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НОВ БЪЛГАРСКИ УНИВЕРСИТЕТ

Танцуват ли гените?

Избрана библиография

КЛЮЧОВИ ДУМИ:

На български език: ДНК, гени, дезоксирибонуклеинова киселина, генетика.

На английски език: DNA, genes, deoxyribonucleic acid, genetics.

ДОКУМЕНТИ: книги, статии, DVD

ХРОНОЛОГИЧЕН ОБХВАТ: 1975 г. - 2023 г.

БИБЛИОГРАФСКИ ИЗТОЧНИЦИ:

1. Каталог на Библиотеката на НБУ

ЕЛЕКТРОННИ РЕСУРСИ:

1. EBSCO: Academic Search Complete
2. EBSCO: eBook Academic Collection
3. EBSCO: eBook Open Access
4. JSTOR
5. ProQuest
6. ScienceDirect

ЕЛЕКТРОННИ РЕСУРСИ С ОТВОРЕН ДОСТЪП:

7. De Gruyter: Open access
8. ScienceDirect: Open access & Open archive
9. SpringerOpen

февруари 2023

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АЙАЛА, Франциско и Джон КИГЕР. *Съвременна генетика*. Прев. от англ. език П. ВЕНКОВ и др. София: Земиздат, 1987.
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Description: RAND researchers explored the U.S. and English forensic DNA analysis systems to find out whether England has capitalized more fully on their crime-fighting potential than the U.S. system, processing samples more quickly and providing more database hits for law enforcement.
Източник: ProQuest

HASLAM, Michael et al. *Archaeological Science Under a Microscope: Studies in Residue and Ancient DNA Analysis in Honour of Thomas H. Loy* [online]. Canberra, ACT: ANU Press, 2009 [viewed 16 February 2023]. EBSCO: eBook Open Access. ISBN 978-192-153-685-4. Available from: http://search.ebscohost.com
Description: These highly varied studies, spanning the world, demonstrate how much modern analyses of microscopic traces on artifacts are altering our perceptions of the past. Ranging from early humans to modern kings, from ancient Australian spears or Mayan pots to recent Maori cloaks, the contributions demonstrate how starches, raphides, hair, blood, feathers, resin and DNA have become essential elements in archaeology's modern arsenal for reconstructing the daily, spiritual, and challenging aspects of ancient lives and for

understanding human evolution. The book is a fitting tribute to Tom Loy, the pioneer of residue studies and gifted teacher who inspired and mentored these exciting projects.
Източник: EBSCO: eBook Open Access

HERRERA, Rene J. and Ralph GARCIA-BERTRAND. *Ancestral DNA, Human Origins, and Migrations* [online]. London: Academic Press, 2018 [viewed 16 February 2023]. ScienceDirect. ISBN 978-0-12-804124-6. Available from: https://www.sciencedirect.com/
Description: Ancestral DNA, Human Origins, and Migrations describes the genesis of humans in Africa and the subsequent story of how our species migrated to every corner of the globe. Different phases of this journey are presented in an integrative format with information from a number of disciplines, including population genetics, evolution, anthropology, archaeology, climatology, linguistics, art, music, folklore and history. This unique approach weaves a story that has synergistic impact in the clarity and level of understanding that will appeal to those researching, studying, and interested in population genetics, evolutionary biology, human migrations, and the beginnings of our species.
Източник: ScienceDirect

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Description: Biological DNA Sensor defines the meaning of DNA sensing pathways and demonstrates the importance of the innate immune responses induced by double stranded DNA (dsDNA) through its influencing functions in disease pathology and immune activity of adjuvants for vaccines.
Though discussed in specific subsections of existing books, dsDNA and its immunogenic properties has never received the complete treatment given in this book. Biological DNA Sensor approaches the impact of dsDNA's immunogenicity on disease and vaccinology holistically. It paints a complete and concise picture on the topic so you can understand this area of study and make more informed choices for your respective research needs. Chapters are authored by researchers who are renowned for their research focus, ensuring that this book provides the most complete views on the topics.
Източник: ScienceDirect

LEE, W. David et al. *From X-Rays to DNA: How Engineering Drives Biology* [online]. MIT Press, 2013 [viewed 16 February 2023]. ProQuest. ISBN 978-026-231-838-9. Available from: https://ebookcentral.proquest.com
Description: Engineering has been an essential collaborator in biological research and breakthroughs in biology are often enabled by technological advances. Decoding the double helix structure of DNA, for example, only became possible after significant advances in such technologies as X-ray diffraction and gel electrophoresis. Diagnosis and treatment of tuberculosis improved as new technologies -- including the stethoscope, the microscope, and the X-ray -- developed. These engineering breakthroughs take place away from the biology lab, and many years may elapse before the technology becomes available to biologists. In this book, David Lee argues for concurrent engineering -- the convergence of engineering and biological research -- as a means to accelerate the pace of biological discovery and its application to diagnosis and treatment. He presents extensive case studies and introduces a metric to measure the time between technological development and biological discovery. Investigating a series of major biological discoveries that range from pasteurization to electron microscopy, Lee finds that it took an average of forty years for the necessary technology to become available for laboratory use. Lee calls for new approaches to research and funding to encourage a tighter, more collaborative coupling of engineering and biology. Only then, he argues, will we see the rapid advances in the life sciences that are critically needed for life-saving diagnosis and treatment.
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NEWTON, David E. *DNA Technology: A Reference Handbook* [online]. Santa Barbara, California: ABC-CLIO, 2017 [viewed 16 February 2023]. EBSCO: eBook Academic

Collection. ISBN 978-144-085-047-9. Available from: http://search.ebscohost.com
Description: The great strides made in our understanding of the structure and function of DNA in recent decades have led to applying this invaluable knowledge to use in serving humanity. For example, recent discoveries in the field of genetic editing have created the potential for the creation of life forms de novo, a possibility that results in profound ethical issues for the human race that are just beginning to be discussed. What other positive - and potentially negative - developments are coming our way with continuing advancements in DNA research? DNA Technology: A Reference Handbook provides an up-to-date historical overview and general technical background to the topic as well as a broad introduction to current issues related to the development of DNA technology, such as genetically modified organisms, the use of DNA technology in the forensic sciences, and genetic testing and genetic therapy.Written by David E. Newton, an author and former teacher who has dedicated a lifetime to authoring educational texts on science and technology, this book examines the history of DNA technology from its discovery in the 1950s to the present day and covers recent advances, such as new methods for gene editing, including CRISP-Cas9 technology. Readers need to have little or no background knowledge of the technology of genetic engineering to improve their understanding of DNA-based technologies and how DNA research influences many current issues and debates in agriculture, food science, forensics, public health, and other fields. The single-volume work is particularly well-suited to students and young adults because of the range of references included that serve further study, such as a glossary of terms, a chronology, and an extensive annotated bibliography.
Источник: EBSCO: eBook Academic Collection

SANJEEVI, Shiv. *Mitochondrial DNA: The Works* [online]. [n.p.]: Delve Publishing, 2019 [viewed 16 February 2023]. EBSCO: eBook Academic Collection. ISBN 978-177-407-441-1. Available from: http://search.ebscohost.com
Description: Mitochondrial DNA: The Works takes into account the overview of mitochondria along with its dna and inheritance. It also comprises the interest aspects and glimpses of research related to the mitochondrial dna. It provides the reader with the insights of mitochondrial dna and its interesting aspects so as to understand the advances in methods for reducing mitochondrial dna disease by replacing or manipulating the mitochondrial genome, reaction of human cells in the absence of mitochondrial dna and variants of mitochondrial dna in case of obesity. This book also discusses about regulation of mitochondrial genome inheritance by autophagy and ubiquitin-proteasome system: implications for health, fitness, and fertility, advances in methods for reducing mitochondrial dna disease by replacing or manipulating the mitochondrial genome, mitochondrial dna variants in obesity and research on plants for the understanding of diseases of nuclear and mitochondrial origin.
Источник: EBSCO: eBook Academic Collection

TSEYTLIN, Yakov M. *Advanced Mechanical Models of DNA Elasticity* [online]. London: Academic Press is an imprint of Elsevier, 2016 [viewed 16 February 2023]. ScienceDirect. ISBN 978-0-12-801999-3. Available from: https://www.sciencedirect.com/
Description: Advanced Mechanical Models of DNA Elasticity includes coverage on 17 different DNA models and the role of elasticity in biological functions with extensive references. The novel advanced helicoidal model described reflects the direct connection between the molecule helix structure and its specific properties, including nonlinear features and transitions. It provides an introduction to the state of the field of DNA mechanics, known and widely used models with their short analysis, as well as coverage on experimental methods and data, the influence of electrical, magnetic, ionic conditions on the persistence length, and dynamics with viscosity influence. It then addresses the need to understand the nature of the non-linear overstretching transition of DNA under force and why DNA has a negative twist-stretch coupling.
Источник: ScienceDirect

WAILOO, Keith, Alondra NELSON, and Catherine LEE. *Genetics and the Unsettled Past: The Collision of DNA, Race, and History* [online]. Rutgers University Press, 2012 [viewed 16 February 2023]. ProQuest. ISBN 978-081-355-336-8. Available from: https://ebookcentral.proquest.com
Description: "Genetics and the Unsettled Past" considers the alignment of genetic science with commercial trends in genealogy, with legal and forensic developments, and with pharmaceutical innovation to examine how

these trends lend renewed authority to biological understandings of race and history. Essays by scholars across a wide range of disciplines--biology, history, cultural studies, law, medicine, anthropology, ethnic studies, sociology--explore the emerging and often contested connections among race, DNA, and history.
Източник: ProQuest

YASHON, Ronnee K. and Michael R. CUMMINGS. *DNA Forensics* [online]. New York: Momentum Press, 2019 [viewed 16 February 2023]. EBSCO: eBook Academic Collection. ISBN 978-194-664-638-5. Available from: http://search.ebscohost.com
Description: This book reveals amazing examples of what has and is happening with science and DNA forensics.The public now knows the DNA molecule by sight and how it can assist in solving crimes such as murder and sexual assaults. In this book, the authors demonstrate how DNA forensics has developed over the years.DNA has assisted in finding criminals and releasing those who were wrongly accused, including prisoners on death row and a few who were already executed!
Източник: EBSCO: eBook Academic Collection

СТАТИИ

AFANASIEVA, K S. et all. DNA loop organization in dorsal root ganglion neurons: effects of peripheral inflammation. *Biopolymers & Cell* [online] 2021, vol. 37(2), pp. 98-104 [viewed 09 February 2023]. ISSN 0233-7657. EBSCO: Academic Search Complete. Available from: https://www.ebscohost.com
Abstract: The loop domain organization of chromatin plays an important role in transcription regulation and is known to be dependent on the cell functional states. The aim of this work was to investigate the possible DNA loop reorganization in dorsal ganglion neurons upon inflammatory pain. Methods. We used single cell gel electrophoresis (the comet assay) to analyze the kinetics of the DNA loop migration from the nucleoids obtained from lysed neurons. Results. Independently of inflammation, the neurons are characterized by relatively low amount of DNA in the comet tails due to a low content of DNA in the loops, which may be resolved by the comet assay (up to ~400 kb). Upon inflammation the contour length of the loops essentially decreases, in parallel with a respective increase of DNA in relatively short (up to ~100 kb) loops. Conclusions. The reorganization of the DNA loops upon inflammation could be suggested to be accompanied by rather significant changes in the transcription regulation.
Източник: EBSCO: Academic Search Complete

BOZKURT, Aliseydi et al. Qualification and quantification of plasma cell-free DNA after long-term storage conditions in patients with benign prostatic hyperplasia (BPH): a pilot study. *Journal of Laboratory Medicine* [online]. 2022, vol. 46(6), pp. 383-389 [viewed 09 February 2023]. De Gruyter: Open access. ISSN 2192-8614. Available from: https://www.degruyter.com/
Abstract: Objectives:Free DNA is used as a cancer biomarker due to its low cost, high applicability, and fast, reliable results compared to invasive methods. This study aimed to evaluate the quantification of plasma-free DNA after long-term storage conditions and perform qualification through single nucleotide polymorphism (SNP) screening based on this DNA.
Methods: Plasma-free DNA samples were quickly isolated from the peripheral blood of both the benign prostatic hyperplasia (BPH) and control group participants and then maintained at −80 °C for four years. Upon thawing, first, free DNA was purified and fluorometric measurements were taken to determine the amount of DNA. Subsequently, the rs6983267, rs12628, and rs1799939 SNPs were screened in the CCAT2, HRAS, and RET genes, respectively.
Results:Significant results were obtained from the fluorometric measurements in terms of single-stranded DNA (ssDNA) ($p<0.001$). However, there was no significant difference in SNPs rs6983267, rs12628, and rs1799939 in the BPH group compared to the healthy individuals.
Conclusions: The data show that fluorometric ssDNA measurements are suitable for quantifying free DNA. The fact that SNP screening can be done successfully in both healthy people and BPH patients suggests that plasma-

free DNA can be stored in the laboratory under appropriate conditions.
Източник: De Gruyter: Open access

CAO, Mengyao. DNA computational device-based smart biosensors. *TrAC Trends in Analytical Chemistry* [online]. 2023, vol. 159, pp. 1-10 [viewed 15 February 2023]. ISSN 0165-9936. ScienceDirect. Available from: https://www.sciencedirect.com/
Abstract: During the past decade, DNA computing has been rapidly developed and made continuous progress. Based on typical DNA functional motifs, DNA computational devices can perform diverse powerful computational functions, such as simple Boolean logics and sophisticated neural network algorithms. Thus, DNA computer is widely regarded as one of the most excellent next-generation molecular computers performing Boolean logic. Benefiting from DNAs' inherent properties of biocompatibility, low-cost, ease of synthesis, and sequence programmability, DNA computational devices have shown great potential in various biosensing applications. In this review, we summarize the recent progress in DNA computational devices-based biosensors. Initially, DNA logic circuit-based in vitro biosensing is outlined. Afterwards, the DNA neural network-based in vitro biosensing is reviewed. Further, employing DNA logical circuits for in vivo biosensing and programming cell behaviors is also elaborated. Finally, we discuss future challenges and offer some insights on potential directions of DNA computational device-based smart biosensors.
Източник: ScienceDirect

CHAKRABORTY, Anirban et al. Human DNA polymerase η promotes RNA-templated error-free repair of DNA double strand breaks. *Journal of Biological Chemistry* [online]. 2023, pp. 1-61 [viewed 16 February 2023]. ISSN 1083-351X. ScienceDirect: Open access & Open archive. Available from: https://www.sciencedirect.com/
Abstract: A growing body of evidence indicates that RNA plays a critical role in orchestrating DNA double strand break repair (DSBR). Recently, we showed that homologous nascent RNA can be used as a template for error-free repair of DSBs in the transcribed genome and to restore the missing sequence at the break site via the transcription-coupled classical non-homologous end-joining (TC-NHEJ) pathway. TC-NHEJ is a complex multistep process in which a reverse transcriptase (RT) is essential for synthesizing the DNA strand from template RNA. However, the identity of the RT involved in the TC-NHEJ pathway remained unknown. Here, we report that DNA polymerase eta (Pol η), known to possess RT activity, plays a critical role in TC-NHEJ. We found that Pol η forms a multi-protein complex with RNAP II and other TC-NHEJ factors, while also associating with nascent RNA. Moreover, purified Pol η, along with DSB repair proteins PNKP, XRCC4 and Ligase IV (Lig IV) can fully repair RNA templated 3'-phosphate-containing gapped DNA substrate. Additionally, we demonstrate here that Pol η deficiency leads to accumulation of R-loops and persistent strand breaks in the transcribed genes. Finally, we determined that in Pol η depleted, but not in control cells, TC-NHEJ-mediated repair was severely abrogated when a reporter plasmid containing a DSB with several nucleotide deletion within the E. coli lacZ gene was introduced for repair in lacZ-expressing mammalian cells. Thus, our data strongly suggest that RT activity of Pol η is required in error-free DSBR.
Източник: ScienceDirect: Open access & Open archive

CHO, YongDeok et al. DNA as grabbers and steerers of quantum emitters. *Nanophotonics* [online]. 2022. [viewed 09 February 2023]. De Gruyter: Open access. ISSN 2567-9449. Available from: https://www.degruyter.com/
Abstract: The chemically synthesizable quantum emitters such as quantum dots (QDs), fluorescent nanodiamonds (FNDs), and organic fluorescent dyes can be integrated with an easy-to-craft quantum nanophotonic device, which would be readily developed by non-lithographic solution process. As a representative example, the solution dipping or casting of such soft quantum emitters on a flat metal layer and subsequent drop-casting of plasmonic nanoparticles can afford the quantum emitter-coupled plasmonic nanocavity (referred to as a nanoparticle-on-mirror (NPoM) cavity), allowing us for exploiting various quantum mechanical behaviors of light–matter interactions such as quantum electrodynamics (QED), strong coupling (e.g., Rabi splitting), and quantum mirage. This versatile, yet effective soft quantum nanophotonics would be further benefitted from a deterministic control over the positions and orientations of each individual quantum emitter, particularly at the molecule level of resolution. In this review, we will argue that DNA nanotechnology

can provide a gold vista toward this end. A collective set of exotic characteristics of DNA molecules, including Watson-Crick complementarity and helical morphology, enables reliable grabbing of quantum emitters at the on-demand position and steering of their directors at the single molecular level. More critically, the recent advances in large-scale integration of DNA origami have pushed the reliance on the distinctly well-formed single device to the regime of the ultra-scale device arrays, which is critical for promoting the practically immediate applications of such soft quantum nanophotonics.
Источник: De Gruyter: Open access

LORD, Mary. Disrudisrupting DNA. *ASEE Prism* [online]. 2018, vol. 27(6), pp. 28-31 [viewed 15 February 2023]. JSTOR. ISSN 1056-8077 Available from: http://www.jstor.org
Источник: JSTOR

MIDDLETON, James. Handy DNA Nucleotide Model. *The American Biology Teacher* [online]. 2019, vol. 81(3), pp. 193-196 [viewed 15 February 2023]. JSTOR. ISSN 0002-7685 Available from: http://www.jstor.org
Abstract: A readily available resource to create a model for the study of DNA is the human hand. Students can recognize how structure and function of nucleotides determine structure and function of the DNA molecule by labeling parts of a gloved hand with the parts of a DNA molecule.
Источник: JSTOR

RODRIGUEZ, Marcella et al. The effect of abnormal placentation on maternal serum fetal fraction of cell-free DNA. *Journal of Perinatal Medicine* [online]. 2023, vol. 51(1), pp. 97-101 [viewed 09 February 2023]. De Gruyter: Open access. ISSN 1619-3997. Available from: https://www.degruyter.com/
Abstract: Objectives: Abnormal placentation may affect the maternal serum fraction of cell-free fetal DNA (fetal fraction) determined as part of non-invasive prenatal screening (NIPS). This study aimed to assess whether the fetal fraction can predict placenta accreta spectrum (PAS) with or without placenta previa (PP). We also investigated the impact of trophoblastic invasion depth on the fetal fraction.
Methods: This is a retrospective case-control study of pregnant women with and without abnormal placentation carrying a singleton and having undergone NIPS prior to 20 weeks of gestation. The eligible subjects were selected from a cohort managed at our institution for PAS suspected antenatally. We compared women with normal placentation (controls) to PAS, PP, or PAS + PP cases. Data were abstracted from electronic medical records, and PAS was confirmed histologically.
Results: Of the 146 patients in our cohort, 8 controls, 10 PP, 6 PAS, and 7 PAS + PP cases were eligible for the study. Among the groups, there were no significant differences in baseline demographic and clinical characteristics except the median number of prior uterine surgeries. Also, the groups did not significantly differ in their median fetal fraction. The fetal fraction did not discriminate any group when stratified according to the depth of placental invasion, i.e., no PAS, abnormally adherent, and abnormally invasive placenta.
Conclusions: The maternal serum fraction of cell-free fetal DNA measured before 20 weeks of gestation is not predictive of PAS with or without concurrent PP or the depth of trophoblastic invasion.
Источник: De Gruyter: Open access

SELVESTREL, Davide et al. DNA methylation of the TPMT gene and azathioprine pharmacokinetics in children with very early onset inflammatory bowel disease. *Biomedicine & Pharmacotherapy* [online]. 2023, vol. 157, pp. 1-9 [viewed 16 February 2023]. ISSN 1950-6007. ScienceDirect: Open access & Open archive. Available from: https://www.sciencedirect.com/
Abstract: Background: Thiopurine methyltransferase (TPMT) is a crucial enzyme for azathioprine biotransformation and its activity is higher in very early onset inflammatory bowel disease (VEO-IBD) patients than in adolescents with IBD (aIBD).
Aims: The aims of this pharmacoepigenetic study were to evaluate differences in peripheral blood DNA methylation of the TPMT gene and in azathioprine pharmacokinetics in patients with VEO-IBD compared to

aIBD.
Methods: The association of age with whole genome DNA methylation profile was evaluated in a pilot group of patients and confirmed by a meta-analysis on 3 cohorts of patients available on the public functional genomics data repository. Effects of candidate CpG sites in the TPMT gene were validated in a larger cohort using pyrosequencing. TPMT activity and azathioprine metabolites (TGN) were measured in patients' erythrocytes by HPLC and associated with patients' age group and TPMT DNA methylation.
Results: Whole genome DNA methylation pilot analysis, combined with the meta-analysis revealed cg22736354, located on TPMT downstream neighboring region, as the only statistically significant CpG whose methylation increases with age, resulting lower in VEO-IBD patients compared to aIBD (median 9.6% vs 12%, p = 0.029). Pyrosequencing confirmed lower cg22736354 methylation in VEO-IBD patients (median 4.0% vs 6.0%, p = 4.6 ×10−5). No differences in TPMT promoter methylation were found. Reduced cg22736354 methylation was associated with lower TGN concentrations (rho = 0.31, p = 0.01) in patients with VEO-IBD and aIBD.
Conclusion: Methylation of cg22736354 in TPMT gene neighborhood is lower in patients with VEO-IBD and is associated with reduced azathioprine inactivation and increased TGN concentrations.
Източник: ScienceDirect: Open access & Open archive

SILVA JUNIOR, Ronaldo C. et all. DNA databases as a tool to improve the search for missing persons in Brazil. *Forensic Science International: Genetics Supplement Series* [online]. 2022, vol. 8, pp. 167-169 [viewed 15 February 2023]. ISSN 1875-1768. ScienceDirect. Available from: https://www.sciencedirect.com/
Abstract: In 2019, based on the publication of Law No. 13,812/2019, the National Policy on the Search for Missing Persons was created in Brazil. In this context, on March 2, 2020 the Steering Committee of the Integrated Network of DNA Databases (RIBPG) created the Working Group on Genetic Identification of Missing Persons. In 2021, the first National Campaign for the Collection of DNA from Relatives of Missing Persons was launched. This action provided the collection of relatives of more than 1700 missing people throughout Brazil. Since the beginning of the work, the number of genetic profiles related to the search for missing persons has increased by 216 % in the National DNA Database. So far, RIBPG has already managed to solve 223 disappearances throughout Brazil.
Източник: ScienceDirect

TSURUTA, Haruka et al. Effects of acetaldehyde-induced DNA lesions on DNA metabolism. *Genes and Environment* [online]. 2020 (42), 2 [viewed 16 February 2023]. SpringerOpen. ISSN 1880-7062. Available from: https://link.springer.com/
Abstract Background: Acetaldehyde, produced upon exposure to alcohol, cigarette smoke, polluted air and sugar, is a highly reactive compound that is carcinogenic to humans and causes a variety of DNA lesions in living human cells. Previously, we reported that acetaldehyde reacts with adjacent deoxyguanosine residues on oligonucleotides, but not with single deoxyguanosine residues or other deoxyadenosine, deoxycytosine, or thymidine residues, and revealed that it forms reversible intrastrand crosslinks with the dGpdG sequence (GG dimer).
Results: Here, we show that restriction enzymes that recognize a GG sequence digested acetaldehyde-treated plasmid DNA with low but significant efficiencies, whereas restriction enzymes that recognize other sequences were able to digest such DNA. This suggested that acetaldehyde produced GG dimers in plasmid DNA. Additionally, acetaldehyde-treated oligonucleotides were efficient in preventing digestion by the exonuclease function of T4 DNA polymerase compared to non-treated oligonucleotides, suggesting structural distortions of DNA caused by acetaldehyde-treatment. Neither in vitro DNA synthesis reactions of phi29 DNA polymerase nor in vitro RNA synthesis reactions of T7 RNA polymerase were observed when acetaldehyde-treated plasmid DNA was used, compared to when non-treated plasmid DNA was used, suggesting that acetaldehyde-induced DNA lesions inhibited replication and transcription in DNA metabolism.
Conclusions: Acetaldehyde-induced DNA lesions could affect the relative resistance to endo- and exo-nucleolytic activity and also inhibit in vitro replication and in vitro transcription. Thus, investigating the effects of acetaldehyde-induced DNA lesions may enable a better understanding of the toxicity and carcinogenicity of acetaldehyde.

Источник: SpringerOpen

WANG, Jing, Mingzhe GAN. DNA Nanoflowers' Amelioration of Lupus Symptoms in Mice via Blockade of TLR7/9's Signal. *International Journal of Molecular Sciences* [online] 2022, vol. 23 Issue 24, p. 16030 [viewed 15 February 2023]. ISSN 1661-6596. EBSCO: Academic Search Complete. Available from: https://www.ebscohost.com

Abstract: Inhibitory oligodeoxynucleotides (INH-ODN) can exert an immunomodulatory effect to specifically block TLR7 and TLR9 signaling in systemic lupus erythematosus (SLE). To extend the half-life of INH-ODN in vivo, the phosphorothioate backbone, instead of the native phosphodiester, is preferred due to its strong resistance against nuclease degradation. However, its incomplete degradation in vivo may lead to potential risk. To solve these problems and enhance the blockage of TLR7 and TLR9, we prepared highly compressed DNA nanoflowers with prolonged native DNA backbones and repeated INH-ODN motifs. Three therapeutic types of nanoflower, incorporating INH-ODN sequences, including IRS 661, IRS 869, and IRS 954, were prepared by rolling circle amplification and were subcutaneously injected into MRL/lpr mice. The TLR7 blocker of the IRS 661 nanoflower and the TLR9 antagonist of the IRS 869 nanoflower could decrease autoantibodies, reduce cytokine secretion, and alleviate lupus nephritis in mice. However, the IRS 954 nanoflower, the TLR7 and TLR9 dual antagonist, did not have additive or opposing effects on lupus nephritis but only showed a decrease in serum IFNα, suggesting that the TLR7 and TLR9 antagonist may have a competition mechanism or signal-dependent switching relationship. INH-ODN nanoflowers were proposed as a novel and potential therapeutic nucleic acids for SLE

Источник: EBSCO: Academic Search Complete

ZHANG, Runrun et al. Identification of DNA methylation-regulated differentially expressed genes in RA by integrated analysis of DNA methylation and RNA-Seq data. *Journal of Translational Medicine* [online]. 2022, (20), p. 481 [viewed 16 February 2023]. SpringerOpen. ISSN 1479-5876. Available from: https://link.springer.com/

Abstract: Objective: To identify novel DNA methylation-regulated differentially expressed genes (MeDEGs) in RA by integrated analysis of DNA methylation and RNA-Seq data.
Methods: The transcription and DNA methylation profiles of 9 RA and 15 OA synovial tissue were generated by RNA-Seq and Illumina 850K DNA methylation BeadChip. Gene set enrichment analysis (GSEA) and Weighted gene co-expression network analysis (WGCNA) were used to analyze methylation-regulated expressed genes by R software. The differentially expressed genes (DEGs), differentially methylated probes (DMPs), differentially methylated genes (DMGs) were analyzed by DESeq and ChAMP R package. The functional correlation of MeDEGs was analyzed by Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG). The protein–protein interaction (PPI) network of MeDEGs was constructed by STRING and Reactome FI Cytoscape Plugin. Correlation analysis between methylation level and mRNA expression was conducted with R software.Results: A total of 17,736 genes, 25,578 methylated genes and 755,852 methylation probes were detected. A total of 16,421 methylation-regulated expressed genes were obtained. The GSEA showed that these genes are associated with activation of immune response, adaptive immune response, Inflammatory response in C5 (ontology gene sets). For KEGG analysis, these genes are associated with rheumatoid arthritis, NF-kappa B signaling pathway, T cell receptor signaling pathway. The WGCNA showed that the turquoise module exhibited the strongest correlation with RA ($R = 0.78$, $P = 1.27 \times 10-05$), 660 genes were screened in the turquoise module. A total of 707 MeDEGs were obtained. GO analysis showed that MeDEGs were enriched in signal transduction, cell adhesion for BP, enriched in plasma membrane, integral component of membrane for CC, and enriched in identical protein binding, calcium ion binding for MF. The KEGG pathway analysis showed that the MeDEGs were enriched in calcium signaling pathway, T cell receptor signaling pathway, NF-kappa B signaling pathway, Rheumatoid arthritis. The PPI network containing 706 nodes and 882 edges, and the enrichment p value $< 1.0 \times 10-16$. With Cytoscape, based on the range of more than 10 genes, a total of 8 modules were screened out. Spearman correlation analysis showed RGS1(cg10718027), RGS1(cg02586212), RGS1(cg10861751) were significantly correlated with RA.
Conclusions: RGS1 can be used as novel methylated biomarkers for RA.

Источник: SpringerOpen