

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 разных направлениях.



ARTICLE

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Integrative epigenetics that DNA methylation in inflammatory

N.T. Ventham¹, N.A. Kennedy¹, A.T. Consortium¹, IBD CHARACTER CON

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 (VMP), IT paired genetic and epigenetic data, v VMP/microRNA-27 methylation associate with a known IBD susceptibility variant hypermethylation within the FXR 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 migration 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 and groups related to East Asians/Indo-Australo-Melanesians (yellow).

RESEARCH ARTICLE SUMMARY

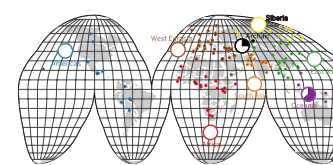
HUMAN GENOMICS

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

Peter H. Sudmant, Swapna Mallik, Bradley J. Nelson, Fereydoon Hormozdizadeh, Niklas Krumh, John Huddleston, Bradley P. Cove, Carl Baker, Susanne Nordfjell, Michael Bamshad, Lynn B. Jorde, Olga I. Poustka, Horstmann Sahakyan, W. Scott Watkins, Leon Veprikopoyan, M. Syarif Abdillah, Claudio M. Bravi, Cristian Capelli, Tor Hervig, Joseph T. S. Wee, Chris Tyler-Smith, George van Driem, Irene Gallego Romero, Anshul K. R. Das, Sona Karasahakyan, Praga Tranchesi, David Comas, Breanna Henn, Tomas Kivikald, Andres Ruiz-Linares, Antti Sajantila, Ene Metspalu, Jitni Parkk, Richard Villem, Elena K. Starikovskaya, George Argyros, Cynthia M. Beall, Anna Di Rienzo, Michael F. Hammer, Rika Khachatryan, Elza Khusnutdinova, William Kilts, Cheryl Winfield, Daniam Laboda, Matt Metspalu, Sarah A. Tishkoff, Stanislav Deryomov, Rem Sukernik, Nick Patterson, David Reich, Evan E. Eichler

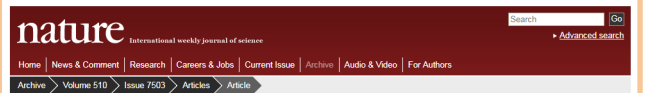
INTRODUCTION: Most studies of human genetic variation have focused on single-nucleotide variants (SNVs). However, copy-number variants (CNVs) affect more base pairs of DNA among humans, and yet our understanding of CNV diversity among human populations is limited.

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



Global human CNV diversity and archaic introgression of a chromosome 16 duplication. (Left) The sampled are indicated on a world map (colored dots). The pie charts show the continental population allele frequencies for polymorphisms found exclusively among Oceanic populations and an archaic Denisovan. (Right) The ancestral site Denisovan duplication structure (2) are shown in relation to their position on chromosome 16. We estimate that 10 years ago (ka) in the Denisova and then introgressed into ancestral Papuan populations ~40 ka.

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The tetraploid genome and the evolutionary origins of neural systems

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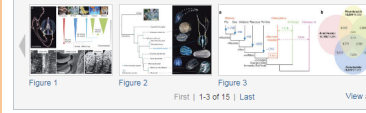
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Abstract
 Abstract | Introduction | Ctenophore phylogeny | Ctenophore innovations | Parallel evolution of neural organization | Discussion | Methods | Accession codes | Change history | References | Acknowledgements | Author information | Extended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

The origins of neural systems remain unresolved. In contrast to other derived metazoans, ctenophores (comb jellies) have both complex nervous and mesoderm-mediated muscle systems. These holoprotistan predators also have sophisticated ciliated locomotion, behaviour and distinct development. Here we present the draft genome of *Platybrachia lachneri*, Pacific sea gossamer, 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



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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