

Публикационная активность

Институт, являясь одним из признанных лидеров российской биологической науки, активно публикует в российских и зарубежных журналах лучшие научные достижения. В результате исследований, проводимых в ИЦиГ СО РАН по фундаментальным направлениям, за последние пять лет (2012–2017) в высокорейтинговых журналах, которые индексируются в международной базе Web of Science (WoS), опубликованы 1194 статьи с авторством наших сотрудников. В число этих журналов входят самые престижные журналы с очень высоким импакт-фактором, и среди таких высокорейтинговых журналов можно перечислить Nature, Nature Genetics, Science, Scientific Reports, Nature Communications, American Journal of Human Genetics и многие другие. За последние пять лет увеличилось количество публикаций сотрудников в иностранных журналах. Если в 2010 году институт опубликовал 139 публикаций в иностранных журналах, то в 2016 году уже появилось 185 статей. За 2011–2015 годы, по данным АСУ РИД – системы, которая раз-

работана Академией наук для учета наукометрических показателей, цитируемость работников нашей организации в РИНЦ, отнесенная к численности исследователей, равна 24,8, то есть на каждого научного сотрудника приходится около 25 цитирований в других публикациях в год. Цитируемость работников научной организации в системе WoS оказалась еще выше: здесь на каждого научного работника приходится 26 цитирований в год. За 2016 г. опубликовано 240 статей, зарегистрированных в WoS, общее количество статей в рецензируемых журналах – более 400. В 2016 году статьи сотрудников института цитировались в WoS более 4227 раз, их совокупный импакт-фактор в этой международной базе данных составил 657 – это очень высокий показатель среди российских институтов. К ноябрю 2017 года опубликовано 205 статей в журналах, которые индексируются в международных базах WoS и Scopus. Тем самым институт продолжает наращивать свою публикационную активность и увеличивать показатели в этом направлении.



ARTICLE

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Integrative epigenetics that DNA methylation in inflammatory

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Epigenetic alterations may provide important inflammatory bowel disease (IBD). Here, differences in 240 newly-diagnosed IBD differentially methylated positions (DMPs) which we study in detail using whole-genome DMP (RP56KAZ) and DMRs (VMPs) paired genetic and epigenetic data, a VMP/microRNA-27 methylation associate with a known IBD susceptibility variant hypermethylation within the TXNIP promoter in whole-blood and CD8⁺ T cells, but methylation changes in IBD relate to an alteration in gene expression.



Population history of present-day Native Americans. The ancestors of all Native Americans entered the Americas as a single migratory wave from Siberia (purple) no earlier than ~23 ka, separate from the 'northern' and 'southern' Native American branches ~13 ka. There is evidence of post-divergence gene flow between some Native American branches and groups related to East Asians/Melanesians (yellow).

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RESEARCH ARTICLE SUMMARY

HUMAN GENOMICS

Global diversity, population stratification, and selection of human copy-number variation

Peter H. Sudmant, Swapan Mallick, Bradley J. Nelson, Pereydom Hormozdiari, Niklas Krumm, John Huddleston, Bradley P. Cove, Carl Baker, Suzanne Nordenfalk, Michael Bamshad, Lynn R. Jorde, Olga L. Poustka, Horstmann Sahakyan, W. Scott Watkins, Leon Vepolevskiy, M. Syarif Abdullah, Claudio M. Bravi, Cristian Capelli, Tor Hervig, Joseph T. S. Wee, Clark Tyler-Smith, George van Deren, Irene Gallego Romero, Anshul K. R. Jha, Sena Karasahin Yankov, Prage Thandava, David Comas, Breanna Hens, Thomas Kivild, Andreia Ruiz-Linares, Anthei Sajnath, Eze Metspalu, Juri Park, Richard Villem, Elena B. Starikova, George Ayuda, Cynthia M. Beall, Anna Di Rienzo, Michael F. Hammer, Rika Khramtsova, Elza Khramtsova, William Kitz, Cheryl Winkler, Damián Labada, Matt Metspalu, Sarah A. Tishoff, Stanislaw Dryomov, Ren Salazar, Nick Patterson, David Reich, Evan E. Eichler

INTRODUCTION: Most studies of human genetic variation have focused on single-nucleotide variants (SNVs). However, copy-number variants (CNVs) affect more base pairs of DNA among humans, and yet our understanding of CNV diversity among human populations is limited.

RATIONALE: We aimed to understand the pattern, selection, and diversity of copy-number variation by analyzing deeply sequenced genomes representing the diversity of all humans. We compared the selective constraints of deletions versus duplications to understand population stratification in the context of the

ancestral human genome and to assess differences in CNV load between African and non-African populations.

RESULTS: We sequenced 296 individual genomes from 125 distinct human populations and identified 14,467 autosomal CNVs and 545 X-linked CNVs with a sequence read-depth approach. Deletions exhibit stronger selective pressure and are better phylogenetic markers of population relationships than duplication polymorphisms. We identified 1000 population-stratified copy-number-variable regions, 205 of which intersect coding regions and 109 of which exhibit extreme signatures of diver-

entiation likely to post-date modern human population splits. The distribution of CNVs is shaped by the interplay of natural selection and drift.

CONCLUSIONS: CNVs have a distinct evolutionary history and are better phylogenetic markers of population relationships than duplication polymorphisms.

KEYWORDS: CNVs, human genome, population stratification, selection, copy-number variation

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日本語要約

The ctenophore genome and the evolutionary origins of neural systems

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Abstract

Abstract | Introduction | Ctenophore phylogeny | Ctenophore innovations | Parallel evolution of neural organization | Discussion | Methods | Accession codes | Change history | References | Acknowledgements | Author information | Extended data figures and tables | Supplementary information

The origins of neural systems remain unresolved. In contrast to other basal metazoans, ctenophores (comb jellies) have both complex nervous and mesoderm-derived muscular systems. These holoplutean predators also have sophisticated ciliated locomotion, behaviour and distinct development. Here we present the draft genome of *Platybrachia pacifica*, Pacific sea gooseberry, together with ten other ctenophore transcriptomes, and show that they are remarkably distinct from other animal genomes in their content of neurogenic, immune and developmental genes. Our integrative analyses place Ctenophora as the earliest lineage within Metazoa. This hypothesis is supported by comparative analysis of multiple gene families, including the apparent absence of Hox genes, canonical microRNA machinery, and reduced immune complement in ctenophores. Although two distinct nervous systems are well recognized in ctenophores, many bilaterian neuron-specific genes and genes of 'classical' neurotransmitter pathways either are absent or, if present, are not expressed in neurons. Our metabolic and physiological data are consistent with the hypothesis that ctenophore neural systems, and possibly muscle specification, evolved independently from those in other animals.

Subject terms: Phylogeny • Phylogenetics • Comparative genomics •

At a glance

Figures | Videos

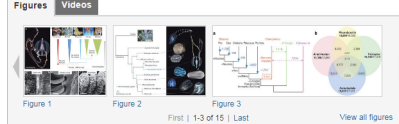


Figure 1 | Figure 2 | Figure 3 | First | 1-3 of 15 | Last | View all figures

Editor's summary

Ctenophores (comb jellies) are enigmatic animals that combine two distinct nervous systems with an elementary brain-like centre and possess mesoderm-derived muscles appropriate to their predatory life.

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