IECGE 2024 Conference

The 2nd International Electronic Conference on Genes

11–13 December 2024 | Online

Program and Abstract Book

Organizers

MDPI

genes

Media Partners

cancers

biomedicines

cardiogenetics

sciforum.net/event/IECGE2024
iecge2024@mdpi.com

The 2nd International Electronic Conference on Genes

11–13 December 2024 | Online

MDPI

Organizing Committee

Conference Chair

Prof. Dr. Selvarangan Ponnazhagan

Session Chairs

Dr. Christos K. Kontos
Dr. Silvia Turroni
Prof. Dr. Dror Sharon
Prof. Dr. Laurent Metzinger
Prof. Dr. Maria Luisa Chiusano

Scientific Committee

Dr. Alexessander Couto-Alves
Dr. Ayse Demirkan
Dr. Dubravka Švob Štrac
Dr. Giovanni Nigita
Dr. Hongjie Li
Dr. Isabel Henriques
Dr. Jyotsna Batra
Dr. Panagiotis Katsonis
Dr. Sudheer Kumar Gara
Dr. Valeria D'Argenio
Dr. Xénia Gonda
Prof. Dr. Cornelia M. Van Duijn
Prof. Dr. Jianping Xu
Prof. Dr. Nicholas Moschonas

Organised by

MDPI

Conference Secretariat

Email: iecge2024@mdpi.com

Table of Contents

Welcome from the Chair

Dear Colleagues,

It is with great enthusiasm that we announce the **2nd International Electronic Conference on Genes (IECGE2024)**. The conference is organized by the MDPI open access journal *Genes* (ISSN: 2073-4425; Impact Factor: 2.8) and will be held **online** from **11th to 13th December 2024**.

This conference will provide leading scientists with an online platform to share their latest research and engage in exciting discussions. The main topics and sessions of the conference are:

1. Non-Coding RNAs in Health and Diseases;
2. Genetic Diagnosis and Targeted Therapy in Cancer;
3. Microbial Genetics and Genomics;
4. Technologies and Resources for Genetics Research;
5. Human Genomics and Genetic Diseases.

This is an excellent opportunity for researchers and scientists to interact with each other, communicate with their colleagues, learn from each other, share ideas and results, help solve problems, and suggest alternative options for a better future. As well as the energetic and dynamic nature of virtual international conferences, another advantage is that you do not need to travel to attend. You can take advantage of this opportunity from wherever you live.

In the virtual conference, there are additional advantages: (1) engagement tools that keep energy levels high, (2) participants are given a voice, (3) far stronger attention is received while one is talking, (4) a Q&A through the Chat is also possible if you do not wish to raise your question verbally, (5) polls, (6) feedback through the Chat, (7) the use of “Reaction” functions to show your voice, appreciation, or a request, (8) greater reach with remote audiences, and (9) the ability to deliver live and pre-recorded presentations simultaneously.

All the accepted abstracts will be available online on Sciforum.net during and after the conference.

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham, Birmingham, AL, USA

Genes (ISSN 2073-4425) is an international, peer-reviewed open access journal which provides an advanced forum for studies related to genes, genetics and genomics. It publishes reviews, research articles, communications and technical notes. There is no restriction on the maximum length of the papers and we encourage scientists to publish their results in as much detail as possible.

Journal Webpage: https://www.mdpi.com/journal/genes

Keynote Speakers

Prof. Dr. Laurent Metzinger
UPJV HEMATIM UR 4666, C.U.R.S, Université de Picardie Jules Verne, CEDEX 1, 80025 Amiens, France

Prof. Dr. Rana Ahmed Youness
Molecular Biology and Biochemistry Department, Molecular Genetics Research Team (MGRT), Faculty of Biotechnology, German International University, Cairo 11835, Egypt.

Prof. Dr. Carlo Rivolta
Institute of Molecular and Clinical Ophthalmology Basel (IOB), University of Basel, Mittlere Strasse 91, 4031 Basel, Switzerland

Prof. Dr. Batsheva Kerem
Department of Genetics, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Edmond J. Safra Campus, Givat Ram, Jerusalem 9190401, Israel

Dr. Yuval Itan
Charles Bronfman Institute for Personalized Medicine, Department of Genetics and Genomic Sciences, Mindich Child Health and Development Institute, Icahn School of Medicine at Mount Sinai, New York, NY, USA

Dr. Federica D'Amico
Department of Pharmacy and Biotechnology, University of Bologna, Via Belmeloro 6, 40126 Bologna, Italy

Prof. Dr. Jianping Xu
Department of Biology, McMaster University, Hamilton, ON, Canada

Invited Speaker

Dr. Leili Rejali

Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran P.O. Box 19875-17411, Iran

Dr. Katerina Katsaraki

Department of Biochemistry and Molecular Biology, Faculty of Biology, National and Kapodistrian University of Athens, Panepistimiopolis, 15701 Athens, Greece

Dr. Mariachiara Mengoli

Human Microbiomics Unit, Department of Medical and Surgical Sciences, University of Bologna, 40138 Bologna, Italy

Program at a Glance

	Day 1	Day 2	Day 3
Morning	**Session B.** Genetic Diagnosis and Targeted Therapy in Cancer	**Session E.** Microbial Genetics and Genomics	**Session C.** Human Genomics and Genetic Diseases
Afternoon	**Session A.** Non-Coding RNAs in Health and Diseases		**Session D.** Technologies and Resources for Genetics Research

IECGE 2024 Program

11th December 2024 (Wednesday)

Session B. Genetic Diagnosis and Targeted Therapy in Cancer

Time: 9:00 (CET, Basel) / 03:00 (EDT, New York) / 16:00 (CST Asia, Beijing)

Time in CET	Speaker	Title
9:00–9:10	**Prof. Dr. Selvarangan Ponnazhagan** Event Chair	*Opening Speech*
9:10–9:20	**Dr. Christos K. Kontos** Session Chair	*Welcome from the session chair*
9:20–9:50	**Prof. Dr. Rana Ahmed Youness** Keynote Speaker	Liquid Biopsy-Guided Precision Immunotherapy: A special focus on LncRNAs in Young Breast Cancer Patients
9:50–10:10	**Dr. Leili Rejali** Invited Speaker	Consensus molecular subgroups (CMS) in colorectal cancer management
10:10–10:30	**Dr. Katerina Katsaraki** Invited Speaker	The Combination of Sequencing Approaches Unravels the Post-transcriptional Regulatory Effect of Proteasome Inhibitors, in Breast Cancer
10:30–10:45	**Amali Thannkoon** Selected Speaker	The role of Iroquois-class homeobox genes in cancer stemness
10:45–11:00	**Saima Firdaus** Selected Speaker	mRNA-Based Biomarker Identification for Targeted Therapy Development in Pancreatic Cancer
11:00–14:00	**BREAK**	

Session A. Non-Coding RNAs in Health and Diseases

Time: 14:00 (CET, Basel) / 08:00 (EDT, New York) / 21:00 (CST Asia, Beijing)

Time in CET	Speaker	Title
14:00–14:10	**Prof. Dr. Laurent Metzinger** Session Chair	*Welcome from the session chair*
14:10–14:40	**Prof. Dr. Laurent Metzinger** Keynote Speaker	Nobel price attributed to microRNAs timeline of the discovery and summarize the inaugural papers of Ambros and Ruvkun
14:40–14:55	**Emma Brisot** Selected Speaker	Uremic toxins levels are associated with miR-223 in Chronic Kidney Disease-associated anemia
14:55–15:10	**Muhammad Safdar** Selected Speaker	Decoding miRNA Interactions and SNP Variability in the 3'UTR of NF-κB: Implications for Gene Regulation and Cancer
15:10–15:25	**Irina Valerievna Pronina** Selected Speaker	Association of the expression level of lncRNAs GAS5, HAND2-AS1, LINC00152, and LINC00339 and tumor size and the lymphogenous metastasis in clear cell renal cell carcinoma
15:25–15:40	**Mateusz Gotowiec** Selected Speaker	miRNA dysregulation in the autophagy response induced by starvation in rat mammary epithelial cells and breast cancer cells

12th December 2024 (Thursday)

Session E. Microbial Genetics and Genomics

Time: 9:00 (CET, Basel) | 03:00 (EDT, New York) | 16:00 (CST Asia, Beijing)

Time in CET	Speaker	Title
9:00–9:10	**Dr. Silvia Turroni** Session Chair	*Welcome from the session chair*
9:10–9:40	**Dr. Federica D'Amico** Keynote Speaker	Gut microbiome in infancy and childhood: a multiomic approach in health and disease
9:40–10:10	**Prof. Dr. Jianping Xu** Keynote Speaker	Population genomic analyses reveal diverse patterns of evolution in human fungal pathogens
10:10–10:30	**Dr. Mariachiara Mengoli** Invited Speaker	Human Microbiome and Infections: (Not) Just the Two of Us
10:30–10:45	**Savanah Senn** Selected Speaker	Artemisia californica draft leaf and flower transcriptome and soil WGS resources
10:45–11:00	**Niraj Kumar Prajapati** Selected Speaker	Genomic basis of mycorrhizal fungal specificity in plant-fungal symbioses
11:00–11:15	**Alexey V. Rakov** Selected Speaker	Regional Variability of Spotted Fever Group Rickettsia Genospecies: Insights from Eight Regions in Russia
11:15–11:30	**Marcos Jessé Abrahão Silva** Selected Speaker	Functional and Structural Characterization of Exonic SNPs associated with Leprosy Risk: an In Silico Analysis

13th December 2024 (Friday)

Session C. Human Genomics and Genetic Diseases

Time: 9:00 (CET, Basel) / 03:00 (EDT, New York) / 16:00 (CST Asia, Beijing)

Time in CET	Speaker	Title
9:00–9:10	**Prof. Dr. Dror Sharon** Session Chair	*Welcome from the session chair*
9:10–9:40	**Prof. Carlo Rivolta** Keynote Speaker	An integrated bioinformatic toolbox for the analysis of rare disease genetic data
9:40–10:10	**Prof. Batsheva Kerem** Keynote Speaker	From gene cloning to mutation specific therapies in cystic fibrosis
10:10–10:25	**Manar Salameh** Selected Speaker	A Founder Homozygous Nonsense Variant in CREB3 Causes a Variable Retinal Degeneration Phenotype
10:25–10:40	**Maria-Anna Kyrgiafini** Selected Speaker	Whole-genome profile of Greek patients with asthenozoospermia: Identification of candidate variants and genes
10:40–10:55	**Husna Irfan Thalib** Selected Speaker	Genetic Insights and Therapeutic Approaches for Epidermolysis Bullosa in the Saudi Arabian Population
10:55–11:10	**Farhan Ikhtiar** Selected Speaker	Genetic analysis of hemochromatosis and its impact on liver function in the population of Lahore, Pakistan
11:10–14:00	**BREAK**	

Session D. Technologies and Resources for Genetics Research

Time: 14:00 (CET, Basel) / 08:00 (EDT, New York) / 21:00 (CST Asia, Beijing)

Time in CET	Speaker	Title
14:00–14:10	**Prof. Dr. Maria Luisa Chiusano** Session Chair	*Welcome from the session chair*
14:10–14:40	**Dr. Yuval Itan** Keynote Speaker	Novel Machine Learning Approaches for Predicting Functional Consequences of Human Genetic Variants
14:40–14:55	**Savanah Senn** Selected Speaker	A draft transcriptome of the climate resilient California native plant Ribes malvaceum
14:55–15:10	**Sakeena Bairamova** Selected Speaker	An approach to identify aggression profiles via machine learning
15:10–15:25	**Tanya Ahmed Sheik** Selected Speaker	Reconstruction of Transcriptome Datasets to Understand the Molecular Basis Behind the Advantageous Effect of Triploid Over Diploid Mulberry (Morus spp.)
15:25–15:40	**Guillaume Pavlovic** Selected Speaker	The LAG-R guidelines, a framework for standardizing and improving laboratory animal genetic reporting
15:40–15:55	**Raju Mondal** Selected Speaker	Elucidation of the molecular basis of phenotype in Seri-genetic resources (Bombyx mori L. and Morus spp.) using repository RNA-Seq datasets: A self-service data mining approach

Poster List

Poster List	
Name	**Title**
Zhengjie Hou	Enhanced iturin A synthesis in Bacillus amyloliquefaciens Through Genetic Modification Targeting Rap Phosphatase Inactivation
Michał Karasek	Occurrence of genetic determinants of resistance to colistin and biofilm in carbapenem-resistant Acinetobacter baumannii isolated from hospitalized patients
Xia Li	Genetic Engineering to Enhance Surfactin Production in Bacillus subtilis via Nitrogen Metabolism and Membrane Transport Pathways
Marcos Jessé Abrahão Silva	Functional and Structural Characterization of COVID-19 Risk-Associated Exonic SNPs: An In Silico Analysis
Vanessa Silva	Resistance gene profiles of multidrug-resistant Klebsiella spp. from poultry samples
Javed Aalam	Machine Learning-Driven Omics Approaches for Diagnostic Biomarker in Tuberculosis based on Differential Gene Expression data
Gauri Awasthi	Relevance of Pharmacogenomics, CYP450 genes and their genetic variations in drug metabolism and toxicity
Natalya Mazanova	The Early Diagnostic of Niemann-Pick Disease Type a Caused by c.996del and c.1252C>T in SMPD1 Gene: A Case Study
Sariya Khan	Genetic and immunological implications in fibromyalgia: A Literature Review
Asodu Sandeep Sarma	A leaky deep intronic splice variant in CLRN1 is associated with non-syndromic retinitis pigmentosa
Maul Shree	Bioinformatics analysis of Gymnema sylvestre and Withania somnifera on insulin resistance pathway targets
Shadab Ahamad	ACE Insertion/Deletion Polymorphism as a Potential Risk Factor for Congenital Heart Disease among North Indians: Insights from a Tertiary Pediatric Cardiac Care Centre Study
Dror Sharon	Non-coding single nucleotide and structural variants affecting the EYS putative promoter cause autosomal recessive retinitis pigmentosa
Pramodkumar P Gupta	To study SUM159 Cell Lines Untreated and Treated with drug Mebendazole and its effect on Transcriptome Level (Rna-Seq Analysis).
Swarna Beesetti	RUNX1 Mutations in Stomach Adenocarcinoma: Unveiling a New Player in Solid Tumors and Its Immune Microenvironment Impact
Milena M. Jovanović	Unsaturated 10H2DA Queen Bee Acid from Royal Jelly Modulate EMT in SW-480 Colorectal Cancer Cells
Elena Voropaeva	Recurrent clinically significant mutations in acute myeloid leukemia: analysis of the cancer genomics database and proprietary data on the CBio portal
Mamatha Bhanu L S	The role of non-coding RNAs (miRNA and lncRNA) in the diagnosis and prognosis of rheumatoid arthritis

Session A. Non-Coding RNAs in Health and Diseases

sciforum-105401: Association of the expression levels of lncRNAs GAS5, HAND2-AS1, LINC00152 and LINC00339 and tumor size with lymphogenous metastasis in clear-cell renal-cell carcinoma

Irina Valerievna Pronina [1,2,*] and Vitaly Loginov [1,3]

[1] Institute of General Pathology and Pathophysiology
[2] Department of Physiology, Human Ecology and Medical and Biological Sciences, State University of Education, 105005 Moscow, Russia
[3] Research Center for Medical Genetics

The frequency of clear-cell renal-cell carcinoma (ccRCC) metastasis has reached 25-30%, which makes the search for prognostic biomarkers urgent. Long non-coding RNAs (lncRNAs) regulate biological processes and may serve as prognostic markers. The aim of our study was to compare the expression levels of lncRNAs GAS5, HAND2-AS1, LINC00152 and LINC00339 in tumors and normal kidney tissue and analyze the association of their changes with clinicopathological parameters of ccRCC.

We used archival RNA samples (RIN>7) from 70 primary tumors with a confirmed diagnosis of ccRCC and 70 adjacent normal kidney tissues. Expression analysis was performed by RT-qPCR. Statistical analysis was performed using a multivariate ANOVA test ($p \leq 0.05$).

A decrease in the expression of GAS5 by 5.25, HAND2-AS1 by 5.92, LINC00152 by 2.04 and LINC00339 by 2.34 times was revealed in the tumor tissues. The expression of LINC00152 did not change at T1, T2 and T3 (the TNM classification) and decreased by 33.43 times when the tumor grew beyond Gerota's fascia (T4). LINC00152 expression was lower in T4 tumors compared to tumors of a smaller size: T1/T4—10.86 times; T2/T4—22.76 times; and T3/T4—27.11 times. LINC00152 expression decreased by 4.71 times in cases with multiple lesions of regional lymph nodes (normal/N2), including compared with tumors with no metastases in the lymph nodes (N0/N2) or one affected lymph node (N1/N2), by 4.36 and 7.26 times, respectively. HAND2-AS1 had a lower level of expression in tumors with multiple lesions of regional lymph nodes: normal/N2—15.02 times; N0/N2—5.84 times; N1/N2—4.04 times.

The significant decrease in the expression of HAND2-AS1 and LINC00152 when more than one regional lymph node is affected (N2 according to the TNM classification) in ccRCC allows us to propose them as prognostic markers of lymphogenous metastasis in the absence of the ability to evaluate regional lymph nodes (Nx).

sciforum-106486: Decoding miRNA Interactions and SNP Variability in the 3'UTR of NF-κB: Implications for Gene Regulation and Cancer

Muhammad Safdar

Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan

Nuclear factor-κB (NF-κB) is a pivotal transcription factor family involved in key biological processes such as inflammation, immune response, cell survival, apoptosis, cellular stress reactions, and tumorigenesis. Dysregulation of NF-κB is increasingly recognized as a critical factor in the initiation and progression of various cancers. Polymorphisms in miRNA genes or their target sites (miRSNPs) can significantly impact miRNA activity. While polymorphisms in miRNA genes are rare, studies have shown that SNPs at miRNA target sites can either enhance or reduce the strength of miRNA–target interactions. The objective of this study was to identify miRSNPs in the NF-κB gene and SNPs in miRNA genes targeting their 3'UTR and to evaluate their potential roles in apoptosis and cancer using computational tools. We identified 121 miRNA binding sites corresponding to 101 distinct miRNAs, as well as 16 SNPs located within miRNA binding regions of the NF-κB 3'UTR. Notably, a binding site for miR-6826-5p in the NF-κB 3'UTR harbors an SNP (rs960795970, A/G), and the same miRNA's genomic sequence contains an SNP (rs6771809, C/T) at the same nucleotide position as rs960795970. Additionally, miR-6826-5p has three other SNPs (rs757908839, A/G; rs746350709, C/T; and rs115693266, A/C), with the first positioned directly at its binding site. This cross-matching between miRSNP (rs960795970) in the NF-κB 3'UTR and an SNP (rs6771809) in the miR-6826-5p genomic sequence in the same binding region suggests potential functional interplay. Moreover, miR-6826-5p was found to target several genes associated with cancer and apoptosis, including HIP1, TRIAP1, GSKIP, NIN, DAP, CAAP1, XIAP, TMBIM1, TMBIM4, TNFRSF10A, RAD21, AKT1, BAG1, and BAG4, despite having no previously established cancer-related interactions. These findings imply that miR-6826-5p may play a critical role in apoptosis through pathways beyond NF-κB, potentially influencing cancer progression via alternative mechanisms.

sciforum-106244: Identification of Biomarkers for Early Diagnosis and Prognosis in Sepsis: A Comprehensive Analysis

Kumari Astha Rupali * and Dhiraj Kishore

Department of General Medicine, Institute of Medical Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh-221005, India

Introduction

Sepsis is a life-threatening disease caused by an excessive immune response to infection, causing inflammation, tissue damage, and organ failure. Globally, sepsis caused 19.7% of all fatalities in 2017, with India having one of the highest rates, with over 4 million cases annually. MicroRNAs (miRNAs) are small, non-coding RNA molecules that regulate gene expression by binding to messenger RNAs (mRNAs) and blocking their transcription. Identifying miRNA as predictive biomarkers could significantly reduce the worldwide burden of sepsis by enhancing patient care, management, and treatment. This study aims to discover potential diagnostic biomarkers implicated in the dysregulated immune response and provide insights for mechanistic illness progression research.

Methods

The Gene Expression Omnibus (GEO) datasets, GSE134364, GSE134358, GSE94717, GSE236713 and GSE131761 were used to identify the differentially expressed genes involved in sepsis. Biological targets were identified that coincide with the identified differentially expressed miRNAs. The biological pathways were analyzed using KEGG and GO. Hub genes were identified for further functional and signaling pathway analysis.

Results

Several differentially expressed miRNA biomarkers were identified between control and Sepsis groups (p0.05 and fold change >2). MiR-146a regulates the immune response, miR-155 promotes pro-inflammatory cytokine expression, miR-150 regulates immune cell function and inflammation, and miR-21 is involved in apoptosis and inflammation. Moreover, we identified matrix metalloproteinase (MMP8 and MMP9) involved in the neutrophil degranulation.

Conclusions

MiRNAs regulating MMP-8 and MMP-9 in sepsis regulate immune responses and inflammation, leading to tissue damage. MiR-21 downregulate MMP-9 expression, while miR-146a indirectly affects MMP expression by targeting upstream signaling molecules. Targeting specific miRNAs that regulate MMPs offers a potential therapeutic strategy for managing sepsis. By modulating the levels of these miRNAs, it may be possible to control the activity of MMPs and reduce the harmful effects of excessive inflammation and tissue damage.

sciforum-106657: miRNA dysregulation in the autophagy response induced by starvation in rat mammary epithelial cells and breast cancer cells

Mateusz Gotowiec *, Antoni Smoliński, Michał Suchecki, Wiktor Pascal and Paweł Włodarski

Department of Methodology, Medical University of Warsaw, Poland

Introduction

Breast cancer (BC) is highly heterogeneous, with varying molecular characteristics. Autophagy, a critical cellular degradation process, helps cells survive under stress, but its regulation can be influenced by altered microRNA (miRNA) expression. Studying miRNA changes during starvation-induced autophagy in both mammary epithelial cells and BC cells could reveal potential molecular targets.

Methods

BC cell lines and rat mammary epithelial cells were subjected to starvation using Earle's Balanced Salt Solution (EBSS) or treated with cell medium (CM). The STRING database identified proteins related to autophagy and starvation, which were cross-referenced with known miRNA interactions. Total RNA from both CM- and EBSS-treated cells was analyzed for miRNA expression changes and validated using the TCGA dataset.

Results

Starvation induced autophagy, reduced cell proliferation in all cell types, and increased the invasive capacity of BC cells. We identified a miRNA signature related to starvation, comprising 27 miRNAs. Six miRNAs had elevated baseline expression, while another six, including miR-218a-5p, were reduced in BC cells compared to healthy cells. Starvation caused significant miRNA dysregulation, with miR-218a-5p being notably affected. Bioinformatic analysis showed that although miR-218a-5p is less expressed in primary BC tissues compared to normal tissues, its expression increases with advanced N status and is higher in metaplastic BC.

Conclusions

The response to starvation varies between rat BC cells and normal cells. Baseline miRNA expression related to starvation and autophagy differs between breast cancer and healthy cells. Starvation induces BC-specific miRNA dysregulation, particularly affecting miR-218a-5p, which could have therapeutic implications through autophagy modulation.

This research was funded by the Medical University of Warsaw (69/M/MG/N/23) and the Polish Ministry of Science and Higher Education (SKN/SP/569610/2023).

sciforum-107515: Predicting Mimotopes of Amyloid beta ($A\beta_{42}$) from Non-Coding DNA as candidates for Synthetic Peptide Vaccine Design against Alzheimer's Disease

Navya Raj [1,*], Shidhi P R [2], Deepthi Varughese [3], Achuthsankar S Nair [4] and Pawan Dhar [5]

[1] Department of Health Informatics, College of Health Sciences, Saudi Electronic University, Dammam, Saudi Arabia
[2] Department of Zoology, University of Kerala, Thiruvananthapuram, Kerala, India
[3] Centre for Development and Aging Research, Inter University Centre for Biomedical Research & Super Speciality Hospital, Mahatma Gandhi University Campus at Thalappady, Kerala, India
[4] Department of Computational Biology and Bioinformatics, University of Kerala, India
[5] School of Biotechnology, Jawaharlal Nehru University, New Delhi, India.

Introduction

What could be an ideal raw material for developing a drug or a vaccine? In line with the research on different biomolecules like DNA, RNA, protein, and peptide, we explore the potential use of non-coding DNA in designing lifesaving vaccines and drugs.

Methods

Using computational approaches, a multi-parametric virtual library of novel peptides from the intergenic regions of the *Escherichia coli* genome was generated, and their therapeutic potential was studied. The potential antigens from the peptides were analyzed for their B cell epitopes and MHC binding T cell epitopes, which find application in epitope-based vaccine design. Alzheimer's disease (AD) immunotherapy was selected as an example to demonstrate the possible application of the non-coding DNA-derived peptides as promising candidates for Synthetic Peptide Vaccine Design.

Results

Sequence and structure comparison studies between toxic amyloid beta ($A\beta_{42}$) peptides and the non-coding DNA-derived peptides revealed promising matches. The structural mimics of $A\beta_{42}$ with potential mimotopes were further studied through mimotope-antibody docking and molecular dynamic simulation for their affinity towards the antibody's antigen-binding fragment (Fab).

Conclusions

Our study put forward a novel method to identify therapeutic peptides from non-coding DNA, which offers a non-obvious source of potential mimotope candidates for designing novel synthetic vaccines against Alzheimer's Disease.

sciforum-106221: The role of non-coding RNAs (miRNA and lncRNA) in the diagnosis and prognosis of rheumatoid arthritis

Mamatha Bhanu L S

Yuvaraj's College, University of Mysore

Rheumatoid arthritis (RA) is a chronic autoimmune disease affecting multiple joints, causing adverse effects on organs. Early diagnosis, aggressive treatment, and disease-modifying anti-rheumatic drugs (DMARDs) have improved management and long-term prognosis of the disease. The global prevalence of RA is increasing, primarily in women, and is associated with disability and mortality. The prognosis depends on the disease stage at diagnosis; early diagnosis can prevent or delay disease progression in 90% of patients, preventing irreversible joint damage and disability. However, non-coding RNA (ncRNA), including microRNA and long ncRNA (lncRNA), are small, non-coding segments of RNA that regulate gene expression, has been discovered to be deregulated in diseases like RA, potentially contributing to its pathogenesis, progression, and treatment. Pre-clinical RA, characterized by auto-antibodies and biomarkers before clinical RA, is a stage of RA research aimed at early diagnosis and control of immunological abnormalities. For instance, SNP rs2850711 in lnc00305 links RA susceptibility, miR-10a response to methotrexate (MTX) treatment, and ncRNA plays a crucial role in refractory RA by regulating drug sensitivity. Lower miR-20a expression in rheumatoid arthritis synovial fibroblasts (RASFs) activates Janus Kinase (JAK)-mediated inflammation, promoting cell proliferation and apoptosis-resistant. This study highlights changes in ncRNAs, disease progression, and novel therapeutic targets and strategies.

sciforum-106177: Uremic toxins levels are associated with miR-223 in Chronic Kidney Disease-associated anemia.

Valérie Metzinger-Le Meuth [1,2], Emma Brisot [1,*], Ophélie Fourdinier [3], Eya Hamza [1], Pierre-Marie Leprêtre [4], Benjamin Brigant [1,5], Hakim Ouled-Haddou [1], Gabriel Choukroun [3], Francis Verbeke [6], Ziad Massy [7,8], Griet Glorieux [6] and Laurent Metzinger [1]

1 UPJV HEMATIM UR 4666, C.U.R.S, Université de Picardie Jules Verne, CEDEX 1, 80025 Amiens, France
2 INSERM UMRS 1148, Laboratory for Vascular Translational Science (LVTS), UFR SMBH, Université Sorbonne Paris Nord, CEDEX, 93017 Bobigny, France
3 Nephrology Dialysis and Transplantation Department, Amiens University Hospital, Amiens, France
4 Université de Rouen Normandie, CETAPS UR 3882, Boulevard André Siegfried, F-76000, Rouen, France
5 Centre of Molecular Inflammation Research (CEMIR), Department of Clinical Research and Molecular Medicine (IKOM), Faculty of Medicine and Health Sciences (MH), Norwegian University of Science and Technology (NTNU), Trondheim, Norway
6 Nephrology Section, Department of Internal Medicine and Pediatrics, Ghent University Hospital, Corneel Heymanslaan 10, 9000, Ghent, Belgium
7 Ambroise Paré Hospital, Division of Nephrology, APHP, Paris Ile de France Ouest (UVSQ) University
8 INSERM 1018 Eq. 5, CESP, Boulogne Billancourt et Villejuif, Paris, France

Chronic kidney disease (CKD) poses a significant global threat, with increased rates of cardiovascular and all-cause mortality. Anemia is common in CKD, and is often associated with the accumulation of uremic toxins in the bloodstream. Previously, we demonstrated that the uremic toxin indoxyl sulfate (IS) has an impact on the regulation of erythropoiesis in both cellular and preclinical CKD models. In this study, the roles of non coding RNAs in this toxin/toxic effect, we measured the effect of IS on microRNA expression in the human erythropoietic cell line UT7/EPO, using nanostring technology. We found a significant increase of miR-223 in cells treated with IS. This finding was further validated in human primary CD34+ cells, a more physiological model for human erythropoiesis. Finally, serum levels of miR-223 correlated with representative uremic toxins, including IS, in patients with various stages of CKD, and also with endothelial dysfunction markers, indicating a link with vascular damage. These findings suggest that miR-223 may contribute to the development of anemia in CKD. Further investigation into the involvement of miR-223 in erythropoiesis is needed for a better understanding of the mechanisms underlying anemia in CKD and the potential role of uremic toxins. Ultimately, this may open up new therapeutic possibilities for the management of anemia in CKD.

Session B. Genetic Diagnosis and Targeted Therapy in Cancer

sciforum-107399: mRNA-Based Biomarker Identification for Targeted Therapy Development in Pancreatic Cancer

Saima Firdaus * and Rafat Parveen

Department of Computer Science, Jamia Millia Islamia, New Delhi-110025, India

Introduction

Pancreatic cancer is one of the highly malignant cancers that have a poor prognosis and limited treatment options. The development of targeted therapies is important for improving the patient's outcome. mRNA-based biomarkers offer a promising avenue for developing the targeted therapies in Pancreatic Cancer as they identify the key genes involved in disease progression.

Methods

In this study, we analyzed the datasets from the GEO database to identify potential mRNA biomarkers for pancreatic cancer. Differentially expressed gene (DEGs) analysis was conducted using R Bioconductor, by applying statistical thresholds of adjusted p-value 0.05 and log2 fold-change > 1 to identify genes that are expressed differentially between tumor and normal samples. Functional enrichment and pathway analysis were carried out to understand the biological roles of the identified DEGs. Additionally, FDA-approved drugs are repurposed as an inhibitor against the upregulated genes, validated through simulations.

Results

TFF1 and CELA2A together emerged as key candidate genes for pancreatic cancer among the identified DEGs. Functional enrichment analysis showed that these genes are involved in cell proliferation, apoptosis, and metastasis. These findings suggest that these genes play a significant role in pancreatic cancer progression and can be utilized as a target for therapeutic intervention. The identified genes are further validated through an independent dataset from the TCGA database.

Conclusions

TFF1 and CELA2A were identified as the potential mRNA-based biomarkers for pancreatic cancer. These biomarkers have potential to serve as molecular elements for targeted therapies, offering hope for improvement in more precise, personalized treatments and minimizing side effects, addressing the complexity of pancreatic cancer.

sciforum-104779: Recurrent clinically significant mutations in acute myeloid leukemia: analysis of the cancer genomics database and proprietary data on the CBio portal

Elena Voropaeva [1,2,*], Irina Chuhontseva [2], Vladimir Maximov [1,3] and Tatyana Pospelova [2]

[1] Research Institute of Internal and Preventive Medicine - Branch of the Federal State Budget Scientific Institution The Federal Research Center Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences
[2] Department of Hematology, Novosibirsk State Medical University
[3] Novosibirsk State Medical University

According to the literature, the frequency of mutations in genes associated with the development of acute myeloid leukemia (AML) varies significantly.

The objective of this study was to obtain up-to-date data on the prevalence of mutations in the "hot spots" of the *FLT3, NPM1, IDH1, IDH2,* and *DNMT3A* genes in AML.

Methods: An analysis of NGS data from 1567 patients with AML presented in the cancer genomics database on C-Bioportal and 124 Russian patients with AML was performed.

Results: According to the database analysis, at the time of the diagnosis of the disease, 46.6% of patients had mutations in *DNMT3A* p.R882, *NPM1* p.W288Cfs*12*, FLT3*-ITD, *FLT3*-TKD1, *IDH1* p.R132, and *IDH2* p.R140. Only in a third of cases (30.1%) did the *DNMT3A* mutation of R.R882 occur in patients in an isolated variant. In 47.4% of cases, it was combined with *NPM1* p.W288Cfs*12, in 34.1% with mutations in the hot spots of the *FLT3* gene, and in 23.0% with recurrent mutations in *IDH1* and *IDH2*. At the same time, the combination revealed by our data remains highly significant (p0.001) even after adjusting for the multiplicity of comparisons (q0.001). In Russian AML patients, the mutation rates in the "hot spots" of genes generally corresponded to the data from the C-Bioportal cancer genomics database and amounted to the following: *DNMT3A* p.R882—7.3%; *NPM1* p.W288Cfs*12—15.3%; *FLT3*-ITD—14.5%; *FLT3*-TKD1—4.0%; *IDH1* p.R132—5.6%; *IDH2* p.R140—10.5%.

Conclusions: The data obtained indicate that in 40-50% of AML cases, clinically significant recurrent mutations in one or more of the studied genes are detected at the onset of the disease. Mutations for which targeted drugs (FLT3, IDH1, and IDH2 inhibitors) have been developed occur in 35% of patients. In one-fifth of cases (18.1%) of AML, *NPM1* p.W288Cfs*12 is detected, which can be used as an independent target for the molecular assessment of minimal residual disease.

sciforum-106109: RUNX1 Mutations in Stomach Adenocarcinoma: Unveiling a New Player in Solid Tumors and Its Immune Microenvironment Impact

swarna beesetti

St jude children's research hospital

Introduction: RUNX1, a transcription factor crucial for hematopoiesis and frequently mutated in myelodysplastic syndrome (MDS) and acute myeloid leukemia (AML), has recently been implicated in solid tumors. This study investigates the role of RUNX1 mutations in stomach adenocarcinoma and their impact on the tumor immune microenvironment.

Methods: Bioinformatic approaches using GEPIA (Gene Expression Profiling Interactive Analysis) and TIMER (Tumor Immune Estimation Resource) were used to analyze gene expression data and immune cell infiltration in stomach adenocarcinoma samples with and without RUNX1 mutations.

Results: Stomach adenocarcinomas harboring RUNX1 mutations exhibited significantly higher levels of macrophage infiltration compared to wild-type tumors. Gene expression analysis revealed upregulation of key inflammatory mediators, including IFNG, TNF, IL1B, and NLRP3, in RUNX1-mutated samples. These findings suggest a strong association between RUNX1 mutations and an enhanced inflammatory tumor microenvironment.

Conclusions: This study establishes a potential link between RUNX1 mutations, increased immune cell recruitment, and elevated expression of pro-inflammatory genes in stomach adenocarcinoma. This altered immune landscape may have important implications for disease progression and the development of targeted therapeutic approaches. Furthermore, these findings extend our understanding of RUNX1's role beyond hematological malignancies, highlighting its significance in solid tumors and opening new avenues for research and potential therapeutic interventions.

sciforum-107658: The role of Iroquois-class homeobox genes in cancer stemness

Amali Thannkoon *, Achala Vitharanage and Jyotsna Batra

[1] School of Biomedical Sciences, Faculty of Health, Queensland University of Technology, QLD 4102, Australia
[2] The centre for Genomics and Personalised Health, Queensland University of Technology, Brisbane, QLD 4059, Australia
[3] Translational Research Institute, Queensland University of Technology, Brisbane, QLD 4102, Australia

Introduction

Cancer poses a global challenge due to aggressive metastasis, treatment resistance, and relapse, often driven by cancer stem cells (CSCs). CSCs evade conventional therapies, emphasizing the need for CSC-targeted strategies. The Iroquois homeobox (*IRX*) gene family is linked to cancer stemness, but the exact roles and therapeutic potential of *IRX* genes in CSC promotion remain unclear.

Methods

Normalized gene expression data from all six IRX genes were downloaded from publicly available databases. Comparison of IRXs expression with cancer stages and drug sensitivity was conducted. All data processing and analysis were performed using GraphPad Prism (10.0.2). A student t-test was used to compare difference between two groups and a one-way ANOVA test was applied to compare multiple groups. The functional role of these IRXs in CSC regulation will be assessed using *in vitro* and *in vivo* models.

Results

In-silico analyses revealed elevated expression of Iroquois homeobox 3 (*IRX3*) and Iroquois homeobox 5 (*IRX5*) in castration-resistant prostate cancer (PCa) patient samples and patient-derived xenografts (PDX) compared to primary tumours, with further upregulation after enzalutamide treatment. Gene set enrichment analysis identified significant enrichment of stemness-associated gene signatures in PCa patients with high *IRX3* expression. Additionally, expression data revealed *IRX5* upregulation with therapy resistance in several breast cancer (BCa) cell lines. Future studies will explore the roles of IRX3 and IRX5 in CSC maintenance, tumour progression, metastasis, and therapeutic resistance in PCa and BCa models.

Conclusions

Given the link between CSCs, therapy resistance, and metastasis, we hypothesize that elevated *IRX3* and *IRX5* expression contributes to CSC maintenance in PCa and BCa. If validated, these IRXs could serve as novel therapeutic targets, inhibiting CSC-driven tumour growth and progression. This would represent a significant advance, as no therapies currently target CSCs and ultimately preventing metastasis, drug resistance, and relapse in PCa and BCa patients.

sciforum-106255: To study SUM159 Cell Lines Untreated and Treated with drug Mebendazole and its effect on Transcriptome Level (Rna-Seq Analysis)

Pramodkumar P Gupta [1,*], Mala M Parab [1], Janhavi Tripathi [1], Mayur Sonkusare [1], Hridhya Yogesh Nair [1], Mrunal Gokhale [1], Amit Kumar Shrivastava [2], Prerona Boruah [1] and Debjani Dasgupta [1]

[1] School of Biotechnology and Bioinformatics, D Y Patil Deemed to be University, Navi Mumbai, Maharashtra, India
[2] Department of Pharmacology, Universal College of Medical Sciences, Bhairahawa, Rupandehi, Nepal.

Breast cancer is a leading cause of cancer-related deaths worldwide. While significant progress has been made in its diagnosis and treatment, it remains a major public health concern. This study aimed to investigate the transcriptomic effects of Mebendazole, an antiparasitic drug, on SUM159 cell lines, a model for triple-negative breast cancer (TNBC). RNA-Seq analysis was conducted to identify differentially expressed genes (DEGs) between untreated and Mebendazole-treated cells. Our analysis revealed significant transcriptional alterations in Mebendazole-treated SUM159 cells, data collected from the NCBI GEO database. GALAXY server NGS data analysis frame work is used followed by FASTQC, FASTP, HISAT2, SAMTOOL_Sort, SAMTOOLs_Dataset, Uploading GTF for Humans standard file from UCSC, Hiseq-Count and analysis in R reported DEGs. The list of 820 DEGs were analysed for enrichment using EnrichR, David tools to understand the involvement of DEGs in biological processes. DEGs were enriched in pathways related to cell cycle regulation, apoptosis, survival signaling, and metabolism, suggesting that Mebendazole exerts its effects through multiple mechanisms. Notably, the identified DEGs were associated with various diseases, including breast cancer and neurodegenerative disorders. The downregulated genes from the analysis reported to be involved with Liver cirrhosis, Atherosclerosis, Neurological disorder, cellular adhesion, extracellular matrix, Transcription factor, Assembly of collagens in Humans. Whereas the upregulated genes were more involved in pathways of Breast cancer, ovarian cancer, cell cycle and cell division process. These findings highlight the potential for Mebendazole to be repurposed as a therapeutic agent beyond its traditional use in parasitic infections. Further research is needed to validate these in vitro findings in vivo and explore the clinical implications of Mebendazole for, cellular mechanism, signal cascade, TNBC and neurodegenerative diseases.

sciforum-105146: Unsaturated queen bee acid from royal jelly 10H2DA modulates the epithelial-to-mesenchymal transition in SW-480 colorectal cancer cells

Milena M. Jovanović [1,*] and Dragana Šeklić [2]

[1] Department for biology and ecology, Faculty of Science, University of Kragujevac, Kragujevac, 34000, Serbia
[2] Institute for Information Technologies Kragujevac, University of Kragujevac, 34 000 Kragujevac, Serbia

Cancer research largely focuses on the epithelial-to-mesenchymal transition (EMT) as a critical mechanism required for the acquisition of the invasive potential of cancer cells, which can culminate in the formation of metastases. This process involves the transformation of epithelial cells into mesenchymal cells by acquiring suppressed levels of E-cadherin, an anti-EMT marker with a role in the establishment of intercellular junctions. Also, the expression of pro-EMT markers, such as the regulatory marker SNAIL, as well as the effectors N-cadherin and Vimentin, rises as cancer advances. Therefore, there is an emerging need for bioactive substances able to target and modulate EMT markers and reverse this process. The unsaturated fatty acid 10H2DA has not been investigated so far regarding its potential to target specific EMT markers in colorectal cancer (CRC), which was the aim of this study.

Colorectal cancer cell line SW-480 isolated from stage II CRC was treated with 10H2DA in two selected concentrations of 10 and 100 μM. After 24 h, the gene expression of *E-cadherin, SNAIL, N-cadherin,* and *Vimentin* markers was assessed by the qPCR method. Additionally, changes in the protein concentration of these markers between control (untreated) and treated cells were evaluated by immunofluorescent assay.

Queen bee acid successfully upregulated the expression of the anti-EMT marker *E-cadherin.* Our results also point towards a downregulated expression of the pro-EMT regulatory marker *SNAIL,* as well as the effector markers *N-cadherin* and *Vimentin.* This successively led to a significant elevation in E-cadherin on the protein level, and also to an inhibition of pro-EMT proteins, namely, SNAIL, N-cadherin, and Vimentin.

The potential of the unsaturated acid 10H2DA to modulate the expression of specific and significant EMT markers in CRC is obvious and prominent, and it should not be neglected in future studies regarding anticancer therapeutic approaches.

Session C. Human Genomics and Genetic Diseases

sciforum-106986: Relevance of Pharmacogenomics, CYP450 genes and their genetic variations in drug metabolism and toxicity

Surbhi Malhotra, Manik Kaushal abd Gauri Awasthi *

Genomics and Personalized Medicine, Tata Consultancy Services

Background

Variations in drug responses are related to inherited characteristics of the genome that cause a wide variability in individual responses to drugs. Pharmacogenetics or pharmacogenomics analyses help us to understand DNA variations that are related to drug action (pharmacodynamics) and drug disposition (pharmacokinetics). Using a pharmacogenomics (PGx) approach, we studied different CYP450 genes that are associated with drug metabolism, along with their genomic variants, thus strengthening our understanding of personalized medicines.

Methods

We downloaded the PGx database from the FDA website and collated the data utilizing various evolutionary tools and software. We also provided an overview of current progress in computational approaches for the prediction of drug metabolism and toxicity using a combination of knowledge graph- and AI-based approaches. Utilizing ethnicity data from published sources, we also correlated the clinical implications of drug metabolism and toxicity variability in different population cohorts.

Results

We observed that 42 unique drugs catering to nine different therapeutic areas are associated with six CYP450 (CYP1A2, CYP2B6, CYP2C9, CYP2C19, CYP2D6 and CYP3A5) genes/biomarkers and 32 unique variants/SNPs. The allelic frequencies (AFs) of the 32 variants were also studied in different population ethnicity groups (from a published database). We observed unique combinations of drugs, biomarkers and variant associations that highlight how the metabolism of a drug is controlled/regulated/metabolized by the genetic basis of an individual. We observed 32 unique combinations where the same CYP biomarker and its variant are shared by different drugs associated with different therapeutic areas.

Conclusions

PGx studies should be inclusive, and policy makers/drug regulators should include such approaches for better understanding the genetic basis of drug-metabolizing genes for better drug response. The PGx approach also highlights a significant association between Precision Medicine and Pharmacovigilance by understanding drug metabolism and toxicity in accordance with an individual's genetic makeup.

sciforum-104505: A Founder Homozygous Nonsense Variant in CREB3 Causes a Variable Retinal Degeneration Phenotype

Manar Salameh [1,*], Ghadeer Abu Tair [1], Samira Mousa [1], Alexey Obolensky [1], Anand Swaroop [2], Susanne Roosing [3], Eedy Mezer [4,5], Shiri Sourdy [6], Marianthi Karali [7,8], Francesca Simonelli [8], Sandro Banfi [7,9], Eyal Banin [1], Tamar Ben-Yosef [4], Dror Sharon [1] and Samer Khateb [1]

1 Department of Ophthalmology, Hadassah Medical Center, Faculty of Medicine, the Hebrew University of Jerusalem, Jerusalem, Israel.
2 Neurobiology, Neurodegeneration and Repair Laboratory, National Eye Institute, Bethesda, MD, United States.
3 Human Genetics Department, Radboud University Medical Center, Nijmegen, The Netherlands.
4 Rappaport Faculty of Medicine, Technion-Israel Institute of Technology, Haifa, Israel.
5 Department of Ophthalmology, Rambam Health Care Center, Haifa, Israel.
6 Department of Ophthalmology, Rabin Medical Center, Petah Tikva, Israel.
7 Department of Precision medicine, University of Campania “Luigi Vavitelli”, Naples, Italy.
8 Multidisciplinary Department of Medical, Surgical and Dental Sciences, Eye Clinic, University of Campania "Luigi Vanvitelli", Naples, Italy.
9 Telethon Institute of Genetics and Medicine (TIGEM), Pozzuoli (NA), Italy.

Purpose

To report *CREB3* as a novel genetic basis of inherited retinal diseases (IRDs) in families mostly of North African Jewish origin.

Methods

Thirteen patients with a clinical diagnosis of retinitis pigmentosa or macular degeneration were analyzed by next-generation sequencing (NGS). Homozygosity mapping was performed on the Franklin platform for 7 patients from 4 unrelated families. Expression analysis was performed on patient-derived skin fibroblasts using the reverse transcription-polymerase chain reaction (RT-PCR) and western blot analysis, as well as by interrogating previously published retinal single-cell RNA-seq data. Immunohistochemistry staining (IHC) was performed on wild-type mouse retinal sections using an anti-CREB3 antibody.

Results

A founder homozygous nonsense variant in *CREB3* (c.881G>A, p.Trp294*) was identified in 13 patients from four unrelated families. All patients manifested retinal degeneration with varying levels of severity. Homozygosity mapping revealed that out of the 7 patients, 6 patients of North African Jewish descent had an identical haplotype. In patients-derived fibroblasts, the mutant mRNA transcript generated a truncated CREB3 protein. Expression analysis and IHC revealed CREB3 RNA and protein expression in various retinal cell types, indicating its vital role in photoreceptor function.

Conclusions

We report here for the first time the involvement of *CREB3* in IRDs. *CREB3* was previously shown to be upregulated following UV radiation, which might contribute to extensive clinical variability observed in this relatively large cohort of homozygous patients for the same truncating variant.

sciforum-106250: A leaky deep intronic splice variant in CLRN1 is associated with non-syndromic retinitis pigmentosa

Asodu Sandeep Sarma [1,*], Maria Abu Elasal [1], Samer Khateb [1], Daan M Panneman [2], Frans PM Cremers [2], Eyal Banin [1] and Dror Sharon [1]

[1] Division of Ophthalmology, Hadassah Medical Center, Faculty of Medicine, The Hebrew University of Jerusalem, 91120 Jerusalem, Israel
[2] Department of Human Genetics, Radboud University Medical Center, Nijmegen, the Netherlands

Introduction

Inherited retinal diseases (IRDs) are clinically complex and genetically heterogeneous visual impairment disorders with varying penetrance and severity. Disease-causing variants in at least 289 nuclear and mitochondrial genes have been implicated in their pathogenesis.

Methods

Genomic DNA was isolated from peripheral blood lymphocytes. Exome sequencing was performed on illumina platform, splicing analysis of performed using pET01 minigene plasmid in Hela cells.

Results

In the current study, we performed exome sequencing on a 51 years-old Ashkenazi Jewish patient with non-syndromic retinitis pigmentosa (RP) and identified compound heterozygous variants in the *CLRN1* gene: a known pathogenic missense [p.(N48K)] and a novel deep intronic variant c.254- 643G>T. A minigene splicing assay that was performed aiming to study the effect of the c.254- 643G>T variant on CLRN1 pre mRNA splicing revealed the inclusion of a pseudo-exon that was also reported to be included in the transcript due to an adjacent variant, c.254-649T>G. However, unlike the reported c.254-649T>G variant, c.254-643G>T showed aberrant splicing in a leaky manner, implying that the identified variant is not totally penetrant.

Conclusions

The non-syndromic phenotype observed in this index case may be attributed to the leaky nature of this variant, which is causing some normal transcripts to be produced. To conclude, we report on a novel deep intronic variant in CLRN1 causing non-syndromic RP due to leaky nature of the identified variant.

sciforum-106139: ACE Insertion/Deletion Polymorphism as a Potential Risk Factor for Congenital Heart Disease among North Indians: Insights from a Tertiary Pediatric Cardiac Care Centre Study

Shadab Ahamad [1,*], Prachi Kukshal [1], Ajay Kumar [1], Subramanian Chellappan [2], Yogesh Sathe [2], Prabhatha Rashmi Murthy [3]

[1] Sri Sathya Sai Sanjeevani Research Foundation, Palwal, Haryana, India-121102
[2] Sri Sathya Sai Sanjeevani International Centre for Child Heart Care & Research, Palwal, Haryana, India-121102
[3] Sri Sathya Sai Sanjeevani Centre for Child Heart Care & Training in Paediatric Cardiac Skills, Navi Mumbai, Maharashtra, India-410210

Background

Congenital heart disease (CHD) is a global health concern, particularly in low- to middle-income countries like India. The renin–angiotensin–aldosterone system (RAAS) plays a crucial role in the development of cardiovascular disorders and hypertension, with the angiotensin-converting enzyme insertion/deletion (ACE I/D) polymorphism being a key genetic factor. Our study aims to elucidate the genetic influence of ACE I/D polymorphism on CHD in a north Indian cohort.

Methods

A total of 667 CHD cases, including 433 individuals with parental data and 104 controls, were enrolled and genotyped by polymerase chain reaction. Case–control association, parental transmission tests, and the association of patients' and parents' clinical parameters with ACE I/D were explored.

Results

The frequencies of the DD, ID, and II genotypes were 0.23, 0.47, and 0.30, respectively. Our findings highlight significant associations, notably the increased CHD risk conferred by the DD genotype in females (p = 0.036; OR = 1.68), its correlation with abnormal hemoglobin (p = 0.049; OR = 1.68), and its impact on primigravida (p = 0.05). Conversely, the II genotype was found to significantly elevate the risk of CHD in the offspring of tobacco-consuming fathers by 2.5-fold (p = 0.029). Notably, cyanotic cases exhibited a heightened prevalence of ACE I/D mutations (p = 0.059), with the Tetralogy of Fallot showing the strongest association (p = 0.024). Additionally, the DD genotype's involvement in conditions such as stenosis (p = 0.026) and pulmonary artery hypertension (p = 0.05) underscores its clinical relevance. The parent-of-origin test showed maternal transmission of the D allele in combined (p = 0.037) and acyanotic cases (p = 0.039) and paternal transmission in ventricular septal defect (p = 0.021).

Conclusions

This is the first study from India and possibly the only study globally that reports a significant association between ACE I/D and CHD, highlighting the importance of genetic factors in CHD susceptibility.

sciforum-106276: Bioinformatics analysis of *Gymnema sylvestre* and *Withania somnifera* on insulin resistance pathway targets

Maulshree Shree * and Dhiraj Kishore

Dept. of Gen. Medicine, IMS, Banaras Hindu University

Ayurvedic medicine offers a holistic approach to managing complex diseases such as Type 2 diabetes mellitus, which is primarily driven by insulin resistance. Bioinformatics has emerged as a powerful tool for understanding the molecular mechanisms underlying the effects of Ayurvedic drugs on insulin resistance pathway targets. This study uses bioinformatics techniques to analyze the pharmacological potential of Ayurvedic herbs traditionally used to treat diabetes, such as *Gymnema sylvestre* and *Withania somnifera*. The key bioactive compound in *G. sylvestre* has been shown to suppress the taste of sugar and reduce glucose absorption in the intestines, promoting better blood sugar control. Also, recent studies highlight *W. somnifera* role in improving insulin sensitivity and reducing blood sugar levels Using databases like DrugBank, STITCH, and PubChem, active compounds in these herbs were identified, and their interactions with key targets in the insulin signaling pathway, including IRS1, PI3K, and GLUT4, were analyzed. Molecular docking, network pharmacology, and gene expression analyses revealed that these phytochemicals potentially modulate glucose uptake, insulin sensitivity, and inflammation, key processes involved in insulin resistance. Our findings suggest that the synergistic effects of these herbs could offer a complementary approach to managing insulin resistance, warranting further experimental validation. The study paves the way for rational drug design based on traditional knowledge. It contributes to the growing field of systems biology in exploring the efficacy of multi-compound, multi-target therapeutic strategies.

sciforum-106061: Genetic analysis of hemochromatosis and its impact on liver function in the population of Lahore, Pakistan

Farhan Ikhtiar

University of Central Punjab

Hemochromatosis is an autosomal recessive iron overload disorder. Hemochromatosis occurs due to the failure of the hepcidin response in the liver. A high level of iron in the plasma is stored in various organs and destroys them. Hemochromatosis in which the HFE gene is involved is called primary hereditary hemochromatosis. The mutation in the HFE gene takes place at p.C282Y. The methodology used in this research was organic DNA Extraction, Gel Electrophoresis, Tetra ARMS PCR, and Sanger's DNA sequencing. This study's findings reveal a significant association between the TFR2 gene variant rs7385804 and hemochromatosis. The genotype frequencies in the case group were 59.3% for C/C, 38.9% for C/G, and 1.8% for G/G, compared to 77.1%, 22.9%, and 0% in the control group. The allelic frequency of the C allele was slightly lower in cases (78.7%) compared to controls (81.6%), while the G allele frequency was higher in cases (21.3%) than in controls (18.4%). This suggests that the C allele of rs7385804 may be a risk factor for developing hemochromatosis. This study investigates the genetic basis of hemochromatosis in the Pakistani population, focusing on the TFR2 gene variant rs7385804. It identifies a significant association between the C allele and disease susceptibility, with demographic data revealing a higher prevalence in males and onset in the mid-40s. While this study highlights the importance of genetic screening, there is a research gap in understanding the interaction between genetic and environmental factors. Future research should focus on larger, ethnically diverse samples and the development of personalized therapies. In conclusion, our study provides valuable insights into the genetic basis and demographic associations of hemochromatosis, focusing on the TFR2 gene variant rs7385804. We found a significant association between the C allele of rs7385804 and the development of hemochromatosis, highlighting the importance of genetic screening in at risk populations.

sciforum-107802: Genetic and immunological implications in fibromyalgia: A Literature Review

Sariya Khan [1,*], Husna Irfan Thalib [1], Dana Kauther [1], Ayesha Jamal [1], Adnan Anas Moallem [1], Samer Safwan Aldera [1], Anisa Abou Touk [1] and Fatma Elsayed Hassan [2]

[1] General Medicine Practice Program, Batterjee Medical College, Jeddah 21442, Saudi Arabia
[2] General Medicine Practice Program, Department of Physiology, Batterjee Medical College, Jeddah 21442, Saudi Arabia

Fibromyalgia (FM), a musculoskeletal condition characterized by widespread pain and numerous associated symptoms, is a complex disorder with uncertain etiology and pathogenesis. Most of the patients suffering from this syndrome are undiagnosed due to a lack of standard diagnostic criteria. Recent studies have shown the involvement of immune dysfunction and various pro-inflammatory cytokines in FM. Since there is so much uncertainty regarding the pathogenesis of FM, treatment modalities are very limited and ineffective. This review aimed to analyze the immunological mechanisms behind FM, attempting to deepen the understanding of its pathogenesis. Additionally, the review elucidates FM's associations with autoimmune diseases, highlighting shared pathophysiological mechanisms and overlapping symptoms. We synthesized current literature available on Google Scholar, PubMed, Springer, and Web of Science, the review explored the intricate interactions between genetic predisposition, immune dysregulation, and environmental factors in FM pathogenesis. The inclusion criteria prioritized studies focusing on the immunological aspect of FM. In conclusion, immune dysfunction has a role to play in the pathogenesis of FM, and immunomodulatory therapies have proven to be beneficial in the treatment of FM. Genetic variants, epigenetic modifications, and gut microbiome alterations are potential triggers for immune system dysfunction, contributing to the manifestation and exaggeration of FM symptoms. This review provided a comprehensive resource for researchers and clinicians, a guide for future investigations and clinical management towards improved outcomes and enhanced quality of life for individuals with FM.

sciforum-107791: Genetic Insights and Therapeutic Approaches for Epidermolysis Bullosa in the Saudi Arabian Population

Nancy Shehata [1], Noor A. Shaikh [2], Husna Irfan Thalib [3,*] and Bayan Al Zoabi [3]

[1] Department of Dermatology, King Abdullah Medical Complex, Jeddah, Saudi Arabia
[2] Department of Genetic Medicine, Faculty of Medicine at King Abdul Aziz University, Jeddah, SAU
[3] General Medicine Practice Program, Batterjee Medical College, Jeddah, Saudi Arabia

Introduction

Epidermolysis bullosa (EB) is a genetic skin disorder characterized by extreme skin fragility and recurrent blister formation, which significantly impacts the quality of life of patients afflicted by this disease. In Saudi Arabia, the diagnosis of EB relies heavily on thorough clinical assessments as well as genetic testing to confirm specific EB subtypes.

Methods

In this review, we conducted a systematic literature search focusing on genetic implications and management strategies for Epidermolysis Bullosa within the Saudi Arabian population. We analyzed peer-reviewed studies and clinical guidelines to synthesize insights on prevalence, genetic mutations, and therapeutic approaches specific to this demographic.

Results

Although prenatal diagnosis is an option for families with a history of EB, its application is limited in the Middle Eastern countries due to a variety of factors, including access to genetic services and cultural considerations. Current management strategies primarily focus on symptomatic relief. However, recent years have seen a significant increase in developing innovative therapeutics. For example, gene modification and stem cell therapy are currently under extensive investigation. These experimental approaches promise far more effective long-term solutions but are faced by numerous challenges.

Conclusions

Further research is necessary to improve diagnostic accuracy and treatment options, as well as to enhance the overall standard of care for patients with EB. This review delves into the genetic basis of EB and its management within the Saudi population, highlighting the critical need for genetic insights to facilitate accurate diagnosis, tailor targeted treatments, and provide effective counseling for patients and their families.

sciforum-105881: Non-coding single nucleotide and structural variants affecting the *EYS* putative promoter cause autosomal recessive retinitis pigmentosa

Dror Sharon [1,*], Shai Ovadia [2], Jaya Krishnan [3], Manon Bouckaert [4], Daan M. Panneman [5], Milton English [3], Johanna Valensi [1], Frans P.M. Cremers [5], Tamar Ben-Yosef [6], L Ingeborgh van den Born [7], Suzanne E. de Bruijn [5], Susanne Roosing [5], Eyal Banin [1], Samer Khateb [1], Ruth Ashery-Padan [2], Frauke Coppieters [4,8], Anand Swaroop [3] and Tamar Hayman [1]

[1] Division of Ophthalmology, Hadassah Medical Center, Faculty of Medicine, The Hebrew University of Jerusalem, Israel.
[2] Department of Human Molecular Genetics and Biochemistry, Faculty of Medical & Health Sciences and Sagol School of Neuroscience, Tel Aviv University, Tel Aviv, Israel.
[3] Neurobiology, Neurodegeneration and Repair Laboratory, National Eye Institute, National Institutes of Health, Bethesda, MD, USA
[4] Center for Medical Genetics Ghent (CMGG), Department of Biomolecular Medicine, Ghent University, Ghent, Belgium
[5] Department of Human Genetics, Radboud University Medical Center, Nijmegen, the Netherlands
[6] Ruth and Bruce Rappaport Faculty of Medicine, Technion-Israel Institute of Technology, Haifa, Israel
[7] The Rotterdam Eye Hospital, Rotterdam, the Netherlands
[8] Department of Pharmaceutics, Ghent University, Ghent, Belgium

Purpose

To characterize the effect of variants identified in the 5'-untranslated region of the *EYS* gene in patients with autosomal recessive retinitis pigmentosa (ARRP).

Methods

Variant screening included gene panels, Sanger, exome and genome sequencing. Functional validation included an electrophoretic mobility shift assay (EMSA) and various luciferase assays. Clinical examination included visual acuity testing, electroretinography (ERG) testing, and retinal imaging.

Results

Patients with RP from six *EYS* biallelic Arab-Muslim families harbored a 5' noncoding *EYS* variant, c.-453G>T, and four harbored a structural variant affecting the 5' noncoding exons. EMSA analysis revealed an effect on binding of transcription factors for c.-453G>T and a neighboring variant c.-454G>T that was reported previously in a patient with RP. Dual luciferase assays using overexpression of various transcription factors showed distinct effects on expression. c.-453G>T was associated with higher luciferase expression with CRX overexpression and c.-454G>C was associated with higher luciferase expression with OTX2 overexpression. In addition, the two variants were found to influence translation by affecting upstream initiation codons. Interestingly, visual function (including age of onset, visual acuity and ERG responses) of *EYS* RP patients who harbor c.-453G>T are better than those with biallelic null *EYS* mutations.

Conclusions

Our analysis revealed both single nucleotide and structural variants in the *EYS* promoter as the cause of ARRP. These variants may affect *EYS* expression via a dual mechanism by altering transcription factor binding affinity at the *EYS* promoter and by affecting upstream open reading frames.

sciforum-105057: The CXCR4/CXCL12 axis contribute to cerebrolysin-induced neuroprotection against staurosporine-treated cortical neurons at 7 days i*n vitro* and prvevented inflammatiion in a N2a cell line exposure to LPS.

Jose Joaquin Merino

UCM (Universidad Complutense de Madrid), Dpto. Farmacología, Farmacognosia y Botánica (UCM), IUIN, Spain

Introduction

Oxidative stress and Inflammation are hallmarks of neurodegenerative diseases, including a reduced repair capacity. Neural progenitor cells (NPCs) from the subventricular zone (SVZ), the dentate gyrus and the olfactory bulb cam migrate and differentiate into neurons or glial cells. CXCL12 chemokine binds to CXCR4 this axis contributes to neuroinflammation. Following CNS insult, chemokines recruit stem cells for repair while the aberrant CXCR4 activation promotes cell death. in fact, NPCs, endotelial cells, neurons (ang glia) express CXCR4, which enhance homing of stem cells for neuronal repair. The CXCL12 attracts neuroblasts and its is also secreted at sites of injury;

Aim

This study evaluate whether cerebrolysin (brain porcine peptide) or recombinant chemokines may protect cortical neurons at 7 DIV against staurosporine-induced cell death or LPS-induced inflammation in a N2a cell line. For this purpose, extracts from cortical neurons or N2a cells were isolated and several inflammatory markers were quantified by pCR (IL-1 beta, CXCR4/SDF1 alpha). Staurosporine or LPS treatment were added during 6 hours in the medium and cerebrolysin or recombinant proteins were o/n added in the presence of these treatments.

Results

The antiapoptotic role of chemokines and/or cerebrolysin were demonstrated in staurosporine-treated cortical neurons at 7 DIV by using a XTT assay. Cerebrolysin prevented staurosporine-induced apoptosis in the N2A cell line also and decreased Il-1 beta leveles in a N2a cell line exposure to LPS duringh 6 h.

Conclusions

The observed correlationship between cerebrolysin and neuroprotective effect of chemokines against apoptosis suggest that CXCR4 chemokine receptor activation by cerebrolysin prevented staurosporine-induced cell death in cortical neurons from rat and also reduced IL-1 beta levels in a N2a murine cell line expose to LPS (Lypolopisacharicde). Although the clinic efficay of cerebrolysin against dementia requiere more clinical evidences, some clinical trials have confirmed its eficacy against neurological diseases.

sciforum-106849: The early diagnostic of niemann-pick disease type a caused by *c.996del* and *c.1252C>T in SMPD1* gene: a case study

Natalya N Mazanova [1,*], Dmitry S Demianov [2], Goar B Movsisyan [3], Anastasya A Rusakova [2], Daria A Chudakova [2], Alexander A Pushkov [2], Ilya S Zhanin [2], Alexandr S Potapov [2], Kirill V Savostyanov [2] and Andrey P Fisenko [4]

1 Laboratory of Medical Genomics, National Medical Research of Children's Health Federal State Autonomous Institution of the Ministry of Health of the Russian Federation, Moscow, 119991, Russian Federation
2 National Medical Research of Children's Health Federal State Autonomous Institution of the Ministry of Health of the Russian Federation
3 Gastroentherology Department, National Medical Research of Children's Health Federal State Autonomous Institution of the Ministry of Health of the Russian Federation, Moscow, 119991, Russian Federation
4 Director of National Medical Research of Children's Health Federal State Autonomous Institution, National Medical Research of Children's Health Federal State Autonomous Institution of the Ministry of Health of the Russian Federation, Moscow, 119991, Russi

Niemann-Pick disease Type A (MIM 257200, NPD type A) is a rare congenital autosomal recessive hereditary condition. It is caused by the presence of causal nucleotide variants in the gene *SMPD1*(NM_000543.5), resulting in deficiency of the enzyme Acid Sphingomyelinase (ASM) encoded by *SMPD1*. This, in turn, leads to an abnormal lysosomal accumulation of sphingomyelin, causing tissue and organ damage. If untreated, it results in severe complications and death. Therefore, early diagnosis of NPD type A is crucial. The multi-methodological diagnostic of NPD type A includes measurements of enzyme activity of ASM, genetic analysis aimed to detect causal nucleotide variants in *SMPD1*, and a genetic and genealogical study of proband's family. The activity of ASM is commonly measured in Dried Blood Spots (DBS) by High-performance liquid chromatography-tandem mass spectrometry (HPLC-MS/MS), as this method outperforms others. The gold standard for detection nucleotide variants in *SMPD1* is Sanger sequencing. Finally, genetic and genealogical study of the proband's family is recommended when possible. As an example of such an approach, here we present the diagnostic journey of one family. The patient was referred to our center based on the overall clinical picture. The HPLC-MS/MS detected significant decrease ASM activity in patient's DBS. Sequencing of *SMPD1* revealed that proband had two heterozygous nucleotide variants: *c.996del, (p.Phe333Serfs*52)* and *c.1252C>T, (p.Arg418*).* Further segregation analysis showed each variant inherited from one of the genetically unrelated healthy parents. The family received genetic counseling regarding the findings. Another two siblings were not carriers of these variants in *SMPD1* and their ASM activity was in the normal range. However, the same nucleotide variants were found in the third sibling whose ASM activity levels were below the normal range. Without the multi-methodological approach, this patient would have missed a timely diagnosis of NPD type A.

sciforum-106227: Whole-genome profile of Greek patients with asthenozoospermia: Identification of candidate variants and genes

Maria-Anna Kyrgiafini [1,*], Chrysi Kontse [1], Alexia Chatziparasidou [1,2] and Zissis Mamuris [1]

[1] Laboratory of Genetics, Comparative and Evolutionary Biology, Department of Biochemistry and Biotechnology, University of Thessaly, Larissa, Greece
[2] Embryolab IVF Unit, Thessaloniki, Greece

Introduction

Nowadays, infertility represents a multifaceted health issue that significantly impacts numerous couples, giving rise to notable psychological and social complexities. Notably, one in six couples experience infertility, with approximately 50% of cases attributed to male factors. Male infertility, a complex disorder influenced by both environmental factors and genetic predisposition, involves the interplay of various genes contributing to its manifestation. It can be categorized into specific subtypes, including asthenozoospermia. The primary aim of this study was to identify novel variants associated with asthenozoospermia within the Greek population and to elucidate the roles of the genes involved.

Materials and Methods

Whole-genome sequencing (WGS) was conducted on both normozoospermic and asthenozoospermic individuals. Following the identification of variants exclusively present in asthenozoospermic men, an extensive range of tools, functional assessments, and predictive algorithms were employed to prioritize these variants.

Results

The investigation unveiled numerous polymorphisms, comprising 155 classified as high-impact and 715 classified as moderate-impact. While several of these variants were found within genes previously linked to male infertility, a notable subset was associated with asthenozoospermia for the first time. Furthermore, pathway enrichment analysis and Gene ontology (GO) analyses revealed polymorphisms on genes implicated in teratozoospermia through various mechanisms and pathways.

Conclusions

This study reaffirms the involvement of previously studied genes in male infertility, while also shedding light on novel molecular mechanisms. By providing a comprehensive list of variants and candidate genes associated with asthenozoospermia within the Greek population, this research contributes significantly to our understanding of male infertility and paves the road for future studies.

Session D. Technologies and Resources for Genetics Research

sciforum-106927: A draft transcriptome of the climate resilient California native plant *Ribes malvaceum*

Savanah Senn [1,*], Xochitl Estrada [1], Steven Carrell [2], Karu Smith [1], Meika Best [1], Daila Melendez [1,3], John Hsieh [1] and Gerald Presley [4]

[1] Los Angeles Pierce College Department of Agriculture Sciences, Plant Science program, Woodland Hills, CA 91371
[2] Oregon State University, Center for Quantitative Life Sciences, Corvallis, OR 97331
[3] Oregon State University, Department of Horticulture, Corvallis, OR 97331
[4] Oregon State University, Department of Wood Science and Engineering, Corvallis, OR 97331

Ribes malvaceum is commonly known as Chaparral Currant. This pilot project aimed to create genomic resources for *R. malvaceum* for phylogenomic studies of secondary metabolite production. The *Ribes* sp. are of interest in this study due to production of bioactive compounds for human health. *R. malvaceum* is of interest due to its desirable climate resiliency traits. Based on known characteristics of closely related cultivated species *Ribes nigrum* and the best BLASTX results, we hypothesize that we will find transcriptomic evidence of similar secondary metabolites produced by *R. malvaceum* in the transcripts.

Ribes malvaceum tissue was collected on the Red Trail at Gold Creek Preserve, Angeles National Forest. Leaf and fruit tissue was snap frozen in the field and sent to BGI Americas for extraction, library preparation, and sequencing. The data pipeline for plant RNAseq consisted of QC, de novo assembly, BUSCO evaluation, quantification, and annotation. The shell script find_transcript_ids.sh was used to find lant transcripts with TPM>10 (Transcripts Per Million) and length>1000. The downstream analysis was performed in order to narrow down interesting secondary metabolite genes which had high length and high TPM. The BUSCO results showed that the transcriptome was 90.63% complete.

Delta (8)-fatty-acid desaturase sequences were closely related to *Helianthus* (70.43% similar), TPM=42.85, length= 2115. Transcripts closely matched Chalcone synthase from *Humulus*, with 90.69% similarity and length of 1506, and were elevated (TPM= 644.85). A transcript related to Flavonoid 3'-monooxygenase in *Petunia* was identified (77.57% similar), length 2075, TPM=132.70. Anthocyanidin reductase ((2S)-flavan-3-ol-forming) was highly similar to *Vitis* (84.57%), TPM=39.75, length=1249. Monothiol glutaredoxin was related to the sequence *Arabidopsis* (70.67% similar, TPM=49.77, effective length=3616). Transcripts related to 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2 were identified that were 87.69% similar to *Vitis* (TPM=231.54, effective length= 1029).

These results are a starting point for further investigation into the species' resiliency and natural products.

sciforum-106172: An approach to identify aggression profiles via machine learning

Sakeena Bairamova * and Konstantin Pavlov

V. Serbsky National Medical Research Centre of Psychiatry and Narcology, Kropotkinsky per. 23, 119034 Moscow, Russia

The complex nature of aggression and challenges in phenotype description often make it difficult to identify genetic variations associated with aggressive behavior. The use of machine learning algorithms and multivariate analysis makes it possible to construct more accurate diagnostic schemes to characterize the underlying causes of aggression. The aim of this study was to develop a method to differentiate aggression profiles among subjects in a heterogeneous sample and to facilitate the association of the obtained profiles with genetic variations of BDNF rs6265, BDNF rs10835210, HTR2A rs6313, DRD4 1800955 later.

Participants' aggressiveness was assessed using the Buss-Durkee Hostility Inventory (BDHI). On the basis of 10 scales of BDHI, 1013 unique subspaces were formed, in which data was clustered. «Cluster neighborhood» plots were constructed for each participant in the study, allowing us to identify the content of each category of subjects in all of the clusters into which the participant fell. This approach demonstrated two dramatically different phenotypes based on all possible combinations of characteristics. However, many study participants exhibited mixed phenotypes, which were separated using the DBSCAN spatial clustering algorithm.

Individuals initially classified as a control group, addiction-prone group, or inmate group (convicted of felony) were often adjacent to each other in newly formed clusters, suggesting the need to reevaluate the sample: 13 individuals from the addiction-prone group and 17 individuals from the inmate group were assigned to the control group, 24 individuals from the inmate group and 6 individuals from the control group were assigned to the addiction-prone group. A total of 140 individuals belonged to the monotype, while the remaining 261 individuals belonged to the mixed phenotype.

Phenotypes defined by indirect traits often create an erroneous picture. It is necessary to identify similar groups of patients based on their psychometric data and then examine their genotypes within the groups.

sciforum-102331: Elucidation of the molecular basis of phenotypes in Seri-genetic resources (*Bombyx mori* L. and *Morus* spp.) using repository RNA-Seq datasets: A self-service data-mining approach

Raju Mondal [1,*], Dr. Ritwika Sur Chaudhuri [1], Dr. Lokesh Gangadharaiah [1], Dr. Nishitha Naik V. [1] and Dr. Manthira Moorthy [2]

[1] CSB-Central Sericultural Germplasm Resources Centre, Central Silk Board, Hosur, Tamil Nadu 635109, India
[2] Central Silk Board, Bengaluru, Karnataka 560068, India

Transcriptomics provides a link between the genome, proteome, and cellular phenotype; therefore, it is regarded as a unique approach to revealing the molecular basis of phenotypes. Despite the availability of huge datasets for a wide range of taxa in public databases, RNA-Seq data analysis and interpretation remain challenging. This is due to factors including limited processing capability and the need for specialized coding expertise and expensive software. Here, we used publicly available RNA-Seq datasets and emphasized an in-depth description of each cutting-edge system/tool, especially Galaxy platform and TRAPID 2. We also conducted a downstream analysis ofthe authenticity of the taxonomic identity, the global transcriptome map/network, and the functional enrichment of overrepresented genes in silkworm (*Bombyx mori* L.) and mulberry (*Morus* spp.). We provided a flexible de novo assembly, annotations, and sufficient visualization to interpret the RNA-Seq analysis data. The current data-mining approach sheds light on the significant influence of silkworm *black dilute* (*bd*) mutants on melanogenesis and tyrosine degradation, which is mediated by *dopachrome tautomerase* (DTC). However, *M. serrata* revealed significant polyploid trade-offs, such as investments in biochemical expenditure, nucleic acid metabolism, the intrinsic activity of transposable elements, and a functional association with chloroplasts. Overall, the current data-mining method reduces costs and requires no prior coding expertise to comprehend the genetic foundation of phenotype variance. The present approach can also help to decode the genetic architecture of novel phenotypes, including trait-specific accessions, ploidy-associated traits, and the hybridity effect of not only Seri-genetic resources but also other model and non-model organisms.

sciforum-107375: Reconstruction of Transcriptome Datasets to Understand the Molecular Basis Behind the Advantageous Effect of Triploid Over Diploid Mulberry (*Morus* spp.)

Tanya Ahmed Sheik [1,*], Raju Mondal [2] and Dr. Nishitha Naik V. [1]

[1] CSB-Central Sericultural Germplasm Resources Centre, Central Silk Board, Hosur, Tamil Nadu 635109, India
[2] Mulberry Tissue Culture Lab, CSB-Central Sericultural Germplasm Resources Centre, Tamil Nadu 635109, India

Polyploidy is a key factor influencing traits such as chloroplast number, stomatal size, and leaf yield. In mulberry *(Morus* spp.), triploids are well known to be superior over other ploidies in terms of yield traits. However, the cellular and molecular processes driving these benefits remain unclear. Transcriptome analysis is a powerful tool used to understand the molecular mechanisms underlying various plant traits, which requires coding skills and high-performance computers that hinder the utilization of publicly available huge RNA-Seq datasets. To address this issue, repository RNA-Seq datasets were analyzed using Galaxy to decode the genetic basis of the superior functionality of triploid mulberry. Leaf transcriptome datasets of diploids and triploids were retrieved and analyzed in Galaxy, where the genome of *M. indica* K2 was used as a reference. A variety of tools, including Trimmomatic, HISAT2, Stringtie, StringtieMerge, Featurecount, DEseq2, and WGCNA, were employed to identify differentially expressed genes, which were further analyzed using iDEP tools. For data interpretation, a PCA, volcano plot, heatmap, dendrogram, and bubble diagram were generated. The analysis revealed that triploid mulberry germplasm yielded a considerable number of up- and downregulated genes compared to diploids. Notably, the upregulated genes were associated with photosynthesis, chlorophyll biosynthesis, and carbon fixation, which in turn relay the molecular basis of the advantageous effect of triploids over diploids. These transcriptome studies indicate that polyploidization enhances photosynthetic capacity and other metabolic attributes. Therefore, this methodology helps to decipher the molecular basis of the advantageous effect of triploids over diploids without coding skills and high-performance computers.

sciforum-100131: The LAG-R guidelines, a framework for standardizing and improving laboratory animal genetic reporting

Guillaume Pavlovic

Institut Clinique de la Souris (ICS), PHENOMIN, CELPHEDIA, CNRS, INSERM, Université de Strasbourg, Illkirch-Grafenstaden, 67404 Strasbourg, France

Introduction

A major problem in biomedical research is poor reproducibility, with many scientific results not being successfully replicated. Many biological factors can explain this, from sampling effects to the influence of environmental factors such as microbiota. But other factors that are much easier to address, such as lack of access to methodological details, raw data, and research materials, are also playing a major role in the reproducibility crisis. In particular, inadequate reporting of the genetics of laboratory animals in research papers is common.

Methods

ARRIVE has been a pioneer in demonstrating to researchers using *in vivo* animals the importance of structured documentation for animal research. In the same vein, we brought together a large number of leading international experts, consortia and learned societies in the field of animal genetics to define the LAG-R recommendations for Laboratory Animal Genetic Reporting.

Results

Our recommendations have been published in Nature Communications (https://doi.org/10.1038/s41467-024-49439-y). This LAG-R framework defines a set of guidelines to support more complete documentation of the genetic make-up of animals that are used in research.

Conclusions

The intent of LAG-R is to help authors better describe the information they should already have in scientific papers, but also to provide reviewers with a checklist of essential genetic information that needs to be included in a publication. LAG-R provides an easy-to-understand list of recommendations with the goal of improving reproducibility, reliability, and overall scientific rigor.

Session E. Microbial Genetics and Genomics

sciforum-106961: *Artemisia californica* draft leaf and flower transcriptome and soil WGS resources

Savanah Senn [1,*], Steven Carrell [2], John Hsieh [1], Daila Melendez [1,3], Karu Smith [1], Meika Best [1], Daniel Moran [1], Ray A. Enke [4], Bruce Nash [5] and Gerald Presley [6]

[1] Los Angeles Pierce College Department of Agriculture Sciences, Plant Science program, Woodland Hills, CA 91371
[2] Oregon State University, Center for Quantitative Life Sciences, Corvallis, OR 97331
[3] Oregon State University, Department of Horticulture, Corvallis, OR 97331
[4] James Madison University, Department of Biology, Harrisonburg, Virginia, 22807
[5] Cold Spring Harbor Laboratory, DNA Learning Center, Cold Spring Harbor, NY 11724
[6] Oregon State University, Department of Wood Science and Engineering, Corvallis, OR 97331

Secondary metabolite production in *Artemisia* has been studied for its anti-parasitic, anti-tumor, and anti-inflammatory actions. *Artemisia californica* is a drought resilient plant with medicinal value used traditionally as a topical for severe pain relief; flavonoids, stilbenes, sesquiterpene lactones, and terpenes are main therapeutic components.

We aimed to create novel genomic resources, including a leaf & flower transcriptome and soil WGS metagenomics from the *A. californica* rootzone. Snap frozen plant tissues and rhizosphere soil were collected from the field and sent to BGIA for extraction, library preparation, and sequencing. Following QC, de novo assembly and quantification, transcripts were annotated with the best SPROT BLASTX and BLASTP hits. The completeness of the assemblies was assessed using BUSCO. Transcripts with TPM>10 and length>1000 were examined for evidence of candidate genes related to production of the expected bioactive compounds.

Assembly summary statistics were computed. There were 212,818 total sequences with a total length of 2.07*10^8. The average sequence length was 908; the length ranged between 193-13,630. L50 value was 41,357, N50 was 1,591, and N80 was 647. The *Artemisia californica* transcriptome was 91.4% complete. In the transcripts, there was evidence of sesquiterpene production, sesquiterpene lactones, and flavonoids. Beta-caryophyllene synthase was related to *Artemisia*, however with low similarity (62.70% ID, TPM= 14.86, length=2889). Multiple sesquiterpenoids and triterpenoids appeared to be elevated. Chalcone synthase transcripts were 96.23% similar to Australasian lineages of Asteraceae.

There was evidence of a distinct rootzone microbial community. *Geodermatophilus* from *Actinomycetes* was well-represented. The Biobakery metagenomics output indicated that there are differences in taxonomy in soil samples from different plant species, although there were few differences in function.

Future studies should focus on Nanopore sequencing of plant RNA and mining for novel bacterial species in the *Artemisia* rootzone using WGS data. Further studies should include biochemical analysis to confirm genomic findings.

sciforum-107342: Resistance gene profiles of multidrug-resistant *Klebsiella spp.* from poultry samples

Vanessa Silva [1,2,3,*], Catarina Freitas [2], Jessica Ribeiro [1,2,3], Pedro Pinto [4], Madalena Vieira-Pinto [5,6], Patrícia Poeta [1,2] and Gilberto Igrejas [1,3,7]

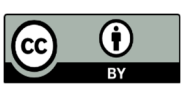
1 Associated Laboratory for Green Chemistry (LAQV-REQUIMTE), University NOVA of Lisboa, Lisboa, Caparica, Portugal
2 Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal
3 Department of Genetics and Biotechnology, Functional Genomics and Proteomics' Unit, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal
4 Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal
5 Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal
6 Veterinary and Animal Science Research Center (CECAV), University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal
7 Functional Genomics and Proteomics Unit, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal

The increasing prevalence of antibiotic-resistant bacteria, especially *Klebsiella spp.*, represents a major threat to both human and veterinary medicine. This study aimed to isolate and characterize the antimicrobial resistance profiles of *Klebsiella spp.* from broilers and broiler bursitis.

A total of 210 samples were collected, including 70 from hens, 40 from free-range chickens, 40 from bursitis, 20 from males, 20 from roosters, and 20 from young chickens. Antimicrobial susceptibility testing was conducted using the disc diffusion method, as recommended by EUCAST and CLSI guidelines, against 14 antibiotics. Additionally, PCR analysis revealed the presence of several resistance genes.

From the 210 samples, 51 isolates of *Klebsiella spp.* were obtained, including 20 from hens, 10 from young chickens, 8 from bursitis, 6 from free-range chickens, 4 from roosters, and 3 from males. Regarding the antimicrobial resistance, 57% of the isolates were classified as multidrug-resistant. The highest levels of resistance were observed for ampicillin (98.04%) and amoxicillin-clavulanic acid (86.27%). Resistance to nalidixic acid, trimethoprim-sulfamethoxazole, ciprofloxacin, gentamicin, and tetracycline was detected in 52.94%, 50.98%, 47.06%, 45.10%, and 23.53% of the isolates, respectively. None of the isolates showed resistance to imipenem, cefotaxime, or ceftazidime. The *sul2* gene was detected in 65.39% of isolates resistant to trimethoprim-sulfamethoxazole, while *sul3* was found in only 3.85%. The bla_{TEM} gene, associated with beta-lactam resistance, was present in 78% of isolates, while bla_{SHV} was detected in 4%. For tetracycline resistance, the *tetA* and *tetB* genes were found in 58.33% and 41.67% of the isolates, respectively.

This study highlights the significant antimicrobial resistance found in *Klebsiella spp.* isolated from poultry, underscoring the public health risks associated with the consumption of poultry products. More than half of the isolates were multidrug-resistant, which calls for ongoing surveillance and responsible antibiotic use in animal production to mitigate the spread of resistant strains.



sciforum-105431: Enhanced iturin A synthesis in *Bacillus amyloliquefaciens* Through Genetic Modification Targeting Rap Phosphatase Inactivation

Zhengjie Hou [1], Chunyang Cao [1], Gengrong Gao [1], Mingzhu Ding [1], Qiuman Xu [2] and Jingsheng Cheng [1]

[1] Tianjin University
[2] Tianjin Normal University

The biosynthesis of Iturin A, a compound with potent antimicrobial properties, has attracted considerable interest. However, challenges persist in achieving high yields from wild-type strains and optimizing *Bacillus amyloliquefaciens* for industrial-scale production. This study investigates the genetic foundations of Iturin A biosynthesis, emphasizing the roles of endogenous plasmids and Rap phosphatases. By optimizing and updating CRISPR/Cas9-based gene-editing tools, the modifications were successfully applied to the genetic manipulation of *Bacillus amyloliquefaciens*. The deletion of the endogenous plasmid plas1 from *B. amyloliquefaciens* HM618 significantly enhances Iturin A production, likely due to the removal of the Rap phosphatase gene located on plas1. Additionally, the targeted inactivation of the *rapC*, *rapF*, and *rapH* genes within the chromosomal DNA further increases Iturin A yield and specific productivity, although this is accompanied by reduced cell growth. By strategically combining plasmid deletion with targeted gene inactivation, a balance between cellular growth and Iturin A production is established. The engineered strain subsequently produced 849.9 mg/L of Iturin A within 48 hours, demonstrating a significant improvement in production efficiency. These findings underscore the crucial role of microbial genetics in optimizing Iturin A biosynthesis and offer a novel approach for enhancing the industrial production of this valuable antimicrobial compound in *B. amyloliquefaciens.*

sciforum-106882: Functional and Structural Characterization of COVID-19 Risk-Associated Exonic SNPs: An *In Silico* Analysis

Marcos Jessé Abrahão Silva [1,*], Sebastião Kauã de Sousa Bispo [2], Rebecca Lobato Marinho [1], Eliete Costa da Cruz [3], Thiago Pinto Brasil [4], Caroliny Soares Silva [1], Cristiane Cunha Frota [4], Diana da Costa Lobato [1], Lilian Cristina Santos Sinfrônio da Silva [5], Everaldina Cordeiro dos Santos [5], Karla Valéria Batista Lima [2] and Luana Nepomuceno Gondim Costa Lima [2]

[1] University of Pará State (UEPA)
[2] Bacteriology and Mycology Section of the Evandro Chagas Institute (IEC)
[3] Federal University of Pará (UFPA)
[4] Federal University of Ceará (UFC)
[5] Evandro Chagas Institute (IEC)

Introduction

The individual host susceptibility to coronavirus disease 2019 (COVID-19) can be attributed in part to single nucleotide polymorphisms (SNPs), which may be in exonic sites of the genome. The objective of this work was to analyze, *in silico*, the functional and structural impact of exonic SNPs related in the literature to susceptibility to COVID-19.

Methods

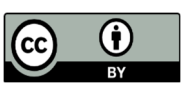
Literature data were retrieved from PubMed and Science Direct in relation to COVID-19-risk associated SNPs and a separate analysis was performed between synonyms (sSNP) and non-synonymous (nsSNP). To characterize the sSNPs, the following predictions were made: effects on mRNA structure (with RNAfold; CycleFold; Kinefold); splicing effects on mRNA (MaxEnt Scan; Ex Skip); effects on miRNA binding (TargetScan Score). Regarding nsSNPs, the following were performed: functional analysis of protein damage (with SIFT, PolyPhen 2, PhD-SNP, SNPs & GO, Predict SNP 2). After passing pathogenicity criteria, 8 nsSNPs were selected to predict their impacts on stability (CUPSAT), functionality and residual evolution (MutPred, ConSurf).

Results

The sampling consisted of 16 exonic SNPs, 4 sSNP and 12 nsSNP. Among the sSNPs, the SNP rs12252 of *IFITM3* had the greatest potential impact on mRNA structure, alternative splicing and miRNA binding, and indicated a moderate impact on post-transcriptional regulation. Regarding nsSNPs, *TYK2* SNP rs34536443 was predicted as deleterious/damaging by all tools used. SNPs predicted as destabilizing by CUPSAT, such as *PLSCR1* SNP rs343320, appear to have a greater negative impact on protein stability. The molecular, structural and evolutionary impacts of each SNP were described.

Conclusions

A total of 9 exonic SNPs (1 sSNP and 8 nsSNPs) were indicated here as potential candidates for further in vivo studies for COVID-19, as they may alter protein stability, interactions, and functional motifs that may be associated with antiviral response pathways.



sciforum-107292: Functional and Structural Characterization of Exonic SNPs associated with Leprosy Risk: an In Silico Analysis

Marcos Jessé Abrahão Silva [1,*], Sebastião Kauã de Sousa Bispo [1], Rebecca Lobato Marinho [2], Eliete Costa da Cruz [3], Keitty Anne Silva Neves [2], Luiza Raquel Tapajós Figueira [2], Diana da Costa Lobato [2], Lilian Cristina Santos Sinfrônio da Silva [4], Marcelo Cleyton da Silva Vieira [2], Everaldina Cordeiro dos Santos [4], Karla Valéria Batista Lima [1] and Luana Nepomuceno Gondim Costa Lima [1]

[1] Bacteriology and Mycology Section of the Evandro Chagas Institute (IEC)
[2] University of Pará State (UEPA)
[3] Federal University of Pará (UFPA)
[4] Evandro Chagas Institute (IEC)

Introduction

Leprosy, caused by *Mycobacterium leprae*, shows variations in individual susceptibility, which may be linked to genetic differences in the exome. Exonic single-nucleotide polymorphisms (SNPs) can influence immune response and disease progression. This study aimed to analyze, in silico, the functional and structural impact of exonic SNPs associated with leprosy susceptibility.

Methods

Data from the literature on leprosy-risk SNPs were retrieved from PubMed and SciELO. Analyses were conducted on synonymous (sSNP) and non-synonymous SNPs (nsSNP). For sSNPs, predictions included effects on mRNA structure (RNAfold, CycleFold, Kinefold), splicing (MaxEnt Scan, Ex Skip), and miRNA binding (TargetScan Score). For nsSNPs, protein damage was assessed using SIFT, PolyPhen 2, PhD-SNP, SNPs and GO, and Predict SNP 2. Pathogenicity filters identified 11 nsSNPs for further analysis of stability (CUPSAT), functionality (MutPred), and evolutionary conservation (ConSurf).

Results

A total of 35 exonic SNPs were analyzed (6 sSNPs, 29 nsSNPs). The sSNP rs2230365 (*NFKBIL1*) showed the highest potential for impacting miRNA regulation and mRNA structure, while no significant changes were observed in splicing. The nsSNP rs5743708 (*TLR2*) was predicted as deleterious by all tools used. SNP rs145562243 (*NCKIPSD*) was shown to be destabilizing with an unfavorable ΔΔG (-5.53 kcal/mol). The molecular, structural and evolutionary impacts of each SNP were reported. Highly conserved and exposed SNPs like rs5743708 suggest that they are critical for protein function.

Conclusions

This study identified 12 exonic SNPs (1 sSNP and 11 nsSNPs) as potential candidates for further in vivo studies on leprosy. These SNPs reveal complex interactions between genetic variations and their functional consequences, contributing to the understanding of disease mechanisms.

sciforum-106648: Genetic Engineering to Enhance Surfactin Production in *Bacillus subtilis* via Nitrogen Metabolism and Membrane Transport Pathways

Xia LI * and Wen Jianping

Tianjin University

Surfactin is a highly effective biosurfactant with broad potential applications in the medical and environmental technology sectors. Its biosynthesis in *Bacillus subtilis* is orchestrated by intricate genetic networks responsive to environmental stimuli. This study explores the enhancement of surfactin production in *Bacillus subtilis* ATCC 21332 through targeted genetic modifications, particularly under nitrate-enriched conditions, resulting in a significant boost in production. Comprehensive systems-level analysis identified pivotal genetic components governing nitrogen metabolism, fatty acid biosynthesis, and membrane transport, which were experimentally validated as key to facilitating increased surfactin output. Specifically, the upregulation of genes including nitrate reductase subunit genes *narG* and *NarH*, long-chain fatty acid β-hydroxylase gene *cypC*, preprotein translocase subunit gene *secA*, and the ATPase involved in cell division, gene *ftsE,* proved critical in optimizing surfactin synthesis. Through systematic engineering and the combination of these gene targets, the engineered strain SURb8 exhibited remarkable improvements in surfactin yield and production efficiency. Furthermore, a tailored feeding regime, designed to align with surfactin biosynthesis pathways, elevated the final production to 14.41 g/L, a 41.4-fold increase over that of the wild-type strain. This research offers valuable insights into the genetic and metabolic regulation of surfactin biosynthesis, highlighting the potential of microbial genetic engineering to enhance biosurfactant production for industrial applications.

sciforum-105415: Genomic basis of mycorrhizal fungal specificity in plant-fungal symbioses

Niraj Kumar Prajapati

Department of Horticulture, School of Agricultural Sciences and Technology, Babasaheb Bhimrao Ambedkar University (A Central University), Lucknow (U.P.) – 226025, India

Mycorrhizal symbioses, crucial for plant nutrition and ecosystem functioning, exhibit varying degrees of specificity between plant hosts and fungal symbionts. This study explores the genomic underpinnings of mycorrhizal fungal specificity, synthesizing recent advances in understanding the molecular mechanisms governing these intricate associations. Comparative genomic analyses of over 100 mycorrhizal fungal species have revealed that the loss of plant cell wall-degrading enzymes is a common feature, with ectomycorrhizal fungi retaining only 10-15% of these enzymes compared to their saprotrophic ancestors. This adaptation reflects the transition from saprotrophic to symbiotic lifestyles. Studies on effector proteins have identified several mycorrhiza-induced small secreted proteins (MiSSPs) that play key roles in symbiosis establishment. For instance, the MiSSP7 gene in Laccaria bicolor is essential for colonization of Populus roots, highlighting the importance of effectors in host specificity. Genomic investigations have also uncovered expansions in certain gene families, such as those encoding for nutrient transporters, with some ectomycorrhizal fungi possessing up to 3 times more ammonium transporter genes than their non-mycorrhizal relatives. Furthermore, analysis of plant genomes has revealed that up to 5% of plant genes are differentially expressed during mycorrhizal colonization, with common symbiosis genes being conserved across 80-90% of land plants. This study underscores the complex genomic landscape underlying mycorrhizal specificity, emphasizing the co-evolution of plant and fungal genomes. Future research directions include functional characterization of candidate genes and exploration of epigenetic mechanisms in symbiosis regulation.

sciforum-107810: Machine Learning-Driven Omics Approaches for Diagnostic Biomarker in Tuberculosis based on Differential Gene Expression data

Javed Aalam * and Rafat Parveen

Department of Computer Science, Jamia Millia Islamia, New Delhi, India – 110025

Background

Tuberculosis (TB) continues to remain a global health challenge, with 10.6 million cases and 1.3 million fatalities reported in 2022. Mycobacterium tuberculosis presents diagnostic difficulties because traditional procedures such as the Tuberculin Skin Test and IGRA are limited. MicroRNAs, including miR-18b and miR-378d, have been identified as prospective biomarkers for tuberculosis.

Method

This extensive review examines the use of OMICS technologies (genomics, transcriptomics, proteomics) with machine learning algorithms to identify and assess tuberculosis biomarkers. The recent literature from PubMed, Scopus, and IEEE Xplore was studied, concentrating on standard techniques such as KNN, SVM, and deep learning models.

Results

Machine learning techniques, especially deep learning, routinely attained elevated accuracy rates (often above 95%) in the classification of tuberculosis infections utilizing OMICS data. Biomarkers like miR-29a, miR-21, and 2-hydroxyglutarate (2-HG) have been recognized as promising diagnostic tools for TB. Additional biomarkers, including IL-8, IL-6, IFN-γ, and FCGR1A from transcriptomics, serum amyloid A (SAA), and lipoarabinomannan (LAM) from proteomics, provide more accurate insights into TB infection and progression.

Conclusions

The integration of machine learning with OMICS data offers a groundbreaking approach for tuberculosis diagnosis and biomarker discovery. Additional research is required to improve feature selection and refine machine learning models for clinical applications, potentially revolutionizing tuberculosis detection and treatment methods.

sciforum-106233: Occurrence of genetic determinants of resistance to colistin and biofilm in carbapenem-resistant *Acinetobacter baumannii* isolated from hospitalized patients

Michał Karasek

Student Research Group at the Department of Pharmaceutical Microbiology, Medical University of Lublin, Lublin, Poland

Carbapenem-resistant *Acinetobacter baumannii* (CRAb) is a priority pathogen, according to the World Health Organization (WHO), that is the most threatening to human health, being responsible for pneumonia, bacteraemia, urinary tract, skin and soft tissue infections, with mortality rates approaching 35%. The aim of this study was to evaluate the occurrence of colistin resistance (*mcr1-5*) and biofilm genes (*surA1*, *bap*, *ompA*, *luxR*, *epsA*) in 26 CRAb isolates collected from hospitalised patients and *Acinetobacter baumanii* ATCC 19606 as the reference strain. Gene prevalence was determined by multiplex or single PCR (polymerase chain reaction), in a 25 µL mixture (12.5 µL of REDTaq® ReadyMix™ PCR Reaction Mix, 1 µL of each primer, 2 µL bacterial DNA). As a result, 92.3% (24/26) and 96.2% (25/26) of the isolates were *mcr1*- and *mcr3*-positive, respectively. None of the isolates possessed the *mcr2*, *mcr4* and *mcr5* genes. All CRAb isolates had the *surA1*, *bap*, *ompA* and *luxR* genes, while 61.5% of isolates (16/26) harboured the *epsA* gene.

CRAb are highly pathogenic bacteria isolated from infections and are increasingly resistant to most available therapies. Every effort should be made to prevent the spread of these microorganisms, including analysing the presence of new genetic determinants in the CRAb genome, and identifying biofilm-related genes whose expression inhibition could more effectively eradicate these pathogens.

sciforum-107408: Regional Variability of Spotted Fever Group *Rickettsia* Genospecies: Insights from Eight Regions in Russia

Alexey V. Rakov *, Tatiana A. Chekanova and Ketevan Petremgvdlishvili

Laboratory for Natural Focal Infections Epidemiology, Central Research Institute of Epidemiology, 111123 Moscow, Russia

Introduction

In recent years, there has been growing interest in tick-borne infections, particularly tick-borne rickettsioses (TBR). Assessing the genospecies composition and regional distribution of spotted fever group rickettsiae (SFGR) is crucial for optimizing risk-based surveillance of TBR. However, the genospecies diversity of SFGR populations in the Russian Federation remains understudied. To address this, we studied ticks collected from vegetation, humans, and animals in eight regions of Russia to identify the SFGR genospecies, which may have significance for human morbidity.

Materials and Methods

From 2020 to 2024, we collected 2,431 ticks from eight regions of Russia, representing Western Siberia (Altai Krai), North Caucasus (Karachay-Cherkessia), Southern Russia (Astrakhan Oblast), the Volga region (Samara Oblast), Central Russia (Moscow, Tula Oblast, Oryol Oblast), and Central Europe (Kaliningrad Oblast). We utilized commercial qPCR kits for SFGR screening and identified genospecies by Sanger sequencing of partial genes for citrate synthase (*gltA*) and outer membrane protein A (*ompA*), comparing results with the GenBank database.

Results

Our findings revealed six distinct genospecies of SFGR across the eight regions of Russia; however, the diversity of these genospecies varied by region. The highest diversity (five genospecies: *R. raoultii*, *R. slovaca*, *R. helvetica*, *R. monacensis*, and *R. aeschlimannii*) was found in the North Caucasus in ticks from three genera. In Western Siberia, we detected three genospecies: *R. sibirica*, *R. raoultii*, and *R. helvetica* in two genera of ticks. In the Volga region, genospecies *R. slovaca* and *R. raoultii* were found in *Dermacentor* ticks, while in Southern Russia, *R. raoultii* and *R. aeschlimannii* were identified in two different genera of ticks. Central Russia (three regions) and Europe showed a similar pattern with *R. raoultii* in *Dermacentor* and *R. helvetica* in *Ixodes*.

Conclusions

Our study highlights significant regional variations in SFGR genospecies diversity in Russia, underscoring the necessity for ongoing research and monitoring for public health.

MDPI AG
Grosspeteranlage 5
4052 Basel
Switzerland
Tel.: +41 61 683 77 34

Genes Editorial Office
E-mail: genes@mdpi.com
www.mdpi.com/journal/genes


MDPI