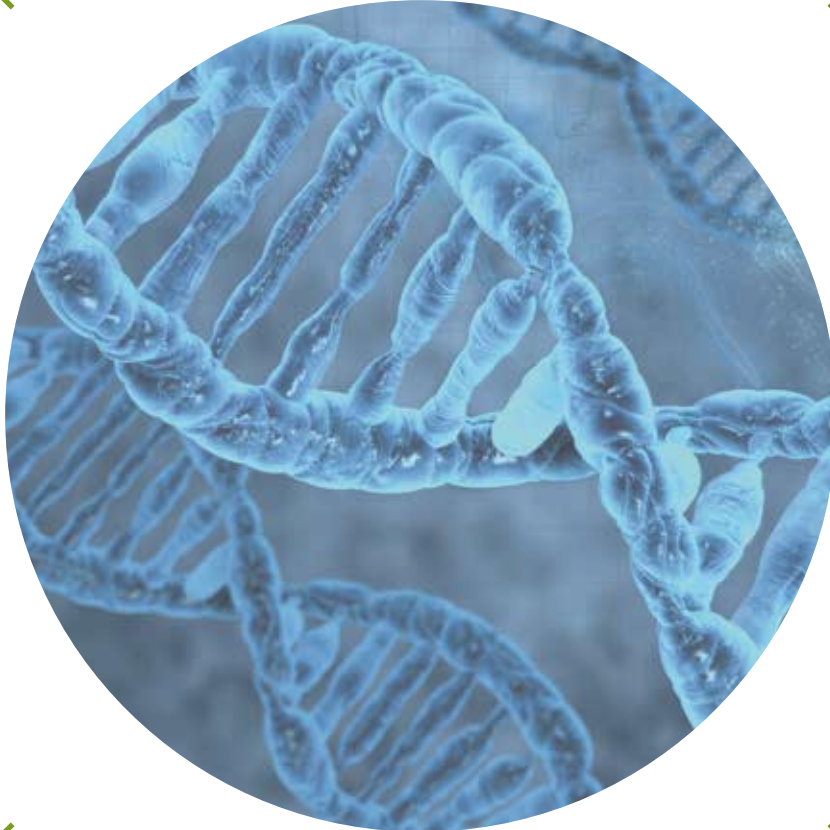


Faculty of Science University of Ostrava



**GENOMIC BIOLOGY**

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## GENOMIC BIOLOGY

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Biology is undergoing a transformation that is unparalleled in the history of this field in its pace and scope. While in the 20th century, physicists were fascinating the world with their revolutionary theories about the nature of the world, our century will apparently belong to biologists. Its first fifth certainly indicates this, and the genome, i.e. a set of all genes of a given organism (according to one of the possible definitions), has become the key concept of biology in this period. The „reading“ of the human genome has become a generally known milestone in the first decade of the 21st century. Nevertheless, this human spirit triumph - in terms of technology and ability of cooperation across nations and cultures - reflects a radical change in the possibilities of the biology as a whole, not only its parts dealing solely with the human. Biology at the University of Ostrava does not stand aside from this development, but, on the contrary, it tries to participate maximally in it. And you can see it for yourself also in this bulletin.

#genome #genomics  
#DNA #organisms  
#evolution #protists

## GENOMIC BIOLOGY

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The development of DNA sequencing methods and the exponentially growing volume of genomic data represent one of the primary impulses in biology development in the last twenty years. The availability of genomic sequences from a rapidly increasing number of organisms and the current possibility to sequence genomes and transcriptomes of organisms of interest also in laboratories outside large genomic centres have entirely changed the nature of the biological research - democratizing it to such an extent that essential discoveries can now be made anywhere with only a computer connected to the Internet. „As I said in an interview for a Czech daily newspaper years ago, after a large study of a genome of one interesting plant had been published in the Science journal, to which I had the honour to contribute, today you can make the excellent science from the living room. This is still true,“ comments the situation prof. Eliáš, the guarantor of the leading research direction „Genomic Biology“ at the University of Ostrava and the head of the Life Science Research Centre (LSRC), the informal research unit within the Faculty of Science of the University of Ostrava, associating several teams connected by the common interests and shared infrastructure.

Genomic and transcriptomic data are real treasury of biology. Their analysis using various methods of bioinformatics, in the first place, enables to know the gene repertoire of organisms and its evolutionary history in an unprecedented way. However, the results of such analyses also represent a starting point for the subsequent research in the field of the functioning of living systems at the level of individual genes, molecular modules, cells, and whole organisms. Here, the genomics and bioinformatics meet with the „traditional“ molecular and cellular biology, biochemistry and genetics, the cultivation of which can no longer be done without the proper background of modern research laboratories.

*„The conditions for the experimental biological research at the Faculty of Science of the University of Ostrava have dramatically improved over the last ten years thanks to the joint efforts of many colleagues and the support from European Union funds and other sources. So, we can immediately develop the results of our computer analyses at home, and we do not just rely on colleagues from elsewhere,“* states prof. Eliáš with pleasure.

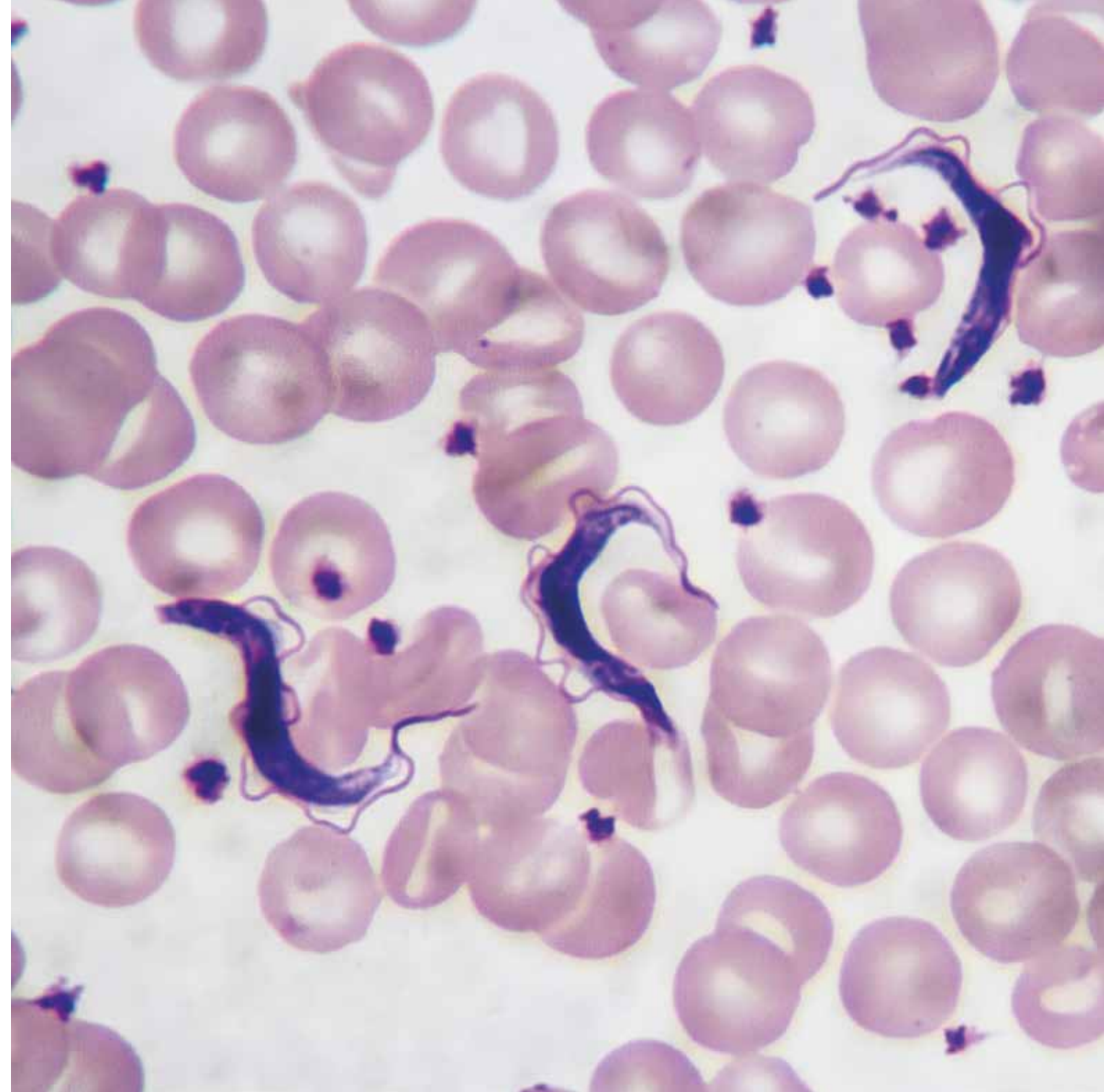
However, the phenomena that biologists mainly study are universal and extremely complex, which automatically means that quality biological research today is unthinkable without extensive cooperation. Therefore, the biologists from LSRC actively cooperate with many teams in the country and abroad, with which they are connected not only by friendly relations and common interests, but also by the complementarity of the owned know-how, and the biological material itself. As regards the domestic workplaces, the most important is the cooperation with the colleagues from the Faculty of Science of Charles University and the Biology Centre of the Czech Academy of Sciences, with whom our researchers solve joint GACR projects and form a joint Centre for Research of Pathogenicity and Virulence of Parasites, that draws the support from the OP RDE sources under the „Excellent Research“ call in the years 2018 to 2022. The foreign cooperation includes the colleagues from Europe (Portugal, Lithuania, Russia), overseas (Canada, USA), but also the Far East (Japan, Singapore). The cooperation of the team of dr. Flegontov with prof. David Reich of Harvard Medical School in Boston, the world's leading expert in the study of the human (pre)history through genomic methods, is very prestigious. This collaboration also resulted in perhaps the greatest publication success to date of the biologists from the University of Ostrava, an article published in the journal Nature in 2019 revising the existing perspectives on peopling of the areas around the Bering Strait.

*„During the few years since our informal group at the University of Ostrava has been active, a number of things have succeeded; not only many interesting discoveries leading to the quality and widely quoted publications or securing financial funds for our scientific activities, but primarily, this concept created an international team of the science-passionate people hard-working in a friendly atmosphere, that has produced and sent to the world many quality doctoral graduates or more experienced post-docs, who spread the good name of our university elsewhere. And I am delighted about that,“* prof. Eliáš concludes.

## FUNCTIONAL GENOMICS AND MOLECULAR BIOLOGY OF HUMAN PATHOGENS

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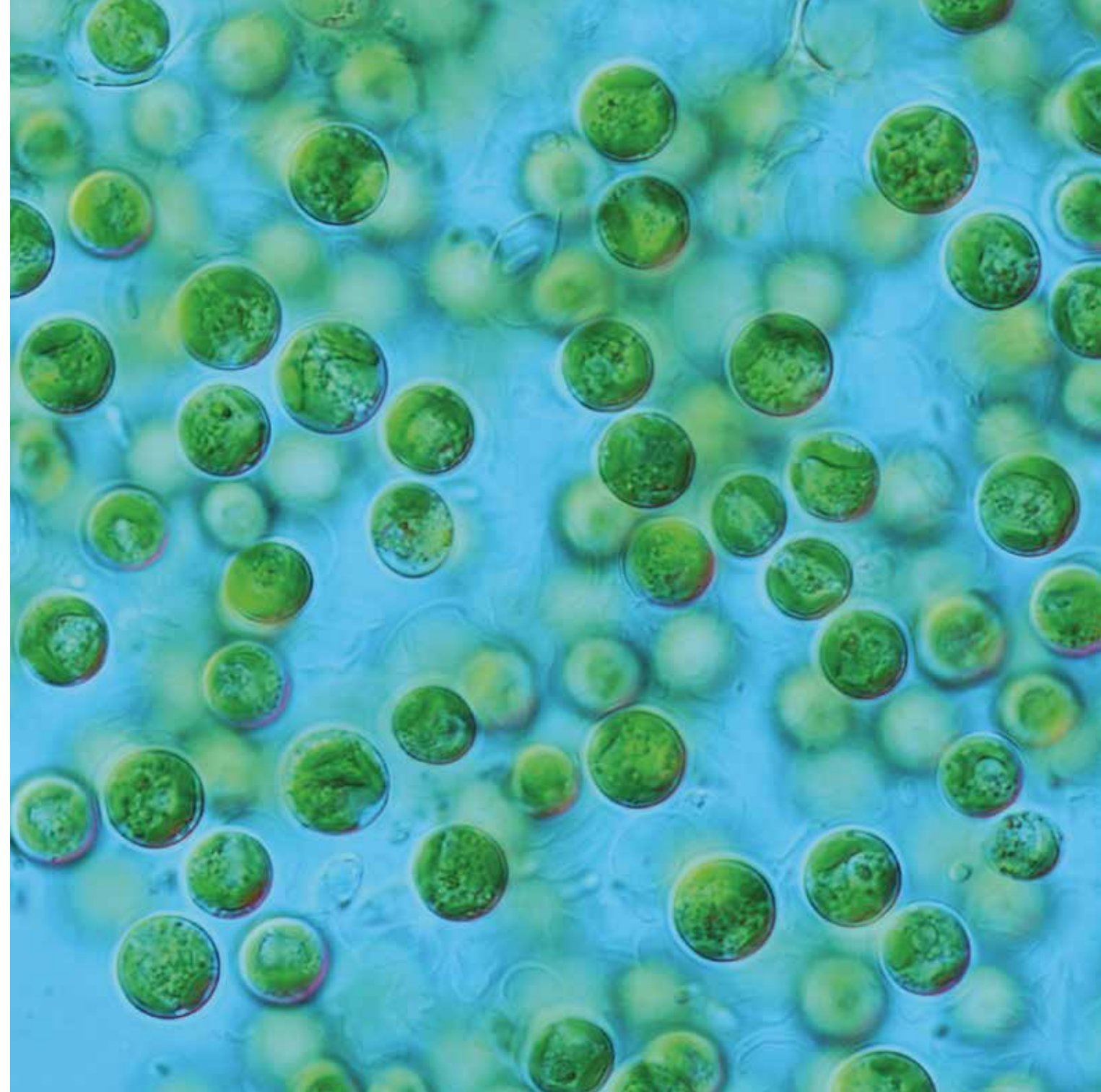
The interest of biologists is not distributed among different organismic groups evenly. In addition to spectacular forms such as elephants or orchids, the special attention is naturally attracted also by those, the research of which is motivated by the motto „know your enemy“. At the University of Ostrava, trypanosomatids are such a group, i.e. parasitic flagella including not only the sleeping sickness originator (*Trypanosoma brucei*), but also other human endangering relatives (*Trypanosoma cruzi* causing Chagas' disease or the leishmaniasis originator, i.e. *Leishmania major*). Therapeutic options are still insufficient in the case of infections caused by trypanosomatids, and, understandably, a careful basic research of the biology of this group is necessary for further development in this area. The research team of prof. Yurchenko concentrates on it, using a wide range of molecular biological and genomic approaches summarized in the term „functional genomics“ to describe the life processes of trypanosomatids at the molecular level. The primary research model is *Leishmania mexicana*, at which our biologists have developed a method of targeted genetic manipulations using a modern tool known as CRISPR / Cas9 (Nobel Prize in Chemistry 2020). One of the goals of the research of prof. Yurchenko is to identify the genes that are responsible for the ability of these pathogens to attack the host organism and cause disease states.



## PHYLOGENOMICS AND COMPARATIVE GENOMICS

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The genomes of organisms are the products of evolution and carry their history with them, hidden in their current form, i.e. the sequence of basic letters of the DNA alphabet. For more than half a century, biologists have been researching genomes as historical documents, from which it is possible to read how individual groups of organisms have gradually changed and differentiated. Whereas in the past, for technical reasons, this research had to be limited to small fragments of genomes, i.e. specific selected genes, today's methods make it possible to analyse practically entire genomes. The result is breath-taking progress in fulfilling Charles Darwin's ancient dream of the „tree of life“ reconstruction, thus an imaginary genealogy depicting the relationship among the single lines of organisms. And not only that: genomics allows to wrap this „phylogenetic skeleton“ with meat, i.e. to learn how the properties of organisms at individual gene levels, proteins, functional pathways, cell structures, etc., were changing in various evolutionary lines. Biologists at the University of Ostrava, mainly (but not only) from the team of prof. Eliáš, contribute to this superb scientific project by their considerable work. Their interest is primarily focused on microbial eukaryotic organisms alias protists (algae and protozoa), whose variety at the molecular and cellular level dramatically exceeds the diversity that we find in plants and animals altogether. Using own newly generated genomic sequences and data, which are available in genomic databases, our biologists uncover the structure of various branches of the eukaryotic tree of life, search for the image of the common ancestor of all eukaryotes, research the evolution of the genetic code, reconstruct the evolutionary history of interesting gene families, and discover much more.



## EVOLUTION AND BIOLOGY OF CELL ORGANELS

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One of the most remarkable findings that biology has made in the last half-century is that eukaryotic cells, including us ourselves, were formed by the connection of at least two initially independent partners, one of which, in dramatically modified form, represents a cellular organelle called mitochondria today. At some eukaryotes - algae and plants, another distinctive organelle, a plastid (also known as a chloroplast), was later developed from another - photosynthesizing - endosymbiont. The origin of organelles from endosymbiotic bacteria is also evidenced by the fact that these cellular structures have kept their own genomes. The history of the origin of these organelles and their subsequent differentiation in different groups of eukaryotes represents a hugely impressive, complex, and still undescribed chapter of biology in which also our scientists, especially the team of prof. Eliáš, are interested. They sequence and analyse the genomes of organelles, identify proteins and functional pathways localized into organelles, and monitor plastid transfers among distant eukaryotic lines. One of the most important outputs of their work is the characterization of new, hitherto unsuspected functional systems of mitochondria, the existence of which further strengthens a „bacterial character“ of this organelle.

## INTERNAL CELL BIOSPHERE: WANTED AND UNWANTED PARTNERS

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The human individual is, in fact, a conglomerate of various organisms, the so-called holobiont, the form of which is surprisingly decided by its microbial component, traditionally said a microflora, in a modern language a microbiome. But, as well, single-celled eukaryotic organisms which inside their bodies - separate cells - can host a surprising diversity of microscopic entities, especially bacteria and viruses, can have their kind of a microbiome. It is often a matter of unwanted partners, explicitly harmful to their host, but, sometimes, such an inhabitant of the cell' interior is a welcome partner, called as a mutualist in the jargon of ecology. The existence of endosymbionts and viruses in protozoan and algal cells has been known for a long time, but only genomics reveals the true extent of this phenomenon and makes it much easier to gain insight into the nature of these entities' relationships with host organisms. A significant part of the research activities of our biologists associated in the Life Science Research Centre is to study just endosymbionts and protist viruses, especially two main model groups - trypanosomatids and eustigmatophyte algae. To give one example of success in this field, the choice is clear: the work result of the team of prof. Yurchenko, who revealed the existence of an entirely new virus infecting trypanosomatids. The virus was named Ostravirus in honour of the site of the discovery, and the relevant study was published in the prestigious *PNAS* journal in 2018.

## HISTORY OF HUMAN POPULATIONS

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Today, archaeology routinely utilizes DNA sequencing possibilities to study ancient human cultures, including domestic animals, crops, and pathogens. The genomes of thousands of ancient human individuals from around the world have already been sequenced, on a timeline from Neanderthals to the recent past, and in geographic space from the poles to the tropics. This influx of new data not only changes the archaeology and allows us to describe our complicated past in an unprecedented way, but also has significant benefits for understanding the genetic origin of human diseases. In the last decade, a standard set of statistical tools for reconstructing demographic history from genomic data was developed, and was used in countless publications. As it has been revealed, also thanks to the work of our dr. Flegontov group' biologists, these tools suffer from significant limitations and shortcomings. Therefore, one of the main activities of our human population genomics' team is the development of new methods and robust protocols for testing models of demographic history, which would overcome the problems of currently popular methods of archaeogenetics. Our experts and their foreign collaborators apply these new methods in the study of the prehistory of America, Siberia, Southeast Asia, and Europe.



## SIGNIFICANT PROJECTS

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Genomic formation of Indo-Europeans: new approaches to genetic admixture modelling guided by simulated data (GAČR 21-27624S), solver: M.Sc. Pavel Flegontov, Ph.D., period: 01.01.2021 – 31.12.2023, the total grant for UO: 5 242 000,- CZK

Trypanosomatids with in-frame sense stop codons: dissecting molecular mechanisms behind the unique ambiguity of the genetic code (GAČR 18-15962S), solver: Assoc. Prof. Vyacheslav Yurchenko, Ph.D., co-solver: prof. RNDr. Julius Lukeš, CSc. (Biology Centre CAS), period: 01.01.2018 – 31.12.2020, the total grant for UO: 3 654 000,- CZK

Catalase: to be or not to be in two hosts (GAČR 21-09283S), solver: prof. Vyacheslav Yurchenko, Ph.D., co-solver: prof. RNDr. Julius Lukeš, CSc. (Biology Centre CAS), period: 01.01.2021 – 31.12.2023, the total grant for UO: 5 622 000,- CZK

Molecular mechanisms and evolution of RNA polyadenylation in euglenophyte plastids (GAČR 21-19664S), solver: prof. Mgr. Marek Eliáš, Ph.D., co-solver: Assoc. Prof. Mgr. Štěpánka Vaňáčková, Ph.D. (CEITEC, MU), period: 01.01.2021 – 31.12.2023, the total grant for UO: 5 172 000,- CZK

The eustigmatophyte endosphere: intracellular bacteria and viruses in the life and evolution of a model group of algae (GAČR 20-27648S), solver: Assoc. Prof. Mgr. Marek Eliáš, Ph.D., period: 01.01.2020 – 31.12.2022, the total grant for UO: 6 419 000,- CZK

Archeogenetická studie lidských populací pevninské Jihovýchodní Asie // Archaeogenetic Study of Human Populations in Mainland Southeast Asia (INTER-EXCELLENCE,

LTAUSA18153), solver: M.Sc. Pavel Flegontov, Ph.D., period: 01.01.2019 – 31.12.2021, the total grant for UO: 3 301 000,- CZK

Centrum výzkumu patogenity a virulence parazitů // Centre for research of pathogenicity and virulence of parasites, OP RDE (CZ.02.1.01/0.0/0.0/16\_019/0000759), the recipient: Charles University, partners: Biology Centre CAS, University of Ostrava, Project Manager: prof. RNDr. Jan Tachezy, Ph.D. (FS CHU), team leader at UO: prof. Vyacheslav Yurchenko, Ph.D., period: 01.03.2018 – 31.12.2022, the total grant for UO: 39 270 000,- CZK

Leishmaniaviruses in trypanosomatids (GAČR 20-22689S), solver: prof. Vyacheslav Yurchenko, Ph.D., period: 01.01.2020 – 31.12.2022, the total grant for UO: 10 725 000,- CZK

Non-standard genetic codes in protists and their evolution (GAČR 18-18699S), solver: Assoc. Prof. Mgr. Marek Eliáš, Ph.D., co-solver: Assoc. Prof. RNDr. Ivan Čepička Ph.D. (FS CHU), period: 01.01.2018 – 31.12.2020, the total grant for UO: 3 970 000,- CZK

Functional genomics of Leishmania virulence (GAČR 17-10656S), solver: Assoc. Prof. Vyacheslav Yurchenko, Ph.D., co-solver: Assoc. Prof. RNDr. Jan Votýpka Ph.D. (FS CHU), period: 01.01.2017 – 31.12.2019, the total grant for UO: 4 327 000,- CZK

The dark side of plastid biology: evolution and function of leucoplasts in algae (GAČR 17-21409S), solver: Assoc. Prof. Mgr. Marek Eliáš, Ph.D., period: 01.01.2017 – 31.12.2019, the total grant for UO: 3 865 000,- CZK

The Algal Microbiome: Friends and Foes (Horizon 2020, H2020-MSCA-ITN-2014, SEP-210135917), solver Dr. Claire M. Gachon (Scottish Marine Institute, Scottish Association for Marine Science, Oban, Great Britain), co-solver for the UO: Assoc. Prof. Mgr. Marek Eliáš, Ph.D., period: 01.01.2015 – 31.12.2018, the total grant for UO: 203 838,- EUR (ca. 5 500 000,- CZK)



## SIGNIFICANT PUBLICATIONS

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**Kostygov AY**, Frolov AO, Malysheva MN, Ganyukova AI, Chistyakova LV, Tashyreva D, Tesařová M, **Spodareva VV**, **Režnarová J**, **Macedo DH**, **Butenko A**, d'Avila-Levy CM, Lukeš J, **Yurchenko V** (2020) Vickermania gen. nov., trypanosomatids that use two joined flagella to resist midgut peristaltic flow within the fly host. *BMC Biology* 18:187.

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human parasite *Leishmania*. *Proceedings of the National Academy of Sciences of the United States of America* 115:E506-E515.

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**Pánek T**, **Žihala D**, **Sokol M**, Derelle R, **Klimeš V**, Hradilová M, Zadrobílková E, Susko E, Roger AJ, Čepička I, **Eliáš M** (2017) Nuclear genetic codes with a different meaning of the UAG and the UAA codon. *BMC Biology* 15:8.

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## THE TEAM STAFF

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