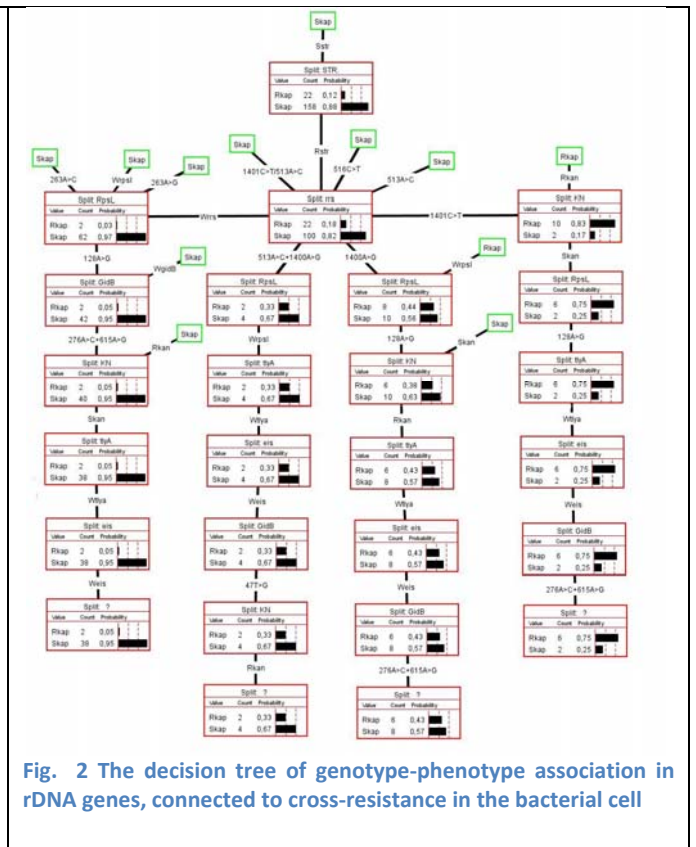
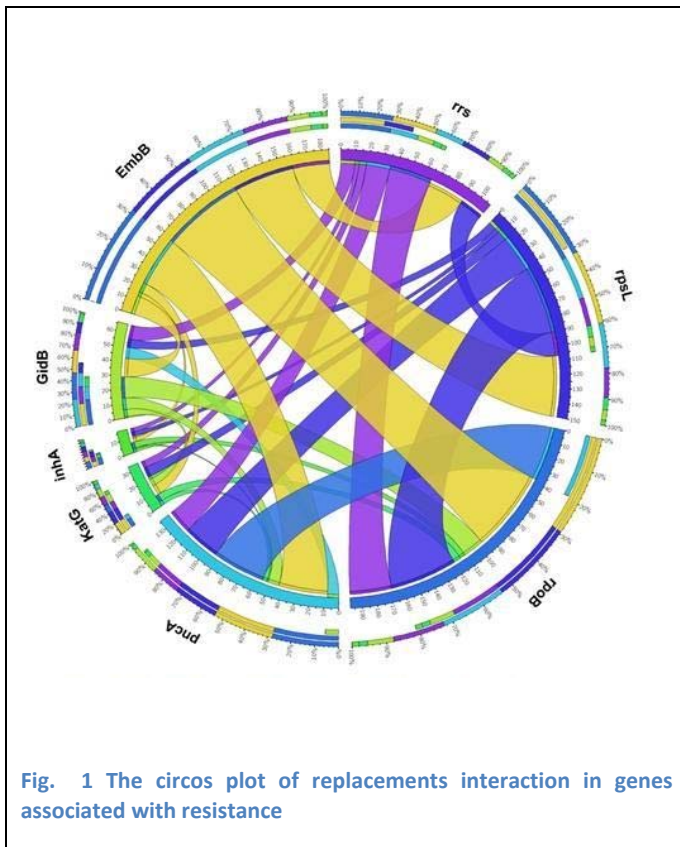
Irena Martirosyan, Ph.D, Scientist, Department of Embryology, Carnegie Institute, Baltimore, USA.
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RESEARCH INTERESTS

The research interests focused on molecular genetics and comparative genomics. One of main interests focused on understanding the logic of interaction between biological events and followed by their visualization. As example, the circos plot and different methods of clusterization (decision tree and multivariate analyses) were used me for detection of relationship between genomic replacements, phenotype expression of cell (resistance and virulence) and evolution rate and events. Genome instability and plasticity is key factor for organism's adaptation. The next generation sequence technology I have applied for investigation. Next step was combine genomics, proteomics and metabolomics data for create accurate and correct a de novo assembly of genome. The superposition of metabolic and genomic maps allowed to detect incorrect and false SNPs in assembly. Additionally, my interests included phylogenetics as instrument of search associations between evolutionary and genetic events, particularly for concerted evolution. Primary, I'm molecular geneticist and field and laboratory experiments are integral part of my research that is 50 % of time. The 40% of my work dedicated to deep statistic analysis of data by genetic software and 10 % is bioinformatics approaches. that is reflection of my skills.

My last projects were strongly associated with genome-wide association between genomic events and phenotypic influence. The first step was postdoc fellow in Freiburg University, where I have studied the genetic basis of malformation in children as genetic alteration in ribosomal genes, that associated with dimond blackfun anemia. This project was directed to detect logic of mutation formation via combination data from different level: genomic, proteomic and crystallographic. Why the disorder's mutations formed in specific points in genes?, and Why the role of this changes might be different as reflection of human diseases?

The second project based on deep analysis of genotype-phenotype association by statistic and bioinformatic analysis. Used the spectra of molecular genetic methods as NGS technology, cloning, detection of expression by realtime and bioinformatic approaches like graph construction and clusterisation of biologic data, the complex of genetic events as complimentary relationship and epistatic effect in genes was observed. The detailed comparison between genetic and metabolic maps allowed to predict silent mutations, which might be affect on function's change in the cell and finally, resulted to change of phenotype. As example , the two pics below, where the genotype-phenotype association were detected in bacterial cell:



The first (Ph.D.) project was aimed on study of genetic processes and events in natural population as influence of concerted evolution. The main aim of project was detection of hot spot points of recombination and mobile elements in fishes from cyprinidae family. Classical population analysis and multivariate statistical methods were involved for study of divergence wild and domestic subpopulation and complex of morphotypes.

Additionally, the info about my projects was published on my web site <http://www.ludanny.ru/> and I'll very gratefull if you take a look. If you will have question or comments, please contact to me at your convenience.

Ruslan Ludanny