

CURRICULUM VITAE

Alexei N. Fedorov, Ph.D.

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RESEARCH FOCUS:

To progress our understanding of the organization and operation of the human genome to new frontiers.

EDUCATION

- 1993 Ph.D. Molecular Genetics - Institute of Molecular Genetics, Russian Academy of Sciences, Moscow, Russia
Thesis Title: "Investigation of beta-hemoglobin gene mutations in certain regions of the Caucasus.
- 1982 M.Sc. Low-temperature Physics - Lomonosov Moscow State University, Moscow, Russia

PROFESSIONAL EXPERIENCE

- 2010-present Vice Director, Bioinformatics and Genomics/Proteomics Program, the University of Toledo College of Medicine, Tenure
- 2008-present Associate Professor, Department of Medicine, the University of Toledo College of Medicine
- 2003-2007 Assistant Professor, Department of Medicine, the University of Toledo College of Medicine
- 1997-2003 Post-doctoral Research Fellow, The Biological Laboratories, Harvard University
Adviser: Walter Gilbert
- 1997-1998 Post-doctoral Research Fellow, Department of Physiology, the University Miami School of Medicine
- 1994-1996 Post-doctoral Research Fellow, Sussex Centre for Neuroscience, University of Sussex, Brighton, UK
- 1982-1994 Research Associate, Department of Human Genetics, Institute of Molecular Genetics, Russian Academy of Sciences, Moscow, Russia

AWARDS AND COMMENDATIONS

- 1986 BDNX medal by the Russian National Government
- 1993 Stipend by the George Soros foundation (program Biodiversity)
- 2007 NSF CAREER Development award MCB-0643542

MENTORING (major advisor)

NAME: Jason Bechtel
DATES UNDER THE GUIDANCE: Sept 2006 - May 2008
DEGREE AWARDED AND DATE: MS Bioinformatics, May 2008
Education awards: Outstanding MSBS in 2008 at HSC UT

NAME: Theodor Rais
DATES UNDER THE GUIDANCE: Sept 2006 – May 2009
DEGREE AWARDED AND DATE: MS Bioinformatics, May 2009

Education awards: Second/Third Poster award by Ohio Bioinformatics Consortium
OCCBIO 2009, Cleveland, June 15-17.

NAME: Samuel Shepard
DATES UNDER THE GUIDANCE: Sept 2007- June 2010
DEGREE AWARDED AND DATE: PhD Molecular Biology, May 2010
Education awards: Outstanding PhD student in 2010 at HSC UT

NAME: Ashwin Prakash
DATES UNDER THE GUIDANCE: Sept 2007- December 2011
DEGREE AWARDED AND DATE: PhD Molecular Biology, December 2011

NAME: David Rearick
DATES UNDER THE GUIDANCE: Sept 2008- Dec 2010, dropped by personal reasons
DEGREE AWARDED AND DATE: Accomplished project: Rearick et al NAR 2010

NAME: Andrew McSweeny
DATES UNDER THE GUIDANCE: May 2009- December 2010
DEGREE AWARDED AND DATE: MS Bioinformatics, December 2010

NAME: Maryam Nabiyouni
DATES UNDER THE GUIDANCE: September 2009- June 2011
DEGREE AWARDED AND DATE: MS Bioinformatics, June 2011

NAME: William TenBrink
DATES UNDER THE GUIDANCE: September 2010- Dropped May 2011
POSITION: MS student

NAME: Shuhao Qiu
DATES UNDER THE GUIDANCE: Septmber 2011 –May 2015
POSITION: PhD Molecular Biology, May 2015

NAME: Arnab Saha Mandal
DATES UNDER THE GUIDANCE: September 2011- August 2013
POSITION: MS Bioinformatics, July 2013
Education awards: Outstanding MS student in 2013 at HSC UT

NAME: Ahmed Al-Khudair
DATES UNDER THE GUIDANCE: September 2012-2014
POSITION: MS Bioinformatics, September 2014
Education awards: Outstanding MS student in 2015 at HSC UT

NAME: Rajib Dutta
DATES UNDER THE GUIDANCE: April 2014- current
POSITION: PhD student

NAME: Yuriy Yatskiv
DATES UNDER THE GUIDANCE: December 2014-present
POSITION: MS student

NAME: Joseph Mainsah
DATES UNDER THE GUIDANCE: December 2014-present
POSITION: MS student

JOURNAL PEER REVIEW

Associate Editor of *BMC Genomics*

Member of Editorial Board *Genomics Discovery*, Herbert Open Access Journals, UK

Member of Editorial Board of *ISRN Computational Biology*

Ad hoc reviewer for:

Nucleic Acids Research; Gene; Bioinformatics; Journal of Molecular Evolution; BMC Bioinformatics, Genomics; Molecular Biology and Evolution; Genetics; Genome Research; Proceedings of National Academy of Science; Trends in Genetics; etc.

REVIEW PANELS:

Biomedical Research Council (BMRC), A*STAR (2006-2007). NSF grant reviewer (2007- 2009);

COMMUNITY SERVICE AND ORGANIZATIONS

Member of student graduate committees

- Xi Cheng (PhD, HSC, current student)
- Eric Haynes (MS, HSC, 2013)
- Tina Agarwal (PhD, UT Main, 2012),
- Shi, Xinhui (PhD, UT Main March 2011),
- Amal Abu Almakarem (PhD student, Bowling Green State University, 2011),
- Jie He (PhD, UT Main Campus December 2009),
- Robert Linter (PhD, UT HSC, April 2007),
- Michael Harr (PhD, UT HSC, 2006),
- Thomas Wittenschlaeger (MS, BGSU May 2007),
- Jesse Stombaugh (PhD, BGSU December 2008),
- Ali Mokdad (PhD, BGSU May 2006),

Training Summer students and volunteers

Mark McCreary (2005, 2007)

Tiara Heisey (2008)

Aaron Walsh (2008)

Ramya Yarlagadda (2009)

Sam Choulet (HSC UT, Medical student 2011)

Lorraine Walters (UT Main, Bioengineering student, 2011)

Eugene Akkuratov (PhD student, Moscow State University, Russia, during his internship at HSC UT, 2011)

Mark Pavlyukovskyy (undergraduate student, Cornell University, 2011)

Jasmine Serpen (2012-1013)

Asare Thelma (2014) (Public Health, HSC UT, internship)

Active participant of the Ohio Bioinformatics Consortium (co-organizer of the OCCBIO conference, Cleveland, OH, June 15-17, 2009).

Member of the Program Committee of the 6th Great Lakes Bioinformatics Conference, May 4-6, 2011, Athens, Ohio (an official conference of the International Society for Computational Biology).

Support of prominent bioinformatics investigations all over the United States and across the World by the following activities:

- Creating and maintaining public databases:
 - the Exon-Intron Database
 - the Alternative Splicing Mutation Database
- Creating and maintaining public computational resources:
 - snoTARGET, a web-based program for finding targets for orphan snoRNAs.
 - Genomic MRI (Mid-Range Inhomogeneity), a resource to study the distribution of genomic regions with inhomogenous composition in any sequence of interest.
 - Splicing Potential, a program for evaluation of pre-mRNA splicing properties.
 - GEMA (genome evolution with matrix algorithms).

COMMITTEES, THE UNIVERSITY OF TOLEDO:

Computer Cluster Management Committee (Head),

Program Bioinformatics and Genomics/Proteomics

INVITED PRESENTATIONS (selected)

- *Intron sliding during evolution*. Chicago University, Department of Ecology and Evolution. January 1998 (Oral presentation).
- *Intron sliding during evolution*. Harvard University, Biological Laboratories. May 1998 (Oral presentation).
- *Correlation of intron positions with protein module boundaries*. MIT, Seminar Series “RNA World” May 1999 (Oral presentation).
- *Hunting for exonic splicing enhancers*. Maryland University, May 14, 2001 (Oral presentation).
- *Introns in gene evolution*. SUNY at Albany, February 2002 (Oral presentation).
- *Introns in gene evolution*. Arizona State University, March 26th 2002 (Oral presentation).
- *Conceptions of intron evolution*. NCBI, December 9th 2003, Bethesda (Oral presentation)
- *Exon scrambling, repetition, and trans-splicing*. July 2005, Cold Spring Harbor (Oral presentation)
- *Bioinformatic investigation of human introns*. December 3rd 2007, Hamilton College, NY (Oral presentation)
- *Symbiotic Intron Doctrine*, May 12th 2009, Georgia Institute of Technology, Atlanta (Oral presentation)
- *Symbiotic Intron Doctrine*, May 27th 2009, Institute of Gene Biology, Moscow, Russia (Oral presentation)

CONSULTATIVE ACTIVITIES

At the University of Toledo

- Provide expertise and assistance for genomic computational problems [latest consultations in 2009 for Dr. Kahaleh (HSC UT), Dr. Cicila (HSC UT), Dr. Rais (HSC UT), Dr. Leisner (Main UT)].
- Provide the necessary computational facilities using the Bioinformatics laboratory workstations.
- Consulting for colleagues and students on gene prediction, exon/intron gene structure, and non-coding RNAs.

Collaboration within the State of Ohio

- Dr. Neocles Leontis and Craig Zirbel (BGSU)
- Dr. Lonnie Welsh (OU)

World-wide

- External Examiner for Bioinformatics, B.Sc, University of Malaya, Kuala Lumpur, Malaysia.
- Co-chairman: Moscow International Conference “Molecular Phylogenetics” May 18-21, 2010, Moscow, Russia

MAJOR SCIENTIFIC INTERESTS

- Principles of mammalian genome organization.
- Origin, evolution, and functioning of introns.
- Computer modeling of the human genome evolution.
- Structure, function, and evolution of non-protein coding RNA.

PAST RESEARCH SUPPORT, TRAINING GRANTS

Start-up funds for Bioinformatics Laboratory, University of Toledo (2003-2006)

NSF CAREER Development award MCB-0643542

Title: “Investigation of intron cellular roles”

Funding agency: National Science Foundation

Period of support: from June 2007 to June 2012

PI: Alexei Fedorov, Department of Medicine, UT

CURRENT RESEARCH SUPPORT, TRAINING GRANTS

Grant #: 5RO1HL108016-04 by National Heart, Lung & Blood Institute (PI: James Willey, MD)

Project Title: Inherited genetic risk factors common to COPD and lung cancer

Project Period: 7/1/2011 – 4/30/15

Role: collaborator

PENDING RESEARCH SUPPORT, TRAINING GRANTS

Peer-reviewed PUBLICATIONS (#40 and #56 are book chapters)

71. Fedorova L, Qiu S, Dutta R, and Fedorov A. “Atlas of cryptic genetic relatedness among 1000 human genomes”.
Submitted, July 23, 2015.

70. Fedorova L and Fedorov A. Impact of mitochondria on inflammation and renal cell death in chronic kidney disease. A review. Submitted to *Biomed Research International*, 2015.
69. Qiu S and Fedorov A. “Maruyama’s allelic age revised by whole-genome GEMA simulations” *Genomics* 105:282-287, 2015.
68. Al-Khudhair A, Qiu S, Wyse M, Chowdhury S, Cheng X, Bekolsynov D, Fedorova L, Fedorov A. An exhaustive computation of the differences between 1092 sequenced human genomes. “Inference Of Distant Genetic Relations In Humans Using “1000 Genomes”” *Genome Biol Evol* 7:481-492, 2015.
67. Gorlova O, Fedorov A, Logothetis C, Amos C, and Gorlov I. Genes with a large intronic burden show greater evolutionary conservation at the protein level. *BMC Evolutionary Biology*. 2014,14(1):50. PMID:24629165
66. Saha-Mandal A, Cheng X, Qiu S, Serpen J, Fedorova L, Fedorov A. What do 1000 genomes tell us about Biased Gene Conversion hypothesis? *Under review in Gene*, 2014.
65. Qiu S, Mcsweeny A, Choulet S, Saha-Mandal A, Fedorova L, and Fedorov A. Genome Evolution by Matrix Algorithms (GEMA): Cellular Automata Approach to Population Genetics. *Genome Biol Evol*. 2014, 6(4):988–999; *PubMed PMID:24723728*.
64. Akkuratov E, Walters L, Saha-Mandal A, Khandekar S, Crawford E, Zirbel CL, Leisner S, Prakash A, Fedorova L, Fedorov A. “Bioinformatics analysis of plant orthologous introns: identification of an intronic tRNA-like sequence”. *GENE*, 2014, 548:81-90.
63. Nabiyouni M., Prakash A., Fedorov A. “Vertebrate codon bias suggest a highly GC-rich ancestral genome”. *Gene*, 2013;519(1):113-119.
62. He J., Shepard S.S., Fedorov A., Leisner S. “Identification of candidate genes regulated through argonaute4-dependent RNA-dependent DNA methylation in Arabidopsis.” *Under revision for Gene*.
61. Shepard S., McSweeney A., Serpen G., Fedorov A. “Binary-absrtacted Markov models and their application to sequence classification.” *Nucleic Acids Research*, 2012, 40(11):4765-4773.
60. Yu B, Fey P, Kestin-Pilcher KE, Fedorov A, Prakash A, Chisholm RL, Wu JY. Spliceosomal genes in the D. discoideum genome: a comparison with those in H. sapiens, D. melanogaster, A. thaliana and S. cerevisiae. *Protein Cell*. 2011, May;2(5):395-409.
59. Prakash A., Bechtel J., Fedorov A. “Genomic MRI – a public resource for studying sequence patterns within genomic DNA”. *J Vis Exp*. 2011; 9;(51) pii: 2663.
58. Rearick D., Prakash A., McSweeney A., Shepard S.S., Fedorova L., and Fedorov A. “Critical association of ncRNA with introns” *Nucleic Acids Research*, 2011;39(6):2357-2366.
57. Fedorova L. and Fedorov A. “Mid-range Inhomogeneity of Eukaryotic Genomes” *TheScientificWorld Journal: Genes & Genomics*. 2011, 11:842-854.
56. Fedorov A., Fedorova L. “An Intricate Mosaic of Genomic Patterns at Mid-range Scale” Chapter for a book “Advances in Genome Sequence Analysis and Pattern Discovery”. *Science, Engineering, and Biology Informatics, Vol. 7; Eds: L. Elnitski, H. Piontkivska, and L.R.Welch. World Scientific Publishing Co. Pte. Ltd. Singapore, 2011.*
55. Shepard S., McCreary M., Fedorov A. “The peculiarities of large intron splicing in animals”, *PLoS ONE*, 2009, 4(11):e7853.
54. Prakash A., Shepard S., Mileyeva-Biebesheimer O., He J., Hart B., Chen M., Amarachiniha S., Bechtel J., Fedorov A. “Molecular forces shaping human genomic sequence at mid-range scales”, *BMC Genomics* 2009, 10:513.
53. Bechtel J.M., Wittenschlaeger T., Dwyer T., Song J., Arunachalam S., Ramakrishnan S.K., Shepard S., Fedorov A. Genomic mid-range inhomogeneity correlates with an abundance of RNA secondary structures. *BMC Genomics* 2008, 9:284.
52. Bechtel J. M., Rajesh P., Ilikchyan I., Deng Y., Mishra P.K., Wang G., Wu X., Afonin K., Grose W., Wang Y., Khuder S., and Fedorov A. Calculation of Splicing Potential from the Alternative Splicing Mutation Database *Research Notes* 2008, 1:4.
51. Bechtel J. M., Rajesh P., Ilikchyan I., Deng Y., Mishra P.K., Wang G., Wu X., Afonin K., Grose W., Wang Y., Khuder S., and Fedorov A. The Alternative Splicing Mutation Database: a hub for investigations of alternative splicing using mutational evidence. *Research Notes* 2008, 1:3.
50. Bazeley P.S., Shepelev V., Talebizadeh Z., Butler M.G., Fedorova L., Filatov V., Fedorov A. snoTARGET shows that human orphan snoRNA targets locate close to alternative splice junctions. *Gene* 2008, 408:172-179.
49. Havlioglu N., Wang J., Fushimi K., Vibranovski M.D., Kan Z., Gish W., Fedorov A., Long M., Wu J.Y. An intronic signal for alternative splicing in the human genome. *PLoS ONE* 2007, 11:e1246.
48. Fedorov A., Fedorova L. Where is the difference in the genomes of humans and annelids? *Genome Biology* 2006, Vol. 7, No. 1, Article 203, pp 1-2.
47. Shepelev V., Fedorov A. Advances in the Exon-Intron Database. *Briefings in Bioinformatics* 2006, 7: 178-185.

46. Shao X., Shepelev V., Fedorov A. Bioinformatic analysis of exon repetition, exon scrambling and trans-splicing in humans. *Bioinformatics* 2006, 22:692-698.
45. Fedorova L., Fedorov A. Puzzles of the human genome: why do we need our introns? *Current Genomics* 2005, Vol. 6, No 8, 589-595.
44. Fedorov A., Stombaugh J., Harr M.W., Yu S., Nasalean L., Shepelev V. Computer identification of snoRNA genes using a Mammalian Orthologous Intron Database. *Nucl. Acids Res.* 2005. 33, 4578-4583.
43. Fedorov A., Fedorova L. Introns: mighty elements from RNA world. *J. Molec. Evol.* 2004, 59, 718-721.
42. Fedorov A. and Hartman H. What does microsporidian *E.cuniculi* tell us about the origin of the eukaryotic cell? *J. Molec Evol.* 2004, 59, 695-702.
41. Fedorov A., Roy S., Fedorova L., Gilbert W. Mystery of intron gain. *Genome Research* 2003, 13, 2236-2241.
40. Fedorov A., Fedorova L. Exonic splicing enhancers. 2003 in *Encyclopedia of the Human Genome*, Nature Publishing Group, London, v 2, 386-391.
39. Fedorova L., Fedorov A. Introns in gene evolution. *Genetica* 2003, 118: 123-131.
38. Roy S*, Fedorov A*, Gilbert W. Large-scale comparison of intron positions in mammalian genes shows intron loss but no gain. *PNAS*, 2003, 100: 7158-7162. (*equal contribution)
37. Fedorov A., Roy S., Cao X., Gilbert W. Phylogenetically older introns strongly correlate with module boundaries in ancient proteins. *Genome Research* 2003, 13: 1155-1157.
36. Fedorov A., Merican A.F., Gilbert W. Large-scale comparison of intron positions between plant, animal and fungal genes. *PNAS*, 2002, 99, 16128-16133.
35. Roy S., Fedorov A., Gilbert W. The signal of ancient introns is obscured by intron density and homolog number. *PNAS* 2002, 99, 15513-15517.
34. Hartman H. & Fedorov A. The origin of the eukaryotic cell – a genomic investigation. *PNAS* 2002, 99, 1420-1425.
33. Fedorov A., Saxonov S., Gilbert W. Regularities of context-dependent codon bias in eukaryotic genes. *Nucl.Acids Res.* 2002, 30 (5), 1192-1197.
32. Endo T., Fedorov A., DeSouza S., Gilbert W. Do introns favor or avoid regions of amino acid conservation? *Mol.Biol.Evol.* 2002, 19, 521-525.
31. Roy S., Lewis B., Fedorov A., Gilbert W. Footprints of primordial introns on the eukaryotic genome *TIG* 2001, 17, 496-499.
30. Fedorov A., Cao X., Saxonov S., DeSouza S., Roy S.W., Gilbert W. Intron distribution difference for 276 ancient and 131 modern genes suggests the existence of ancient introns. *PNAS* 2001, 98, 13177-13182.
29. Fedorova L., Daizadeh I., Fedorov A., Ryskov A.P. *In silico* analysis of the restriction fragment length distribution of the human genome. *Genetika (Russian)* 2001, 37, 456-466.
28. Fedorov A., Saxonov S., Fedorova L., Daizadeh I. Comparison of intron-containing and intron-lacking genes elucidates putative exonic splicing enhancers. *Nucl. Acids Res.* 2001, v. 29, 1464-1469.
27. Saxonov S., Daizadeh I., Fedorov A., Gilbert W. EID: The Exon-Intron Database: An exhaustive database of protein-coding intron-containing genes. *Nucleic Acids Res.*, 2000, 28, 185-190.
26. Fedorov A., Fedorova L., Grechko V.V., Ryabinin D., Sheremet'eva V.A., Bannikova A.A., Lomov A.A, Ryskov A.P, Darevsky I.S. Variable and invariable DNA repeat characters revealed by taxonprint approach is useful for molecular systematics. *J Mol. Evol.* 1999, 48, 69-76.
25. Fedorov A., Johnston H., Korneev S., Blackshaw S., Davies J. Cloning, characterization and expression of the alpha-tubulin genes of the leech *Hirudo medicinalis*. *Gene*, 1999, 227, 11-19.
24. Fedorov A., Starshenko V., Fedorova L., Filatov V., Grigor'ev E. Influence of exon duplication and shuffling on intron phase distribution. *J. Mol. Evol.* 1998, 46, 263-271.
23. Korneev S., Fedorov A., Collins R., Blackshaw S.E., Davies J.A. A subtractive cDNA library from an identified regenerating neuron is enriched in sequences up-regulated during nerve regeneration. *Invertebrate Neuroscience*, 1997, 3, 185-192.
22. Grechko V.V., Fedorova L.V., Fedorov A.N., Slobodyanyuk S.Ya., Ryabinin D.M., Melnikova M.N., Bannikova A.A., Lomov A.A., Sheremet'eva V.A., Gorshkov V.A., Sevostyanova G.A., Semenova S.K., Ryskov A.P., Mednikov B.M., Darevsky I.S. Restriction endonuclease analysis of highly repetitive DNA as a phylogenetic tool. *J. Mol. Evol.* 1997, 45, 332-336.
21. Grechko V.V., Ryabinin D.M., Fedorova L., Fedorov, A., Ryskov A.P., Darevski I.S. Parentage of Caucasian parthenogenetic rock lizard species (*Lacerta*) as revealed by restriction endonuclease analysis of highly repetitive DNA. *Amphibia-Reptilia* 1997, 18, 407-418.
20. Fedorov A., Nasyrova F., Bocharova T., Smirnova E., Limborska S.A. G - C in IVS-I,-I, and C - G in -42 of promoter region of beta-globin gene in Tajikistan. *Hemoglobin*, 1993, 17, 275-278.
19. Fedorov A., Suboch G., Bujakov M., Fedorova L. Analysis of nonuniformity in intron phase distribution. *Nucleic Acids Res.*, 1992, 20, 2553-2557.

18. Fedorov A.N., Rasulov E.M., Smirnova E.A., Bocharova T.N., Limborska S.A. The T-A mutation at position -30 of the β -globin gene found in a Karachai patient with β -thalassemia intermedia. *Hemoglobin*, 1992, 16, 521-523.
17. Limborska S.A., Fedorov A.N., Prosnjak M.I., Vlasov M.S., Barysheva E.V., Rasulov E.M. The investigation of mutant genes and human normal polymorphism. in: *Metabolism and enzymology of nucleic acids including gene and protein engineering*, edited by J. Balan, 1991, 7, 247-253, Slovak Academy of Sciences, Bratislava, Czechoslovakia.
16. Limborska S.A., Fedorov A.N., Bukhman V.L., Prosnjak M.I. Detection of beta-globin intron mutation in a beta-thalassemic patient from Azerbaijan. in: *Metabolism and enzymology of nucleic acids including gene manipulations*, edited by J. Zelinka and J. Balan, 1988, 6, 197-201, Plenum Press, New York and London.

PUBLICATIONS IN INTERNATIONALLY RECOGNISED RUSSIAN JOURNALS:

15. Grechko V.V., Ryabinin D.M., Fedorova L.V., Rudykh I.A., Fedorov A.N., Ryskov A.P., Semenova S.K., Darevskii I.S. DNA –taxonprints of some Lacertidae lizards – taxonomic and phylogenetic implications. *Molecular Biology* (Russian), 1998, 32, 151-160.
14. Grechko V.V., Fedorova L.V., Fedorov A.N., Slobodyanyuk S.Y., Ryabinin D.M., Melnikova M.N., Bannikova A.A., Lomov A.A., Sheremeteva V.A., Gorshkov V.A., Sevostyanova G.A., Semenova S.K., Ryskov A.P., Mednikov B.M., Darevskii I.S. Restriction endonuclease analysis of highly repeated DNA sequences sheds light on genetic relatedness of lower taxa of animals. *Molecular Biology* (Russian), 1997, 31, 202-209.
13. Bannikova A.A., Dolgov V.A., Fedorova L.V., Fedorov A.N., Lomov A.A., Mednikov B.M. Divergence of shrews (Insectivora, Soricidae) from the data of DNA restriction analysis. *Zoologicheskyy zhurnal* (Russian), 1996, 75, 256-270.
12. Bannikova A.A., Dolgov V.A., Fedorova L.V., Fedorov A.N., Troitsky A.V., Lomov A.A., Mednikov B.M. Taxonomic relationships among hedgehogs of the subfamily Erinaceinae (mammal, Insectivora) determined basing on the data of restriction-endonuclease analysis of total DNA. *Zoologicheskyy zhurnal* (Russian), 1995, 74, 95-106.
11. Bannikova A.A., Fedorova L.V., Fedorov A.N., Troitsky A.V., Grechko V.V., Dolgov V.A., Lomov A.A., Mednikov B.M. Comparison of DNA repeats elements of mammals fam. Erinacea using restriction analysis. *Genetika* (Russian), 1995, 31, 1498-1506.
10. Slobodyanyuk S.Y., Pavlova M.E., Fedorov A.N., Belikov S.I. Bsp-family of tandemly repeated DNA-sequences of Baikal cottoid fishes (Cottoidea). *Molecular Biology* (Russian), 1994, 28, 282-288.
9. Lebedeva I.V., Ivanovskaya M.G., Fedorov A.N., Limborskaya S.A., Shabarova Z.K. New method of nonradioactive labeling of oligonucleotides and their use as allele-specific probes for mutations causing beta-thalassemia. *Molecular biology* (Russian), 1994, 28, 521-526.
8. Grechko V.V., Ryabinin D.M., Fedorova L.V., Fedorov A.N., Darevskii I.S., Ryskov A.P. DNA taxonprint analysis of family Lacertidae species. *Molecular Biology* (Russian), 1993, 27, 883-890.
7. Grechko V.V., Ryabinin D.M., Fedorova L.V., Fedorov A.N., Darevskii I.S., Ryskov A.P. DNA taxonprint analysis of certain lizard species from the Lacertidae family. *Molecular Biology* (Russian), 1993, 27, 1404-1414.
6. Fedorov A.N., Suboch G.M., Buiakov M.I., Fedorova L.V. Study of the minimum frequency of phase 2 introns. . *Molecular Biology* (Russian), 1993, 27, 519-530.
5. Fedorov A.N. Investigation of beta-globin gene mutations in certain regions of the Caucasus and Central Asia. In: Autoreferat, Moscow, 1992.
4. Fedorov A.N., Grechko V.V., Slobodyanyuk S.Ya., Fedorova L.V., Timochina G.I. Taxonomic analysis of DNA repeated sequences. *Molecular Biology* (Russian), 1992, 26, 464-469.
3. Limborskaya S.A., Bukhman V.L., Prosnjak P.M., Fedorov A.N., Slominsky P.A., Ninkina N.N., Ryskov A.P. Molecular investigation of thalassemia .4. Cloning of beta-globin gene of beta-thalassemic patient from Azerbaijan and determination of a point mutation in minor intron. *Genetika* (Russian), 1987, 23, 228-238.
2. Moskaleva E.I., Iliushina N.A., Zakharov V.N., Fedorov A.N., Karaulov A.V. DNA repair capacity of peripheral blood lymphocytes from healthy donors. *Terapevticheskii Arkhiv* 57 116-118, 1985.
1. Egorov V.S., Fedorov A.N. Anomaly in lithium-magnesium alloys. *JETP letters*, 1982, 35, 462-465.