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Vás pozývajú na **103. prednášku** v rámci Kuželových seminárov:

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MONOXENOUS TRYPANOSOMATIDS ARE MODEL ORGANISMS TO STUDY ORIGIN OF PARASITISM AND ENDOSYMBIOSIS

ktorá sa uskutoční **4. apríla 2016** (piatok) o **14:00**

v miestnosti CH1-222 Prírodovedeckej fakulty UK

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Education

Moscow State University, Moscow, Russia

- B. Sc., Molecular Biology (*Cum Laude*) (1993)
- M. Sc., Molecular Biology (*Cum Laude*) (1994)
- Ph.D. with Honors, Biochemistry (1999)

Research and training

- Picower Institute for Medical Research, Manhasset, NY (1999 – 2001) – postdoctoral researcher
- Albert Einstein College of Medicine, Bronx, NY (2001 – 2007) – research fellow
- Rockefeller University, New York, NY (2008 – 2012) – research associate
- Pfizer Inc., New York, NY (2012 – 2013) – senior research scientist
- University of Ostrava, Ostrava, Czech Republic (2013 – 2015) – assistant professor, lab head
- University of Ostrava (2016 – present) – associate professor, lab head

Abstract of the lecture

Kinetoplastid protists offer a unique opportunity for studying the evolution of parasitism. While all their close relatives are either photo- or phagotrophic, a number of kinetoplastid species are facultative or obligatory parasites, supporting a hypothesis that parasitism has emerged within this group of flagellates. They are evolutionarily more ancestral compared to the majority of other groups of parasitic protists, widespread and adaptable, which is an apparent reflection of their extremely successful life style. Subclass Metakinetoplastina unites 4 Orders: Trypanosomatida, Neobodonida, Eubodonida, and Parabodonida. The order Trypanosomatida encompasses representatives responsible for human diseases and contains the largest number of described genera and species.

Trypanosomatids parasitize either insects (monoxenous) or shuttle between insects and secondary hosts (vertebrates for *Trypanosoma* and *Leishmania*, or plants for *Phytomonas* spp. = dixenous). My lab is working on delineating genetic factors distinguishing monoxenous and dixenous species using Next-Generation Sequencing techniques. I will also present new data on virulence factors in *Leishmania* infection. Using comparative genomics approach, we have identified and characterized several proteins potentially involved in *Leishmania* pathogenicity.

The final part of my lecture will deal with bacterial endosymbionts in trypanosomatids. We have described a novel symbiotic association between a kinetoplastid protist *Novymonas esmeraldas* gen. n., sp. n. and an intracytoplasmic bacterium *Ca. Pandoraea novymonadis* sp. n. We characterized this association by describing the morphology of both organisms, as well as their interactions, and by establishing their phylogenetic affinities. This symbiotic association seems to be relatively recent, as the host does not exert a stringent control over the number of bacteria harbored in its cytoplasm. We argue that this unique relationship may represent a suitable model for studying the initial stages of establishment of endosymbiosis between a single-cellular eukaryote and a prokaryote. Based on phylogenetic analyses, *Novymonas* could be considered a proxy for the monoxenous ancestor of the dixenous genus *Leishmania*, and shed light on the origin of the two-host life cycle within the subfamily Leishmaniinae.

Recent references

- 1) Kraeva, N., Butenko, A., Hlaváčová, J., Kostygov, A., Myškova, J., Grybchuk, D., Leštinová, T., Votýpka, J., Volf, P., Opperdoes, F., Flegontov, P., Lukeš, J., Yurchenko, V. *Leptomonas seymouri*: adaptations to the dixenous life cycle analyzed by genome sequencing, transcriptome profiling and co-infection with *Leishmania donovani*. PLOS Path., 2015, 11(8): e1005127.
- 2) Kostygov, A., Dobáková, E., Grybchuk-Ieremenko, A., Váhala, D., Maslov, D., Votýpka, J., Lukeš, J., Yurchenko, V. Novel trypanosomatid–bacterium association: evolution of endosymbiosis in action, mBio, 2016 (in press).