

INTRODUCTION

Open Access



Computational models in genetics at BGRS-2018

Yuriy L. Orlov^{1,2*}, Tatiana V. Tatarinova^{3,4,5} and Alex V. Kochetov¹

From 11th International Multiconference “Bioinformatics of Genome Regulation and Structure\Systems Biology” - BGRS\SB-2018

Novosibirsk, Russia. 20-25 August 2018

This Special Issue of *BMC Genetics* assembles papers on genetics presented at the biannual summit in Bioinformatics and Systems Biology BGRS\SB (Bioinformatics of Genome Regulation and Structure\Systems Biology) – 2018 (<http://conf.bionet.nsc.ru/bgrssb2018/en/>). BGRS\SB-2018 was XI-th in the conference series in Novosibirsk since 1998. Genetics models as well as computational genomics were presented at the conference from the beginning and highlighted at BioMed Central special journal issues since 2014 (<https://bmccgenomics.biomedcentral.com/articles/supplements/volume-15-supplement-12>) [1–3]. It also included *BMC Genetics* Supplement (<https://bmccgenet.biomedcentral.com/articles/supplements/volume-16-supplement-1>) [4], selected papers in microbiology models (<https://bmccmicrobiol.biomedcentral.com/articles/supplements/volume-16-supplement-1>), structural biology (<https://bmccstructbiol.biomedcentral.com/articles/supplements/volume-18-supplement-1>). To accompany this Special Issue, other Supplements compiling selected BGRS-2018 articles in the fields of genomics, bioinformatics, plant biology, evolutionary biology and systems biology are published as a part of following journal series: *BMC Genomics*, *BMC Bioinformatics*, *BMC Systems Biology*, *BMC Medical Genomics*, *BMC Evolutionary Biology* and *BMC Plant Biology* [5–9]. In the past, respective highlights were organized into the Special Issues with reports from “Belyaev Readings-2017” memorial event (<http://conf.bionet.nsc.ru/belyaev100/en>) [10–15]. The Belyaev Conference-2017 (“Belyaev Readings - 2017”) was devoted to science legacy of outstanding scientist, evolutionist and geneticist, full member of the USSR Academy of Sciences, Professor Dmitry K. Belyaev (1917–1985) to mark the 100-th anniversary since his birth [16]. Such science problems include selection works on fox and rat lines [17], search

for genes related to climate adaptation [18] including published earlier at *BMC Genetics* [4].

This year we have attracted presentations covering a variety of topics – from plant and animal genetics to climate adaptation. The best papers were selected for publication in this special issue, and the brief summary is presented below.

Igoshin et al. focused their research on the cold stress in Siberian cattle [19] continuing climate adaptation topic [18]. Siberia is notoriously known for its cold climate with long snowy winters and short summers. Design of new highly productive livestock breeds adapted to harsh climatic conditions is therefore an important aim of modern agriculture and breeding. However, our knowledge of the genetic mechanisms of adaptation to local environments is still scarce. To address this issue for cold climates Igoshin and colleagues used an integrated approach for detecting genomic intervals related to body temperature maintenance under acute cold stress. The team was able to detect a single candidate region on cattle chromosome 15 overlapping between the GWAS results and the results of scans for selective sweeps. This important finding will allow breeders to create cattle breeds thriving in the cold climate of Siberia as well as in other cold regions of the world.

Andreyeva et al. [20] continued the topic of fruit fly research, discussing the role dCNDP2 plays in G2/M transition of the cell cycle in *Drosophila melanogaster*. This work is another application of animal models for analysis of human disease. Expression of the CNDP2 gene is frequently up- or down-regulated in different types of human cancers. The authors demonstrated that one of the dCNDP2 isoforms is expressed throughout the different tissues tested, and detected in both the cytoplasm and the nucleus. The presented approach will allow further functional characterization of the conserved CNDP2 protein using *D. melanogaster* as a model system.

* 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



The next group of papers is dedicated to plant genetics. Glagoleva et al. [21] investigated the evolution of the chalcone synthase gene family in bread wheat and relative species. The authors investigated structural and functional organization of the chalcone synthase genes and discussed evolution of this gene family in bread wheat and relative species. Putative members of this family were examined using genomic and transcriptomic approaches, resulting in the final list of well-characterized eight genes. Transcriptional assay along with a comparative analysis of the cis-regulatory elements revealed their functional diversification. The multiple functions supported by the chalcone synthase family are assumed to be a driving force for duplications of the chalcone synthase gene and their retention in plant genome. Wheat genes analysis papers by the groups from the same institute were published at *BMC Genetics* [22] and *BMC Plant Biol* [23, 24] special post-conference issues including 2019 issue [25].

Strygina et al. [26] were interested in genetic control of anthocyanin pigmentation of potato tissues. Potato is one of the most important crops worldwide, and a main component in diets in many cultures worldwide. Anthocyanins synthesis and accumulation in potato tissues are considered as one of important traits related to stress resistance and nutritional value. Strygina and co-authors investigated the genetic control of pigmentation of different potato tissues and concluded that that StAN1 is the major regulatory gene controlling potato anthocyanin synthesis, however, other genes are also involved in formation of potato pigmentation patterns. This is the first step in developing of a pigmentation diagnostic assay. This work continues potato resistance analysis presented earlier at *BMC Plant Biol* special issue after Belyaev Conference - 2017 [27].

The final paper of this Special Issue, written by Khlestkin et al. [28] discusses potato GWAS to find starch phosphorylation associated SNPs. Potato tubers cannot be stored for long periods of time, therefore, the use of potatoes in the form of starch and products from starch modification appears as a reasonable alternative. To increase the appeal of potato starch as a feedstock for various industries, substantial attempts to improve its molecular composition and physical and chemical properties are being made. Physical and chemical properties of potato starch gels is dependent on its phosphate content; phosphorus is important for proper nutrition, and potatoes and starch high in phosphate would be valuable as food. Kleshkin et al. performed a genome-wide association study using a 22 K SNP potato array to find novel genomic regions associated with starch phosphorylation. The researchers found eight novel genomic regions associated with starch phosphorylation. This study will support selection of the most informative SNPs for developing convenient diagnostic markers to accelerate

the breeding of potatoes with predetermined levels of starch phosphorylation.

We offer to our readers a wide range of reports describing recent breakthrough in genetics presented at the conference as well as science trends in related fields. Young scientists gathered in Novosibirsk for a School “Systems Biology and Bioinformatics” (SBB-2018) co-authored current issue and parallel Supplements 2019 [5–9]. In previous years, the materials of SBB Schools were published in Special Issues [29] including *BMC Genetics* [30]. Genomics field will be highlighted at VII Congress of Vavilov Society of Geneticists and Breeders organized by Saint Petersburg State University 18–22 June 2019 (<https://events.spbu.ru/events/genetic-selection-2019>). Soon after, 24–29 June 2019, 5th International scientific conference “Plant genetics, genomics, bioinformatics and biotechnology” (PlantGen2019) will be organized in Novosibirsk, Russia (<http://conf.bio-net.nsc.ru/plantgen2019/en/>) focusing on plant genomics field together with SBB-2019 School. Next BGRS\SB-2020 event is scheduled to June 2020 in Novosibirsk, Russia. We invite our readers worldwide to attend our next events!

Acknowledgements

We are grateful to Professors N.A. Kolchanov for organization of the multi-conference and providing platform for international genetics research. We thank the Russian Foundation of Basic Research for the conference organization support, Zhejiang Bioinformatics Society, China, for logistic support of conference participants, Institute of Cytology and Genetics SB RAS and Novosibirsk State University for hosting the conference. The conference was supported by RFBR and ICG SB RAS budget project (0324-2019-0040). The guest editors of the special issue are grateful to the conference committee members and reviewers who helped in the peer-review of the articles as well as in editing and issue preparation: Ancha Baranova (George Mason University, Fairfax, USA), Nikolai Barlev (Institute of Cytology of the RAS, St.Petersburg, Russia), Hongyu Yang (Peking University, China), Andre Marakhonov (Research Centre for Medical Genetics, Moscow, Russia), Elza Khusunudinova (Institute of biochemistry and genetics, Ufa, Russia), Ranajit Das (Manipal Academy of Higher Education of India), Juha Kantanen and Ruslan Kalendar (both - Finland Natural Resources Institute, Finland), Mikhail Smaragdov (Research institute of genetics and breeding farm animals, St.Petersburg, Russia), Denis Baranenko and Mariam Muradova (ITMO University, St.Petersburg, Russia), Sergii Tukaiev (National Taras Shevchenko University of Kyiv, Ukraine), Giorgio Prantera (Tuscia University, Viterbo, Italy), Michael Goldberg (Cornell University, USA), Tamara Khlebodarova, Svetlana Fedorova, Olga Redina and Nataliya Dorogova (all - Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia), Alexander Konev (St. Petersburg Nuclear Physics Institute, Russia), Casey Bergman (University of Manchester, UK), Edward Dubrovsky (Fordham University, USA), Elena Pasyukova (Institute of molecular genetics RAS, Moscow, Russia), Mirjana Stajić (Belgrade University, Serbia), Robert Brueggeman (North Dakota State University, USA), Mehraj Abbasov (National Academy of Sciences, Azerbaijan), Saule Abugalieva and Yerlan Turuspekov (Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan), Gilda Eslami (Yazd University, Iran), Yonghai Luo (Jiangsu Normal University, China), Yuri Shavrukov (Flinders University, Adelaide, Australia).

Funding

This article did not receive sponsorship for publication.

About this supplement

This article has been published as part of *BMC Genetics Volume 20 Supplement 1, 2019: Selected articles from BGRS\SB-2018: genetics*. The full contents of the supplement are available online at <https://>

bmccentral.com/articles/supplements/volume-20-supplement-1.

Authors' contributions

TT and YO are guest editors of the special post-conference issue and Program Committee members of BGRS\SB-2018 conference. AK is Program Committee member and Chairman of genetics session at BGRS\SB-2018. All the authors read, revised and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Author details

¹Institute of Cytology and Genetics SB RAS, 630090 Novosibirsk, Russia. ²Novosibirsk State University, 630090 Novosibirsk, Russia. ³Department of Biology, University of La Verne, La Verne, CA, USA. ⁴Vavilov Institute for General Genetics, Moscow, Russia. ⁵Siberian Federal University, Krasnoyarsk, Russia.

Published: 18 March 2019

References

- Orlov YL, Baranova AV, Markel AL. Computational models in genetics at BGRS\SB-2016: introductory note. *BMC Genet.* 2016;17(Suppl 3):155.
- Orlov YL, Baranova AV, Hofstadt R, Kolchanov NA. Computational genomics at BGRS\SB-2016: introductory note. *BMC Genomics.* 2016;17(Suppl 14):996.
- Orlov YL, Baranova AV, Salina EA. Computational plant bioscience at BGRS\SB-2016: introductory note. *BMC Plant Biol.* 2016;16(Suppl 3):243.
- Redina OE, Smolenskaya SE, Klimov LO, Markel AL. Candidate genes in quantitative trait loci associated with absolute and relative kidney weight in rats with inherited stress induced arterial hypertension. *BMC Genet.* 2015;16(Suppl 1):S1.
- Baranova AV, Klimontov VV, Letyagin YL, Orlov YL. Medical genomics research at BGRS-2018. *BMC Medical Genomics.* 2019;12(Suppl 2) <https://doi.org/10.1186/s12920-019-0480-0>
- Tatarinova TV, Chen M, Orlov YL. Bioinformatics research at BGRS-2018. *BMC Bioinformatics.* 2019;20(Suppl 1):33. <https://doi.org/10.1186/s12859-018-2566-7>.
- Orlov YL, Baranova AV, Kolchanov NA, Moroz LL. Evolutionary biology research at BGRS-2018. *BMC Evolutionary Biology.* 2019;19(Suppl 1) doi: <https://doi.org/10.1186/s12862-019-1368-5>
- Orlov YL, Hofstadt R, Baranova AV. Systems biology research at BGRS-2018. *BMC Systems Biology.* 2019;13(Suppl 1) doi: <https://doi.org/10.1186/s12918-019-0685-z>
- Orlov YL, Salina EA, Eslami G, Kochetov AV. Plant biology research at BGRS-2018. *BMC Plant Biol.* 2019;19(Suppl 1):56. <https://doi.org/10.1186/s12870-019-1634-0>.
- Orlov YL, Baranova AV, Tatarinova TV, Kolchanov NA. Genetics at Belyaev conference - 2017: introductory note. *BMC Genet.* 2017;18(Suppl 1):116.
- Orlov YL, Baranova AV, Hofstadt R, Kolchanov NA. Genomics at Belyaev conference - 2017. *BMC Genomics.* 2018;19(Suppl 3):79.
- Orlov YL, Baranova AV, Herbeck YE. Evolutionary biology at Belyaev conference - 2017. *BMC Evol Biol.* 2017;17(Suppl 2):260.
- Orlov YL, Baranova AV, Chen M, Salina EA. Plant biology at Belyaev conference - 2017. *BMC Plant Biol.* 2017;17(Suppl 2):257.
- Orlov YL, Moroz LL, Baranova AV. Neuroscience researches at Belyaev conference-2017. *BMC Neurosci.* 2018;19(Suppl 1):14.
- Orlov YL, Fernandez-Masso JR, Chen M, Baranova AV. Medical genomics at Belyaev conference - 2017. *BMC Med Genet.* 2018;11(Suppl 1):11.
- Shumny VK. To the centenary of the birth of outstanding evolutionist Dmitri Konstantinovich Belyaev. *Vavilovskii Zhurnal Genetiki i Seleksii = Vavilov. J Genet Breed.* 2017;21(4):387–91. <https://doi.org/10.18699/VJ17.256> (In Russian).
- Trut LN, Kharlamova AV, Vladimirova AV, Herbeck YE. On selection of foxes for enhanced aggressiveness and its correlated implications. *Vavilovskii Zhurnal Genetiki i Seleksii = Vavilov. J Genet Breed.* 2017;21(4):392–401. <https://doi.org/10.18699/VJ17.257> (In Russian).
- Yudin NS, Larkin DM, Ignatieva EV. A compendium and functional characterization of mammalian genes involved in adaptation to Arctic or Antarctic environments. *BMC Genet.* 2017;18(Suppl 1):111.
- Igoshin AV, Belonogova NM, Yurchenko AA, Yudin NS, Larkin DM. Genome-wide Association Study for Body Temperature Maintenance Under the Cold Stress in Siberian Cattle. *BMC genetics.* 2019;20(Suppl 1).
- Andreyeva EN, Ogienko AA, Dubatolova TD, Alekseeva AL, Kozhevnikova EN, Ivankin AA, Pavlova GA, Kopyl SA, Pindyurin AV. dCNDP2 is both cytoplasmic and nucleus protein playing role in G2/M transition of the cell cycle in *Drosophila melanogaster*. *BMC genetics.* 2019;20(Suppl 1).
- Glagoleva AY, Ivanisenko NV, Khlestkina EK. Organization and evolution of the chalcone synthase gene family in bread wheat and relative species. *BMC genetics.* 2019;20(Suppl 1).
- Vavilova V, Konopatskaia I, Kuznetsova AE, Blinov A, Goncharov NP. DEP1 gene in wheat species with normal, compactoid and compact spikes. *BMC Genetics.* 2017;18(Suppl 1):106.
- Dobrovolskaya OB, Amagai Y, Popova KI, Dresvyannikova AE, Martinek P, Krasnikov AA, et al. Genes WHEAT FRIZZY PANICLE and SHAM RAMIFICATION 2 independently regulate differentiation of floral meristems in wheat. *BMC Plant Biol.* 2017;17(Suppl 2):252.
- Dobrovolskaya O, Pont C, Sibout R, Martinek P, Badaeva E, Murat F, et al. FRIZZY PANICLE drives supernumerary spikelets in bread wheat. *Plant Physiol.* 2015;167(1):189–99.
- Strygina KV, Khlestkina EK. Myc-like transcriptional factors in wheat: structural and functional organization of the subfamily I members. *BMC Plant Biol.* 2019;19(Suppl 1):50.
- Strygina KV, Kochetov AV, Khlestkina EK. Genetic control of anthocyanin pigmentation of potato tissues. *BMC genetics.* 2019;20(Suppl 1).
- Kochetov AV, Glagoleva AY, Strygina KV, Khlestkina EK, Gerasimova SV, Ibragimova SM, et al. Differential expression of NBS-LRR-encoding genes in the two transcriptomes of two *Solanum phureja* genotypes with contrasting resistance to *Globodera rostochiensis*. *BMC Plant Biol.* 2017;17(Suppl 2):251.
- Khlestkin VK, Rozanova IV, Efimov VM, Khlestkina EK. Starch phosphorylation associated SNPs found by genome-wide association studies in potato (*Solanum tuberosum* L.). *BMC genetics.* 2019;20(Suppl 1).
- Orlov YL, Tatarinova TV, Zakhartsev MV, Kolchanov NA. Introduction to the 9th young scientists school on systems biology and bioinformatics (SBB'2017). *J Bioinforma Comput Biol.* 2018;16(1):1802001.
- Baranova AV, Orlov YL. The papers presented at 7th young scientists school "systems biology and bioinformatics" (SBB'15): introductory note. *BMC Genet.* 2016;17(Suppl 1):20.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more bmccentral.com/submissions

