**1) Chaos and Hyperchaos in a Model of Ribosome Autocatalytic Synthesis**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5151018/>

Likhoshvai VA, Kogai VV, Fadeev SI, Khlebodarova TM

**SCIENTIFIC REPORTS**  
Том: 6  
Номер статьи: 38870  
DOI: 10.1038/srep38870  
Опубликовано: DEC 12 2016  
**iF 5.228**

**2) A quantitative method for determination of PPDK concentration in miscanthus leaves**

<http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12361/full>

Meshcheryakova IA, Bannikova SV, Rozanov AS, Demidova EV, Demidov EA, Goryachkovskaya TN, Burmakina NV, Shekhovtsov SV, Bryanskaya AV, Kolchanov NA, Peltek SE

**GLOBAL CHANGE BIOLOGY BIOENERGY**  
Том: 9 Выпуск: 1 Стр.: 262-269 Специальный выпуск: SI  
DOI: 10.1111/gcbb.12361  
Опубликовано: JAN 2017  
**iF 6.151**

Abstract:

          In this study, we used ELISA for quantification of PPDK in photosynthesizing leaves of miscanthus. We cloned a fragment of the gene encoding PPDK, purified the resulting protein by affinity chromatography, identified it using MALDI mass spectrometry, and obtained monoclonal antibodies by immunizing BALB/c mice. Selectivity of monoclonal antibodies was assessed by Western blot using the protein extracts of Soranovskii. The presence of PPDK was again verified by MALDI mass spectrometry. Therefore, we developed and tested the method for determining PPDK quantity in miscanthus using ELISA.

**3) Evaluation of the SeedCounter, A Mobile Application for Grain Phenotyping**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5151018/>

Komyshev E, Genaev M, Afonnikov D

**FRONTIERS IN PLANT SCIENCE**  
Том: 7  
Номер статьи: 1990  
DOI: 10.3389/fpls.2016.01990  
Опубликовано: JAN 4 2017  
**iF 4.495**

Abstract:

Grain morphometry in cereals is an important step in selecting new high-yielding plants. Manual assessment of parameters such as the number of grains per ear and grain size is laborious. One solution to this problem is image-based analysis that can be performed using a desktop PC. Furthermore, the effectiveness of analysis performed in the field can be improved through the use of mobile devices. In this paper, we propose a method for the automated evaluation of phenotypic parameters of grains using mobile devices running the Android operational system. The experimental results show that this approach is efficient and sufficiently accurate for the large-scale analysis of phenotypic characteristics in wheat grains. Evaluation of our application under six different lighting conditions and three mobile devices demonstrated that the lighting of the paper has significant influence on the accuracy of our method, unlike the smartphone type.

**4) The Interplay of Chromatin Landscape and DNA-Binding Context Suggests Distinct Modes of EIN3 Regulation in Arabidopsis thaliana**

<http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12361/full>

Zemiyanskaya EV, Leyitsky VG, Oshchepkov DY, Grosse I, Mironova VV

**FRONTIERS IN PLANT SCIENCE**  
Том: 7  
Номер статьи: 2044  
DOI: 10.3389/fpls.2016.02044  
Опубликовано: JAN 9 2017  
**iF 4.495**

Abstract:

The plant hormone ethylene regulates numerous developmental processes and stress responses. Ethylene signaling proceeds via a linear pathway, which activates transcription factor (TF) EIN3, a primary transcriptional regulator of ethylene response. EIN3 influences gene expression upon binding to a specific sequence in gene promoters. This interaction, however, might be considerably affected by additional co-factors. In this work, we perform whole genome bioinformatics study to identify the impact of epigenetic factors in EIN3 functioning. The analysis of publicly available ChIP-Seq data on EIN3 binding in Arabidopsis thaliana showed bimodality of distribution of EIN3 binding regions (EBRs) in gene promoters. Besides a sharp peak in close proximity to transcription start site, which is a common binding region for a wide variety of TFs, we found an additional extended peak in the distal promoter region. We characterized all EBRs with respect to the epigenetic status appealing to previously published genome-wide map of nine chromatin states in A. thaliana. We found that the implicit distal peak was associated with a specific chromatin state (referred to as chromatin state 4 in the primary source), which was just poorly represented in the pronounced proximal peak. Intriguingly, EBRs corresponding to this chromatin state 4 were significantly associated with ethylene response, unlike the others representing the overwhelming majority of EBRs related to the explicit proximal peak. Moreover, we found that specific EIN3 binding sequences predicted with previously described model were enriched in the EBRs mapped to the chromatin state 4, but not to the rest ones. These results allow us to conclude that the interplay of genetic and epigenetic factors might cause the distinct modes of EIN3 regulation.

**5) Contributions of age-related alterations of the retinal pigment epithelium and of glia to the AMD-like pathology in OXYS rats**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5278403/>

Telegina, DV, Kozhevnikova, OS, Bayborodin, SI, Kolosova, NG

**SCIENTIFIC REPORTS**  
Том: 7  
Номер статьи: 41533  
DOI: 10.1038/srep41533  
Опубликовано: JAN 30 2017  
**iF 5.228**

Abstract:

Age-related macular degeneration (AMD) is a major cause of blindness in developed countries, and the molecular pathogenesis of early events of AMD is poorly understood. It is known that age-related alterations of retinal pigment epithelium (RPE) cells and of glial reactivity are early hallmarks of AMD. Here we evaluated contributions of the age-related alterations of the RPE and of glia to the development of AMD-like retinopathy in OXYS rats. We showed that destructive alterations in RPE cells are a primary change during the development of retinopathy in OXYS rats. Furthermore, a defect of retinal maturation and decreased immune function at the preclinical stage of retinopathy were observed in OXYS rats in addition to the impairment of RPE cell proliferation and of their capacity for division. At the active stage of the disease, the atrophic alterations increased, and reactive gliosis was observed when disease progressed, but immune function stayed weakened. Unexpectedly, we did not observe migration of microglia and macrophages into the photoreceptor layer. These results and the wide spectrum of age-related retinal alterations in humans as well as individual differences in the risk of AMD may be attributed to genetic factors and to differences in the underlying molecular events.

**6) Gene expression profiling of tumor-initiating stem cells from mouse Krebs-2 carcinoma using a novel marker of poorly differentiated cells**

https://www.ncbi.nlm.nih.gov/pubmed/28031533

Potter EA, Dolgova EV, Proskurina AS, Efremov YR, Minkevich AM, Rozanov AS, Peltek SE, Nikolin VP, Popova NA, Seledtsov IA, Molodtsov VV, Zavyalov EL, Taranov OS, Baiborodin SI, Ostanin AA, Chernykh ER, Kolchanov, NA, Bogachev SS.

**ONCOTARGET  
Том: 8 Выпуск: 6 Стр.: 9425-9441  
DOI: 10.18632/oncotarget.14116  
Опубликовано: 2017  
iF 5.008**

Abstract:

Using the ability of poorly differentiated cells to natively internalize fragments of extracellular double-stranded DNA as a marker, we isolated a tumorigenic subpopulation present in Krebs-2 ascites that demonstrated the features of tumor-inducing cancer stem cells. Having combined TAMRA-labeled DNA probe and the power of RNA-seq technology, we identified a set of 168 genes specifically expressed in TAMRA-positive cells (tumor-initiating stem cells), these genes remaining silent in TAMRA-negative cancer cells. TAMRA+ cells displayed gene expression signatures characteristic of both stem cells and cancer cells. The observed expression differences between TAMRA+ and TAMRA- cells were validated by Real Time PCR. The results obtained corroborated the biological data that TAMRA+ murine Krebs-2 tumor cells are tumor-initiating stem cells. The approach developed can be applied to profile any poorly differentiated cell types that are capable of immanent internalization of double-stranded DNA.

**7) Nonsynonymous Variation in NKPD1 Increases Depressive Symptoms in European Populations**

<https://www.ncbi.nlm.nih.gov/pubmed/27745872>

Amin N, Belonogova NM, Jovanova O, Brouwer RWW, van Rooij JGJ, van den Hout MCGN, Svishcheva GR, Kraaij R, Zorkoltseva IV, Kirichenko AV, Hofman A, Uitterlinden AG, van IJcken WFJ, Tiemeier H, Axenovich TI, van Duijn CM.

**BIOLOGICAL PSYCHIATRY**  
Том: 81 Выпуск: 8 Стр.: 702-707  
DOI: 10.1016/j.biopsych.2016.08.008  
Опубликовано: APR 15 2017  
**iF 11.212**

Abstract:

BACKGROUND: Despite high heritability, little success was achieved in mapping genetic determinants of depression-related traits by means of genome-wide association studies.

METHODS: To identify genes associated with depressive symptomology, we performed a gene-based association analysis of nonsynonymous variation captured using exome-sequencing and exome-chip genotyping in a genetically isolated population from the Netherlands (n = 1999). Finally, we reproduced our significant findings in an independent population-based cohort ( n 5 1604).

RESULTS: We detected significant association of depressive symptoms with a gene NKPD1 (p = 3.7\*102(-08)). Nonsynonymous variants in the gene explained 0.9% of sex-and age-adjusted variance of depressive symptoms in the discovery study, which is translated into 3.8% of the total estimated heritability (h(2) = 0.24). Significant association of depressive symptoms with NKPD1 was also observed ( n = 1604; p = 1.5 \* 10(-03)) in the independent replication sample despite little overlap with the discovery cohort in the set of nonsynonymous genetic variants observed in the NKPD1 gene. Meta-analysis of the discovery and replication studies improved the association signal (p = 1.0 \* 10(-09)).

CONCLUSIONS: Our study suggests that nonsynonymous variation in the gene NKPD1 affects depressive symptoms in the general population. NKPD1 is predicted to be involved in the de novo synthesis of sphingolipids, which have been implicated in the pathogenesis of depression.

**8) The age-associated loss of ischemic preconditioning in the kidney is accompanied by mitochondrial dysfunction, increased protein acetylation and decreased autophagy**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5353572/>

Jankauskas SS, Pevzner IB, Andrianova NV, Zorova LD, Popkov VA, Silachev DN, Kolosova NG, Plotnikov EY, Zorov DB.

**SCIENTIFIC REPORTS**  
Том: 7  
Номер статьи: 44430  
DOI: 10.1038/srep44430  
Опубликовано: MAR 15 2017  
**iF 5.228**

Abstract:

In young rats, ischemic preconditioning (IPC), which consists of 4 cycles of ischemia and reperfusion alleviated kidney injury caused by 40-min ischemia. However, old rats lost their ability to protect the ischemic kidney by IPC. A similar aged phenotype was demonstrated in 6-month-old OXYS rats having signs of premature aging. In the kidney of old and OXYS rats, the levels of acetylated nuclear proteins were higher than in young rats, however, unlike in young rats, acetylation levels in old and OXYS rats were further increased after IPC. In contrast to Wistar rats, age-matched OXYS demonstrated no increase in lysosome abundance and LC3 content in the kidney after ischemia/reperfusion. The kidney LC3 levels were also lower in OXYS, even under basal conditions, and mitochondrial PINK1 and ubiquitin levels were higher, suggesting impaired mitophagy. The kidney mitochondria from old rats contained a population with diminished membrane potential and this fraction was expanded by IPC. Apparently, oxidative changes with aging result in the appearance of malfunctioning renal mitochondria due to a low efficiency of autophagy. Elevated protein acetylation might be a hallmark of aging which is associated with a decreased autophagy, accumulation of dysfunctional mitochondria, and loss of protection against ischemia by IPC.

**9) AltORFev facilitates the prediction of alternative open reading frames in eukaryotic mRNAs**

<https://www.ncbi.nlm.nih.gov/pubmed/28039164>

Kochetov AV, Allmer J, Klimenko AI, Zuraev BS, Matushkin YG, Lashin SA.

**BIOINFORMATICS**  
Том: 33 Выпуск: 6 Стр.: 923-925  
DOI: 10.1093/bioinformatics/btw736  
Опубликовано: MAR 15 2017  
**iF 5.766**

Abstract:

Motivation: Protein synthesis is not a straight forward process and one gene locus can produce many isoforms, for example, by starting mRNA translation from alternative start sites. altORF evaluator (altORFev) predicts alternative open reading frames within eukaryotic mRNA translated by a linear scanning mechanism and its modifications (leaky scanning and reinitiation). The program reveals the efficiently translated altORFs recognized by the majority of 40S ribosomal subunits landing on the 50-end of an mRNA. This information aids to reveal the functions of eukaryotic genes connected to synthesis of either unknown isoforms of annotated proteins or new unrelated polypeptides.

**10) Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe**

<https://www.ncbi.nlm.nih.gov/labs/articles/28256537/>

Unterlander M, Palstra F, Lazaridis I, Pilipenko A, Hofmanova Z, Gross M, Sell C, Blocher J, Kirsanow K, Rohland N, Rieger B, Kaiser E, Schier W, Pozdniakov D, Khokhlov A, Georges M, Wilde S, Powell A, Heyer E, Currat M, Reich D, Samashev Z, Parzinger H, Molodin VI, Burger J.

**NATURE COMMUNICATIONS**  
Том: 8  
Номер статьи: 14615  
DOI: 10.1038/ncomms14615  
Опубликовано: MAR 3 2017  
**iF 11.329**

Abstract:

During the 1st millennium before the Common Era (BCE), nomadic tribes associated with the Iron Age Scythian culture spread over the Eurasian Steppe, covering a territory of more than 3,500 km in breadth. To understand the demographic processes behind the spread of the Scythian culture, we analysed genomic data from eight individuals and a mitochondrial dataset of 96 individuals originating in eastern and western parts of the Eurasian Steppe. Genomic inference reveals that Scythians in the east and the west of the steppe zone can best be described as a mixture of Yamnaya-related ancestry and an East Asian component. Demographic modelling suggests independent origins for eastern and western groups with ongoing gene-flow between them, plausibly explaining the striking uniformity of their material culture. We also find evidence that significant gene-flow from east to west Eurasia must have occurred early during the Iron Age.

**11) The Systems Biology of Auxin in Development Embryos**

<https://www.ncbi.nlm.nih.gov/pubmed/28131745>

Mironova V, Teale W, Shahriari M, Dawson J, Palme K.

**TRENDS IN PLANT SCIENCE**  
Том: 22 Выпуск: 3 Стр.: 225-235  
DOI: 10.1016/j.tplants.2016.11.010  
Опубликовано: MAR 2017  
**iF 10.899**

Abstract:

Systems biology orientates signaling pathways in their biological context. This aim invariably requires models that ignore extraneous factors and focus on the most crucial pathways of any given process. The developing embryo encapsulates many important processes in plant development; understanding their interaction will be key to designing crops able to maximize yield in an ever-more challenging world. Here, we briefly summarize the role of auxin during embryo development. We highlight recent advances in our understanding of auxin signaling and discuss implications for a systems understanding of development.

**12) The effect of long-term hindlimb unloading on the expression of risk neurogenes encoding elements of serotonin-, dopaminergic systems and apoptosis; comparison with the effect of actual spaceflight on mouse brain**

<https://www.ncbi.nlm.nih.gov/labs/articles/28088578/>

Kulikova EA, Kulikov VA, Sinyakova NA, Kulikov AV, Popova NK.

**NEUROSCIENCE LETTERS**  
Том: 640 Стр.: 88-92  
DOI: 10.1016/j.neulet.2017.01.023  
Опубликовано: FEB 15 2017  
**iF 2.107**

Abstract:

The study of spaceflight effects on the brain is technically complex concern; complicated by the problem of applying an adequate ground model. The most-widely used experimental model to study the effect of microgravity is the tail-suspension hindlimb unloading model; however, its compliance with the effect of actual spaceflight on the brain is still unclear. We evaluated the effect of one month hindlimb unloading on the expression of genes related to the brain neuroplasticity brain neutotrophic factors (Gdnf, Cdnf), apoptotic factors (Bcl-xl, Bax), serotonin- and dopaminergic systems (5-HT2A, Maoa, Maob, Th, D1r, Comt), and compared the results with the data obtained on mice that spent one month in spaceflight on Russian biosatellite Bion-M1. No effect of hindlimb unloading was observed on the expression of most genes, which were considered as risk neurogenes for long-term actual spaceflight. The opposite effect of hindlimb unloading and spaceflight was found on the level of mRNA of D1 dopamine receptor and catechol-O-methyltransferase in the striatum. At the same time, the expression of Maob in the midbrain decreased, and the expression of Bcl-xl genes increased in the hippocampus, which corresponds to the effect of spaceflight. However, the hindlimb unloading model failed to reproduce the majority of effects of long-term spaceflight on serotonin-, dopaminergic systems and some apoptotic factors. (C) 2017 Elsevier B.V. All rights reserved.

**13) High-resolution three-dimensional macromolecular proton fraction mapping for quantitative neuroanatomical imaging of the rodent brain in ultra-high magnetic fields**

<https://www.ncbi.nlm.nih.gov/pubmed/27646128>

Naumova AV, Akulov AE, Khodanovich MY, Yarnykh VL.

**NEUROIMAGE**  
Том: 147 Стр.: 985-993  
DOI: 10.1016/j.neuroimage.2016.09.036  
Опубликовано: FEB 15 2017  
**iF 5.463**

Abstract:

A well-known problem in ultra-high-field MRI is generation of high-resolution three-dimensional images for detailed characterization of white and gray matter anatomical structures. T-1-weighted imaging traditionally used for this purpose suffers from the loss of contrast between white and gray matter with an increase of magnetic field strength. Macromolecular proton fraction (MPF) mapping is a new method potentially capable to mitigate this problem due to strong myelin-based contrast and independence of this parameter of field strength. MPF is a key parameter determining the magnetization transfer effect in tissues and defined within the two-pool model as a relative amount of macromolecular protons involved into magnetization exchange with water protons. The objectives of this study were to characterize the two-pool model parameters in brain tissues in ultra-high magnetic fields and introduce fast high-field 3D MPF mapping as both anatomical and quantitative neuroimaging modality for small animal applications. In vivo imaging data were obtained from four adult male rats using an 11.7 T animal MRI scanner. Comprehensive comparison of brain tissue contrast was performed for standard R-1 and T-2 maps and reconstructed from Z-spectroscopic images two-pool model parameter maps including MPF, cross-relaxation rate constant, and T, of pools. Additionally, high-resolution whole-brain 3D MPF maps were obtained with isotropic 170 mu m voxel size using the single-point synthetic-reference method. MPF maps showed 3-6-fold increase in contrast between white and gray matter compared to other parameters. MPF measurements by the single-point synthetic reference method were in excellent agreement with the Z-spectroscopic method. MPF values in rat brain structures at 11.7 T were similar to those at lower field strengths, thus confirming field independence of MPF. 3D MPF mapping provides a useful tool for neuroimaging in ultra-high magnetic fields enabling both quantitative tissue characterization based on the myelin content and high-resolution neuroanatomical visualization with high contrast between white and gray matter. (C) 2016 Elsevier Inc. All rights reserved.

**14) Nanoparticles Associate with Intrinsically Disordered RNA-Binding Proteins**

<https://www.ncbi.nlm.nih.gov/pubmed/28122180>

Romashchenko AV, Kan TW, Petrovski DV, Gerlinskaya LA, Moshkin MP, Moshkin YM

**ACS NANO**  
Том: 11  Выпуск: 2  Стр.: 1328-1339  
DOI: 10.1021/acsnano.6b05992  
Опубликовано: FEB 2017  
**iF 13.334**

Abstract:

Nanoparticles are capable of penetrating cells, but little is known about the way they interact with intracellular proteome. Here we show that inorganic nanoparticles associate with low-complexity, intrinsically disordered proteins from HeLa cytosolic protein extracts in nondenaturing in vitro nanoparticle pull-down assays. Intrinsic protein disorder associates with structural mobility, suggesting that side-chain flexibility plays an important role in the driving of a protein to nanoparticle absorption. Disordered protein domains are often found in a diverse group of RNA-binding proteins. Consequently, the nano particle-associated proteomes were enriched in subunits of RNA-processing protein complexes. In turn, this indicates that within a cell, nanoparticles might interfere with protein synthesis triggering a range of cellular responses.

**15) Origin and spread of human mitochondrial DNA haplogroup U7**

<https://www.ncbi.nlm.nih.gov/pubmed/28387361>

Sahakyan H., Kashani B.H., Tamang R., Kushniarevich A., Francis A., Costa M.D., Pathak A.K., Khachatryan Z., Sharma I., van Oven M., Parik J., Hovhannisyan H., Metspalu E., Pennarun E., Karmin M., Tamm E., Tambets K., Bahmanimehr A., Reisberg T., Reidla M., Achilli A., Olivieri A., Gandini F., Perego U.A., Al-Zahery N., Houshmand M., Sanati M.H., Soares P., Rai E., Sarac J., Saric T., Sharma V., Pereira L., Fernandes V., Cerny V., Farjadian S., Singh D.P., Azakli H., Ustek D., Ekomasova N., Kutuev I., Litvinov S., Bermisheva M., Khusnutdinova E.K., Singh N.R.M., Singh V.K., Reddy A.G., Tolk H.V., Cvjetan S., Lauc L.B., Rudan P., Michalodimitrakis E.N., Anagnou N.P., Pappa K.I., Golubenko M.V., Orekhov V., Borinskaya S.A., Kaldma K., Schauer M.A., Simionescu M., Gusar V., Grechanina E., Govindaraj P., Voevoda M., Damba L., Sharma S., Singh L., Semino O., Behar D.M., Yepiskoposyan L., Richards M.B., Metspalu M., Kivisild T., Thangaraj K., Endicott P., Chaubey G., Torroni A., Villems R.

**SCIENTIFIC REPORTS**  
Том: 7  
Номер статьи: 46044  
DOI: 10.1038/srep46044  
Опубликовано: APR 7 2017  
**IF 5.528**

Abstract:

Human mitochondrial DNA haplogroup U is among the initial maternal founders in Southwest Asia and Europe and one that best indicates matrilineal genetic continuity between late Pleistocene huntergatherer groups and present-day populations of Europe. While most haplogroup U subclades are older than 30 thousand years, the comparatively recent coalescence time of the extant variation of haplogroup U7 (-16-19 thousand years ago) suggests that its current distribution is the consequence of more recent dispersal events, despite its wide geographical range across Europe, the Near East and South Asia. Here we report 267 new U7 mitogenomes that -analysed alongside 100 published ones -enable us to discern at least two distinct temporal phases of dispersal, both of which most likely emanated from the Near East. The earlier one began prior to the Holocene (-11.5 thousand years ago) towards South Asia, while the later dispersal took place more recently towards Mediterranean Europe during the Neolithic (-8 thousand years ago). These findings imply that the carriers of haplogroup U7 spread to South Asia and Europe before the suggested Bronze Age expansion of Indo-European languages from the Pontic-Caspian Steppe region.

**16) Potential importance of B cells in aging and aging-associated neurodegenerative diseases**

https://www.ncbi.nlm.nih.gov/pubmed/28083646

Biragyn A., Aliseychik M., Rogaev E.

**SEMINARS IN IMMUNOPATHOLOGY**  
Том: 39  Выпуск: 3  Стр.: 283-294  
DOI: 10.1007/s00281-016-0615-8  
Опубликовано: APR 2017  
**IF 6.394**

Abstract:

Our understanding of B cells as merely antibody producers is slowly changing. Alone or in concert with antibody, they control outcomes of seemingly different diseases such as cancer, rheumatoid arthritis, diabetes, and multiple sclerosis. While their role in activation of effector immune cells is beneficial in cancer but bad in autoimmune diseases, their immunosuppressive and regulatory subsets (Bregs) inhibit autoimmune and anticancer responses. These pathogenic and suppressive functions are not static and appear to be regulated by the nature and strength of inflammation. Although aging increases inflammation and changes the composition and function of B cells, surprisingly, little is known whether the change affects aging-associated neurodegenerative disease, such as Alzheimer's disease (AD). Here, by analyzing B cells in cancer and autoimmune and neuroinflammatory diseases, we elucidate their potential importance in AD and other aging-associated neuroinflammatory diseases.

**17) Histological validation of fast macromolecular proton fraction mapping as a quantitative myelin imaging method in the cuprizone demyelination model**

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5402392/

Khodanovich M.Y., Sorokina I.V., Glazacheva V.Y., Akulov A.E., Nemirovich-Danchenko N.M., Romashchenko A.V., Tolstikova T.G., Mustafina L.R., Yarnykh V.L.

**SCIENTIFIC REPORTS**  
Том: 7  
Номер статьи: 46686  
DOI: 10.1038/srep46686  
Опубликовано: APR 24 2017  
**iF 5.228**

Abstract:

Cuprizone-induced demyelination in mice is a frequently used model in preclinical multiple sclerosis research. A recent quantitative clinically-targeted MRI method, fast macromolecular proton fraction (MPF) mapping demonstrated a promise as a myelin biomarker in human and animal studies with a particular advantage of sensitivity to both white matter (WM) and gray matter (GM) demyelination. This study aimed to histologically validate the capability of MPF mapping to quantify myelin loss in brain tissues using the cuprizone demyelination model. Whole-brain MPF maps were obtained in vivo on an 11.7T animal MRI scanner from 7 cuprizone-treated and 7 control.57BL/6 mice using the fast single-point synthetic-reference method. Brain sections were histologically stained with Luxol Fast Blue (LFB) for myelin quantification. Significant (p < 0.05) demyelination in cuprizone-treated animals was found according to both LFB staining and MPF in all anatomical structures (corpus callosum, anterior commissure, internal capsule, thalamus, caudoputamen, and cortex). MPF strongly correlated with quantitative histology in all animals (r = 0.95, p < 0.001) as well as in treatment and control groups taken separately (r = 0.96, p = 0.002 and r = 0.93, p = 0.007, respectively). Close agreement between histological myelin staining and MPF suggests that fast MPF mapping enables robust and accurate quantitative assessment of demyelination in both WM and GM.

**18)A Sacrifice-for-Survival Mechanism Protects Root Stem Cell Niche from Chilling Stress**

https://www.ncbi.nlm.nih.gov/pubmed/28648662

Hong J.H., Savina M., Du J., Devendran A., Ramakanth K.K., Tian X., Sim W.S., Mironova V.V., Xu J.

**CELL**  
Том: 170  Выпуск: 1  
DOI: 10.1016/j.cell.2017.06.002  
Опубликовано: JUN 29 2017  
**iF 30.41**

Abstract:

Temperature has a profound influence on plant and animal development, but its effects on stem cell behavior and activity remain poorly understood. Here, we characterize the responses of the Arabidopsis root to chilling (low but above-freezing) temperature. Chilling stress at 4 degrees C leads to DNA damage predominantly in root stem cells and their early descendants. However, only newly generated/differentiating columella stem cell daughters (CSCDs) preferentially die in a programmed manner. Inhibition of the DNA damage response in these CSCDs prevents their death but makes the stem cell niche more vulnerable to chilling stress. Mathematical modeling and experimental validation indicate that CSCD death results in the re-establishment of the auxin maximum in the quiescent center (QC) and the maintenance of functional stem cell niche activity under chilling stress. This mechanism improves the root's ability to withstand the accompanying environmental stresses and to resume growth when optimal temperatures are restored.

**19) Modulation of proteostasis counteracts oxidative stress and affects DNA base excision repair capacity in ATM-deficient cells**

https://www.ncbi.nlm.nih.gov/pubmed/28973444

Poletto M., Yang D., Fletcher S.C., Vendrell I., Fischer R., Legrand A.J., Dianov G.L.

**NUCLEIC ACIDS RESEARCH**  
Том: 45  Выпуск: 17  Стр.: 10042-10055  
DOI: 10.1093/nar/gkx635  
Опубликовано: SEP 29 2017  
**iF 10.162**

Abstract:

Ataxia telangiectasia (A-T) is a syndrome associated with loss of ATM protein function. Neurodegeneration and cancer predisposition, both hallmarks of AT, are likely to emerge as a consequence of the persistent oxidative stress and DNA damage observed in this disease. Surprisingly however, despite these severe features, a lack of functional ATM is still compatible with early life, suggesting that adaptation mechanisms contributing to cell survival must be in place. Here we address this gap in our knowledge by analysing the process of human fibroblast adaptation to the lack of ATM. We identify profound rearrangement in cellular proteostasis occurring very early on after loss of ATM in order to counter protein damage originating from oxidative stress. Change in proteostasis, however, is not without repercussions. Modulating protein turnover in ATM-depleted cells also has an adverse effect on the DNA base excision repair pathway, the major DNA repair system that deals with oxidative DNA damage. As a consequence, the burden of unrepaired endogenous DNA lesions intensifies, progressively leading to genomic instability. Our study provides a glimpse at the cellular consequences of loss of ATM and highlights a previously overlooked role for proteostasis in maintaining cell survival in the absence of ATM function.

**20)Mutational re-modeling of di-aspartyl intramembrane proteases: uncoupling physiologically-relevant activities from those associated with Alzheimer's disease**

https://www.semanticscholar.org/paper/Mutational-re-modeling-of-di-aspartyl-intramembran-Grigorenko-Moliaka/58c5c0d034128d4c8c41253953e4e06b9dbdee44

Grigorenko A.P., Moliaka Y.K., Plotnikova O.V., Smirnov A., Nikishina V.A., Goltsov A.Y., Gusev F., Andreeva T.V., Nelson O., Bezprozvanny I., Rogaev E.I.

**ONCOTARGET**  
Том: 8  Выпуск: 47  Стр.: 82006-82026  
DOI: 10.18632/oncotarget.18299  
Опубликовано: OCT 10 2017  
**IF 5.168**

Abstract:

The intramembrane proteolytic activities of presenilins (PSEN1/PS1 and PSEN2/PS2) underlie production of beta-amyloid, the key process in Alzheimer's disease (AD). Dysregulation of presenilin-mediated signaling is linked to cancers. Inhibition of the gamma-cleavage activities of PSENs that produce A beta, but not the epsilon-like cleavage activity that release physiologically essential transcription activators, is a potential approach for the development of rational therapies for AD. In order to identify whether different activities of PSEN1 can be dissociated, we designed multiple mutations in the evolutionary conserved sites of PSEN1. We tested them in vitro and in vivo assays and compared their activities with mutant isoforms of presenilin-related intramembrane di-aspartyl protease (IMPAS1 (IMP1)/signal peptide peptidase (SPP)). PSEN1 autocleavage was more resistant to the mutation remodeling than the epsilon-like proteolysis. PSEN1 with a G382A or a P433A mutation in evolutionary invariant sites retains functionally important APP epsilon- and Notch S3-cleavage activities, but G382A inhibits APP.-cleavage and A beta production and a P433A elevates A beta. The G382A variant cannot restore the normal cellular ER Ca2+ leak in PSEN1/PSEN2 double knockout cells, but efficiently rescues the loss-of-function (Egl) phenotype of presenilin in C. elegans. We found that, unlike in PSEN1 knockout cells, endoplasmic reticulum (ER) Ca2+ leak is not changed in the absence of IMP1/SPP. IMP1/SPP with the analogous mutations retained efficiency in cleavage of transmembrane substrates and rescued the lethality of Ce-imp-2 knockouts. In summary, our data show that mutations near the active catalytic sites of intramembrane di-aspartyl proteases have different consequences on proteolytic and signaling functions.

**21) Education and coronary heart disease: mendelian randomisation study**

https://www.ncbi.nlm.nih.gov/pubmed/28855160

Tillmann T., Vaucher J., Okbay A., Pikhart H., Peasey A., Kubinova R., Pajak A., Tamosiunas A., Malyutina S., Hartwig F.P., Fischer K., Veronesi G., Palmer T., Bowden J., Smith G.D., Bobak M., Holmes M.V.

**BMJ-BRITISH MEDICAL JOURNAL**  
Том: 358  
Номер статьи: j3542  
DOI: 10.1136/bmj.j3542  
Опубликовано: AUG 30 2017  
**IF 20.785**

Abstract:

OBJECTIVE

To determine whether educational attainment is a causal risk factor in the development of coronary heart disease.

DESIGN

Mendelian randomisation study, using genetic data as proxies for education to minimise confounding.

SETTING

The main analysis used genetic data from two large consortia (CARDIoGRAMplusC4D and SSGAC), comprising 112 studies from predominantly high income countries. Findings from mendelian randomisation analyses were then compared against results from traditional observational studies (164 170 participants). Finally, genetic data from six additional consortia were analysed to investigate whether longer education can causally alter the common cardiovascular risk factors.

PARTICIPANTS

The main analysis was of 543 733 men and women (from CARDIoGRAMplusC4D and SSGAC), predominantly of European origin.

EXPOSURE

A one standard deviation increase in the genetic predisposition towards higher education (3.6 years of additional schooling), measured by 162 genetic variants that have been previously associated with education.

MAIN OUTCOME MEASURE

Combined fatal and non-fatal coronary heart disease (63 746 events in CARDIoGRAMplusC4D).

RESULTS

Genetic predisposition towards 3.6 years of additional education was associated with a one third lower risk of coronary heart disease (odds ratio 0.67, 95% confidence interval 0.59 to 0.77; P=3x10(-8)). This was comparable to findings from traditional observational studies (prevalence odds ratio 0.73, 0.68 to 0.78; incidence odds ratio 0.80, 0.76 to 0.83). Sensitivity analyses were consistent with a causal interpretation in which major bias from genetic pleiotropy was unlikely, although this remains an untestable possibility. Genetic predisposition towards longer education was additionally associated with less smoking, lower body mass index, and a favourable blood lipid profile.

CONCLUSIONS

This mendelian randomisation study found support for the hypothesis that low education is a causal risk factor in the development of coronary heart disease. Potential mechanisms could include smoking, body mass index, and blood lipids. In conjunction with the results from studies with other designs, these findings suggest that increasing education may result in substantial health benefits.

**22) Infection with Opisthorchis felineus induces intraepithelial neoplasia of the biliary tract in a rodent model**

https://www.ncbi.nlm.nih.gov/pubmed/28910999

Gouveia M.J., Pakharukova M.Y., Laha T., Sripa B., Maksimova G.A., Rinaldi G., Brindley P.J., Mordvinov V.A., Amaro T., Santos L.L., da Costa J.M.C., Vale N.

**CARCINOGENESIS**  
Том: 38  Выпуск: 9  Стр.: 929-937  
DOI: 10.1093/carcin/bgx042  
Опубликовано: SEP 2017  
**IF 5.105**

Abstract:

The liver fluke Opisthorchis felineus is a member of the triad of epidemiologically relevant species of the trematode family Opisthorchiidae, and the causative agent of opisthorchiasis felinea over an extensive range that spans regions of Eurasia. The International Agency for Research on Cancer classifies the infection with the liver flukes Opisthorchis viverrini and Clonorchis sinensis as group 1 agents and a major risk factor for cholangiocarcinoma. However, the carcinogenic potential of the infection with O. felineus is less clear. Here, we present findings that support the inclusion of O. felineus in the Group 1 list of biological carcinogens. Two discrete lines of evidence support the notion that infection with this liver fluke is carcinogenic. First, novel oxysterol-like metabolites detected by liquid chromatography-mass spectroscopy in the egg and adult developmental stages of O. felineus, and in bile, sera, and urine of liver fluke-infected hamsters exhibited marked similarity to oxysterol-like molecules known from O. viverrini. Numerous oxysterols and related DNA-adducts detected in the liver fluke eggs and in bile from infected hamsters suggested that infection-associated oxysterols induced chromosomal lesions in host cells. Second, histological analysis of liver sections from hamsters infected with O. felineus confirmed portal area enlargement, inflammation with severe periductal fibrosis and changes in the epithelium of the biliary tract characterized as biliary intraepithelial neoplasia, BilIN. The consonance of these biochemical and histopathological changes revealed that O. felineus infection in this rodent model induced precancerous lesions conducive to malignancy.

**23) Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation**

https://www.ncbi.nlm.nih.gov/pubmed/28878392

Shen X., Klaric L., Sharapov S., Mangino M., Ning Z., Wu D., Trbojevic-Akmacic I., Pucic-Bakovic M., Rudan I., Polasek O., Hayward C., Spector T.D., Wilson J.F., Lauc G., Aulchenko Y.S.

**NATURE COMMUNICATIONS**  
Том: 8  
Номер статьи: 447  
DOI: 10.1038/s41467-017-00453-3  
Опубликовано: SEP 6 2017  
**IF 12.124**

Abstract:

Joint modeling of a number of phenotypes using multivariate methods has often been neglected in genome-wide association studies and if used, replication has not been sought. Modern omics technologies allow characterization of functional phenomena using a large number of related phenotype measures, which can benefit from such joint analysis. Here, we report a multivariate genome-wide association studies of 23 immunoglobulin G (IgG) N-glycosylation phenotypes. In the discovery cohort, our multi-phenotype method uncovers ten genome-wide significant loci, of which five are novel (IGH, ELL2, HLA-B-C, AZI1, FUT6-FUT3). We convincingly replicate all novel loci via multivariate tests. We show that IgG N-glycosylation loci are strongly enriched for genes expressed in the immune system, in particular antibody-producing cells and B lymphocytes. We empirically demonstrate the efficacy of multivariate methods to discover novel, reproducible pleiotropic effects.

**24) Linagliptin alleviates podocyte injury and enhances glomerular nephrin expression in a model of type 2 diabetes**

https://www.researchgate.net/publication/320149611\_Linagliptin\_alleviates\_podocyte\_injury\_and\_enhances\_glomerular\_nephrin\_expression\_in\_a\_model\_of\_type\_2\_diabetes

Korbut A.I., Klimontov V.V., Bgatova N.P., Gavrilova Y.S., Ischenko I.Y., Orlov N.B., Dozenko A.S., Zavjalov E.L.

**DIABETOLOGIA**  
Том: 60 Стр.: S550-S550 Приложение: 1 Аннотация к встрече: 1194  
Опубликовано: SEP 2017  
Конференция  
Конференция: 53rd Annual Meeting of the European-Association-for-the-Study-of-Diabetes (EASD)   
Местоположение: Lisbon, PORTUGAL  
публ.: SEP 11-15, 2017  
Спонсоры:European Assoc Study Diabet  
**IF 12.124**

**25) FEATURES OF TELOMERE LENGTH DISTRIBUTION ON INDIVIDUAL CHROMOSOMES IN RHEUMATOID ARTHRITIS**

http://ard.bmj.com/content/76/Suppl\_2/206.2.info

Barkovskaya M., Bogomolov A., Knauer N., Blinova E., Sizikov A., Rubtsov N., Kozlov V.

**ANNALS OF THE RHEUMATIC DISEASES**  
Том: 76 Стр.: 206-207 Приложение: 2 Аннотация к встрече: THU0019  
DOI: 10.1136/annrheumdis-2017-eular.3649  
Опубликовано: JUN 2017  
Конференция  
Конференция: Annual European Congress of Rheumatology  
Местоположение: Madrid, SPAIN  
публ.: JUN 14-17, 2017  
**IF 12.811**

Abstract:

Ataxia telangiectasia (A-T) is a syndrome associated with loss of ATM protein function. Neurodegeneration and cancer predisposition, both hallmarks of AT, are likely to emerge as a consequence of the persistent oxidative stress and DNA damage observed in this disease. Surprisingly however, despite these severe features, a lack of functional ATM is still compatible with early life, suggesting that adaptation mechanisms contributing to cell survival must be in place. Here we address this gap in our knowledge by analysing the process of human fibroblast adaptation to the lack of ATM. We identify profound rearrangement in cellular proteostasis occurring very early on after loss of ATM in order to counter protein damage originating from oxidative stress. Change in proteostasis, however, is not without repercussions. Modulating protein turnover in ATM-depleted cells also has an adverse effect on the DNA base excision repair pathway, the major DNA repair system that deals with oxidative DNA damage. As a consequence, the burden of unrepaired endogenous DNA lesions intensifies, progressively leading to genomic instability. Our study provides a glimpse at the cellular consequences of loss of ATM and highlights a previously overlooked role for proteostasis in maintaining cell survival in the absence of ATM function.