

INTRODUCTION

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Evolutionary biology and biodiversity research at BGRS-2018

Yuriy L. Orlov^{1,2,3*}, Ancha V. Baranova^{4,5}, Nikolay A. Kolchanov^{1,2} and Leonid L. Moroz⁶

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In this Special Issue of BMC Evolutionary Biology we present the materials from the Bioinformatics and Systems Biology summit BGRS\SB (Bioinformatics of Genome Regulation and Structure\Systems Biology) – 2018 (<http://conf.bionet.nsc.ru/bgrssb2018/en/>). This summit is conducted in Novosibirsk every other year, since 1998. This Special Issue accompany other BioMed Central journal issues, which highlight recent breakthroughs in the fields of genomics, bioinformatics, plant biology, and genetics, being published as BMC Genomics, BMC Bioinformatics, BMC Systems Biology, BMC Genetics, BMC Medical Genomics and BMC Plant Biology supplements [1–6]. Previous year’s highlights are described in the special issues which followed the presentations made at Belyaev Readings-2017 (<http://conf.bionet.nsc.ru/belyaev100/en>) [5–8].

A majority of the papers collated within current issue of BMC Evolutionary Biology were discussed at the BGRS\SB–affiliated symposium “Biodiversity: genomics and evolution” (BioGenEvo-2018). Below is a brief summary of the papers presented.

Georgy Slivko-Koltchik, Victor Kuznetsov and Yuri Panchin [9] delved into evolutionary history of gap junctions to show that the genomes of some metazoans lack both connexins and pannexins, while their 2-cell embryo’ blastomeres are electrical coupled. It seems that LRCC8 family of pannexin homologues [10] is not the final addition to happy family: gap junction treasure troves still keep some surprises to be unearthed.

Sergey Shekhovtsov et al. [11] presented a result of a challenging project – RNA-seq based assessment of the genetic lineages of five isolates of polyploid earthworm *Eisenia nordenskioldi nordenskioldi* and two outgroups

from the family Lumbricidae, the congenetic *E. andrei*, and *Lumbricus rubellus*. Detailed analysis of these lineages indicates complexity of earthworm evolution, with evidence of deep and ancient divergence of the lineages within *Eisenia nordenskioldi* species complex, possibly representing species which are phenotypically similar but genetically distinct.

Anastasia Kuzminkova et al. [12] presented an interactive resource which describes evolutionary analysis of epistatic interactions in protein families involved in mitochondrial function of vertebrata. In particular, they showed that rodents and primates differ in the rates of evolution for the components of various functional protein complexes and pathways.

Roman Bykov and co-authors [13] analyzed more than fifteen hundreds Paleoarctic *Drosophila* isolates for their mtDNA lineages as well as prevalence, genetic diversity and distribution patterns of their Wolbachia symbionts. Researchers concluded that the genetics structure of the population of symbionts found in subsequent fly generations is made by Wolbachia carried by the flies that survive the winter. Moreover, in study of Bykov et al., no evidences in support of so-called global Wolbachia genotype replacement hypothesis [14] were found.

Elena Kotenkova and co-authors [15] showed that the odor of mother affects the level of MRI signal in the assessor olfactory bulb neurons (AOB) to greater degree than the genetic relationships of the recipient to the donor of the odor. In related *Mus* taxa, early postnatal experiences influence subsequent choice of mates, thus, opening possibility to epigenetic origin of pre-copulatory reproductive isolation in rodent species.

Marina Rutovskaya [16] performed a comparison of the distress signals of the hybrid and parent species of the voles, created a reliable discriminator and showed that the paternal heritage has substantial influence on the sound signals observed in hybrids.

* Correspondence: orlov@bionet.nsc.ru

¹Institute of Cytology and Genetics SB RAS, 630090 Novosibirsk, Russia

²Novosibirsk State University, 630090 Novosibirsk, Russia

Full list of author information is available at the end of the article



Nadezhda Bolsheva et al. [17] advanced our understanding of the evolution of the genus *Linum*, which is characterized unusual variability in size, morphology and karyotypes. The key to this diversity was found in the repeatomes of flax species. Researchers show that evolution of species comprising the genus *Linum* was accompanied by multiple waves of satellite DNA and LTR retrotransposon amplification. In fact, evolutionary tree of the *Linum* species may be built based on sole comparison of repeatomes, largely ignoring non-repetitive fraction of their genomic DNA. Note that previous publication of this research group employed high-throughput sequencing of multicopy rRNA gene families for substantial adjustments in the phylogeny of blue-flowered flax species [18].

Ksenia Strygina and Elena Khlestkina [19] analyzed structural and functional divergence of the *Mpc1* genes in wheat and barley. This study resulted in identification of regulatory R2R3-Myb genes involved in anthocyanin synthesis in Triticeae tribe species.

Taken together, this issue comprises a wide array of reports describing recent insight in evolution of various life forms, covering a spectrum from plants to invertebrates and vertebrates. At BGRS-2018, the symposium “Biodiversity: genomics and evolution” was also attended by young scientists who gathered in Novosibirsk for a School “Systems Biology and Bioinformatics” (SBB-2018) (<http://conf.bionet.nsc.ru/bgrsb2018/en/school/>). BioMed Central previously had published special issues by materials of SBB Schools. We invite our readers worldwide to attend our next event - Young Scientists School Systems Biology and Bioinformatics (SBB-2019) which will be held in Novosibirsk, Russia in summer of 2019 (<http://conf.bionet.nsc.ru/sbb2019/en/>). Evolutionary biology researches will be discussed as well at VII Congress of Vavilov Society of Geneticists and Breeders organized by of St.-Petersburg State University 18–22 June 2019 (<https://events.spbu.ru/events/genetic-selection-2019>). Welcome to next events!

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AVB and YLO are guest editors of the special post-conference issues and Program Committee members of BGRS\SB-2018 conference. NAK is Chairman of BGRS\SB-2018 multi-conference and LLM is Chairman of the “Biodiversity: genomics and evolution” Symposium. All the authors read, revised and approved the final manuscript.

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Author details

¹Institute of Cytology and Genetics SB RAS, 630090 Novosibirsk, Russia. ²Novosibirsk State University, 630090 Novosibirsk, Russia. ³The A.O.Kovalevsky Institute of Marine Biological Research of RAS, Moscow, Russia. ⁴Research Centre for Medical Genetics, Moscow 115478, Russia. ⁵School of Systems Biology, George Mason University, Fairfax, VA, USA. ⁶University of Florida, Gainesville, FL, USA.

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