UFV Universidad Francisco de Vitoria

II CONGRESO SAN ALBERTO MAGNO

LA REVOLUCIÓN HUMANA DESDE LA CIENCIA

ISBN: 978-84-09-70173-5

Índice

1. Introducción

El proyecto educativo de la Facultad de Ciencias Experimentales de la Universidad Francisco de Vitoria es referente universitario en la formación de una nueva generación de hombres y mujeres de ciencia que reflexionen sobre el sentido de la solidaridad, conocedores del hombre y de la cultura en la que viven, capacitados para desarrollar su ejercicio profesional reconociendo la dignidad de la persona como pilar fundamental.

El Congreso San Alberto Magno surge como una iniciativa de la Facultad para promover el encuentro entre alumnos, alumni, profesores, con profesionales de la investigación, industria, administración pública, etc.

Este congreso fue concebido como un espacio para la reflexión, el diálogo y la colaboración, donde las fronteras entre la academia y el mundo profesional se desdibujan, generando una interacción enriquecedora que permite la creación de soluciones innovadoras a los desafíos del presente y del futuro. La ciencia, entendida en su sentido más amplio, es un vehículo fundamental para transformar la realidad y construir una sociedad más equitativa, inclusiva y sostenible.

Bajo la consigna:" La Revolución Humana desde la Ciencia", en esta tercera edición hemos sido testigos a través de las presentaciones que se recogen en estas páginas, del trabajo y el compromiso de quienes, desde distintas disciplinas, se esfuerzan por llevar a cabo una revolución humana basada en el conocimiento científico. Este encuentro ha sido, sin duda, una oportunidad única para aprender de las experiencias de egresados y profesionales, pero también para fortalecer los lazos entre la academia y el sector privado, y fomentar la colaboración con los servicios públicos en la construcción de un futuro mejor.

El presente libro de abstracts reúne el esfuerzo y la creatividad de quienes participan en esta revolución del conocimiento, reflejando la diversidad de enfoques y el rigor científico que caracterizan a nuestra comunidad académica.

Agradecemos a todos los que han hecho posible este encuentro, a los autores por compartir su trabajo, a los organizadores por su dedicación y a los asistentes por ser parte activa de este espacio de crecimiento y reflexión.

¡Bienvenidos a esta revolución humana desde la ciencia!

1.1 Comité Organizador

Dra. Maite Iglesias Badiola. Decana Ciencias Experimentales, Profesora de Técnicas Instrumentales Básicas, Grado Biotecnología, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dr. Cruz Santos Tejedor. Director Escuela Internacional de Doctorado. Vicedecano de Investigación de Ciencias Experimentales. Profesor de Microbiología, Universidad Francisco de Vitoria.

Dra. Lourdes Rufo Nieto. Vicedecana de Gestión Académica y Calidad. Profesora de Biología Vegetal y Farmacognosia, Grados de Farmacia y Genética, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dra. Águeda M. Tejera. Directora Grado Genética, Profesora Genética e Ingeniería Genética, Grados en Genética, Biomedicina y Biotecnología, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dr. Ramiro Perezzan Rodríguez. Profesor Química Orgánica, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dra. Esther Grueso Hierro. Profesora Histología, Grado Biomedicina, Facultad Ciencias Experimentales Universidad Francisco de Vitoria.

Dra. Elena Pascual Vega. Coordinadora del Grado en Biomedicina. Profesora de Bioquímica, Grado en Biomedicina, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dr. Ismael Santa María Pérez. Profesor Genética, Grado Biotecnología y Grado Genética, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria

.

Estefanía del Valle López. Responsable de Nuevos Proyectos y RRSS, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dra. Noemí García Romero. Profesora Genética, Grado Biomedicina, Universidad Francisco de Vitoria.

Dra. Teresa de Asúa Corchado. Profesora de Biología Celular. Mentora de alumnos de Experimentales. Universidad Francisco de Vitoria.

Dr. José María Bueno Calderón. Profesor de Química General y Química Farmacéutica I y II en el Grado de Farmacia. Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dra. Marian Mellén Rodríguez. Profesora de Genómica, Grado Biotecnología, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

1.2 Comité Científico

Dra. Esther Grueso Hierro. Profesora Histología, Grado Biomedicina, Facultad Ciencias Experimentales Universidad Francisco de Vitoria.

Dra. Elena Pascual Vega. Coordinadora del Grado en Biomedicina. Profesora de Bioquímica, Grado en Biomedicina, Facultad Ciencias Experimentales, Universidad Francisco de Vitoria.

Dra. Noemí García Romero. Profesora Genética, Grado Biomedicina, Universidad Francisco de Vitoria.

2. Listado de Abstracts

1. Automated detection of anatomical positions in hip radiographs for Wiberg´s angle
2. Multiresistant *Mycobacterium tuberculosis*: the silent threat
3. Implication of the 5-HT2C serotonin receptor in somatosensory filtering as a posible therapeutic target for psyshosis
4. Acinetobacter baumannii
5. Analysis of viral epitopes from B lymphocytes reveals the need for extensive antigen processing for recognition
6. Potential targeted therapy against triple-negative breast cancer
7. Analysis of H2AX, Caspase 3 and Cleaved Caspase 3 expression in CSCs from patients with Diffuse Midline Gliomas (DMG) by Western Blotting
8. Nanoparticles. Are they potential solution for a direct and specific drug delivery?
9. Multilayer Mesoporous Catalysts Modified for the Eco-Efficient Synthesis of Bioactive Heterocycles
10. Analysis of a drug effect on diffuse midline glioma (DMG) cells using Western blot
11. The podoplain/CD44/MT1-MMP axis as a regulator of invadopodia-mediated invasión in squamous cell carcinoma
12. Regulation of the Hair Follicle Growth Cycle Through the Photoproduction of Activating Levels of ROS
13. *Pseudomonas aeruginosa*: implication of the expresión of beta-lactamases in the mechanism of antibiotic resistance
14. Investigating the immunomodulatory properties of probiotics through their sugar metabolism and epigenetics
15. ASR92: Low-cost, sustainable analog incubator
16. Effects of grape must polyphenols on meduloblastoma cell lines
17. Validation of an ATP Probe as a Biomarker for Intranuclear Activity and Chromatin Dynamics
18. Stimulation of cell proliferation through direct photoproduction of reactive oxygen species (ROS)
19. Effect of High-Intensity Interval Exercise-Conditioned Human Serum on Breast Cancer Cells
20. Unraveling biomechanical control mechanisms in the cells nucleus through thermodynamic mapping
21. MECP2 Duplication Syndrome, a mouse model to understand the molecular mechanisms of this rare neurodevelopmental disorder
22. Generation of Animal Models of Fragility Skin Diseases Epidermal
23. Piezoelectric Nanoparticles for Deep Brain Stimulation
24. Impact of Podoplanin on the Initiation and Progression of SCCs
25. Molecular insights and functional study of a patient MDA5 variant
26. Antimicrobial activity análisis of plant extracts from extremophile plants

3. Abstracts

Automated detection of anatomical positions in hip radiographs for Wiberg's angle.

Fernando Pocino Martín[1], Paula Méndez de Inza[1], Luis Novoa Rodrígez[2], Alberto de Santos Sierra [1]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Hip Unit, Clínica CEMTRO

*Correspondence: alberto.desantos@ufv.es

Abstract

Hip dysplasia is a complex orthopaedic condition characterized by an improperly shaped acetabulum, leading to structural and anatomical alterations in the hip joint. This creates a static problem, that compromises the joint's, resulting in hip instability due to abnormal load transmission and anomalous concentration of forces within the weight-bearing zone. To detect this condition using X-rays the key indicators include: displacement of the femoral head with its coverage percentage, lateral center-edge (LCE) angle of Wiberg, acetabular roof angle of Tönnis, acetabular index (AI), acetabular depth-to-width ratio, acetabular angle of Sharp and the anterior center-edge angle of Lequesne. These measurements are detected manually in radiographic images, which may lead to variability in the interpretations of the results obtained among doctors of the same specialty and experience levels. Therefore, we present the development of a software that, through artificial intelligence, identifies anatomical positions in hip radiographs and, with mathematical relations, facilitates the interpretation and diagnosis of this condition as a complementary tool. Primarily it is focused on evaluating the angle of Wiberg. Future enhancements are intended to include the detection of additional clinical indicators, improving its diagnostic capabilities for this condition. The model is based on a convolutional neural network (CNN) that has demonstrated good accuracy in identifying positions, achieving a high confidence rate in 80% of the tests performed. While initial results are promising, expanding the training dataset would improve the model's performance and robustness contributing to the advancement of automated diagnosis in traumatology. Furthermore, the application increases accessibility by not restricting users to specific medical formats like DICOM files, thus enabling broader adaptability and facilitating greater integration in different environments.

Keywords: *Automated Detection; Hip Dysplasia; Complementary Tool*

Multiresistant Mycobacterium tuberculosis: the silent threat

Laura Gimeno Tello[1*], Sara González Sánchez[1], Íñigo Mancho Calleja[1], Alexia Maria Maté Galaup [1]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: lgimenotello@gmail.com

Abstract

Tuberculosis (TB) is an endemic disease caused by Mycobacterium tuberculosis (Mtb), which represents a public health threat and affects approximately one-quarter of the world's population. We highlight the alarming increase in the incidence of multidrug-resistant Mycobacterium tuberculosis (MDR-TB), especially in regions with high population density, as well as in vulnerable groups such as prisoners, health care workers, homeless people, migrants, intravenous drug users, and people with weakened immune systems.
Virulence and resistance factors of MDR-TB, either inherent to Mtb or resulting from specific adaptive genetic mutations that confer resistance to first-line drugs such as isoniazid and rifampicin, are analyzed.
In addition, the etiopathogenesis (cause and mechanism of TB development) is explored, the main actor being the interaction between the microorganism and the human immune system. This highlights how the mycbacterium can persist in a latent state and reactivate under favorable conditions.
The poster also reviews the different therapeutic targets of currently used drugs, indicating that, in a prolonged multi-drug combination treatment regimen, TB is successfully combated, albeit with significant side effects.
Prospects are equally discussed, including developing new drugs, vaccines, and treatment strategies that are more effective and less toxic to the patient. However, despite advances in developing new antimicrobials, treatment of these individuals is often expensive and very complex, with variable success rates. This limits its accessibility to populations with limited healthcare resources, who are most affected by MDR-TB.
This analysis underlines the urgent need for innovative and collaborative strategies to combat this silent threat. Implementing an early diagnosis, appropriate treatment, and prevention programs, along with continued research, is crucial to improving global health and reducing the burden of MDR-TB.

Keywords: *Mycobacterium tuberculosis, resistance, virulence factors, therapy*

Implication of the 5-HT2C serotonin receptor in somatosensory filtering as a possible therapeutic target for psychosis

Alba Tejada de Mesa[1], C. Izquierdo-Luengo[1], M. Ponce-Renilla[1], I. Pereda-Pérez[2], M. Ten-Blanco[1], R. Mª Tolón[1], F. Berrendero[1]*

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Departamento de Psicobiología, Facultad de Psicología, Universidad Complutense de Madrid, España

*Correspondence: fernando.berrendero@ufv.es

Abstract

Psychosis is a set of symptoms (hallucinations and delusions) common to several pathologies, mainly psychiatric, which represent a major public health problem. Although the pathophysiology of this condition is not fully understood, the most accepted theory points to alterations in the dopaminergic system, which has directed most treatments towards modulating it. However, recent research has highlighted the relevance of the serotonergic system, particularly the 5-HT2C receptor in the appearance of psychotic symptoms. This work aims to delve deeper into the role of this receptor in psychosis, as well as its possible pharmacological modulation, in order to find new potential therapeutic targets. To do so, the prepulse inhibition test (PPI) will be used, an indicator of somatosensory filtering which is altered in both patients and rodents with psychotic symptoms. JWH-018, a synthetic cannabinoid present in commonly consumed herbal preparations such as Spice, has been shown to induce acute psychotic effects. Modulation of the serotonergic system in this context through 5-HT2C allows us to explore the involvement of this receptor in psychotic-like behaviors induced by certain drugs of abuse. On the other hand, the 129S1/SvImJ mouse strain, which presents high inhibition levels compared to C57BL/6J mice in the PPI test, is proposed as an alternative model to investigate the relationship between the 5-HT2C receptor and a correct somatosensory filtering. The conclusions obtained with both approaches indicate that modulation of the 5-HT2C receptor could be a promising therapeutic target for the management of psychotic symptoms present in numerous pathologies.

Keywords: *psychosis; 5HT2C; somatosensory filtering*

Acinetobacter baumannii

Alexandra Bru[1], Paula Carromero[1], Elsa González[1], Claudia María Moreno[1], Jone Pisabarro[1], Paula Zamorano[1]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: alexandrabrcasahuga@gmail.com

Abstract

(Background: Acinetobacter baumannii is a gram-negative coccobacillus of significant medical importance, particularly as a pathogen in nosocomial infections. Its resistance to multiple antibacterial agents poses critical challenges in healthcare, especially in intensive care units (ICUs) where it is often associated with high mortality rates. Methods: This study highlights the structural components, mechanisms of pathogenicity, and transmission pathways of A. baumannii. It also reviews environmental reservoirs, emphasizing its adaptability to hospital settings and potential contamination of medical equipment and surfaces. (3) Results: Key findings include its survival and persistence on various surfaces, its resistance mechanisms linked to β-lactamase production, and membrane proteins enhancing virulence. Effective hygiene practices, isolation protocols, and equipment sterilization are essential preventive strategies. (4) Conclusions: Understanding the bacterium's transmission, habitat, and resistance mechanisms is crucial for developing targeted therapeutic interventions and minimizing nosocomial outbreaks.

Keywords: *nosocomial infections; multidrug resistance; hospital hygiene*

Analysis of viral epitopes from B lymphocytes reveals the need for extensive antigen processing for recognition

Álvaro Ras-Carmona[1] and Pedro A. Reche[1]*

[1]Laboratory of Immunomedicine, Department of Immunology & O2, Faculty of Medicine, University Complutense of Madrid, Pza Ramon y Cajal S/N, 28040 Madrid, Spain

*Correspondence: parecheg@med.ucm.es

Abstract

B-cell epitopes (B epitopes) must be accessible for recognition by B lymphocytes and related antibodies. In this work, we have attempted to study this premise for B epitopes recognized in infectious processes in humans. Most of these B epitopes were virus-specific linear epitopes, so we focused on them by first analyzing the localization of the antigens that include them. This localization could be unequivocally assigned to 26498 linear B epitopes. Of these, 18832 B epitopes belonged to antigens that remain enclosed in host cells and/or viral particles, hidden from antibody recognition, while only 7666 are found in ectodomains of viral envelope antigens and/or mature secreted antigens, visible to antibody recognition. We then selected B epitopes corresponding to antigens with known tertiary (3D) structures. We determined the accessibility of each epitope (eRSA) and compared these values with eRSAs of conformational B epitopes obtained from available 3D structures of antigen-antibody complexes. We observed that only 32.72% of linear B epitopes had eRSA values minimally comparable to those of conformational B epitopes. In summary, our results suggest that most of the targeted virus-specific B epitopes recognized in infectious processes are unreachable for antibody recognition on intact viral particles and/or host cells. Therefore, we must conclude that antigen recognition by antibodies must be preceded by degradation/processing of viral particles and infected cells.

Keywords: *Linear B cell epitope; virus; structural analysis*

Potential targeted therapy against triple-negative breast cancer

Fabiola Carretero Bellver[1]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: fcbsabc@gmail.com

Abstract

Triple-negative breast cancer (TNBC) is characterized by the absence of estrogen receptor (ER) and progesterone receptor (PR) expression, as well as the lack of amplification of the human epidermal growth factor receptor 2 (HER2). This type of cancer also exhibits a high capacity for invasiveness, significant metastatic potential, and a tendency to relapse. Metastases often involve the brain and visceral organs. The mortality rate among patients is 40% within five years of diagnosis.

To understand the management of this condition, it is important to note that standardized treatment regimens for TNBC are still lacking, which is why chemotherapy remains the primary systemic treatment.

Although there is still much research to be done to uncover the intrinsic mechanisms of this condition, new approaches and studies are being conducted to design targeted therapies.

Conclusion: This poster presents recent advancements in the treatment of triple-negative breast cancer through targeted therapies. It seeks to emphasize the significance of understanding this condition and the critical role of research in identifying new opportunities for targeted treatment approaches.

Keywords: *Triple-negative breast cancer, targeted therapies, advancements*

Analysis of H2AX, Caspase 3 and Cleaved Caspase 3 expression in CSCs from patients with Diffuse Midline Gliomas (DMG) by Western Blotting

Lucía Parejo Celadilla[1], Raquel De La Flor Laserna[1], Alvaro Monago Sanchez[1,2], Noemí García Romero[1,2], Angel Ayuso Sacido[1,2*]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2] Brain Tumor Laboratory, Fundación Vithas, Grupo Hospitales Vithas, 28043-Madrid, Spain.

*Correspondence: noemi.garcia@ufv.es

Abstract

(Background: Diffuse Midline Glioma (DMG) is a highly aggressive subtype of pediatric glioma. It is found in the midline structures of the brain (thalamus, brainstem, spinal cord and the brainstem, spinal cord and the Pons area), resulting in symptoms such as difficulty walking, balance, vision and speech problems, among others. These tumors are classified as grade IV glioblastomas due to their high malignancy, diffuse infiltration and resistance to therapies. Treatment is extremely challenging due to their delicate localization in the brainstem and diffuse infiltration, it precludes safe surgical resection, therefore the main treatment strategies include fractionated focal radiotherapy as the most common standard treatment or the use of chemotherapy (temozolomide, TMZ). The purpose of this study is to investigate the sensitivity of DMG cells to a specific drug and explore its potential synergistic effect when combined with radiation therapy. Methods: DMG CSCs were subjected to a drug and then irradiated with the standard therapy (4Gy) and at a higher dose (30Gy) to ensure cell damage. Then, protein extraction was performed 1h, 3h and 24h after radiation and was analyzed by Western Blot. Results: Tumor cells show a large amount of DNA damage 1h after radiation, but appear to have repair mechanisms, as the proportion of H2AX appears to decrease with time. However, the apoptosis is stimulated in cells that have been treated with the drug in all conditions (1h, 3h and 24h after radiation). In addition, no noticeable difference was observed in cells when given the drug and the standard treatment (4Gy) allowing the possibility to suppress radiotherapy in future clinical trials.

Keywords: *Diffuse Midline Glioma (DMG); Radiation therapy; Chemotherapy*

Nanoparticles. Are they a potencial solution for a directed and specific drug delivery?

Mariia Krivenkova[1]*

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: mariakrivenkova6@gmail.com

Abstract

Nanoparticles are nanostructures that have a transformative potential in the biomedical field due to their ability to interact with cellular structures in a unique way. Bio-imaging, vaccination, data storage, and targeted drug delivery are only a few already existing applications of nanoparticles, although their maximal potential has not yet been reached. This material can be associated with cytochrome proteins as a potential treatment for targeted cancer treatment of solid tumors. Nanoparticles exhibit exceptional versatility, allowing them to revolutionize various aspects of modern medicine, particularly in oncology, where precision is crucial.

In this poster, we have analyzed a theoretical application of amine MSNPs in this field based on their chemical and physical properties, as well as a given a general description and classification of nanoparticles as a biomaterial. Through analyzing existing investigations on the topic and the unique properties of these nanoparticles, we have described a potential application to decrease adverse secondary effects of cancer treatment through the precise and localized liberation of drugs. This targeted approach reduces damage to healthy tissues, addressing a significant limitation of current treatments. If turned into reality, such mechanisms would propose efficient, personalized oncological solutions, representing a significant step forward in patient care and outcomes, enhancing treatment success rates and quality of life.

***Keywords**: Nanoparticles; MSNPs; targeted drug delivery*

Multilayer Mesoporous Catalysts Modified for the Eco-Efficient Synthesis of Bioactive Heterocycles

Erika Margüello[1], Isabel Carballo[1], Daniel González[1]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain

*Correspondence: daniel.gonzalez@ufv.es.

Abstract

Nowadays, the twelve principles of green chemistry outlined by Paul Anastas are the core elements in the development of sustainable chemical processes. Particularly, heterogeneous catalysis is a key tool in this field. The fact that the catalysts are in a different phase from the reactants and products allows their recovery and reuse after the reaction occurs, contributing significantly to waste reduction and the approach to a more environmentally and friendly chemistry. In this research, a series of multilayer catalysts based on mesoporous silica SBA-15 have been designed and developed for the synthesis of 2-amino-4*H*-chromenes in a tricomponent reaction. The thermal stability of the SBA-15, altogether with its mesoporous structure and the possibility of anchoring various catalytically relevant molecules makes it a tool with great potential in the field of heterogeneous catalysis.

The SBA-15 has been functionalized with the ionic liquid 1-Methyl-3-(3-trimethoxysylil)-propyl)-1H-imidazolum chloride and modified with four different amino acids whose basic properties significantly enhance the yields of the reaction. Samples from the reaction were taken at different times, and once the catalyst was removed, they were prepared for the analysis with nuclear magnetic resonance.
Chromenes are molecules of great interest in the pharmaceutical context due to their applications in the synthesis of drugs with antitumor or antioxidant properties for the central nervous system, however, its synthesis in the absence of catalysts is challenging due to the low yields reached and the use of contaminant solvents. In this regard, our four basic catalysts have proven to be efficient in synthesizing 2-amine-4*H*-chromenes, all of them reaching yields above 90% and being reusable more than once. This confirms that heterogeneous catalysis is an effective and promising technique aligned with green chemistry principles for developing environmentally friendly processes.

Keywords: *Green Chemistry; heterogeneous catalysis; mesoporous silica; SBA-15; Ionic liquid; 2-amino-4H-chromenes*

Analysis of a drug effect on diffuse midline glioma (DMG) cells using Western blot

Raquel De La Flor Laserna[1]; Lucía Parejo Celadilla[1]; Monago-Sánchez Álvaro[1,2]; Carrión-Navarro, Josefa[1,2]; García-Romero, Noemí[1,2]; Ayuso-Sacido, Ángel[1,2].

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Brain Tumor Laboratory, Fundación Vithas, Grupo Hospitales Vithas, 28043-Madrid, Spain.

*Correspondece: noemi.garcia@ufv.es

Abstract

Diffuse midline gliomas (DMG) are highly aggressive pediatric brain tumors located in critical areas of the central nervous system such us the pons, spinal cord, and thalamus. These tumors predominantly affect children aged 4-7 years, presenting with severe neurological symptoms and an estimated survival of 9-12 months post-diagnosis. Approximately 80% of DMGs harbour the H3K27M mutation, which disrupts normal histone methylation, resulting in epigenetic dysregulation and tumor growth. Surgical resection is not feasible due to the tumor's delicate location, leaving fractionated radiotherapy as the only palliative treatment. However, the urgent need for innovative therapeutic strategies remains unfulfilled.

This study investigates the effects of a novel pharmacological agent on DMG cells harbouring the H3K27M mutation. Using Western blot analysis, we evaluated DNA damage and apoptosis induced by this drug in combination with ionizing radiation at different time points (1h, 3h, and 24h post-treatment). Protein markers such as γH2AX (DNA damage) and cleaved caspase-3 (apoptosis) were analyzed and normalized against GAPDH as a control.

Our findings indicate that the drug enhances apoptotic responses in DMG cells at all evaluated time points. Notably, untreated tumor cells displayed significant DNA damage shortly after irradiation, but apoptosis does not remain at 3 and 24h without the drug. In contrast, the drug-treated cells maintained higher levels of DNA damage with and without the implementation of the radiation, which indicates that the drug alone could have an effect in cancerous cells even with the suppression of the standard treatment. Despite these promising results, further studies are required to validate the long-term efficacy of this therapeutic approach.

Key words: *Glioma, γH2AX, apoptosis*

The podoplanin / CD44 / MT1-MMP axis as a regulator of invadopodia-mediated invasion in squamous cell carcinoma

Santiago Garcés-Fernández[1], Lucía Montero-Montero[1], Diego Megías[2], Sara Temprano-Carazo[1], Rocío Jarcovsky[1], Susana Álvarez[1], Esther Grueso and Ester Martín-Villar [1,*].

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Advanced Optical Microscopy Unit, Instituto de Salud Carlos III, Madrid, Spain

*Correspondence: ester.martin@ufv.es

Abstract

Squamous cell carcinoma (SCC) originates from stratified epithelial cells, including those of the skin and oral cavity. A hallmark of SCC is its ability to degrade and breach the basement membrane, a process likely mediated by dynamic, actin-rich cellular protrusions known as invadopodia. These structures exhibit high proteolytic activity, as they concentrate extracellular matrix (ECM)-degrading metalloproteinases, particularly MT1-MMP, which is crucial for invadopodia-mediated ECM degradation. Our laboratory has previously linked the transmembrane glycoprotein podoplanin (PDPN) to SCC malignancy progression and identified its role in promoting invadopodia stability and ECM degradation. Recently, we observed that podoplanin co-localizes with the adhesion molecule CD44, with which it interacts, in the adhesion ring of invadopodia. However, the cooperative role of PDPN and CD44 in the formation and function of invadopodia remains unexplored. Given that both proteins are known to interact with MT1-MMP in other cellular contexts, this study investigates the functional relationship of the PDPN/CD44/MT1-MMP axis with invadopodia. To address this, SCC cells were genetically modified to conduct gain- and loss-of-function studies, coupled with fluorescent gelatin degradation assays. Our findings expand on previous results from our lab, demonstrating that CD44 plays a pivotal role in concentrating the activity of MT1-MMP, MMP2, and MMP9 at the invadopodia. Additionally, although not previously reported, podoplanin also contributes to this process. Using *in vivo* pre-embedding assays, we observed that CD44, and to a lesser extent podoplanin, modulate the localization of MT1-MMP at the cell surface. Furthermore, co-immunoprecipitation assays revealed that MT1-MMP interacts with multiple CD44 isoforms, including CD44s, CD44v3-10, and to a lesser degree CD44v6-10 and CD44v8-10, suggesting potentially significant functional implications.

Keywords: *Squamous Cell Carcinoma (SCC), invadopodia, podoplanin/CD44/MT1-MMP*

Regulation of the Hair Follicle Growth Cycle Through the Photoproduction of Activating Levels of ROS

M. Duprado[1]*, L.V. Sauvaire[1]*, S. Fernández-Martos[1,3], A. Lobo-Aldezabal[1], M. Escobar[1], M.I. Calvo-Sánchez[1,3], J. Espada[2,3]****

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Foundation for Biomedical Research of the Gregorio Marañón Hospital (FIBHGM), Madrid

[3]Skin Target BD, Madrid.

*Co-authorship. **Correspondence: maria.calvo@ufv.es

Abstract

Reactive oxygen species (ROS) are unstable molecules due to the presence of unpaired electrons. They are produced incidentally in mitochondria during oxidative phosphorylation in aerobic metabolism or deliberately by certain enzymes with physiological functions. Elevated levels of ROS, which exceed the antioxidant capacity of ROS-detoxifying enzymes, promote the development of human diseases, such as cancer, and neurodegenerative, psychiatric, and cardiovascular disorders. However, low levels of ROS play a signaling role with activating functions.

Laboratory results demonstrate that the controlled production of low ROS levels through photodynamic treatment using PPIX as a photosensitizer and 635 nm light stimulates cellular proliferation in in vitro cultures, promotes burn and wound regeneration, and enhances hair follicle (HF) growth both *in vivo*, in mouse skin, and *in vitro*, in hair follicles derived from hair transplant procedures.

Based on these findings, we hypothesize that direct photoproduction of ROS, in the absence of the photosensitizer PPIX, could generate physiological levels of ROS capable of inducing the anagen (growth) phase in hair follicles *in vivo* in C57Bl6 mice in the telogen (resting) phase. The results obtained suggest that photoproduction of physiological ROS levels induces hair follicle entry into the anagen phase, accompanied by an increase in skin thickness. Additionally, ROS photoproduction increases the expression of the proliferation marker PCNA in the hair bulb of anagen-phase HFs without causing nuclear damage, as indicated by the absence of an increase in the expression of the damage marker H2AX.

Keywords: *Reactive oxygen species; hair follicles; proliferation*

Pseudomonas aeruginosa: implication of the expression of beta-lactamases in the mechanism of antibiotic resistance

Iris Rioseras Tardón[1], Blanca Gómez Barahona[1], Estela Pérez-Lago[1], Olga Zafra *[1], Cruz Santos-Tejedor *[2]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: olga.zafra@ufv.es, c.santos@ufv.es

Abstract

Pseudomonas aeruginosa is an opportunistic Gram-negative rod-shaped pathogen known for its virulence, intrinsic resistance to multiple antibiotics, and high capacity to acquire resistance genes. The World Health Organization (WHO) has prioritized the development of effective treatments against these multi-resistant strains. In this study, we analyzed 20 carbapenem-resistant clinical strains of *P. aeruginosa* isolated at the San Carlos Clinical Hospital. These strains exhibited resistance to ceftazidime/avibactam (CAZ/AVI) and aztreonam (ATM) individually but were susceptible when both drugs were used in combination. To investigate this resistance phenotype, we hypothesized that constitutive derepression of the chromosomal beta-lactamase AmpC, regulated by the repressor AmpR, could be responsible. AmpR binds to the promoter region of *ampC* and inhibits its transcription under normal conditions. To test this, RNA was extracted from clinical isolates of the 20 strains and gene expression was quantified using specific oligonucleotides by qPCR. Our results demonstrated no overexpression of *ampC* or its repressor *ampR*, refuting the initial hypothesis that the observed resistance phenotype was due to increased AmpC expression. To further understand the resistance mechanisms, we propose sequencing the *ampC* and *ampR* genes to identify potential mutations affecting their function. Additionally, we expanded the study to analyze the expression of other beta-lactamases, including NDM, KPC, and TEM-1. Interestingly, while many strains had positive amplification, discrepancies between the expected and observed amplification product sizes suggest possible chromosomal rearrangements. These findings underscore the complexity of resistance mechanisms in *P. aeruginosa* and highlight the need for further genetic and molecular analyses to uncover the underlying factors contributing to multidrug resistance.

Keywords: *Pseudomonas aeruginosa; beta-lactamases; antibiotic resistance*

Investigating the immunomodulatory properties of probiotics through their sugar metabolism and epigenetics

Lucía Hontanilla[1], Selvin Solís[2] and Jorge Gutiérrez-Merino[2]*

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2] Biosciences School (University of Surrey)

* Correspondence: j.gutierrez@surrey.ac.uk

Abstract

The human gut microbiota is a dense and diverse microbial community colonizing the gastrointestinal tract from birth, maintaining stability throughout life. Dysbiosis, an imbalance in this ecosystem, is linked to inflammatory gut disorders. Type-I interferon (IFN-I) cytokines, produced in response to microbial infections and autoimmune diseases, are being explored alongside probiotic commensal bacteria as a complementary strategy to mitigate gut inflammation thanks to its immunomodulatory properties. This study focuses on a high interferon-inducing strain of Lactiplantibacillus plantarum (LP), identified with an over-activated galactose pathway through transcriptional analysis. The main objective was to understand the immunomodulatory properties of LP and their association with monosaccharide metabolism and epigenetics. We hypothesize that galactose metabolism enhances cell wall surface proteins, modulating immune interactions and inducing a stronger IFN-I response. LP cultured with different monosaccharides exhibited varying self-aggregation, with galactose showing the highest levels. Flow cytometry revealed that this enhanced aggregation increased bacterial uptake by macrophages, inducing higher IFN-I levels. Surprisingly, macrophages transfected with genomic DNA from fructose-grown LP elicited the highest IFN-I response. Epigenetic analysis of LP genomic DNA revealed distinct methylation patterns dependent on the sugar metabolized. DNA with fewer methylation sites had a greater impact on intracellular DNA-sensing pathways, enhancing IFN-I production. These results suggest that both self-aggregation and DNA methylation, influenced by sugar metabolism, are critical determinants of LP's immunomodulatory properties. These findings highlight the potential of LP to modulate immune responses through sugar metabolism, self-aggregation, and DNA methylation. Understanding these mechanisms enables the development of targeted probiotic formulations with precise immunomodulatory effects, offering a therapeutic approach for inflammatory gut disorders.

***Keywords**: gut microbiota, IFN-I response, sugar metabolism*

ASR92: Low-cost, sustainable analog incubator

Carlos López Valverde[1], Noelia Redondo Bort[1] and Álvaro Sanz Rozas[1]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: asr.covers@gmail.com

Abstract

An incubator is an essential medical device in the care of newborns, especially premature babies or those with health problems who require specialized attention. These devices allow the temperature to be regulated within a specific range, usually around 37ºC, providing a safe and controlled environment for the newborn.
This poster presents the development of a low-cost, sustainable analog incubator, designed for developing countries with limited access to high-priced incubators. The aim of our project is to create an incubator that is easy to assemble and replicate, while maintaining a low production cost.
For its development, the electronic circuit was first designed in LTSpice software. Common electronic components (resistors, operational amplifiers, diodes, and transistors) and a temperature sensor were used for assembly. Finally, the physical assembly of the circuit was carried out on prototyping boards.
The results obtained show an incubator that meets the basic requirements of functionality, accessibility, and sustainability, with an estimated cost of 100 euros. Therefore, this project proposes this incubator as an efficient alternative for neonatal care in areas with limited resources, offering advantages such as low energy consumption and easy repair. Additionally, this initiative is aligned with some of the Sustainable Development Goals of the 2030 Agenda of the European Union. Furthermore, future improvements such as the incorporation of a scale, as well as other medical devices to measure vital signs of the newborn or better control of other parameters, such as oxygen, carbon dioxide, and humidity, are suggested.

Keywords: *incubator, low-cost, sustainable, newborn, LTSpice*

Effects of grape must polyphenols on medulloblastoma cell lines

Galián-Guevara, E.[1], Soto-Sainz, A.[1], Santos Tejedor, C.[2], Tejera, AM.[1]

[1]Biology of Ageing Lab, Institute of Life Sciences, Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Microbial Biotechnology Lab, Institute of Life Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: agueda.tejera@ufv.es

Abstract

Medulloblastoma (MB) is the most common brain cancer and one of the leading causes of cancer-related death in children. Current therapies usually produce adverse effects, including an increased risk of the appearance of new tumors. For this reason, advanced precision therapy is urgently needed. Meanwhile, it is necessary to explore all options aimed at alleviating the harmful effects of cancer treatments, for example, with dietary supplements of proven efficacy. Polyphenols are a group of molecules characterized by the presence of several phenolic rings, which have been found in numerous foods such as grapes. Recent studies have shown that most polyphenols can slow down the proliferation of various cancers. The main goal of this study is to study the potential of polyphenols as natural agents to be used as adjuvants in the treatment of pediatric tumors, such as MB. Based on previous results, we will continue our research with the aim of analyzing the effect of polyphenols on the proliferation and apoptosis of MB cells. We have focused on quercetin and catechin, which are the main polyphenols of the Airén variety of grapes, widely used in the production of must for baby food. We have analyzed the effects of these polyphenols on proliferation and apoptosis on two MB cell lines (Daoy, from the SHH MB group; and D283, from the more aggressive MB group 3). Our preliminary results suggest that catechin induces proliferation on both cell lines and that the reduction in the cell number observed in MB cells treated with resveratrol was possibly due to apoptosis. Quercetin seemed to promote proliferation first in D283, but finally it induced apoptosis, coinciding with the preliminary results obtained in the less aggressive MB cell line Daoy. The effects of quercetin on D283 could be somewhat controversial. Initially, it appears to induce proliferation, but we have also found evidence of apoptosis, like the previous results obtained in the less aggressive MB cell line Daoy. The pathways for apoptosis induction have yet to be determined. Together, these findings indicate that it is worthwhile to continue investigating to assess whether these compounds could serve as adjuvants for MB treatment.

***Keywords**: Medulloblastoma, Polyphenols, Apoptosis*

Validation of an ATP Probe as a Biomarker for Intranuclear Activity and Chromatin Dynamics

Celia M. Lirola[1], Judith Ortega[2], Macarena Calero[2], Francisco Monroy[2], Diego Herráez-Aguilar[1,*]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Departamento de Química Física, Facultad de Ciencias Químicas, Av. Complutense s/n, 28240 Madrid.

*Correspondence: diego.herraez@ufv.es

Abstract

Cell dissemination and extravasation in lymphomas are associated with alterations in the mechanical and dynamic properties of nuclear structures, driven by increased metabolic activity within the nucleus. This study aims to develop a method employing intranuclear activity as a biomarker for the diagnosis and treatment of leukemia through its correlation with chromatin dynamics. Using an experimental ATP probe and chromatin staining (Hoechst), ATP signals were analysed in HeLa cells, revealing differences between nuclear and extracellular regions. However, the limited nuclear penetration of the probe hindered intranuclear detection, highlighting the need to optimize the protocol for enhanced accuracy.

To establish a correlation between intranuclear activity and chromatin mobility, several computational methods were applied, including Particle Image Velocimetry (PIV) to assess velocity fields, particle tracking (PT) to trace the dynamics of specific points, and optical flow analysis to represent apparent chromatin movement across sequential images. Preliminary results indicated a modest correlation between ATP concentration and chromatin mobility, though the relationship remains inconclusive due to the low ATP signal within the nucleus.

Future optimization of the probe is expected to improve nuclear penetration and provide a stronger signal, enhancing its potential utility as an intranuclear biomarker for lymphoma detection and analysis. This approach could not only refine diagnostic precision but also offer critical insights into nuclear rheology and its role in leukemia progression.

Keywords: *chromatin dynamics; computational microscopy; microrheology*

Stimulation of cell proliferation through direct photoproduction of reactive oxygen species (ROS)

L.V. Sauvaire-Muñoz[1]*, M. Duprado[1]*, S. Fernández-Martos[1,3], A. Lobo-Aldezabal[1],
M. Escobar[1], M.I. Calvo-Sánchez[1,3], J. Espada[2,3]****

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2] Foundation for Biomedical Research of the Gregorio Marañón Hospital, Madrid

3 Skin Target BD, Madrid.

* Co-authorship. ** Co-corresponding author

Correspondence: maria.calvo@ufv.es

Abstract

Reactive oxygen species (ROS) are reactive metabolic intermediates generated in the mitochondria during aerobic metabolism. Due to their high reactivity, the body relies on enzymes such as superoxide dismutase, catalase, and glutathione peroxidase for their elimination. However, when these systems are overwhelmed, oxidative stress can damage lipids, proteins, and DNA, leading to the development of chronic and degenerative diseases. Recently, it has been discovered that ROS also act as signaling molecules, regulating processes such as cell proliferation and differentiation, tissue repair, and cell survival. In previous laboratory results, it has been shown that controlled ROS activation through photodynamic treatment, using Protoporphyrin IX (PPIX) as a photosensitizer and light at a wavelength of 635 nm, promotes cell proliferation both *in vivo* and *in vitro*, accelerating wound healing and promoting the entry of hair follicles into the anagen phase. Our hypothesis focuses on studying whether, through the direct photoproduction of ROS, in the absence of the PPIX photosensitizer, physiological levels of ROS could be generated. In this context, our objective is to analyze whether these ROS are sufficient to activate cell proliferation programs *in vitro*, while ruling out the generation of nuclear damage. The results obtained suggest that the irradiation of NIH 3T3 fibroblast cultures with red light induces the production of ROS, detected through the fluorescence of the DHF-DA and NucPe1 probes. At the evaluated time points, the photoproduction of ROS in the presence of these compounds increased the expression of the cell proliferation marker KI67 in NIH 3T3 mouse fibroblasts, without showing cellular damage. Furthermore, it was recorded that the generation of ROS-activating levels, through irradiation for 5 minutes, promotes cell proliferation 72 hours after irradiation, suggesting a potential bio-stimulatory effect under these conditions.

Keywords: *Reactive oxygen species; Photodynamic Treatment; Cell proliferation*

Effect of High-Intensity Interval Exercise-Conditioned Human Serum on Breast Cancer Cells

Mayalen Valero-Bretón[1], Pablo Ledesma-Roncero[2], María Rodríguez-Mirón[1] Daniel García-Martínez[2], Miguel Ángel López-Moreno[1], Jorge Gutierrez-Hellín[1], Maite Iglesias-Badiola[2], Nuria Mendoza-Laiz[1], Cruz Santos-Tejedor[2], Hermann Zbinden-Foncea[1,*]

[1]Facultad de Ciencias de la Salud, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: herman.zbinden@ufv.es

Abstract

Physical exercise, particularly high-intensity interval exercise (HIIE), has demonstrated benefits in the prevention and treatment of several chronic diseases, including breast cancer. These positive effects are partly attributed to myokines, proteins released during muscle contraction, which facilitate inter-organ communication and regulate essential biological processes. Previous studies suggest that exercise training can improve the tumor microenvironment by enhancing immune function, reducing inflammation, and modulating hormonal factors. In breast cancer research, exposure of cancer cells to exercise-conditioned human serum has been associated with reduced viability and proliferation. However, the precise molecular mechanisms underlying these benefits remain unclear, highlighting the need to investigate the effects of exposure to HIIE-conditioned serum. This study investigates the mechanisms by which MCF-7 and MDA-MB-231 breast cancer cell lines respond to human serum collected before and after HIIE. The cells were incubated with the conditioned serum for 48 and 72 hours, after which the respective analyses were conducted. Methods included MTT viability assay at 48 and 72 hours and Western-Blot analysis at 48 hours focusing on the Akt/mTOR signaling pathway. Main findings indicate reduced viability in MCF-7 cells at 72 hours, with MDA-MB-231 cells appearing to exhibit a similar trend. Additionally, changes in phosphorylated 4EBP1 were observed in MDA-MB-231 cells, showing a decrease with post-exercise serum, while pro-caspase 9 levels increased in MCF-7 cells. Differential responses between cell lines highlight the importance of studying multiple breast cancer types in exercise-related research.

Keywords: *Exercise-conditioned human serum; Breast Cancer cells; Cell viability; Akt/mTOR signaling pathway*

Unraveling biomechanical control mechanisms in the cell nucleus through thermodynamic mapping

Lucía Benito-Barca [1], Macarena Calero [2], Ramiro Perezzan[1], Sandra Montalvo-Quirós[1], Francisco Monroy [2*] and Diego Herráez-Aguilar [1*]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2] Department of Physical Chemistry, Universidad Complutense de Madrid, Spain.

* Correspondence: diego.herraez@ufv.es

Abstract

Recent discoveries suggest that the biomechanical properties of the cell nucleus are significantly influenced by its biological activity. This is because they act as modulators of matter and energy transport phenomena. Numerous studies have demonstrated a direct relationship between viscoelastic properties and metabolic state or physiological disorders. Additionally, the formation of small domains with highly correlated dynamics, controlled by local stiffness and nuclear activity, has been observed. Can these domains be interconnected through elastic elements that link them?

To explore intranuclear dynamics, a series of computational microscopy techniques capable of performing single-cell in vivo thermodynamic mapping of cell nuclei have been developed. HUVEC cells were used as a biological model and observed with high-resolution spatiotemporal microscopes. The captured biological signals were analyzed in terms of statistical mechanics and Graph Theory, constructing graphs based on the dynamics of local chromatin domains obtained from particle tracking trajectories.

Two distinct biological scenarios were tested: live cells in complete cell culture environments and cells fixed with paraformaldehyde, serving as a negative control for cellular activity.

The efficiency of the hypothetical chromatin network was evaluated through betweenness centrality in the graphs. These measures were then correlated with mechanical characteristics such as local stiffness, diffusion coefficient, viscosity, and activity indicators such as spectral entropy or physical entropy production.

When comparing live and fixed cells, we observed a greater number of nodes with significant betweenness centrality in live cells. This implies that chromatin domains are more interconnected in live cells. This interconnection is facilitated by lower levels of stiffness and viscosity in live cells, allowing both biological activity and information transmission.

The development of a particle tracking methodology allows for the biomechanical phenotyping of cell nuclei, which, along with various simulations, can explain the transmission of mechanical information between the different chromatin domains in the nucleus.

Keywords: *Particle tracking; Cell nucleus; Biomechanical phenotyping*

MECP2 Duplication Syndrome, a mouse model to understand the molecular mechanisms of this rare neurodevelopmental disorder.

Cristina Izquierdo-Luengo[1], Inmaculada Pereda-Pérez[2] María Ponce-Renilla[1], Rosa María Tolón[1], Marc Ten Blanco[1], Fernando Berrendero[1*]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Department of Psychobiology, Faculty of Psychology, Universidad Complutense de Madrid, Spain.

*Correspondence: fernando.berrendero@ufv.es

Abstract

Tau-MECP2 knock-in mice is a model that contributes to the understanding of an X-linked rare neurodevelopmental disorder in human characterized by muscular hypotonia, impaired fear extinction, epilepsy, and autistic behaviour among others. In this work, we have characterized the mouse line with neuron-restricted MeCP2 overexpression (Tau-MECP2). Our studies reveal that Tau-MECP2 mice shows phenotypic alterations similar to those described in humans with MECP2 Duplication Syndrome such as low weight, anxiety, hypotonia, audiogenic hypersensitivity, altered somatosensory filter and impaired emotional and non-emotional memories, among others. Interestingly, after several neurobiochemical studies in different brain areas (prefrontal cortex, amygdala, hippocampus and cerebellum) we found important alterations in the orexinergic system in Tau-MECP2 male mice, specifically, a raised tone was described. Therefore, we re-evaluate the behavioural phenotype of naive Tau-MECP2 mice after a sub-chronic treatment of SB334867, an orexin receptor antagonist, finding interesting reversals of some previously described alterations. These data suggest that the orexinergic system could be involved in the phenotype observed in Tau-MECP2 mice. This preliminary work represents the beginning of a new research line involving two closely linked systems that could be a therapeutic target in this disorder.

***Key words**: MECP2, Orexins, Behaviour*

Generation of Animal Models of Fragility Skin Diseases Epidermal

Andrea López Casanova[1,2,3,*], Rosa A. García Fernández[2]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[2]Anatomía Patológica, Facultad de Veterinaria, Universidad Complutense de Madrid.

[3]Oncología Molecular CIEMAT.

*Correspondence: 9204368@alumnos.ufv.es

Abstract

Skin diseases that cause epidermal fracture, such as the different types of pemphigus[1], greatly reduce the quality of life of patients, since these conditions are very painful and only palliative treatments exist for them. Acantholisis (disunion and detachment of keratinocytes) is a hallmark of pemphigus and is caused by functional defects in the desmosomes, and by detraction and reduction of keratin filaments, which ultimately leads to the formation of blisters. Until now, pemphigus were considered autoimmune diseases, since patients develop autoantibodies against desmosomal proteins: Desmoglein 3 (Dsg 3) and Dsg 1 in pemphigus vulgaris and foliaceus, respectively; as well as antibodies against hemidesmosomal proteins: BPAG1 and Collagen XVII in pemphigoid and paraneoplastic pemphigus. As a result of the secretion of these autoantibodies, defective cell-cell or cell-basement membrane junctions occur, leading to skin fractures[3] and blisters. However, there is currently evidence indicating that autoimmunity in these diseases is secondary to a genetic alteration, although the nature of this molecular change remains unknown. This makes it urgent to investigate which molecular mechanism(s) cause the development of pemphigus in order to achieve a curative treatment. To achieve this, we have generated in this work transgenic mice (K5-N-IKKα mice) that express the human IKKα protein in the nucleus of keratinocytes.
Nuclear IKKα[2] is known to play an essential role in epidermal differentiation, and the results reported here describe how overexpression of IKKα in the nucleus of keratinocytes inhibits the expression of Dsg 1, Dsg3 and keratin 5 (K5) in the skin of transgenic mice, causing epidermal fragility and blister formation. Therefore, the regulation of the expression of these proteins and keratin K5 by IKKα suggests that IKKα could be an effective therapeutic target for the treatment of pemphigus.

Keywords: *pemphigus 1; IKKα 2; skin fractures 3*

Piezoelectric Nanoparticles for Deep Brain Stimulation

Abollado C. [1], Manjón C.[1], Maroto C.-[1], Sierra A.-[1], Vallet G.[1*]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: ggv16180@gmail.com

Abstract

Deep brain stimulation (DBS) is a technique that involves delivering electrical impulses to stimulate specific regions of the brain through the surgical implantation of electrodes, aimed at treating certain neurodegenerative diseases. Given the inherent risks associated with such surgeries, alternative methods have been developed to achieve stimulation in a less invasive manner using nanoparticles. In this work, we introduce the theoretical framework and foundations of this technique, exemplified by one of the many ongoing studies conducted by various researchers. This study utilizes the piezoelectric properties of barium titanate nanoparticles (BTNPs) to assemble a nanoparticle capable of releasing nitric oxide (NO) into the bloodstream when exposed to high-frequency ultrasound-induced electric fields. These nanoparticles exploit the unique capacity of NO to act as a signaling molecule, facilitating temporary disruption of the blood-brain barrier (BBB). This enables targeted delivery of therapeutic agents or direct stimulation of neural tissues in a highly controlled manner. The effectiveness of the technique was evaluated through experiments on mice with induced models of neurodegenerative diseases such as Parkinson's disease. Across all measurements, clear neuronal stimulation was observed, evidenced by indicators such as Ca2+ influx or dopamine release in targeted brain regions. Further analysis demonstrated significant improvements in motor function recovery, correlating these findings with the activation of specific dopaminergic pathways. This and similar studies have concluded that this technique holds significant promise for non-invasively stimulating specific neurons, such as dopaminergic neurons, thereby aiding in the recovery of motor function lost due to diseases like Parkinson's, which affect a substantial number of individuals annually. Moreover, this approach underscores the potential of nanotechnology to revolutionize neurological treatments, offering safer and more efficient alternatives to conventional invasive procedures.

Keywords: *Deep Brain Stimulation; Nanoparticles; Neuronal Disorders Treatment*

Impact of Podoplanin on the Initiation and Progression of SCCs

Sara Temprano-Carazo[1], Alejandro Lozano[1], Santiago Garcés-Fernández[1], Rocío Jarcovsky[1], Lucía Montero-Montero[1], Esther Grueso[1], Ester Martín-Villar[1*]

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

* Correspondence email: ester.martin@ufv.es

Abstract

Squamous Cell Carcinoma (SCC) is a type of cancer that originates in stratified squamous epithelia, such as the skin, the oral cavity and upper respiratory tract. It has a high incidence and significant invasive potential. Our laboratory identified podoplanin (PDPN) as a transmembrane glycoprotein associated with the malignant progression of SCCs. However, the exact role of this glycoprotein in the multistep development of these tumors *in vivo* remains unclear due to the lack of animal models that allow the study of tumor development in adult animals, as podoplanin-deficient mice die at birth. Our laboratory has generated a haploinsufficient mouse model for podoplanin, where the absence of one copy of the Pdpn gene does not result in neonatal lethality. Using this model, our goal is to investigate the relevance of podoplanin in tumor initiation and progression in a chemical skin carcinogenesis model that mimics the multistep development of SCCs. Our results obtained show a significant difference in tumor initiation in the haploinsufficient podoplanin animal model with a reduction in the number and tumor size. However, it remains to be investigated whether podoplanin plays a role in the progression from benign (papillomas) to malignant tumors (SCCs). Nevertheless, our results highlight the potential of podoplanin as a therapeutic target for SCC treatment.

Keywords: *Podoplanin; SCCs; Carcinogenesis*

Molecular insights and functional study of a patient MDA5 variant

Sara Izpura-Luis[1,2,*], Sergio Rius-Rocabert[1], Óscar de la Calle-Martin[3] and Estanislao Nistal-Villan[1].

[1] Universidad San Pablo CEU, IMMA (Instituto de Medicina Molecular Aplicada).

[2]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

[3] Hospital de la Santa Creu i Sant Pau

*Correspondence: saraizpura@gmail.com

Abstract

Pandemic SARS-CoV-2 is a positive-sense single-stranded RNA virus, primarily detected by key pattern-recognition receptors including the MDA5 protein, which acts as sensor by recognizing double-stranded RNA (dsRNA) structures produced during SARS-CoV-2 replication. Upon detecting dsRNA, MDA5 triggers the production of type I interferons (IFNs), initiating a robust antiviral response. This mechanism is well-documented across several viral infections, including Encephalomyocarditis virus, rhinovirus, Coxsackie B virus, hepatitis C virus, West Nile virus, and Zika virus. The MDA5 protein is encoded by the IFIH1 (Interferon Induced with Helicase C Domain 1) gene. Loss-of-function mutations in IFIH1 have been reported in children, who present with severe, often life-threatening respiratory infections, indicative of primary immunodeficiency.
We report a case involving a patient who experienced a severe COVID-19 infection with the Delta variant in 2021, following a previous infection with the Alpha variant of mild effects, and also a COVID-19 vaccination process early in 2021. NGS and Sanger sequencing identified a heterozygous 20-base pair deletion in exon 4 and a single base-pair deletion in intron 4-5 of the IFIH1 gene, resulting in a frameshift and a truncated MDA5 protein. This mutation leads to the generation of three non-native amino acids at the C-terminal end (Glycine-Threonine-Alanine) not present in the wild-type protein. To characterize this variant, we performed transient expression in HEK293T cells, promoter assays and Western Blot. Overexpression of the mutant MDA5 protein via plasmid transfection revealed that the mutant fails to induce IFN-β and functions as a dominant-negative inhibitor of wild-type MDA5, promoting its degradation. This dominant-negative effect of the mutant MDA5 protein potentially underlies the patient's heightened susceptibility to severe COVID-19, providing a mechanistic insight into the observed phenotype.

Keywords: *MDA5/ifih1, SARS-CoV-2, dominant-negative*

Antimicrobial activity analysis of plant extracts from extremophile plants

Ana Martín Secades, Juan Toledano García, Iris Rioseras Sardón, Olga Zafra Amorós, Jose María Bueno Calderón, Marisa León Díaz, Ángela Sáez Somolinos, Cruz Santos-Tejedor[1], and Lourdes Rufo Nieto[2].

[1]Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain.

*Correspondence: c.santos@ufv.es, l.rufo.prof@ufv.es

Abstract

Multi-resistance to antibiotics in bacterial strains is one of the main health problems nowadays, therefore, the search for new antimicrobial compounds is a priority research topic. In this work, the ability of different plant extracts to inhibit the growth of three bacteria has been measured*: Escherichia coli, Staphylococcus aureus and Pseudomonas aeruginosa*. These extracts come from plants adapted to extreme environments, such as salt marshes or areas with high concentrations of metals like Río Tinto (Huelva, Spain) or Laguna del Taray (Toledo, Spain), which implies the production of characteristic secondary metabolites that might have special and different activities. The aim of this research is to find extracts with antibacterial ability, in order to later search for the secondary metabolites responsible for the activity.

The extracts were obtained by on-site recollection of the plants. The extraction method involved the Soxhlet, in which different molecules were obtained depending on the affinity to different solvents (chloromethane, hexane, acetone and methanol) and the rotatory evaporator, in order to evaporate the previously used solvent. After carrying out tests in LB agar and soft LB agar, similar to antibiograms, of the 64 extracts tested, disolved in 100% DMSO (proved as negative control in plates), 34 showed some type of activity, especially against *Pseudomonas aeruginosa*, highlighting species such as *Imperata cylindrica*, *Sarcocornia carinata, Suaeda* vera or *Suaeda braun-blanquetii.*

Considering the obtained results, quorum sensing, biofilm and fractionation tests of the different extracts with activity are proposed as future work, in order to further understand the inhibition mechanisms and the molecules involved.

Keywords*: Pseudomonas aeruginosa; extremophile plants; antibiogram.*

ISBN: 978-84-09-70173-5