

Genomová biologie: studium evoluce a funkce živých organismů pomocí genomických a bioinformatických přístupů

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Složení týmu:

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Vybrané publikace členů týmu v roce 2013:

- Bartáková V, Reichard M, Janko K, Poláčik M, Blažek R, Reichwald K, Cellerino A, Bryja J (2013) Strong population genetic structuring in an annual fish, *Nothobranchius furzeri*, suggests multiple savannah refugia in southern Mozambique. *BMC Evolutionary Biology* 13:196 (EVOLUTIONARY BIOLOGY 19/47, GENETICS & HEREDITY 61/161)
- Bolfíková B, Konečný A, Pfäffle M, Skuballa J, Hulva P (2013) Population biology of establishment in New Zealand hedgehogs inferred from genetic and historical data: Conflict or compromise? *Molecular Ecology* 22: 3709–3720. (BIOCHEMISTRY & MOLECULAR BIOLOGY 38/290, ECOLOGY 10/136, EVOLUTIONARY BIOLOGY 6/47)
- Collén J, Porcel B, Carré W, Ball S, Chaparro C, Tonon T, Barbeyron T, Michel G, Noel B, Valentin K, Eliáš M, Artiguenave F, Arun A, Aury JM, Barbosa-Neto JF, Bothwell JH, Bouget FY, Brillet L, Cabello-Hurtado F, Capella-Gutierrez S, Charrier B, Cladiere L, Cock JM, Coelho SM, Colleoni C, Czjzek M, Da Silva C, Delage L, Denoëud F, Deschamps F, Dittami SM, Gabaldón T, Gachon CMM, Groisillier A, Hervé C, Jabbari K, Katinka M, Kloareg B, Kowalczyk N, Labadie K, Leblanc C, Lopez PJ, McLachlan D, Meslet-Cladiere L, Moustafa A, Nehr Z, Nyval-Collén P, Panaud O, Partensky F, Poulain J, Rensing SA, Rousvoal S, Samson G, Symeonidi A, Weissenbach J, Zambounis A, Wincker P, Boyen C (2013) Genome structure and metabolic features in the red seaweed *Chondrus crispus* shed light on evolution of the Archaeplastida. *Proceedings of the National Academy of Sciences of the United States of America* 110:5247-5252. (MULTIDISCIPLINARY SCIENCES 4/56)
- Dool SE, Puechmaille SJ, Dietz C, Juste J, Ibáñez C, Hulva P, Roué SG, Petit EJ, Jones G, Russo D, Toffoli R, Viglino A, Martinoli A, Rossiter SJ, Teeling EC (2013) Phylogeography and postglacial recolonization of Europe by *Rhinolophus hipposideros*: Evidence from multiple genetic markers. *Molecular Ecology* 22: 4055–4070. (BIOCHEMISTRY & MOLECULAR BIOLOGY 38/290, ECOLOGY 10/136, EVOLUTIONARY BIOLOGY 6/47)
- Eliáš M, Neustupa J, Pažoutová M, Škaloud P (2013) A case of taxonomic inflation in coccoid algae: *Ellipsoidion parvum* and *Neocystis vischeri* are conspecific with *Neocystis* (= *Nephrوديella*) *brevis* (Chlorophyta, Trebouxiophyceae). *Phytotaxa* 76:15-27. (PLANT SCIENCES 98/197)
- Flegontov P, Votýpka J, Skalický T, Logacheva MD, Penin AA, Tanifuji G, Onodera NT, Kondrashov AS, Archibald JM, Lukeš J (2013) Paratrypanosoma is a novel early-branching trypanosomatid. *Curr Biol.* 23:1787-93. (BIOCHEMISTRY & MOLECULAR BIOLOGY 19/290, CELL BIOLOGY 22/185)
- Fulnečková J, Ševčíková T, Fajkus J, Lukešová A, Lukeš M, Vlček Č, Lang BF, Kim E, Eliáš M, Sýkorová E (2013) A broad phylogenetic survey unveils the diversity and evolution of telomeres in eukaryotes. *Genome Biology and Evolution* 5:468-483. (EVOLUTIONARY BIOLOGY 10/47, GENETICS & HEREDITY 27/161)
- Gaysina L, Němcová Y, Škaloud P, Ševčíková T, Eliáš M (2013) *Chloropyrula uraliensis* gen. et sp. nov. (Trebouxiophyceae, Chlorophyta), a new green coccoid alga with a unique ultrastructure, isolated from soil in South Urals. *Journal of Systematics and Evolution* 51:476-484. (PLANT SCIENCES 70/197)

- Grskovic B, Zidkova A, Stenzl V, Popović M, Primorac D, Mršić G (2013) Analysis of 8 X-chromosomal markers in the population of central Croatia. *Croat Med J* 54:238-247. (MEDICINE, GENERAL & INTERNAL 72/155)
- Choleva L, Musilova Z, Kohoutova-Sediva A, Paces J, Rab P, Janko K (2013) Distinguishing between incomplete lineage sorting and genomic introgressions: complete fixation of allospecific mitochondrial DNA in a sexually reproducing fish (Cobitis; Teleostei), despite clonal reproduction of hybrids.. 2013. Plos ONE, accepted MS. (MULTIDISCIPLINARY SCIENCES 7/56)
- Iakovenko N, Kasparova E, Plewka M, Janko K (2013). Key to species of the Genus *Otostephanos* Milne, 1916 (Rotifera, Bdelloidea, Habrotrichidae) with the description of two new species. *Systematics and Biodiversity*, in press. (BIODIVERSITY CONSERVATION 15/40)
- Janko K (2013) Let's not be unfair to asexuals; their ephemerality may be explained by neutral models without invoking any evolutionary constraints of asexuality. *Evolution*, in press (ECOLOGY 17/136, EVOLUTIONARY BIOLOGY 9/47, GENETICS & HEREDITY 24/161)
- Janouškovec J, Sobotka R, Lai DH, Flegontov P, Konik P, Komenda J, Ali S, Prášil O, Pain A, Oborník M, Lukeš J, Keeling PJ (2013) Split photosystem protein, linear-mapping topology, and growth of structural complexity in the plastid genome of *Chromera velia*. *Mol Biol Evol*. 2013 Sep 18 [Epub ahead of print]. (BIOCHEMISTRY & MOLECULAR BIOLOGY 14/290, EVOLUTIONARY BIOLOGY 4/47, GENETICS & HEREDITY 8/161)
- Kočárek P, John V, Hulva P (2013) When the body hides the ancestry: Phylogeny of morphologically modified epizoic earwigs based on molecular evidence. *PLOS ONE* 8, e66900. (MULTIDISCIPLINARY SCIENCES 7/56)
- Koubínová D, Irwin N, Hulva P, Koubek P, Zima J (2013) Hidden diversity in Senegalese bats and associated findings in the systematics of the family Vespertilionidae. *Frontiers in Zoology* 10: 48. (ZOOLOGY 2/151)
- Porcel BM, Denoëud F, Opperdoes F, Noel B, Hammarton TC, Field MC, Da Silva C, Couloux A, Poulain J, Jabbari K, Aury JM, Campbell DA, Cintron R, Dickens N, Docampo R, Sturm NR, Koumandou VL, Fabre S, Flegontov P, Lukeš J, Michaeli S, Mottram JC, Szöör B, Zilberstein D, Bringaud F, Wincker P, Dollet M (2013) Comparison of *Phytomonas* genomes reveals genome contraction with minimal changes of gene repertoire, regardless of pathogenic or non-symptomatic life styles. *PloS Genetics*, in press. (GENETICS & HEREDITY 12/161)
- Ptáčková E, Kostygov AY, Chistyakova LV, Falteisek L, Frolov AO, Patterson DJ, Walker G, Cepicka I (2013) Evolution of Archamoebae: Morphological and Molecular Evidence for Pelobionts Including Rhizomastix, Entamoeba, Iodamoeba, and Endolimax. *Protist* 164:380-410. (MICROBIOLOGY 26/116)
- Schlacht A, Mowbrey K, Elias M, Kahn RA, Dacks JB (2013) Ancient complexity, opisthokont plasticity and discovery of the 11th subfamily in the Arf GAP proteins. *Traffic* 14:636-649. (CELL BIOLOGY 54/185)
- Ševčíková T, Bišová K, Fojtová M, Lukešová A, Hřčková K, Sýkorová E (2013) Completion of cell division is associated with maximum telomerase activity in naturally synchronized cultures of the green alga *Desmodesmus quadricauda*. *FEBS Letters* 587:743-748. (BIOCHEMISTRY & MOLECULAR BIOLOGY 97/290; BIOPHYSICS 18/72; CELL BIOLOGY 80/185)
- Votýpka J, Suková E, Kraeva N, Ishemgulova A, Duží I, Lukeš J, Yurchenko V (2013) Diversity of trypanosomatids (Kinetoplastea: Trypanosomatidae) parasitizing fleas (Insecta: Siphonaptera) and description of a new genus *Blechomonas* gen. n. *Protist* 164:763-781. (MICROBIOLOGY 26/116)
- Zidkova A, Capek P, Coufalova P (2013) X-STR Decaplex study on population of the Czech Republic. *Int J Leg Med*, in press, (MEDICINE, LEGAL 3/16)
- Zidkova A, Horinek A, Kebrdlova V, Korabecna M (2013) Application of the new insertion-deletion polymorphism kit for forensic identification and parentage testing on the Czech population. *Int J Leg Med* 127:7-10. (MEDICINE, LEGAL 3/16)
- Zidkova A, Horinek A, Stenzl V, Popovic M, Primorac D, Mršić G (2013) Analysis of multifactor dimensionality reduction analysis and bayesian networks for eye color and ancestry prediction for forensic purposes in the Czech Republic. *Forensic Sci Int Genet*, in press (MEDICINE, LEGAL 5/16)

Anotace výzkumného programu

Life Science Research Centre as the platform for genomics and bioinformatics at the University of Ostrava

The interests of the individual researchers of the LSRC are broad. Below we provide an overview of main directions of research to be pursued in the next three years (2014-2016):

Area 1 – genomics and transcriptomics of evolutionarily of biotechnologically significant groups of protists (principal investigator M. Eliáš):

The research in Eliáš lab focuses on the biology of unicellular eukaryotes (protists) using molecular biological and genomics approaches. The majority of the research activities will relate to two projects supported by the Czech Science Foundation – “Unravelling the early evolution of the eukaryotic cell through exploring the genomes of the eukaryotic superphylum Discoba” (PI M. Eliáš) and “A genomic approach to unravelling the biology and evolution of eustigmatophyte algae” (co-PI M. Eliáš, PI Miroslav Oborník, Biology centre ASCR, České Budějovice). The primary goal of these projects is to characterize the genomes and gene complements in several groups of protists interesting from the evolutionary or biotechnological perspective.

Area 2 – genome biology of kinetoplastid parasites (principal investigator V. Yurchenko):

- Comparative transcriptomic analysis of virulent and avirulent isolates of *Leishmania*.
- Whole expression profiles for different developmental stages of *Leishmania* differentiation.
- Mechanisms of high-temperature adaptation in monoxenous Trypanosomatidae.
- Population genetics in Trypanosomatidae.
- Comparative transcriptomic analysis of different morphotypes of *Paratrypanosoma sp.*
- Comparative genomics of dixenous (*Leishmania*) and monoxenous (*Leptomonas*) Trypanosomatidae.
- Functional genomics..

Area 3 – population genomics (principal investigator P. Hulva):

Understanding the processes behind speciation and adaptive radiation is the basis for understanding the mechanisms of evolution. Within the rising paradigmatic shift, the level of population biology and process-based interpretations are key approaches for understanding the species phenomenon. Many marked evolutionary changes, which could culminate into speciation, are connected with demography of bottleneck, as described in the shifting balance theory and models connected with the founder effect, that is, genetic revolutions model, founder flush model or transience model.

Area 4 – genomic approaches towards understanding the evolution of clonal vertebrates (principal investigator K. Janko)

The primary aim of my team focuses at evolution of asexual reproduction in a model group of spined loaches. This group of fish comprises several sexually reproducing species as well as their hybrids with clonal reproduction. We have adopted a multidisciplinary approach towards understanding the evolutionary history of asexually reproducing clones, including ecological investigations, reproductive experiments, and genomic analyses.

Area 5 – using genomics and bioinformatics to address salient biological questions (principal investigator P. Flegontov)

- Evolutionary genomics of protists, especially of the super-phylum Excavata.
- Development of accessory tools for genome assembly finishing and genome annotation.
- Genetic anthropology.