SEBBM

LIBRO DE RESÚMENES / BOOK OF ABSTRACTS

46º Congreso de la Sociedad Española de Bioquímica y Biología Molecular

A Coruña

3 al 6 de septiembre 2024

CINBIO Universidade de Vigo

USC Universidade de Santiago de Compostela

Universidade da Coruña

CSIC Consejo Superior de Investigaciones Científicas

COMITÉ EJECUTIVO

Presidenta

María D. Mayán
CINBIO, UV, Vigo

Vicepresidenta

Diana Valverde Pérez
CINBIO, UV, Vigo

Vicepresidente

Manuel Becerra
UDC, CICA, A Coruña

Tesorera

Carmen Rivas Vázquez
CSIC/CiMUS, Santiago de Compostela

Secretaría Científica

Fernando Torres
INIBIC, A Coruña

Vocales

Isabel Varela Nieto
IIIBM, CSIC-UAM, IdiPaz, Madrid
(Presidenta SEBBM)

Irene Díaz Moreno
IIQ-cicCartuja, US-CSIC, Sevilla
Vicepresidenta SEBBM

Raúl Estevez Povedano
IDIBELL, UB, Barcelona
Vocal SEBBM Mentoría y Comunicación

Antonio Ferrer Montiel
IDiBE, UMH, Alicante
Presidente Electo SEBBM

Sara García Linares
UCM, Madrid
Vocal SEBBM Educación y Jóvenes

José Manuel García Pichel
CIBIR, Logroño
Tesorero SEBBM

María Monsalve Pérez
IIBM, CSIC-UAM, Madrid
Vocal SEBBM Empresas

Lluís Montoliu José
CNB-CSIC, Madrid
Secretario SEBBM

María del Mar Orzáez Calatayud
CIPF, UV, Valencia
Coordinadora de Grupos de la SEBBM

Guadalupe Sabio Buzo
CNIO, Madrid
Vocal SEBBM Congresos, Premios y Eventos

Inmaculada Yruela Guerrero
EEAD-CSIC, Zaragoza

COMITÉ CIENTÍFICO

María José Alonso
CiMUS/USC, Santiago de Compostela

Ángel Carracedo
DIS, CiMUS/USC, Santiago de Compostela

Isabel Fariñas Gómez
UV, Valencia

Diana Guallar
CiMUS/USC, Santiago de Compostela

Maite Huarte
Cima Universidad de Navarra, Pamplona

Mabel Loza
CiMUS/USC, Santiago de Compostela

Malu Martínez Chantar
CIC Biogune, Bizkaia

José Luis Mascareñas
USC, Santiago de Compostela

Ángela Nieto
CSIC-UMH, Alicante

Rubén Nogueiras
CiMUS/USC, Santiago de Compostela

José Rivas Rey
USC, Santiago de Compostela

Sara Sdelci
CRG, Barcelona

Arantxa Tabernero
InstiINCYL, Salamanca

COMITÉ LOCAL

Manuel Becerra
UDC, CICA, A Coruña

José Manuel Castro Tubío
CiMUS, Santiago de Compostela

Esperanza Cerdán
UDC, CICA, INIBIC, A Coruña

Manuel Collado
CNB, CSIC, CIMUS (USC), IDIS

Juan Fafián
INIBIC/UDC, A Coruña

Francisco Fernández Trillo
CICA, A Coruña

María de la Fuente
IDIS/CiMUS, Santiago de Compostela

Miguel Ángel García González
IDIS/FPGMX, Santiago de Compostela

Aurora Gómez Durán
CiMUS, Santiago de Compostela

Saida Ortolano
IISGS, Vigo

Margarita Poza Domínguez
INIBIC/UDC, A Coruña

Carmen Rivas Vázquez
CSIC/CiMUS, Santiago de Compostela

Rosana Simón Vázquez
CINBIO, Vigo

Carlos Spuch
IISGS, Vigo

Fernando Torres Andon
INIBIC, A Coruña

Anxo Vidal Figueroa
CiMUS/USC, Santiago de Compostela

Surface Display (YSD) to identify high-affinity HLA-peptide complexes, thereby facilitating the identification of novel neoantigens.

References:
(1) Torre, L. A. et al. CA. Cancer J. Clin. 68, 284–296 (2018) 10.3322/caac.21456

(2) Bobisse, S. et al. Nat. Commun. 9, 1092 (2018) 10.1038/s41467-018-03301-0

Keywords: Epithelial Ovarian Cancer (EOC), Tumor-Infiltrating Lymphocytes (TILs), Single-Cell Sequencing, T-Cell Receptor Sequencing

G03 - 190 - P

Serum Proteome Responses in Sea Bass (Dicentrarchus labrax) Following Immunization

NATALIA MALLO[1], SANTIAGO CABALEIRO[2], BELÉN BUDIÑO[2], PABLO RIERA[2], ANTÓN VILA SANJURJO[1]

[1] *Universidade da Coruña, A Coruña, La Coruña, España*

[2] *CETGA, Ribeira, La Coruña, España*

Finding correlates of protection after fish vaccination is highly dependent on factors such as genetics, immunological history, type of vaccine...

As immunization is the main preventive strategy used in aquaculture, defining the traits that provide protection could be a stepping stone towards the rational design of vaccines, as well as the monitoring of fish immune status, which would lead onto the improvement of vaccine efficiency.

In the present study, the serum protein response after immunization with a Photobacterium damselae subsp. piscicida vaccine was analyzed in individually marked sea bass. Fish were finally challenged against the pathogen. Fish sera of immunized and control groups were classified depending on fish survival. Groups were compared by qualitative and semi-quantitative (label- free liquid chromatography mass spectrometry) proteomic analysis.

A great variation in serum proteins was observed. This correlates with heterogenity of fish populations.

Protein groups specific of fish survival in immunized fish were identified. Besides, protein groups present on survivor fish, regardless of being vaccinated, were also identified as traits of fitness. These proteins clustered into groups showing different responses to vaccination, with identification of protein groups belonging to classical immune system, acute phase molecules, other proteins, (many related to immune system) and some uncharacterized proteins (which shows the status of the lack of information contained in fish protein databases).

Overall, this study provides new knowledge of fish serum proteome improving our underestanding of sea bass immunization and providing prospective paths of study for correlates of protection identification, as well as for vaccine development.

Keywords: Proteomics, Serum, Seabass, Photobacterium, Vaccine

G03 - 225 - P

Identification of immunogenic proteins in the pathogen Aeromonas salmonicida for inclusion in a subunit vaccine.

MANUEL GONZÁLEZ-VEIGA[1], NATALIA MALLO-SEIJAS[1], ANTÓN VILA-SANJURJO[1], SANTIAGO CABALEIRO[2], ANA RIAZA[3], ÓSCAR GONZÁLEZ[3]

[1] *Universidad de A Coruña, A Coruña, La Coruña, España*

[2] *Centro Tecnológico del Cluster de Acuicultura (CETGA), Ribeira, La Coruña, España*

[3] *Stolt Sea Farm, Santiago De Compostela, La Coruña, España*

Furunculosis is one of most common fish diseases on aquaculture, and it is caused by Gram-Negative bacterium *Aeromonas salmonicida*. *A. salmonicida* causes septicemia and wounds in the musculature, called furuncles, increasing the probability of colonization by opportunistic pathogens, worsening the infection. Although furunculosis affects different fish species, in this study we focused on its occurrence in turbot, since currently, the number of proteins studied related to the adhesion of *A. salmonicida* to this host is scarce. Expanding the number of known proteins found within the infectious pathway of this bacterium would help to develope a subunit vaccine, which roughly speaking, is a vaccine designed from virus or bacterial components, usually proteins. In this study, a search for outer membrane proteins of A. salmonicida was carried out for subsequent incorporation into a subunit vaccine effective against different isolates of this pathogen in turbot. For this purpose, we approached a strategy based on bioinformatics, a second based on proteomic analysis, and finally, a third based on a literature search, including in our list of antigens several *A. salmonicida* proteins whose expression on the outer surface of the bacterium is well established. Thus, by combining these three strategies, we tried to maximize the accuracy in the search for these membrane antigens.

Keywords: Shaving, Inmunoinformatics, Vaccines, Aeromonas, Turbot

G03 - 249 - P

Evaluation of DNA-metabarcoding as a new approach for honey's botanical authentication

MÓNICA HONRADO[1,2,3], ANDREIA QUARESMA[1,2], JOANA SANTOS[1,2], M. ALICE PINTO[1,2], JOANA S. AMARAL[1,2]

[1] *Centro de Investigação de Montanha, Instituto Politécnico, Bragança, Portugal*

[2] *SusTEC, Instituto Politécnico de Bragança, Bragança, Portugal*

[3] *LAQV-REQUIMTE & Department of Chemistry, University of Aveiro, Aveiro, Portugal*

Honey is one of the foods most prone to be adulterated, with botanical origin mislabelling being one of the most frequent frauds. Honey's botanical origin is traditionally determined by microscopic analysis of pollen grains, a laborious method requiring expertise and often providing only family-level identification. Pollen identification by DNA-metabarcoding would allow for a faster, simpler, and more accurate determination. However, the reliability of using the number of sequences reads to estimate pollen percentages in honey remains unclear.

To address this issue, the number of pollen grains per mg in 13 pollen samples was determined using a Neubauer chamber. Then, four pollen mock mixtures were created, two containing 5 species and two 13 species. In each case, one of the mock mixtures was prepared with an equal mass of each pollen species (corresponding to varying amounts of grains), and the other was prepared using a similar percentage of each pollen species. Each mock mixture was also added to agave syrup (naturally pollen-free) to simulate the honey matrix. The pollen and agave mock mixtures were subjected to DNA extraction, PCR and ITS2-metabarcoding, and parallelly to pollen microscopic analysis.

DNA-metabarcoding results aligned well between the pollen mixtures and the agave syrup mixtures. In both cases, a few species were overrepresented and others underrepresented but, in general, the quantitative profile was according to the expected. In contrast, microscopy results closely matched the expected composition of the pollen mock mixtures, but significant discrepancies were observed in the agave samples.

Acknowledgment: to project "Mel I.D" financed by PNASA 2023-2027, PRIMA project "MEDIBEES" and FCT PhD scholarships (2021.08119.BD, 2020.05155.BD)

Keywords: DNA-Metabarcoding, Honey, Authentication

G03 - 250 - P

Comparison of different sequencing approaches to uncover botanical adulteration in herbal products

JOANA SANTOS[1,2], MÓNICA HONRADO[1,2,3], ANDREIA QUARESMA[1,2,4], JOSÉ RUFINO[4], M. ALICE PINTO[1,2], JOANA S. AMARAL[1,2]

[1] *Centro de Investigação de Montanha, Instituto Politécnico de Bragança, Bragança, Portugal*

[2] *SusTEC, Instituto Politécnico de Bragança, Bragança, Portugal*

[3] *LAQV-REQUIMTE & Department of Chemistry, University of Aveiro, Aveiro, Portugal*

[4] *CeDRI, Instituto Politécnico de Bragança, Bragança, Portugal*

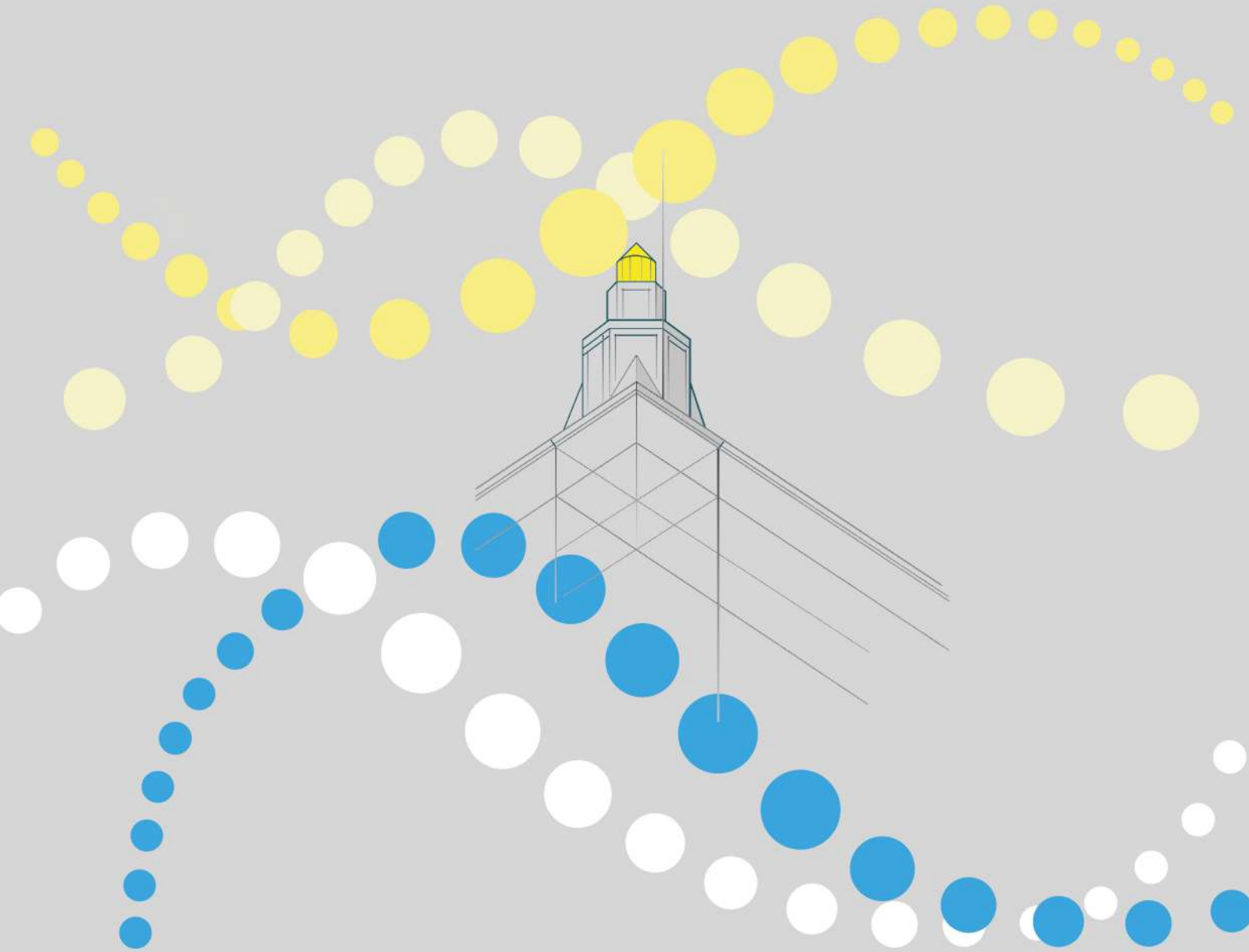
Due to the increasing demand for popular medicinal plants, herbal products are prone to botanical adulteration. Aiming for fraud detection, DNA-barcoding emerges as one of the most suitable approaches for species identification in medicinal plants.

In this study, 58 commercial herbal products labelled with plant species traditionally used for cognitive, mood, or sleep improvement were submitted to DNA extraction and PCR targeting three barcodes. MatK and rbcLa amplicons were sequenced by Sanger, while ITS2 amplicons were sequenced by NGS for plant species identification. The Sanger sequences were identified by BLAST using a custom script. The NGS sequences were identified using a bioinformatic pipeline that included three ITS2 custom databases: one containing sequences of plants traditionally used for improving brain health, one containing medicinal plant sequences, and the third was a curated global database containing 307,977 sequences representing 111,382 species of vascular plants. NGS results were analysed by a script that sequentially went through these databases to ensure that a maximum number of sequences were identified as accurately as possible. Of the evaluated samples, MatK was able to correctly identify 62% labelled samples, rbcLa 76%, and ITS2 68%, with only 28% of the samples being correctly identified by the three barcodes simultaneously. NGS revealed that 29% of samples with a correct identification by Sanger sequencing were in fact mixtures of species, with the labelled one being the most representative. Overall, only 34% of samples conformed to the label, while 56% were mixtures containing the labelled species.

Acknowledgments: FCT project POIROT (PTDC/SAU-PUB/3803/2021) and PhD scholarships (2021.08119.BD, 2020.05155.BD)

Keywords: DNA Barcoding, Botanical Adulteration

INDICE



SE BBM

CINBIO
Universidade Vigo

USC
UNIVERSIDADE DE SANTIAGO DE COMPOSTELA

UNIVERSIDADE DA CORUÑA

CSIC
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTÍFICAS