Under the auspices of the University of Sfax
ADRÏC association organizes

ONE HEALTH CONCEPT

INTERNATIONAL CONFERENCE

FOR PLANT, ANIMAL & HUMAN SAFETY AND ENVIRONMENT IMPROVEMENT

Université de Sfax
TUNISIE

ADRÏC
Association du Développement de la Recherche, de l'Innovation et de l'Insertion des Compétences
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PRIMA
PARTNERSHIP FOR RESEARCH AND INNOVATION IN THE MEDITERRANEAN AREA

May 8th, 9th and 10th, 2025

Les Oliviers Palace hotel,
Sfax, Tunisia

ADRIC

ADRIC tunisie

كلية الطب بصفاقس
Faculté de Médecine de Sfax
معهد باستور تونس
Institut Pasteur de Tunis
CBS CENTRE DE BIOTECHNOLOGIE DE SFAX
Centre de Recherche en Numérique de Sfax
Médis Au service de la santé
الناعورة LE MOULIN
SOTEME
UGFS North Africa
Pharmaghreb
MEDIBIO
Ribosite Biotechnology

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TUNISIE
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Les Oliviers Palace Hotel, SFAX

8th to 10th May, 2025

Thursday, May 8th

14:00 - 14:30 | Registration

14:30 - 14:40 | Opening Ceremony : Welcoming Address

Pr Ahmed Hadj Kacem, President of Sfax University
Pr Hammadi Ayadi, President of ADRÏC

14:40 - 16:10 | Round Table : What Governance for the One Health Ecosystem : Challenges and Perspectives

Moderator : *Mr Mondher Khanfir*

Panellists :

- *WOAH :* ***Dr Nadia Brik*** - One Health Programme Officer
- *WHO :* ***Dr Kaouther Oukaili*** - Responsible One Health
- *M. Health :* ***Dr Kaouther Harabech*** - One Health and IHR focal point
- *M.Environment :* ***Dr Taoufik Gargouri*** - ANPE Sfax
- *Private Sector :* ***Dr Razi Miliani*** - Vice-president of the TPDU

16:10 - 17:50 | Session 1 : European Projects in One Health

Moderators : *Pr Leila Ammar Keskes & Dr Kaouther Harabech*

16:10 - 16:35 | ***Pr Ahmed Hannachi (ENIG, Gabes)***
Innovative solutions for Mediterranean Ecosystem Remediation via Monitoring and decontamination from Chemical Pollution (iMERAID)

16:35 - 17:00 | ***Dr Youmna Mghirbi (PI,Tunis)***
Focus on Medilabsecure and Unihealth European projects

17:00 - 17:25 | ***Dr Chantal Ebel (ISBS, Sfax)***
Strenghening capacities and promoting innovation in inplantomics at the University of Sfax (INPLANTOMICS)

17:25 - 17:50 | ***Pr Slim Tounsi (CBS, Sfax)***
From next generation sequencing microorganisms towards ecofriendly biotech-based products (NGS-4-ECOPROD)

17:50 - 18:30 | Coffee break & Networking

18:30 - 19:30 | Opening Conference :

Moderators : *Pr Hammadi Ayadi & Pr Samia Mnif Marrakchi*

Pr. Hechmi Louzir (PI, Tunisia) *: Santé Unique et Emergence. Approche «One Health» avec quelques exemples : Rage, Leishmanioses et COVID-19*

Friday, May 9th

09:00 - 12:30 | Session 2 : Crop Protection & One Health Concept

Moderators : *Pr Souad Rouis, Pr Radhia Gargouri & Pr Dhouha Ghribi*

09:00 - 09:20 | ***Pr Souad Rouis (CBS, Tunisia)*** : Project introduction : Alternative Biopesticides for SAFe Integrated Pest and WAter Management around Mediterranean SAFWA

09:20 - 09:45 | ***Pr Dietrich Stephan (JKI, Germany)*** *: Industrial bioprocess*

09:45 - 10:10 | ***Pr José.Miguel Compos (IRTA, Spain)****: Field assay, farmer education*

10:10 - 10:35 | ***Pr Michele Fontefrancesco (UM, Italy)****: Farmer's Cultural Practices*

10:35 - 11:05 | Coffee break & Poster session (Digital version)

11:05 - 12:30 | Oral Communications

- ***Oumèma Nouri-Ellouz***
Plant growth-promoting Bacteria as a strategy to promote potato growth in Tunisia
- ***Oumaima Bouazizi***
Towards sustainable agriculture: isolation and characterization of beneficial bacteria for crops and food
- ***Jaweher Sdiri Ghidawi***
Plant growth promoting bacteria (Bacillus mojavensis14) helps in enhancing salt tolerance of somatic hybrid and commercial potatoes
- ***Emna Sellami***
An exopolysaccharide synthesized by the plant growth-promoting bacterium Erwinia sp. STN24: Its role in enhancing potato plant tolerance to abiotic stress
- ***Fatma Driss***
Structure elucidation, biological and molecular docking studies of a new bacillus thuringiensis protoxin active against Lepidopteran pests
- ***Ines Chouaibi***
Effects of nitrous acid mutagenesis on the genomic diversity and adaptation of Bacillus thuringiensis: Towards innovative biopesticides
- ***Hichem Kacem***
Crowding effect on the cestode Gerbillitaenia psammomi (Mikhail & Fahmy, 1968) parasitizing the gerbilline rodent Psammomys obesus Cretzschmar, 1828 in Tunisia
- ***Oumaima Ardhaoui***
Novel bacterial biocontrolagents for sustainable agriculture: High efficacy of Tunisian isolates against prickly pear pest and camel ticks
- ***Ichrak Ben Amor***
Evaluation of cytotoxicity and anti-HSV-1 activity of Olea European leaf extracts
- ***Maroua Gdoura Ben Amor***
Efficacy of Phage Application as an Alternative Biocontrol Strategy for Pathogenic and Spoilage B. cereus group in the Food Industry

12:30 - 14:00 | Lunch

14:00 - 17:30 | Session 3 : Health Care & One Health Concept

Moderators : *Pr Hechmi Louzir & Dr Idriss Ben Neila*

14:00 - 14:45 | ***Pr Ahmed Rejeb (ENMV, Tunisia)***
Le Concept « One Health »

14:45 - 15:30 | ***Pr Noël Tordo (Institut Pasteur de Guinée, Fance/Guinée)***
Rabies : a successful example of the "One Heath" concept and of a continuum between fundamental research and field application"

15:30 - 16:30 | Oral Communications

- **Makram Essafi**
WHO mRNA Tech Transfer Programme in Tunisia : Toward the construction of the first R&D unit for mRNA vaccines and therapeutics

- **Malek Trimèche**
Live attenuated vaccines for canine leishmanasis
- **Radhia Hamdi**
Interconnexion entre les changements de méthylation du gène redox p66shc et l'environnement alimentaire chez des malades rénaux chroniques
- **Fatma Arrari**
Anti-inflammatory and antioxidants Effects of Spirulina Against Lipid Micelles and LPS-Induced Intestinal Epithelium damage in Caco-2 Cells

- **Fatma Ben Mansour**
Effets protecteurs des exopolysaccharides de Halamphora sp. Contre la toxicité du nickel chez le rat
- **Nadia Trimeche**
Les cryptozonoses transmises par le chat domestique

16:30 - 17:30 | Poster Session

Saturday, May 10th

09:00 - 11:00 | Session 4 : IA & One Health Concept

Moderators : *Pr Ahmed Fakhfakh & Dr Wael Ouarda*

09:00 - 09:30 | ***Pr Hassen Drira (FSS/U.Strasbourg, France)***
Apprentissage profond géométrique pour la détection de la maladie d'Alzheimer caractéristiques de la marche

09:30 - 10:00 | ***Pr Imene Magdich (Université Jean-François Champollion Touolouse, France)***
Artificial Intelligence and One Health : Challenges and Solutions for a Global Integrated Health System

10:00 - 10:40 | Oral Communications

- ***Fathia Boubakri***
XAI-PulmoNet : An Explainable AI Framework for Multi-Class Lung Disease Classification

- ***Khouloud Guemri***
A real time Multimodel System for Elderly Human Activity Recognition : Case of Fall detection

- ***Emira Kechiche***

Sequence to Sequence (Seq2SeQ) Models for Breast Cancer image Deblurring Segmentation and Classification

- ***Raja Rezg***

Artificial Intelligence : A transformative tool for predicting Endocrine Disrupting Chemicals potential in the one health concept

10:40 - 11:30 | Coffee Break & Poster Session (Digital version)

11:30 - 13:30 | Session 5 : One Health Concept for environment

Moderators : *Pr Mohamed Chamkha & Pr Mohamed Trigui*

11:30 - 12:00 | *Pr Sonia Khoufi (CBS, Tunisia)*
Sustainable Waste Management : A Key Pillar of One Health Approach to Environmental Well-Being

12:00 - 12:30 | *Pr Asma Sakka (FSB, Tunisia)*
Microalgae : Potentiality and Risks for Environmental Health of Aquatic Ecosystems

12:30 - 13:30 | Oral Communications

- ***Nabil Belaid***

Assessment of radiological risk around the old site of the fertilizer and phosphoric acid plant of Sfax-Tunisia

- ***Yamina Romdhani***

Valorization of Boujaber mining waste through geopolymerization: sustainable management and rehabilitation of polluted sites

- ***Fatma Hadrich***

Olive mill waste water (OMW): potentiel of biomethane production and a source of high value added molecules to alleviate some metabolic diseases

- ***Jihen Elgazel***

Exploring Extremophiles for Green Innovation: Metagenomic Mining of Hypersaline Microbiomes for PHA Bioplastic Potential

- ***Hela Ghorbel***

Olive bioactive molecules protect from nonylphenol toxicity induced hepatic NAFLD and related metabolic disorders

- ***Wiem Elloumi***

Wound healing potential of Pistacia lentiscus distilled Leaf extract, quercetin-3-O-rhamnoside, and myricetin-3-O-rhamnoside in a Rat model

- ***A.Lamis Saidane***

L'approche «One Health» en Tunisie : Etat des lieux

13:30 | Closing Ceremony

SPECIAL THANKS TO THE SCIENTIFIC COMMITEE

Pr. Souad ROUIS
Pr. Hammadi AYADI
Pr. Dhafer AOUINI
Pr. Ahmed FAKHFAKH
Pr. Sonia KHOUFI
Pr. Leila KESKES
Pr. Radhouane GDOURA
Mr. Mondher KHANFIR

SPECIAL THANKS TO THE ORGANIZATION COMMITEE

Hammadi Ayadi - President of ADRÏC

Fatma Abdelhedi
Bochra Ben Rhouma
Rihab Derbel
Radhouane Gdoura
Mohamed Hadj Kacem
Rim Keskes
Nacim Louhichi
Nadia Marrakchi
Syrine Nebli

Souhir Bouaziz
Noura Bougacha
Nadia Daoud
Hela Gargouri
Mounira Hmani
Leila Keskes
Samira Majdoub
Myriam Ghorbel
Souad Rouis
Najeh Zekri

Round Table:

What Governance for One health Ecosystem: Challenges and Perspectives

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ROUND TABLE: WHAT GOVERNANCE FOR THE ONE HEALTH ECOSYSTEM: CHALLENGES AND PERSPECTIVES

Dr. Nadia Brik
One Health Programme Officer
WOAH

Dr. Kaouther Oukaili
Responsible One Health
WHO

Dr. Kaouther Harabech
One Health and IHR focal point
M. Health

Dr. Taoufik Gargouri
ANPE-Sfax
M.Environment

Dr. Razi Miliani
Vice-president of the TPDU
Private Sector

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8th to 10th May, 2025

Dr. Nadia Brik

WORLD ORGANISATION FOR ANIMAL HEALTH

n.brik@woah.org

Dr. Nadia Brik is a Tunisian veterinarian and expert in the "One Health" approach, which integrates animal, human, and environmental health. Since September 2, 2024, she has served as One Health Programme Officer at the World Organisation for Animal Health (WOAH) Sub-Regional Representation for North Africa, based in Tunis. A graduate of the National School of Veterinary Medicine in Sidi Thabet, she also holds a master's degree in animal genetics and reproduction. Dr. Brik previously held various positions at the Tunisian Ministry of Agriculture, working on animal health, epidemiology, veterinary public health, sustainable development, and animal production. She also contributed to capacity building through the Central Agency for Agricultural Training and Extension. Known for her commitment to public service, she emphasizes compassion, generosity, and collaboration in veterinary medicine. Her work continues to strengthen regional coordination in One Health initiatives, supporting disease prevention and health security across North Africa.

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Dr. Kaouther Harabech

ONE HEALTH AND IHR FOCAL POINT AT M. OF HEALTH

kaouther.harabech@rns.tn

Kaouther Harabech is a principal sanitary veterinarian in the Primary Health Care from 2013, in charge of zoonotic diseases within the epidemiologic and communicable diseases unit and from 2018 nominated as the IHR national focal point and responsible of border health control and One Health focal point for the ministry of health.

She leads the national IHR committee for building and strengthening IHR core capacities and the co-chair of the national zoonotic disease committee. She is a Field Epidemiology Training Programme (FETP) graduate and trained on RRT and EMT. She is a member of the Medilabsecure network. Kaouther participate in national COVID response especially in PoE. She has an MSc in Biostatistics, Epidemiology and Clinical trials.

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Dr. Razi Miliani

CEO OF COGEPHA

Mr. Miliani is the Chief Executive Officer of COGEPHA, the largest pharmaceutical distribution company in Tunisia. A trained pharmacist, he also holds an Executive MBA jointly awarded by IAE Sorbonne Business School and Paris-Dauphine University.

Actively involved in shaping the pharmaceutical sector, he serves as Vice President of both the Tunisian Syndicate of Pharmaceutical Distribution and the African Association of Pharmaceutical Distribution. In these roles, he closely monitors major technological trends that are transforming the supply chain, with a strong focus on innovations that streamline operations and improve logistical efficiency. He is also a strong advocate for generative artificial intelligence, frequently speaking at conferences and in the Tunisian media about its impact on businesses. His expertise has also led him to work as a consultant on innovation projects for the Tunisian government.

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Dr. Taoufik Gargouri

NATIONAL AGENCY FOR ENVIRONMENTAL PROTECTION (ANPE) - TUNISIA

Taoufik Gargouri is a Doctor-Engineer in Hydrology and currently serves as Regional Director for the South-East at the National Agency for Environmental Protection (ANPE) in Tunisia.

He is the former Director General of the International Center for Environmental Technologies of Tunis (CITET). Mr. Gargouri is also President of the Environment Commission at the Union of Arab Engineers, and Head of the Governance and Audit Office at the Order of Tunisian Engineers.

Session 1:

European Projects in One Health

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Dr. Leila Ammar Keskes

MODERATOR / FACULTY OF MEDICINE OF SFAX-UNIVERSITY OF SFAX

Dr. Kaouther Harabech

MODERATOR / ONE HEALTH AND IHR FOCAL POINT AT M. OF HEALTH

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Pr. Ahmed HANNACHI

NATIONAL ENGINEERING SCHOOL OF GABES UNIVERSITY OF GABES, TUNISIA

Ahmed Hannachi, was born October 17, 1962 in Feriana-Tunisia. He holds a chemical engineering degree from the National Engineering School of Gabes (ENIG)-Tunisia and a PhD in the same field from University of Ottawa-Canada. He is currently a full chemical engineering professor at the Chemical-Process Department and head of the Research laboratory on Process Engineering and Industrial Systems (GPSI) at ENIG, University of Gabes-Tunisia.

He has published over 250 research contributions in scientific journals and conference proceedings. The main research focus is on Desalination, Water treatment, and design of integrated processes for wise management of water and energy resources.

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Pr. Youmna MGHIRBI

LABORATORY OF MEDICAL ENTOMOLOGY, PASTEUR INSTITUTE OF TUNIS, TUNISIA.

Youmna Mghirbi is an associate professor and permanent scientist researcher at Pasteur Institute of Tunis, Tunisia. She has been working there since at least 2009, focusing her research on parasitology, immunobiology, and infectious diseases, particularly studying the human immune response to Leishmania infections and the development of vaccine candidates against leishmaniasis

She is involved in the Laboratory of Transmission Control and Immunobiology of Infection (LTCII) at the institute. Her work includes large-scale longitudinal studies on Leishmania major transmission and the immune correlates of protection against zoonotic cutaneous leishmaniasis

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Dr. Chantal Ebel

THE INSTITUTE OF BIOTECHNOLOGY OF SFAX, TUNISIA

Dr. Chantal Ebel received her PhD in Cell and Molecular Biology in 2000 from the University of Strasbourg, France and her HDR in 2017 in Biological Engineering from the National School of Engineering of Sfax, Tunisia. She has been working in internationally renowned research centers like ETH-Zurich where she did a post-doc on the comprehension of the control of the plant cell cycle.

Her main research interest aims at fighting against the deleterious effects of climate change on crop growth and productivity. She has been leading several collaborative projects with France, Spain, UK and she is part of the team coordinating the Horizon Europe Twinning project INPLANTOMICS. Dr. Ebel is a Team Leader in the Plant Functional Genomics and Physiology Research Unit (UGFP2) at ISBS where she is focusing on maintaining crop growth and productivity via engineering the plant cell cycle and hormonal signaling pathways.

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Prof. Slim TOUNSI

LABORATORY OF BIOPESTICIDES
CENTRE OF BIOTECHNOLOGY, SFAX-TUNISIA

slim.tounsi@cbs.rnrt.tn

Pr. Slim Tounsi is Professor of Biological Engineering and Director General of the Centre of Biotechnology of Sfax (CBS), Tunisia, since 2019. He previously headed the Biopesticides Laboratory (2009–2019) and currently serves as President of the CBS Scientific Council. He holds two PhDs: one in Biological Engineering and another in Biological Sciences and Biotechnology.

His research focuses on microbial and plant-based biopesticides for controlling fungal, bacterial, and insect pathogens. He has authored over 100 publications in international journals and holds 8 national patents. He has coordinated several national and international projects (H2020, Horizon Europe, ERANETMED). He received multiple awards, including the Presidential Prize for Best Lab in Tunisia (2018) and the PASRI Innovation Award (2014).

Opening Conference

Santé unique et Emergence. Approche “One Health” avec quelques exemples: Rage, Leishmanioses et COVID-19

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Pr. Hammadi Ayadi

MODERATOR / PRESIDENT OF ADRIC, PIONEER IN IMMUNOLOGY AND SENIOR ADVISOR

Pr. Samia Mnif Marrakchi

MODERATOR / GENERAL DIRECTOR OF PASTEUR INSTITUT OF TUNIS

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Prof. Hechmi LOUZIR

hechmi.louzir@gmail.com

Prof. Hechmi Louzir is Professor of Medicine & Immunology at the Faculty of Medicine of Tunis / Univ. Tunis El Manar, and served as DG of the Pasteur Institute of Tunis (IPT) from 2007 to 2023. A graduate of the Tunis Medical School, he trained at Institut Pasteur (Paris) and joined IPT in 1988. He led major research on host-pathogen interactions, authored 80+ publications, and supervised over 40 students, including 6 PhDs.

He coordinated 30+ internationally funded research projects and contributed significantly to immunology education. Prof. Louzir held leadership roles in the Institut Pasteur network, including as coordinator of the MATI region and Euro-Med region. He has served as expert for the EU and WHO-EMRO and is a member of The Lancet Commission on 21st-Century Threats.

During COVID-19, he played a central role in Tunisia’s pandemic response, leading both the scientific vaccination committee and the national campaign.

Session 2 :

Crop Protection & One Health Concept

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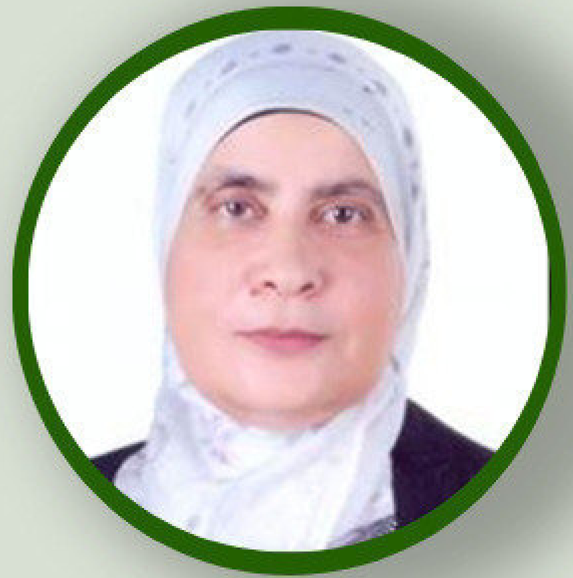
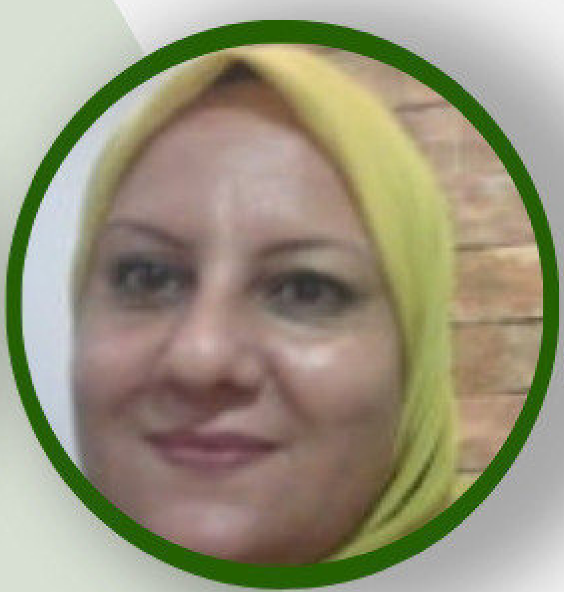


Prof. Souad ROUIS

MODERATOR / HEAD OF LABORATORY OF BIOPESTICIDES, CENTRE OF BIOTECHNOLOGY, SFAX

Pr. Radhia Gargouri

MODERATOR / NATIONAL ENGINEERING SCHOOL OF SFAX - UNIVERSITY OF SFAX



Pr. Dhouha Ghribi

MODERATOR / HIGHER INSTITUT OF BIOTECHNOLOGY OF SFAX, UNIVERSITY OF SFAX

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Prof. Souad ROUIS

LABORATORY OF BIOPESTICIDES
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Pr Souad Rouis works as a full professor in the Centre of Biotechnology of Sfax. She started working in this centre as engineer since 1991, obtained her PhD in 2001 and her habilitation in 2009. She is currently the head of the laboratory of Biopesticides and is specialized in innovation management and tech transfer.

Pr Souad Rouis is a team member of the startup IZAGRI (agriculture field) and was the cofounder of the startup BiotechRDP (human and animal diagnosis devices). Currently, she is Expert/mentor for innovative projects and post creation acceleration and for SMEs open innovation development. She is coordinator of National and European projects

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Dr. Dietrich Stephan

JULIUS KÜHN-INSTITUT (JKI), GERMANY

Dr. Dietrich Stephan is a Senior Scientist and Head of the Laboratory for Microbiology and Bioengineering at the Julius Kühn-Institut (JKI), Institute for Biological Control in Germany. He holds a Ph.D. in Agricultural Sciences from the University of Bonn and has over 30 years of research experience in biological pest control. His expertise includes the biodiversity and application of entomopathogenic fungi and microbial-based pesticides for sustainable agriculture.

Dr. Stephan has led several international and national projects, including EU Horizon 2020 IPM-4-Citrus, BIO-ENTOSOURCE (Germany/Brazil), and the SAFWA initiative. He has published extensively in peer-reviewed journals and is an active member of several scientific societies, including IOBC, VAAM, and SIP. His work focuses on bridging microbial ecology and applied biological control to develop eco-friendly solutions for crop protection.

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Dr. José Miguel CAMPOS RIVELA

UNIVERSITAT JAUME I, CASTELLÓ - SPAIN

José Miguel Campos Rivela holds a PhD in Agricultural Engineering from Universitat Jaume I, Castelló, Spain. His research focuses on entomology within the framework of Integrated Pest Management (IPM). He has studied the population dynamics of several key pest species, their natural enemies, and the impact of ecological infrastructures.

He has contributed to the implementation of various biotechnological techniques in the field, such as mating disruption and mass trapping. He has participated in 16 national and 3 international competitive research projects and is the author of 18 SCI-indexed papers and 76 technical publications. With extensive experience in knowledge transfer, he has delivered 59 training courses, seminars, and workshops targeting technicians and farmers. Additionally, he has presented 62 communications at national and international conferences.

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Dr. Michele Filippo FONTERANCESCO

UNIVERSITÀ CATTOLICA DEL SACRO CUORE IN MILAN, ITALY

Michele Filippo Fonterancesco is an associate professor of cultural anthropology at the Università Cattolica del Sacro Cuore in Milan. He is a member of the EASA (European Association of Social Anthropology), where he is part of the Integrity Committee and coordinates the networks of Economic Anthropology and Food Anthropology.

He is a social anthropologist whose research focuses on cultural heritage protection and promotion, and local development in European and African contexts.

Session 2:

Crop Protection & One Health Concept

Abstracts for Oral Communications

Plant Growth-Promoting Bateria as a Strategy to Promote Potato Grown in Tunisia

Oumèma Nouri-Ellouz[a,b], Jaweher Sdiri Ghidawi[a], Imen Ghazala[a],
Mariem Samet[a], Anissa Haddar[a], Radhia Gargouri-Bouzid[a]

[a] *Laboratory of Plant Improvement and Valorization of Agro-resources (LAPVA),*
National Engineering School of Sfax (ENIS), University of Sfax, Tunisia
[b] *Preparatory Institute for Engineering Studies of Sfax (IPEIS), University of Sfax, Tunisia*
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Background and Aim: Potato is the third most important food crop in the world and a strategic culture in Tunisia. However, this species is sensitive to environmental stresses such as salinity, drought and temperature linked to climate change, which hamper its growth and productivity. Genetic improvement can be employed to ensure better production. More sustainable plant production can be supported by the interaction with beneficial microorganisms such as plant growth-promoting bacteria (PGPB). In this context our laboratory decided to investigate the effect of selected PGPB strains on different potato plants submitted to standard culture conditions or in the presence of drought and salinity.

Methods: PGPB strains isolated from different sources in the laboratory were tested on potato varieties grown in Tunisia and on somatic hybrids characterized in the laboratory, in the presence or in the absence of NaCl (100 mM) or drought stress. Plant morphology (length, foliage…), and physiology (chlorophyll, proline…) as well as tuber yield, caliber and quality (aspect and chemicals) were monitored in the inoculated and non inoculated plants submitted or not to the environnemental stress in greenhouse and field experiments.

Results: Inoculation of potato plants with selected strains of PGPB enhanced plant growth and vigor under standard and stress conditions. This was associated with increased tuber yield and caliber under greenhouse and field culture conditions, thus mitigating the effect of stresses. In addition, an improvement in nutritional and processing qualities of tubers were achieved following inocultaion with some bacteria thereby adding new dimensions to the beneficial impacts of these strains.

Conclusion: Applications of PGPB isolates are promising methods for promoting potato in Tunisia. Data suggest that these strains can be tested in formulation of biostimulants.

Keywords: Potato, plant growth-promoting bacteria, plant growth, tuber yield, quality

Towards Sustainable Agriculture: Isolation and Characterization of Beneficial Bacteria for Crops and Food

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Background and aim:

Salinity is a critical environmental stress that impairs plant growth, reduces crop yield and compromises postharvest quality and shelf life. Moreover, the widespread use of chemical pesticides to manage stress related diseases further degrades soil microbial diversity, harms beneficial organisms, and poses long term-risks to food safety and ecosystem health. In this context, plant growth-promoting bacteria (PGPB), especially halotolerant strains have emerged as promising bioinoculants capable of mitigating the adverse effect of salinity. Their use not only enhances crop resilience and postharvest quality but also reduces the dependence on chemical inputs, contributing to more sustainable agriculture.

Methods:

This study aimed to isolate, identify, and characterise bacteria that exhibit robust plant growth-promoting properties. Deferent samples were collected from saline environments and the bacterial strains were isolated using serial dilution and cultured on nutrient agar supplemented with 3.5 % NaCl. The isolated bacteria were screened for plant growth-promoting traits such as IAA production, phosphate solubilization and siderophore production. Molecular identification was performed using 16S rRNA gene sequencing.

Results:

A total of 16 bacterial isolates from saline environment were selected based on their tolerance to salinity. Several strains demonstrated robust growth at NaCl concentration up to 15%.
All isolates showed plant growth-promoting bacteria (PGPB) based via their ability to produce indole-3-acetic acid (IAA), siderophores, hydrogen cyanide (HCN), solubilize phosphate and secretion of extracellular enzymes. Among them, two strains were further characterized through 16S rRNA gene sequencing. Additionally, five other isolates exhibited notable antimicrobial activities along with functional traits commonly associated with plant growth promotion, underscoring their potential for dual applications in biocontrol and biofertilization.

Conclusion:

The multifunctional traits exhibited by the bacterial strains isolated in this study highlight their strong potential as bioinoculants, capable of boosting plant growth and resilience under saline conditions.

Keywords: Salinity, PGPB, Biocontrol, Biofertilizer

Plant Growth Promoting Bacteria (*Bacillus mojavensis* I4) helps in enhancing salt tolerance of somatic hybrid and commercial potatoes

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Background: Potato (*Solanum tuberosum* L.) is regarded as the future major food crop by FAO to ensure food security due to its high productivity compared to cereals. Among abiotic stresses, salinity is a major global threat to potato, causing damage to its growth and production. The use of plant growth-promoting bacteria (PGPB) is an efficient tool for sustainable production under such adverse conditions. In this context, the present study aims to evaluate the effects of *Bacillus mojavensis* I4 (Bm I4) strain on the response to salinity in somatic hybrid and commercial potatoes.

Material and Methods: Study was conducted on Spunta (Sp) variety and two somatic hybrid lines called H506 and H101, acclimated in greenhouse under salt stress (100 mM NaCl) or standard (0 mM) conditions. The impact of inoculation with BmI4 (10^6 ufc/ml) on response of the different plants to salinity was investigated by monitoring agronomical and physiological parameters.

Results: Inoculation with BmI4 led to a better adaptation of the different potato plants to salinity. Inoculated plants exhibited high growth rates in comparison to non inoculated plants in the presence of salinity. Furthermore, inoculation of H101 and Sp resulted in an increase of tuber yield in association with early tuberization under salt stress conditions, thus was able to attenuate the effect of salinity. Promoting of vegetative growth seems not have significant repercussion on final yield, in H506. These beneficial effects of BmI4 were associated with enhanced control of oxidation in the different plants submitted to salinity.

Conclusions: The overall results prove beneficial effects of BmI4 on the different plants submitted to salinity. The higher yield capacity retained in H101 compared to Sp proves that the BmI4 strategy looks more promising to promote potato when combined with somatic hybridization.

Key words: Potato, Plant growth-promoting bacteria, Salt stress

An exopolysaccharide synthesized by the plant growth-promoting bacterium *Erwinia* sp. STN24: Its role in enhancing potato plant tolerance to abiotic stress

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Background and aim:

Potato (*Solanum tuberosum L.*) is a plant of great economic importance in Tunisia and throughout the world. However, this crop is subject to a number of environmental constraints, such as drought and salinity, which cause significant yield reduction and abnormal plant development. For this reason, plant growth-promoting bacterium *Erwinia sp.*STN24 and its exopolysaccharides (EPS) have shown profound effects on plant growth and abiotic stress tolerance.

Methods:

Erwinia sp.STN24, a bacterial strain exhibiting high exopolysaccharide production, was isolated from wheat seeds and identified based on its 16S-rDNA sequence, as well as its morphological and biochemical characteristics. The EPS was extracted from the fermentation broth via alcohol precipitation, followed by dialyses and freeze-drying. The protective effect of the EPS from *Erwinia* sp.STN24 was evaluated on potato plants under *in vitro* drought and salinity stress conditions. The STN24-EPS (5 mg/mL) inoculated plants were submitted to 100 mM NaCl or 10% polyethylene glycol treatement, for a period of 20 days. To assess the protective role of the EPS, several physiological parameters and antioxidant enzyme activities were measured.

Results:

After treatment, the application of STN24-EPS significantly improved plant elongation and chlorophyll content under stress conditions, compared to both control plants. These findings indicate not only the absence of any phytotoxic effect of the EPS, but also its potential to promote plant tolerance to abiotic stress.

Furthermore, treatment with STN24-EPS led to a clear reduction in hydrogen peroxide (H_2O_2) and malondialdehyde (MDA) levels, as well as in the activation of the antioxidant enzymes activities (SOD, CAT and GPX) compared to untreated plants. These results suggest a mitigation of oxidative stress in response to drought and salinity.

Conclusion:

Erwinia sp.STN24-EPS shows promising potential as a natural biocontrol agent to enhance potato plant tolerance to abiotic stress.

Keywords: Exopolysaccharide, *Erwinia* sp.STN24, salinity, drought.

Structure elucidation, biological and molecular docking studies of a new Bacillus Thuringiensis protoxin active against Lepidopteran pests

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Background and Aim: The isolation of novel *Bacillus thuringiensis* (Bt) strains and the discovery of novel toxins is a continuous action that falls within the framework of pest control and prevention of pest resistance. This entomopathogenic bacterium has become an alternative to chemical insecticides in commercial agriculture to control pests and mosquitoes.

Methods: Identification of the indigenously BUPM14 was made by conventional techniques and 16S rDNA sequencing. Its insecticidal activity against Lepidopteran pests was determined. One Cry1Ca type protoxin was subjected to further studies: The corresponding gene was cloned and sequenced; Structural and biological studies were conducted using bioinformatics analysis; Molecular docking studies using activated toxins were carried out to study the toxin-receptor complex.

Results: BUPM14, identified as a Bt strain, exhibited significant insecticidal toxicity to Lepidopteran insects that are members of families Pyralidae [*Ephestia kuehniella* (35.28 ± 21.91 µg/g)] and Noctuidae [*Agrotis ipsilon* (1.04 ± 0.25 µg/mL)]. Interest has focused on a novel Cry1Ca-like protoxin called Cry1Ca17. The corresponding gene has 3573 bp nucleotides and codes for a 1190-amino acid protein with a calculated molecular mass of 134.673 kDa. Five conserved domains, typical features of the Lepidoptera-active crystal proteins, were detected. Molecular docking studies were carried out using the 600 aa- trypsin-activated toxin. The key amino acid residues involved in the toxin-receptor interaction at two levels, *viz.* the receptor toxin binding site (toxin-binding site) and the catalytic site (toxin-catalytic site), were compared to those of the to-date known toxin-receptor complexes.

Conclusion: This study describes the selection and identification of a promising Bt strain. It produces a novel Cry1Ca-like protoxin called Cry1Ca17. The differences in amino acid residues involved in the toxin-receptor complex revealed when compared to the to-date known ones could be an asset for the use of this protoxin and its mother strain for pest control and prevention of pest resistance.

Keywords: *Bacillus thuringiensis*, Cry1C, Bioinformatics analysis, Molecular docking, insecticide activity

Crowding effect on the cestode *Gerbillitaenia psammomi* (Mikhail & Fahmy, 1968) parasitizing the gerbilline rodent *Psammomys obesus* Cretzschmar, 1828 in Tunisia

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Summary:

In most animal species, individuals live in groups of varying sizes, either due to social behaviors or limited habitat availability. The same applies to parasites, which form an infrapopulation within a host, and the size of this infrapopulation is used to measure density. Each host can harbor a variable number of parasites, ranging from a few individuals to many parasites. The size of the group of conspecifics with which an individual parasite can interact plays a crucial role in parasite ecology. This density factor has important implications, particularly concerning parasite growth and their chances of reproduction (Poulin, 2007).

In the present parasitological study, we investigated the potential crowding effect by examining the size of *Gerbillitaenia psammomi*, assessed through body length and the number of proglottids, in 25 naturally infected Fat sand rats (*Psammomys obesus*) from Southern Tunisia. To do so, we performed Linear Mixed Models (LMMs) on size parameters (log-transformed response variables) as a function of tapeworm abundance (log-transformed fixed effect). Host identity was included as a random factor in the models to account for non-independence among observations from the same host. These LMMs were conducted using the MIXED procedure in SAS (SAS Institute, 2008).

The analysis was based on data from 25 infected rats, with tapeworm counts per host ranging from 1 to 118 individuals. Morphological measurements were obtained from a total of 72 tapeworms, with the number of specimens sampled per rat ranging from 1 (in cases of single infection) to 9. Tapeworm lengths varied from 5.694 mm to 87.000 mm (n = 72, mean ± SD = 35.860 ± 23.741 mm), and the number of proglottids per individual ranged from 4 to 36 (mean ± SD = 16 ± 9). The results of the LMMs revealed highly significant negative relationships between tapeworm abundance and both tapeworm length ($\beta \pm SE = -0.504 \pm 0.058$, t46 = -8.640, $P < 0.001$) and the number of proglottids ($\beta \pm SE = -0.395 \pm 0.041$, t46 = -9.570, $P < 0.001$), suggesting a significant crowding effect.

Thus, this negative density-dependent growth (crowding effect) observed in *G. psammomi* showed the smaller tapeworms in hosts with a high parasite burden, whereas hosts with fewer parasites harbored larger tapeworms. Thus, the crowding effect could explain the variability in the body length of *G. psammomi* according to different findings of the species (Joyeux et al., 1951; Mikhail and Fahmy, 1968; Haukisalmi and Elmahy, 2025). The crowding effect has already been documented by several authors in other tapeworm species (Read, 1951; Heins et al., 2002; Fichet-Calvet et al., 2003). For example, Fichet-Calvet et al. (2003) described a crowding effect in the davaineid tapeworm *Raillietina trapezoides* (Janicki, 1904) parasitizing naturally infected Fat sand rats from Tunisia.

Keywords: *Gerbillitaenia psammomi, Psammomys obesus,* Crowding effect

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Laboratoire Biotechnologie & Valorisation des Bio-Géo Ressources
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Novel Bacterial Biocontrol Agents for Sustainable Agriculture: High Efficacy of Tunisian Isolates Against Prickly Pear Pest and Camel Ticks

Oumaima Ardhaoui, Essia Sebai, Tasnim Hajri, Meriem M’saad, Ameur Cherif, Mohamed Aziz Darghouth, Amor Mosbah.

Abstract

Public concern over the ecological and economic damage caused by *Dactylopius opuntiae* in prickly pear plantations, alongside the threats posed by chemical-resistant ticks like *Hyalomma dromedarii*, has intensified the need for sustainable control strategies. This study evaluated the biocontrol potential of 84 Tunisian bacterial isolates against both pests, emphasizing efficacy and environmental safety. Primary screening via brine shrimp (*Artemia salina*) bioassay identified 28 isolates with high toxicity (75–100% mortality within 24 h). Secondary screening through direct contact assays revealed three actinobacterial strains exhibiting 100% mortality against adult *D. opuntiae* females within 24 hours. These same isolates also demonstrated significant acaricidal activity against *H. dromedarii*, suggesting dual utility in integrated pest and tick management. Our findings highlight the promise of Tunisian actinobacteria as eco-friendly alternatives to chemical pesticides, offering a sustainable approach to mitigate agricultural losses and reduce reliance on synthetic inputs while safeguarding biodiversity and human health.

Keywords *Dactylopius opuntiae*, prickly pear cactus, *Hyalomma dromedarii*, actinobacteria.

Efficacy of Phage Application as an Alternative Biocontrol Strategy for Pathogenic and Spoilage *B. cereus* group in the Food Industry

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Background and Aim:

Food contamination by pathogenic and spoilage bacteria, including *Bacillus cereus* group members, significantly contributes to foodborne diseases and global food spoilage. Despite advancements in food safety, the incidence of foodborne illnesses continues to rise, further aggravated by antimicrobial resistance, a growing public health concern. Developing alternative antibacterial agents is therefore crucial. Bacteriophage (phage) biocontrol approache offers a natural, eco-friendly solution that effectively targets pathogens and enhances food safety throughout production and bio-sanitation of food contact surfaces.

This study aims to characterize the biological and lytic properties of two phages, previously isolated for their activity against *B. cereus* group members, and to evaluate their potential as biocontrol agents in food safety.

Methods:

The study involved the characterization of two bacteriophages, PBC_MG88 and PBC_MG99, including assessments of their stability across a range of pH values and temperatures to determine their suitability for food industry applications. Key biological parameters such as adsorption rate, latent period, burst size, and optimal MOI were evaluated. The phages were tested for their lytic activity against *Bacillus cereus* group strains, including biofilm-forming and cereulide-producing isolates. Their capacity to inhibit and disrupt biofilms was also examined using stainless steel surfaces.

Results:

PBC_MG88 and PBC_MG99 exhibited robust stability over a wide pH range (4–12) and maintained infectivity at temperatures up to 70 °C, suggesting their potential suitability for various food matrices and industrial environments. Both phages exhibited a short latent period and an extended burst phase, with burst sizes of 59 and 63 PFU/cell, respectively, and maintained effective lytic activity even at low multiplicity of infection (MOI). In vitro biofilm assays revealed that both bacteriophages effectively inhibited and disrupted *B. cereus* group biofilms.

Conclusion:

These features make PBC_MG88 and PBC_MG99 promising candidates for phage-based formulation to control *B. cereus* strains, enhancing microbial safety in agro-food systems.

Keywords: Bacteriophage biocontrol, *Bacillus cereus* group, Phage characterization, Biofilm inhibition, Food safety

Session 2:

Crop Protection & One Health Concept

Abstracts for Poster Presentations

Genomic and structural investigation of a novel metalloprotease "inhA3" from *Bacillus thuringiensis* BLB30AF

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Background and Aim: Immuno-inhibitor metalloproteases (InhA) are key virulence factors in *Bacillus cereus* and *Bacillus thuringiensis*, enabling immune evasion and host tissue degradation. This study aims to analyze the inhA3 gene of *B. thuringiensis* strain BLB30AF, which includes genetic characterization, structural evaluation, and potential role in virulence.

Methods: In this study, we focused in the first part on genome sequencing of BLB30AF. Subsequently, we investigated the gene identification and characterization. The second part of this study was dedicated to bioinformatics and structural analysis.

Results: The analysis of the whole genome of BLB30AF, newly isolated, showed the presence of four virulent genes, one of which codes for an "inhA3" type metalloprotease. This gene, which is 2388 bp in size, codes for a protein of 795 aa. The comparison of the nucleotide sequence of the gene shows a 98% identity with the inhA3 gene of *Bacillus thuringiensis* strain 407. The bioinformatic analysis of the sequence shows that this protein contains a 32 aa signal sequence (cleavage between Ala32-Glu33). A modeling was performed based on the crystal structure of the Bacillus anthracis inhA2 peptidase zymogen protein (pdb: 4yu6) with a 71% identity percentage. The obtained structure shows 4 domains including: a propeptide, a catalytic domain, a VEG domain, and a MAM domain grafted into the latter. For the metzincin family, of which InhA3 is a member, this protein has an N-terminal domain and a C-terminal domain that are separated by a cleft containing the active site.

Conclusion: The *inhA3* gene in BLB30AF encodes a structurally conserved metalloprotease with features typical of virulence-associated InhA proteins. Its catalytic domain architecture and regulatory profile suggest a role in immune evasion, potentially through cleavage of host defense molecules. While functional studies are needed, its homology to InhA2 and structural similarity to InhA1 highlight its likely contribution to pathogenesis.

Keywords: inhA3; *Bacillus thuringiensis*; crystal structure; metalloprotease.

Diversity of nematode fauna of *Ctenodactylus gundi* (Rothmann, 1776) in Southern Tunisia

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Summary:

Ctenodactylus gundi (Rothmann, 1776) is a small, herbivorous, and diurnal rodent endemic to the arid and semi-arid regions of North Africa. It typically inhabits rocky environments and forms small, stable colonies that tend to remain distant from human settlements (Seguignes, 1979). Several studies have examined various aspects of the species' biology (Grenot, 1973; George, 1979, 1985; Seguignes, 1979; Gouat, 1988), and have provided valuable breeding guidelines as well as insights into population dynamics of individuals currently held in zoological institutions (Sandra and Hartmut, 2025). However, few studies have focused on the diversity of its parasitic fauna (Ghawar et al., 2018; Meddour et al., 2022). The present study constitutes the first comprehensive investigation of the diversity of intestinal nematodes infecting *C. gundi* populations in Tunisia, thereby contributing valuable insights into parasite-host interactions in arid ecosystems. Between March 2023 and February 2025, a total of 69 individuals of *C. gundi* were captured using hand-forged snap traps placed in various localities across Southern Tunisia: Ksar El Hallouf (n=17), Menzelet Mogr (n=1), El Medhar (n=8), Douiret (n=13), El Fejij (n=13), Toujane (n=8), and Tamaghza (n=9). Following capture, the rodents were humanely euthanized by cervical dislocation in a field laboratory and immediately examined for intestinal parasites under a stereomicroscope.

Specimens were mounted in Amann lactophenol on slides and then observed under the light microscope Leitz Orthoplan microscope (Leitz GmbH, Wetzlar, Germany).

A total of four nematode species were identified: *Nematodirus spathiger*, *Hilgertia hilgerti*, *Ctenodactylina tunetae*, and *Trichuris gundii*, with an overall prevalence of 68.12%. Among these, *N. spathiger* was the most prevalent and abundant species (P=55.07%; A=8.03), followed by *H. hilgerti* (P=44.93%; A=6.03), *C. tunetae* (P=34.78%; A=1.62), and *T. gundii* (P=17.39%; A=0.35). These findings highlight a relatively rich and diverse parasitic fauna of nematodes associated with *C. gundi*, underlining the ecological importance of parasite-host dynamics in arid environments. Further studies are needed to assess the pathological impact of these helminths and their potential role in ecosystem health and host population regulation.

Keywords: *Ctenodactylus gundi,* nematodes, Tunisia

Beauveria bassiana blastospores as bio-pesticide: Production and Formulation

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Background and Aim: The need to reduce the impact of chemical insecticides on human health and environment has led to a steady increase in the use of bio-insecticides such as entomopathogenic fungi (EPF). To use EPF as biological control agents, they must be mass-produced in an economically and cost-effectively method. Currently, EPF are primarily produced using two methods: solid-state fermentation, which produce aerial conidia, and liquid fermentation, which produces blastospores and submerged conidia.

Methods: To achieve this, native virulent fungal isolates should be selected, multiplied extensively and efficiently, and then prepared to obtain a stable product. In this case, an isolate of a local strain of *Beauveria bassiana* (P1 strain) was mass-produced using submerged liquid fermentation and prepared as a wettable powder.

Results: This study compared blastospores production by P1 strain in liquid culture media with different glucose concentrations and stirring speeds. The highest level (1,2 10^{10} blastospores/ml) was obtained after 3 days at a glucose concentration of 100 g/l and an agitation speed of 300 rpm. Then, we investigated the effect of drying on the survival of the produced blastospores, formulated in in wettable powder with certain additives. Furthermore, we showed that the stability of P1 formulated blastospores, after 4 months of storage, is better at a low temperature (4°C) than at room temperature.

Conclusion: P1 blastospores are produced at high level and in a short time at high glucose concentration. However, those infectious propagules, formulated in wettable powder, are sensitive during drying and storage.

Keywords: biopesticides, *Beauveria bassiana*, entomopathogenic fungi

The effect of plant growth-promoting rhizobacteria (PGPR) strain *Serratia liquefaciens* (B.A10) on durum wheat germination under salt stress conditions

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Background and aim:

Durum wheat production is an important component of Tunisian agriculture. However, its yield is irregular due to climatic fluctuations, limited water resources and salty lands. Salinity reduces crop productivity by affecting growth yielding and germination potentialities. To ensure sustainable production of this crop under salt stress conditions the application of plant growth-promoting rhizobacteria (PGPR) can be an efficient strategy. In this context, the effects of PGPR strain *Serratia liquefaciens* (B.A10) isolated in the laboratory from compost tea was investigated on the germination performance of two wheat cultivars from Tunisian market, Aouija and Bidi, under salt stress conditions.

Methods:

Seeds from each cultivar were inoculated with B.A10 (10^7 CFU/ml for 30 min and 1.5 h). Treated and untreated seeds (control) were then germinated on moistened filter paper in the presence or absence of NaCl (100 and 150 mM). Percentage and average germination time, as well as velocity coefficient and vigor were monitored.

Results:

Seeds from Bidi cultivar showed rapid germination compared to Aouija under standard conditions, but were more sensitive to salinity. Inoculation of seeds with B.A10 mitigated salt effect on germination. Inoculation improved germination percentage, reduced time and increased coefficient of velocity and vigor index compared to untreated seeds in both cultivars under saline conditions (from 100 mM in Bidi and only at 150 mM in Aouija). In addition, seeds treatment with bacteria enhanced seedlings growth under salinity. The dry weight of inoculated seedlings was significantly higher than that of uninoculated seedlings under salt stress particularly for Aouija.

Conclusion:

This study proves the beneficial effect of B.A10 on seeds germination and seedlings growth in durum wheat under salinity conditions. Therefore, it can be promising to enhance productivity of this crop in saline areas.

Keywords: Durum wheat, germination, salt stress, PGPR

Protective effect of *Urtica urens* L. against hepatotoxicity induced by imidacloprid in Rats

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Background and Aim: Imidacloprid (IMI) has been known to cause hepatotoxicity. Some reports claim that *Urtica urens* L. (UU) can reduce toxicity. The present study was undertaken to evaluate the protective effect of UU against this toxicity.

Methods: Rats were divided into control group, 3 groups treated with IMI at 50, 200 or 300 mg/kg/day and three groups injected with IMI (50, 200 or 300 mg/kg/day) + 100 mg/kg/day of UU, for 60 days. Urine and blood samples were collected for dosage of biochemical levels. Livers were removed for oxidative stress and histological examination.

Results: IMI caused an acute renal and liver injury, increased the biochemical and tissular levels of MDA, and decreased the levels of antioxidant enzyme activities. UU injection improved the histological and all biochemical parameters.

Conclusion: IMI induced an acute liver injury accompanied with disturbance of oxidant status. UU injection provided a significant protection thanks to antioxidant properties.

Keywords: Imidacloprid, *Urtica urens*, liver, oxidative stress.

Effect of Plant Growth-Promoting Bacteria strains on Potato growth, physiology and tuber yield under field culture conditions

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Background and aim:

As an alternative to conventional chemical fertilizers, the use of biofertilizers has gained significant attention, particularly Plant Growth-Promoting Bacteria (PGPB), which are promising candidates due to their ability to enhance plant productivity and induce their innate resisitance. Potato plant (*Solanum tuberosum* L.) is a major global food crop, widely cultivated all over the world. However, it is highly sensitive to drought stress. In this context, this study aims to evaluate the effect of potato seeds inoculation with selected PGPB strains on plant growth and yield under field conditions, submitted to water scarcity.

Methods:

Three PGPB strains (*Bacillus mojavensis* I4, *Serratia liquefaciens* A10, and *Virgibacillus halodenitrificans*) previously isolated and identified in the laboratory, were used to inoculate potato seeds of Spunta variety prior to planting. The plants were then cultivated under field conditions and submitted to reduced water supply. During the cultivation period, morphological and physiological parameters were assessed monthly. Potato yields were evaluated after harvesting and compared to those of non-inoculated control plants.

Results:

PGPB-treated potato plants exhibited significantly higher fresh biomass, longer stems, increased leaf area, and greater chlorophyll content compared to the control. Physiological assays revealed reduced oxidative stress (lower MDA, H_2O_2) related to better antioxidant enzyme activities (SOD, catalase, GPX) in inoculated plants compared to control ones, indicating their improved capacity to overcome drought stress. These plants displayed higher tuber yield in terms of number and weight per plant.

Conclusion:

This study demonstrated that inoculation of potato tuber seeds with PGPB strains enhanced plant growth, yield, and stress tolerance, offering a sustainable strategy to improve productivity. Consequently, applying these strains represents a promising approach for promoting potato cultivation in drought-affected areas.

Keywords: Field, PGPB, Potato, drought, Yield.

Characterization of *Bacillus velezensis* 32a metabolites and their synergistic bioactivity against crown gall disease

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Abstract

Background: Crown gall disease caused by *Agrobacterium tumefaciens* is considered the main bacterial threat of stone fruit plants in Mediterranean countries. In a previous study*, Bacillus velezensis* strain 32a was isolated from Tunisian rhizosphere soil and revealed high antagonistic potential against *A. tumefaciens* strains.

Material methods: In order to better characterize the antagonistic activity of this strain against this important plant pathogen, the production of secondary metabolites was analyzed using liquid chromatography coupled with mass spectrometry. The involvement of lipopeptides in the antagonistic activity was studied by performing agar and broth dilution tests with pure molecules. Moreover, the construction of *B. velezensis* 32a mutants defective in polyketides and bacilysin biosynthesis and their antagonistic activity was performed and compared to a set of derivative mutants of a comparable strain, *B. velezensis* GA1.

Results: *Bacillus velezensis* strain 32a produced different compounds identified as surfactins, fengycins, iturins and bacillibactin belonging to the lipopeptide group, three polyketides (macrolactins, oxydifficidin and bacillaenes), bacilysin and its chlorinated derivative; chlorotetaine. The involvement of lipopeptides in this antagonistic activity was ruled out by performing agar and broth dilution tests with pure molecules. *B. velezensis* 32a mutants defective in polyketides and bacilysin biosynthesis construction and their antagonistic activity revealed that the defective difficidin mutants (△*dfnA* and △*dfnD)* were unable to inhibit the growth of *A. tumefaciens,* indicating the high-level contribution of difficidin in the antagonism process. While the macrolactin deficient mutant (Δ*mlnA)* slightly decreased the activity, suggesting a synergetic effect with difficidin. Remarkably, the mutant △*dhbC* only deficient in bacillibactin production showed significant reduction in its capacity to inhibit the growth of *Agrobacterium.*

Conclusion: Taken collectively, our results showed the strong synergetic effect of difficidin and macrolactins and the significant implication of siderophore to manage crown gall disease.

Keywords: *Agrobacterium tumefaciens*, Lipopeptides, Polyketides, Oxydifficidin, Macrolactin.

Improving Field Production and Storage of Potatoes Using Biological Biofertilizer Based on Plant Growth-Promoting Rhizobacteria (PGPR)

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Background and Aim

Potato cultivation in Tunisia is essential but faces several challenges, including low productivity and dependence on imported seeds. To address these issues, an innovative solution relies on the use of PGPR, beneficial bacteria that enhance plant growth and resistance. An experimental project is testing these bacteria over two generations to evaluate their impact on tuber production and storage, with trials conducted directly with farmers.

Methods

This study aims to assess the effects of two selected PGPR bacterial strains with beneficial properties on potato cultivation. Field trials will be conducted on plants derived from inoculated or non-inoculated seeds, subjected or not to water stress. Plant growth will be monitored through various parameters such as fresh biomass, chlorophyll content, leaf surface area, and oxidative stress response (MDA, H_2O_2, enzymatic activities). Yield will be evaluated by measuring the number, weight, and size of tubers. Finally, harvested potatoes will be stored, and their dormancy and sprouting will be analyzed during storage.

Results

The results obtained align with the initially set objectives. Indeed, two bacterial strains (Bacillus mojavensis and Serratia grimessi) isolated in the laboratory were used to treat seed potatoes. Monitoring the growth parameters of inoculated and non-inoculated plants confirmed the beneficial effects of these bacteria on plant development and improved water stress response.

Conclusion

The obtained results confirm the initial objectives, demonstrating that Bacillus mojavensis and Serratia grimessi promote potato plant growth and enhance their resistance to water stress.

Keywords

Potato, PGPR, Biofertilizer

Experimental Study on the Nutritional Importance of Marine Algae

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Background and Aim :

Seaweeds, traditionally consumed in Asian cultures, are gaining global attention due to their exceptional nutritional value. They represent a sustainable, natural, and diverse source of essential nutrients with proven health benefits. As part of a personal research project on sustainable food, this small-scale experimental study aimed to analyze and compare the nutritional contributions of three edible seaweed species: *Ulva lactuca* (sea lettuce), *Porphyra* (nori), and *Laminaria digitata* (kombu).

Methods :

Three dehydrated seaweed samples were collected from the Bizerte region in Tunisia. Each was weighed to 100 g and analyzed using basic nutritional tests: Biuret test for proteins, orthophenanthroline reagent for iron, and iodine content measured using starch solution and sodium thiosulfate titration. The results were compared with standard nutritional values.

Results

- *Ulva lactuca*: 14.8 g protein / 100 g, 1.9 mg iron, 30 µg iodine
- *Porphyra*: 28.3 g protein / 100 g, 3.2 mg iron, 55 µg iodine
- *Laminaria digitata*: 9.5 g protein / 100 g, 2.5 mg iron, 1200 µg iodine

Porphyra showed the highest protein content, surpassing some legumes. *Laminaria digitata* was notable for its extremely high iodine levels, making it a valuable source for thyroid function. *Porphyra* showed the highest protein content, surpassing some legumes. *Laminaria digitata* is an excellent iodine source, vital for thyroid function. Moderate consumption can help address iron and iodine deficiencies, especially in vegetarian diets.

Conclusion :

This personal experimental study confirms that marine algae are highly promising foods—nutritious, sustainable, and health-promoting. Their integration into daily diets could help address deficiencies, especially in iron and iodine, in vegetarian or low-animal-product diets.

Keywords :

Nutrition, Sustainable Food, Marine Algae.

Session 3 :

Health Care & One Health Concept

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Pr. Ahmed REJEB

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Professor Rejeb Ahmed is a Doctor of Veterinary Medicine, with MSc, and PhD from ENMV Sidi Thabet, specializing in Histology and Anatomical Pathology at the University of Manouba. He holds significant leadership roles as the President of the Tunisian Veterinary Council and Vice-President of CLIOV Francophones. With around 120 publications and contributions to 150 academic supervisions.

Pr. Ahmed is actively involved in research, including EU H2020 projects like Volatolomics (bovine tuberculosis diagnosis) and CANLEISH (canine leishmaniasis diagnosis). He also contributed to the "Sehat Awledna" project focusing on One Health. Furthermore, Pr. Ahmed has organized international scientific events and serves on numerous national committees related to health, ethics, and environmental issues. He is a recognized expert, frequently participating in television programs to address zoonotic diseases and antimicrobial resistance.

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Pr. Noël TORDO

PASTEUR INSTITUTE OF GUINEA

Noël Tordo is a French virologist and the Director of the Institut Pasteur de Guinée since 2004. He also heads the antiviral strategies unit at the Virology Department of the Institut Pasteur in Paris. His expertise includes the pathophysiology, epidemiology, vaccines, and elimination strategies of the rabies virus.

Under his leadership, the Institut Pasteur de Guinée has developed modern training and research facilities, notably the Pasteur Laboratory in Conakry, which focuses on diagnostics, research, and training to strengthen local expertise in emerging infectious diseases, especially following the 2014 Ebola outbreak. He is also a member of the Board of the Pasteur Network and serves as President of the French Society for Virology

Session 3:

Health Care & One Health Concept

Abstracts for Oral Communications

WHO mRNA Tech Transfer Programme in Tunisia: Toward the construction of the first R&D unit for mRNA vaccines and therapeutics

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Background and Aim: In April 2021, the Tunisian Ministry of Health expressed, through the Pasteur Institute of Tunis (IPT), its interest in acquiring mRNA-based vaccine technology. One year later, Tunisia was declared as a recipient country (currently named Partner) of the mRNA-based vaccine technology.

Methods: IPT has chosen to focus on the Research and Development (R&D) component through the creation of an R&D unit, which will be dedicated to the development of mRNA-based vaccines. The goal is to create a platform, with all the necessary equipments, which will be put at the service of all Tunisian researchers and those in the North African region in order to support them in developing mRNA-based vaccines against a range of pathogens that particularly affect Africa and the other partners countries (15) involved in the programme

Results: A selected short committee (the authors) was subsequently created to monitor the installation of the future structure. In august 2023, a site assessment of IPT was performed by a delegate from Medecine Patent Pool (MPP), the foundation in charge of the implementation of the programme. After several meetings between MPP and the IPT local committee, a detailed work-plan along with a final agreement were signed by the different parties in August 2024. In October 2024, a 60% of the funding was received and ordering of all needed equipment, consumables and reagent along with the laboratory planning started.

Conclusion: We expect to have a well-equipped, fully functional and autonomous R&D unit dedicated to the development of mRNA-based vaccines and therapeutics by the end of this year.

Keywords : WHO, Institut Pasteur de Tunis, Vaccines, mRNA, Therapeutics.

LIVE ATTENUATED VACCINES FOR CANINE LEISHMANASIS

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Background and aim: Zoonotic visceral leishmaniasis (ZVL) affecting canine and human, is a major veterinary and public health problem. The prevalence of ZVL in dogs plays a crucial role in triggering transmission to humans. Therefore, reducing *L. infantum* in dogs through vaccination is a key strategy for controlling ZVL in emerging foci. Thus, we have developed an attenuated vaccine consisting of the genetically modified *Leishmania major* parasite, with a deletion of the centrin gene using the CRISPR-cas9 technique (*Lm*Cen$^{-/-}$).

Methods: In this study, we assessed the safety, immunogenicity, and efficacy of this vaccine candidate in dogs within a natural ZVL focus. The *Lm*Cen$^{-/-}$ vaccine was administered intradermally using a prime-boost regimen. Dogs received the *Lm*Cen$^{-/-}$ vaccine one month before being relocated to a CVL-endemic area in Northern Tunisia, where they were exposed to sand fly bites over three consecutive transmission seasons. Humoral and cellular immune responses were evaluated, and parasite load in naturally exposed dogs was analyzed using qPCR.

Results: Our results showed that the vaccine induced high level of IgG anti-*Leishmania* and exhibited strong antigen-specific cellular responses with IFN- γ production by CD4+T cells one-month post-immunization. One among the vaccinated dogs (n=11) developed clinical signs of CVL with positive PCR for *Leishmania*. In contrast, 4/11 unvaccinated dogs were tested PCR positive for *Leishmania* and displayed oligosymptomatic CVL, demonstrating that immunization with *Lm*Cen$^{-/-}$ vaccine confers long-term protection with an efficacy of 82.5% against CVL in natural transmission settings.

Conclusion: Our results show that live attenuated *L. major* parasites *Lm*Cen$^{-/-}$ vaccine is safe and efficacious against *L. infantum* in dogs resulting in the control of CVL development in natural transmission settings. Since dogs are the main reservoir host of *L. infantum,* development of an effective vaccine against CVL will help the control and elimination of ZVL.

Key words: Live Attenuated Vaccine, *Leishmania major,* Dog, Leishmaniasis, Natural Challenge.

Interconnexion entre les changements de méthylation du gène redox p66shc et l'environnement alimentaire chez des malades rénaux chroniques

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Introduction

L’insuffisance rénale chronique (IRC) est une pathologie multifactorielle, fréquente, grave et couteuse. Elle contribue à l’augmentation de l’incidence et la prévalence des maladies cardiovasculaires(MCV). Malgré les stratégies thérapeutiques et préventives considérées efficaces, l’IRC demeure un problème majeur de santé non résolu. L’IRC est largement associée au stress oxydatif et inflammatoire. Bien que les causes exactes soient diverses et complexes, des données récentes suggèrent que l’interaction entre divers facteurs environnementaux, comportementaux et génétiques, pourraient expliquer le développement de l’IRC.

L’épigénétique fait référence à un ensemble de mécanismes de régulation de l’expression génique, en dehors de toute modification de séquences basiques de l’ADN. La méthylation de l’ADN constitue le mécanisme épigénétique le plus étudié et le plus caractérisé chez les mammifères. C’est un mécanisme dynamique, hautement spécifique au gène à réguler et très sensible aux stimuli environnementaux, notamment les altérations alimentaires. Il est bien admis que les altérations métaboliques sont fortement liées au stress oxydatif et inflammatoire, contribuant aux maladies rénales chroniques. Cependant, les mécanismes reliant ces différents processus ne sont pas encore bien élucidés.

La protéine adaptatrice p66shc est nouvellement reconnue comme médiateur clé de la transduction des signaux oxydatifs, en réponse aux différents stimuli environnementaux conduisant à la surproduction des ROS (Reactive Oxygen Species) mitochondriaux, à des lésions inflammatoires et à l’apoptose cellulaire.

Dans un objectif d’identifier un mécanisme moléculaire reliant les altérations alimentaires aux changements de méthylation de l’ADN de la p66shc et le développement de l’IRC, nous avons analysé la méthylation de l’ADN du gène p66shc dans des cellules immunitaires périphériques chez des patients ayant des MRC (PMRC) comparés avec des contrôles.

Matériels et méthodes

Dans une étude transversale, nous avons choisi 61 PMRC, suivis au service de néphrologie à l’hôpital régional de Sidi Bouzid et 47 personnes de contrôles. Des paramètres cliniques, oxydatifs et inflammatoires ont été analysés. La méthylation du gène p66shc dans des leucocytes périphériques a été réalisée par PCR Spécifique à la Méthylation (PSM).

Résultats

Dans un environnement d’altération métabolique (diabète, dyslipidémie, HHcyst), nous avons démontré une corrélation positive entre l’hypométhylation du p66shc dans des cellules immunitaires et des paramètres cliniques, oxydatifs et inflammatoires chez des PMRC comparés aux contrôles. De plus, l’hypométhylation de la p66shc a montré une corrélation positive et stable avec le MDA (indicateur oxydatif), la CRP (marqueur inflammatoire) et les stades de la MRC.

Conclusion

La corrélation positive et stable de l’hypométhylation de la p66shc avec le MDA, la CRP et les stades de la MRC, nous a permis de déchiffrer l’effet oxydatif suggéré aux altérations métaboliques et la génération du stress oxydatif coassocié d’un état inflammatoire systémique chronique chez des PMRC. La détermination de méthylation de l’ADN du gène p66shc chez les patients susceptibles de développer des MRC, pourrait être utilisée comme marqueur clé de dépistage et de diagnostique à des stades précoces même avant l’apparition de la maladie.

Mots clés : IRC, méthylation de l’ADN, environnement alimentaire, p66shc, stress oxydatif et inflammatoire, épigénétique

Abstract

Domesticated animals have played a significant role in the life of humans for thousands years. Cats are one of pets who are more and more adopted and most people will own a cat, especially kids, at some time during their lives. This is why; we focus in this study on the adoption of cats and the multitude of benefits it provides mainly for children and elderly. Subsequently, we develop the concept of zoo therapy by a cat.

Risks are related to the possibility of contracting zoonotic infections. We reviewed therefore three infectious diseases caused by bacteria: Bartonella, Pasteurella and Capnocytophaga. These bacteria are more severe and occasionally lethal in immunocompromised patients.

As part of personal contribution, we conducted a survey about cat’s adoption among 150 persons on Google Forms which aims to evaluate the quality of cat’s adoption and the exposure risks of crypto zoonosis transmitted by cats. We mainly discussed the results and the risk that might be occurred due to cat adoption particularly for persons at risk. We estimated that it is a low risk.

Finally, we concluded that to mitigate the risks and allow the owner to keep his cat, cooperation between the veterinarian, the physician and the owner is recommended and fundamental.

Résumé

Les animaux domestiques jouent un rôle important dans la vie des humains depuis des milliers d'années. Les chats sont l'un des animaux de compagnie qui sont de plus en plus adoptés et appréciés. La plupart des gens vont posséder un chat, surtout les enfants, à un moment donné au cours de leur vie. C'est pourquoi, dans cette étude nous mettons l'accent sur l'adoption des chats et la multitude d'avantages que procure principalement aux enfants et aux personnes âgées. Par la suite, nous développons le concept de zoothérapie par un chat.

Les risques sont liés à la possibilité de contracter des infections zoonotiques. Nous avons donc traité trois maladies infectieuses causées par des bactéries : Bartonella, Pasteurella et Capnocytophaga. Ces bactéries sont plus sévères et parfois mortelles chez les patients immunodéprimés.

Dans le cadre d'une contribution personnelle, nous avons mené une enquête sur l'adoption du chat chez 150 personnes sur Google Forms qui vise à évaluer la qualité de l'adoption du chat et les risques d'exposition des cryptozoonoses transmises par les chats. Nous avons principalement discuté des résultats et du risque qui pourrait se produire en raison de l'adoption de chat, en particulier pour les personnes à risque. Nous avons estimé que le risque était faible.

Finalement, nous avons conclu que pour atténuer les risques et permettre au propriétaire de garder son chat, la coopération entre le vétérinaire, le médecin et le propriétaire est recommandée et fondamentale.

Session 3:

Health Care & One Health Concept

Abstracts for Poster Presentations

Molecular Docking Analysis of the Antibacterial Activity of Eco-Friendly-Extracted Hydroxytyrosol from Olive Leaves against human pathogens

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Abstract

Context/Purpose: The rise of bacterial resistance, particularly from Extended-Spectrum Beta-Lactamase (ESBL)-producing bacteria, poses a significant threat to public health. These bacteria have evolved mechanisms to resist a broad range of antibiotics, making infections harder to treat and resulting in higher mortality rates. ESBL-producing strains pose particular risks in hospitals, complicating treatments and limiting therapeutic options. As antibiotic resistance continues to grow, exploring alternative solutions like plant-derived compounds becomes crucial.

Methods: The Hydroxytyrosol extract was obtained from the leaves of a Chemlali olive tree (*Olea europaea*) using a simple eco-friendly acid hydrolysis process. To assess its antibacterial properties, *in vitro* analysis was conducted using the well diffusion method and MIC/MBC calculations, followed by *in silico* confirmation through molecular docking simulations.

Results: The results from MIC and MBC measurements confirmed that the phenolic extract exhibits a bactericidal effect, indicating its ability to eradicate ESBL-producing bacteria rather than just inhibiting their growth. Such a mechanism is particularly important in clinical settings, where ESBL-producing bacteria can cause severe infections and complications. *In silico* studies revealed that hydroxytyrosol binds to key bacterial proteins, such as the gyrase B subunit and the DD-transpeptidase domain. These interactions could inhibit the functions of these proteins, subsequently resulting in bacterial death.

Conclusion: These findings support the antimicrobial potential of hydroxytyrosol and highlight its potential as a treatment option against resistant bacteria. Given the rising prevalence of antibiotic resistance globally, the development and use of plant-derived compounds like hydroxytyrosol could provide innovative strategies to combat infections and improve public health outcomes effectively.

Keywords: hydroxytyrosol, antibacterial activity, molecular docking.

Validation of Colorimetric Methods for Measuring Peroxynitrite as an Oxidative Stress Biomarker in Human Plasma peroxynitrite

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Background and Aim: The objective of our work was to ensure the reliability and quality of results obtained during the assay of peroxynitrite, an important parameter of oxidative stress. A well-structured quality document is fundamental to standardize the procedure, ensure traceability, and facilitate data interpretation.

Methods: The determination of peroxynitrite levels in plasma is performed according to the method described by Beckman et al. (1992. This method is based on the nitration of phenol by peroxynitrite, a reaction that leads to the formation of nitrophenol. The concentration of nitrophenol, and consequently of peroxynitrite, is quantified by spectrophotometry at 412 nm. The measured absorbance is directly proportional to the peroxynitrite concentration, using a molar extinction coefficient (ε) of 4400 $M^{-1}cm^{-1}$ for the nitrophenol formed.

Results: The extinction coefficient of the nitrophenol solution was determined to be 0.005 µmol/L using Excel, following the construction of the calibration curve, which yielded a strong correlation coefficient (R^2) of 0.9973.

Conclusion: These findings demonstrate that this colorimetric approach is a validated and dependable tool for quantifying peroxynitrite as a key biomarker of oxidative stress in human plasma.

Keywords (max 5 words): Peroxynitrite, human plasma, oxidative stress.

Abstract core 300 words max (except title, authors and affiliations), Times New Roman, simple interline

Subchronic exposure to Thiophanate-Methyl: Implications for reproductive health

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Keywords: Thiophanatemethyl, histopathology, toxicity, reproductive health.

Background

Thiophanate-methyl (TM) is a widely used pesticide, with its use in Tunisia increasing over the past decade, raising concerns about its potential toxic effects on the environment and human health. While studies on its general toxicity exist, there is limited data on its effects on ovarian function. This study aimed to assess the subchronic impact of TM exposure on ovarian histopathology and function in adult Wistar rats. Given that a significant percentage of agricultural workers are female, this research highlights potential risks to female reproductive health.

Material and Methods

Adult female Wistar rats were orally exposed to TM at different doses for 30 days. The rats were divided into three groups: a control group, a low-dose group (100 mg TM/kg body weight), and a high-dose group (300 mg TM/kg body weight). Histological and biochemical analyses were conducted to evaluate ovarian tissue and oestrogen levels.

Results

Significant decreases in food and water intake and body weight were observed in TM-treated groups, accompanied by signs of general toxicity, including diarrhea, vomiting, fatigue, anxiety, and renal dysfunction biochemically confirmed.

Histological analysis revealed ovarian disorganization, reduced follicle numbers at all stages of maturation, and increased follicular atresia, with more severe changes in the high-dose

group. Biochemical analysis showed significantly lower oestrogen levels. These results suggest that TM exposure leads to ovarian structural and functional changes, potentially affecting reproductive health.

Conclusion

Subchronic TM exposure induces histopathological and hormonal alterations in the ovaries, contributing to reproductive dysfunction. Additionally, TM exposure resulted in general toxicity signs. Further research is needed to explore the underlying mechanisms and evaluate long-term reproductive effects, which will help in the rational use of TM and promote safer agricultural practices.

Development of tools for detecting cross-contamination by anticoccidials in turkey feed.

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Background and Aim: Animal feed plays a critical role in the global food industry, enabling cost-effective production of animal-derived food worldwide. Coccidiosis is the primary parasitic disease in poultry, and anticoccidial feed additives are used for its control. These medications are categorized into synthetic chemical anticoccidials and biological ionophore antibiotics. Narasin, an ionophore, works by altering ion transport across the cell membranes of coccidia, disrupting their physiological processes. While narasin is used in broiler chicken farming within specific dosage limits, it is specifically toxic to turkeys. Considering the risk of cross-contamination with poultry feed supplemented with anticoccidials, the transfer of contamination by narasin into the ingredients of turkey products can prevent significant harm to the turkey animal. The aim is to optimize detection protocols for ionophore anticoccidials in turkey feed.

Results: Different optimization approaches were used for the detection protocols of ionophore anticoccidials in turkey feed. The initial method was qualitative coulometric analysis using Vanillin and DMAB. Although rapid and indicative of certain ionophores through color changes, these methods lack quantitative ability and may not be highly specific. Since narasin cannot be detected by UV and does not possess electrochemical properties, HPLC analysis requires post-column derivatization using vanillin or DMAB. The following technique was Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS). This quantitative analysis stands out for its increased sensitivity and specificity, along with the benefit of easy and rapid sample preparation. Alternative methods such as Near-infrared (NIR) spectroscopy and immunochromatography can also be employed.

Conclusion: For the quantification of ionophores in livestock feed, the most suitable method is LC-MS/MS. This technique enables efficient separation of ionophores within the feed matrix and provides accurate quantification. Regular application of this method can prevent cross-contamination issues and thereby ensure the quality and safety of animal feed.

Keywords: anticoccidial, turkey feed, toxicity, quantification, food safety

Molecular and in silico investigation of a novel ECHS1 gene mutation in a consanguine family with short-chain enoyl-CoA hydratase deficiency and Mt-DNA depletion: effect on trimer assembly and catalytic activity

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Background and Aim: Short-chain enoyl-CoA hydratase deficiency (ECHS1D) is a rare congenital metabolic disorder that follows an autosomal recessive inheritance pattern. It is caused by mutations in the ECHS1 gene, which encodes a mitochondrial enzyme involved in the second step of mitochondrial β-oxidation of fatty acids. The main characteristics of the disease are severe developmental delay, regression, seizures, neurodegeneration, high blood lactate, and a brain MRI pattern consistent with Leigh syndrome.

Methods: Whole exome sequencing was performed in all patients followed by segregation analysis in their parents using sanger sequencing. Whole mitochondrial DNA sequencing was also carried out. The effects of identified variants were predicted using several in silico tools 3D modelling, molecular docking and Experimental analysis

Results: Here, we report three patients belonging to a consanguineous family who presented with mitochondrial encephalomyopathy. Whole-exome sequencing revealed a new homozygous mutation c.619G>A (p.Gly207Ser) at the last nucleotide position in exon 5 of the ECHS1 gene. Experimental analysis showed that normal ECHS1 pre-mRNA splicing occurred in all patients compared to controls. Furthermore, three-dimensional models of wild-type and mutant echs1 proteins revealed changes in catalytic site interactions, conformational changes, and intramolecular interactions, potentially disrupting echs1 protein trimerization and afecting its function. Additionally, the quantification of mtDNA copy number variation in blood leukocytes showed severe mtDNA depletion in all probands.

Conclusion: The overall findings from multiple bioinformatics tools and 3D modeling suggested that the identified mutation might change the echs1 enzyme's stability and flexibility, which would then hinder the formation of trimers, which would impair the enzyme's function and eventually cause mtDNA depletion in all patients. These results demonstrate how, in our cases, treatment with DNs could help to enhance overall mitochondrial respiratory function

KEYWORDS: Short-chain enoyl-CoA hydratase deficiency · ECHS1 · mtDNA depletion

First time investigation of MTBC infection in Tunisian wild boar using culturomic and metagenomic analysis

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Abstract

Background:

Tuberculosis (TB) is a major zoonotic disease at the wildlife-livestock-human interface, and wild boars (*Sus scrofa algira*) are increasingly recognized as potential reservoirs for *Mycobacterium tuberculosis* complex (MTBC) infections. In Tunisia, the role of wild boars in TB epidemiology remains poorly understood. This study aimed to investigate the presence of MTBC in wild boar populations in Tunisia and to characterize the lymph node microbiota using metagenomic analysis.

Materials and Methods:

Submandibular lymph nodes were collected from 52 wild boars harvested during the 2024–2025 hunting season in Tunisia. Samples were subjected to bacteriological culture and DNA extraction. Detection of MTBC was performed using real-time PCR targeting the IS1081 insertion sequence. Additionally, metagenomic analysis was conducted to explore the microbial communities within the lymph nodes, although these results are not included in the current report.

Results:

Out of 52 samples analyzed, 15 tested positive for MTBC by real-time PCR, resulting in a positivity rate of 28.8%. Bacteriological culture results are pending. The metagenomic data, which aim to provide further insight into the microbial ecology of lymph nodes, will be detailed in a subsequent analysis.

Conclusions:

This study confirms the presence of MTBC infection in Tunisian wild boar populations, suggesting that wild boars may serve as reservoirs and contribute to TB transmission in Tunisia. These findings underscore the importance of establishing integrated surveillance and control strategies to mitigate potential zoonotic risks.

Keywords:
Wild boar, *Mycobacterium tuberculosis* complex, Tunisia, Zoonosis, Metagenomics

In vitro and in vivo antibacterial activity of *Spirulina platensis* extracts against *Salmonella* *spp and *E .coli* isolated from bivalve mollusc

Zormati Sonia (Institut de recherche Vétérinaire), Hanen Sallemi, **Pr.Radhouene Gdoura** (faculté de science de Sfax)

Abstract :

Spirulina platensis (Arthrospira platensis) is considered as a natural source of various biologically and pharmacologically active compounds with structurally complex molecules, which are difficult or impossible to be produced by chemical synthesis. Spirulina has gained an importance and international demand for its high phytonutrients value and pigments, which have applications in healthy foods, animal feed, therapeutics and diagnostics.

The aim of the present work was to study the antimicrobial activity of crude and ethanolic extract of Spirulina platensis against isolates Salmonella spp and E. coli from bivalve mollusc. The diameter of inhibition of the ethanolic extract on *E. coli* for the concentration of 5µl is Zi=7mm. The effect of crude extract for the same concentration is Zi=9mm. Also the effect of crude extract on Salmonella spp (Zi= 10mm) is more than the ethanolic extract (Zi=8mm). In addition, our study demonstrated the antibacterial activity in vivo of Spirulina platensis extracts against *Salmonella spp*.We contaminated the seawater from tank N°1 of the experimental purification system developed with a bacterial suspension of approximately 5.10^5 CFU. By real-time PCR technique we had an initial concentration of 10^3 copies/ml on day1, which increased to a concentration of 10^2 on day 2, then to a concentration of 10 on day 3, and finally to a concentration of less than one DNA copy from day 4 onward.

The present study suggested that extract of Spirulina platensis, which proved to be potentially effective can be used as natural alternative preventives to improve the stations of purification for the elimination of enterobacteria and also to give a nutritional impact during the filtration period.

Keywords: *Spirulina platensis*, *E. coli*, *Salmonella spp*, Bivalve mollusc, Antimicrobial activity.

Short-Chain Fatty Acids as Key Mediators of the Microbiota-Gut-Brain Axis in Infantile Epileptic Spasms Syndrome

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Introduction: The microbiota-gut-brain (MGB) axis plays a potential role in modulating cognitive and motor functions. This bidirectional communication involves multiple microbial metabolites, primary short-chain fatty acids (SCFAs). These volatile products caintain one to six carbons arranged in a straight or branched-chain and are predominantly abundant in the colon. Straight SCFAs are produced from the fermentation of undigested dietary fibers and primarily include acetate, propionate, and butyrate. Branched-chain fatty acids (BCFAs), which constitute about 5% of total SCFAs, are produced from protein degradation and mainly include isobutyrate, isovalerate and 2-Methylbutyric acid. SCFAs promote various local and systemic effects. Indeed, SCFAs can enter the bloosdstream and reach the CNS, where they regulate the activation of microglia, promote the neurogenesis and modulate excitatory/inhibitory neurotransmitters. All these effects underline the role of SCFAs in the pathophysiology of brain disorders. The aim of this study is the exploration of the roles of SCFAs in the context of infantile epileptic spasm syndrome (IESS).

Participants and Methods : It was a case-controlled study including IESS patients and healthy controls (HC). The mesearment of SCFAs, in plasma samples, was performed using Gas Chromatography-Mass Spectrometry (GC-MS). The obtained results were statistically compared between IESS patients and HC using student t-test.

Results: 16 IESS patients (mean-age 9,3 ± 6,08 months) and 16 HC (mean-age 9,3± 5,5 months) were included. IESS patients had significantly reduced level of acetate (*P*= 0,022), butyrate (*P* =0,025) and propionate (*P*= 0,022) compared to HC. Regarding the baranched SCFAs we found also a significant reduction in isovalerate (*P*= 0,022), isobutyrate (P= 0,022) and 2-methybutyric acid (P= 0,009) in IESS comapred to HC. Overall, the total SCFAs in the IESS plasma significantly decreased (*P*= 0,022) comapred to HC.

Conclusion: Our findings revealed a reduction in beneficial SCFAs in IESS patients compared to HC, suggesting a potential link to the pathophysiology of IESS and its comorbidities

Keywords : Short-chain fatty acids, Microbiota-gut-brain axis, Infantile epileptic spasm syndrome

Machines à Vecteurs de Support (SVM) : Modèle pour prédire le diagnostic des troubles psychotiques et de l'humeur

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Résumé

Introduction. La schizophrénie (SCZ), le trouble schizo-affectif (TSA) et le trouble bipolaire (TBP) sont des affections mentales chroniques invalidantes qui affectent chacune environ 1% de la population mondiale. Les personnes atteintes de ces troubles ont une espérance de vie plus courte que la moyenne en raison de taux plus élevés de maladies physiques et de suicides. Ces conditions sont fréquemment mal diagnostiquées, ce qui entraîne un traitement inapproprié ou tardif et, par conséquent, une détérioration du pronostic. Par conséquent, l'identification de biomarqueurs pour ces troubles serait très bénéfique pour un diagnostic précis et une intervention précoce. Ces biomarqueurs pourraient même révéler une prédisposition physiopathologique justifiant un traitement préventif. Dans l'ère actuelle des sciences des données, les techniques d'apprentissage automatique sont devenues des outils précieux pour le diagnostic et la prédiction de l'évolution clinique des troubles psychiatriques. Dans ce cadre, notre travail explore l'utilisation d'une de ces techniques, " Machines à Vecteurs de Support ", pour analyser les données issues des tests biochimiques et identifier une signature métabolique spécifique à ces trois troubles psychiatriques. Ce modèle statistique pourrait offrir un support au diagnostic de ces affections.

Patients et méthodes. Il s'agit d'une étude de cas-témoins portant sur des individus présentant des troubles de santé mentale tels que la schizophrénie (SCZ), le trouble bipolaire (BD) et le trouble schizo-affectif (TSA). Le diagnostic de ces troubles a été établi en conformité avec les critères du Manuel diagnostique et statistique des troubles mentaux (DSM-5), et une évaluation des symptômes positifs et négatifs a été effectuée à l'aide de l'échelle des syndromes positifs et négatifs (PANSS). Les sujets témoins, sélectionnés pour cette étude, ont été appariés aux patients en fonction de leur âge et de leur sexe. Un profil biochimique comprenant des mesures telles que le cholestérol total (Tchol), le cholestérol des lipoprotéines de haute densité (HDL-C), le cholestérol des lipoprotéines de faible densité (LDL-C), les triglycérides (TG), l'albumine, la protéine C réactive ultrasensible (CRP), la créatine kinase (CK), l'aspartate aminotransférase (ASAT), l'alanine aminotransférase (ALAT) et les produits oxydatifs avancés des protéines (AOPP) a été réalisé pour tous les patients et témoins. L'analyse a été effectuée à l'aide d'un arbre de décision appliqué à nos données.

Résultats. La base de données regroupe, 99 malades et 55 témoins. Seules les variables communes aux deux groupes d'études ont été conservées pour l'analyse des données et la réalisation des modèles statistiques. Celle-ci contient 20 variables (1 catégorielle et 19 quantitatives). nous avons utilisé l'approche de machines à vecteurs de support (SVM) en testant différentes fonctions de noyau. Ces modèles ont été réalisés par cross validation (n= 10) répétée (n= 3) afin de déterminer les valeurs optimales des hyperparamètres. Pour le modèle SVM à noyau radial (RBF), les valeurs optimales des paramètres coût et sigma étaient respectivement de 1 et 0,1. Pour le modèle SVM linéaire, la valeur optimale du paramètre coût était de 1. Les deux modèles testés ont présentées des performances validés : accuracy et sensibilité et AUC élevés. En termes d'importance des variables incluses dans ces modèles

SVM, presque les mêmes variables étaient caractérisées par le même niveau d’importance quel que soit la fonction du noyau utilisée. Le variable le plus important était l’AOPP.

Conclusion. Dans cette étude, nous avons cherché à construire un modèle statistique en utilisant la méthode d'apprentissage automatique, plus précisément le SVM. Notre objectif principal était de découvrir les biomarqueurs les plus étroitement liés aux troubles psychotiques et de l'humeur, et de développer un outil d'aide à la prise de décision pour le diagnostic.

From Mutation to Manifestation: A Multidisciplinary Study of Genotype-Phenotype Correlations and Gut Microbiota in Familial Hypercholesterolemia

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Background and Aim: Autosomal recessive hypercholesterolemia (ARH) is a rare lipid disorder caused by LDLRAP1 mutations. We investigated a Tunisian family in which only two brothers were affected by ARH, both also presenting with the rare congenital anomaly of a quadricuspid aortic valve (QAV). Clinical evaluation showed elevated LDL cholesterol and tendon xanthomas. Whole-exome sequencing identified a rare homozygous LDLRAP1 mutation (c.161G>A; p.Gly54Asp) in both brothers, confirmed by Sanger sequencing. In silico analysis predicted a damaging effect on protein structure and LDL receptor interaction. No pathogenic variants were found in key valvulogenesis genes. Gut microbiome analysis via 16S rRNA sequencing revealed distinct microbial profiles in the affected brothers, suggesting a role in lipid metabolism and treatment response.

Methods and Results:

1) Identification of rare mutation in the LDLRAP1 gene involved in ARH using WES, and confirmed by Sanger sequencing
2) In *Silico* Analysis: Functional annotation was performed using UniProt, Ensembl, PDB, and STRING. Protein stability and dynamics were evaluated with DynaMut2, MUpro, and DDGun. Structural analysis using NetSurfP-2.0, AlphaFold2, and ConSurf showed that the G54D mutation in LDLRAP1 alters secondary structure and disrupts interaction with LDLR, as visualized in PyMOL. Pathogenicity predictions using MutationTaster, MetaSNP, and MutPred2 indicated a significant deleterious effect.

3) Metagenomic DNA was extracted from patients' stool samples for targeted 16S rRNA gene sequencing. Gut microbiota composition and diversity were analyzed using the Galaxy Europe platform, allowing detailed characterization of microbial communities.
1) Evaluation of Candidate Genes Related to Valvulogenesis (*NKX2-5, GATA4/5/6, TBX5, NOTCH1, BMPs, FGFs, TGF-β, MMPs, FOXC1/2, NOTCH1, MMP2,* etc.,) to explore genetic susceptibility to quadricuspid aortic valve (QAV).

Conclusion:

This multidisciplinary study highlights the importance of integrating genetic, clinical, and microbiome data for personalized management of autosomal recessive hypercholesterolemia (ARH) and related aortic valve anomalies. A pathogenic LDLRAP1 mutation was identified and shown to impact protein structure and function. Gut microbiota analysis suggested a role in modulating lipid-lowering therapy responses. These findings support a tailored therapeutic approach based on individual genetic and microbiome profiles to improve outcomes in ARH patients.

Keywords: ARH, QAV, FH, LDLRAP1, NGS

Session 4 :

IA & One Health Concept

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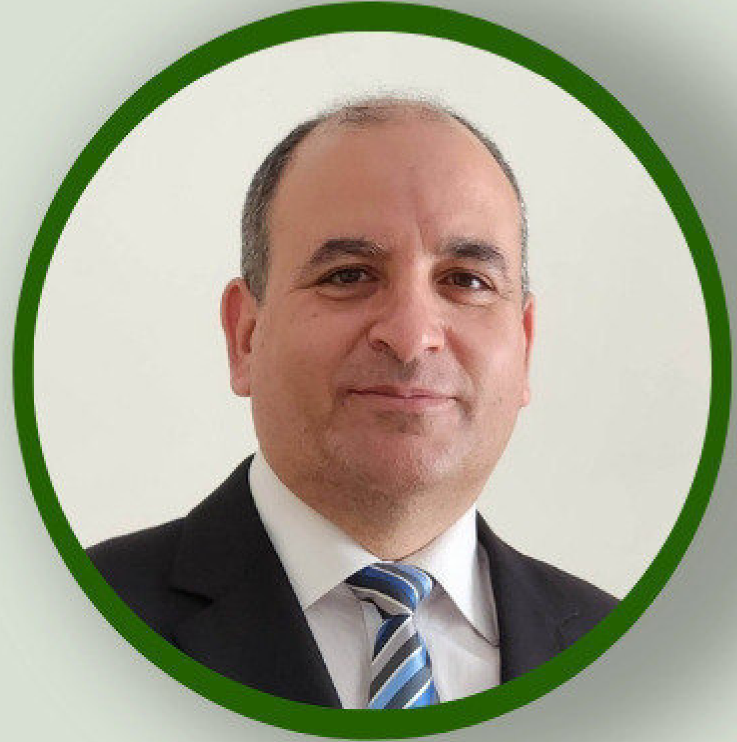

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Prof. Hassen DRIRA

UNIVERSITY OF STRASBOURG (TÉLÉCOM PHYSIQUE STRASBOURG), STRASBOURG - FRANCE

Hassen Drira is a Professor of Computer Science at the University of Strasbourg (Télécom Physique Strasbourg) and a member of the ICube Laboratory (UMR CNRS 7357) in France. He earned his PhD in 2011 from the University of Lille and holds a Master's (2007) and an Engineering degree (2006) from the National School of Computer Science (ENSI) in Tunisia.

His research interests include pattern recognition, shape analysis, computer vision, and medical image analysis, with numerous peer-reviewed publications in these fields. He co-leads the IMAGeS team at ICube and is the academic coordinator of the Image, Signals, and Data Science (ISSD) track within the general engineering program at Télécom Physique Strasbourg. He also coordinates the "Image and Data" (ID) Master's program. From 2019 to 2022, he led the "Cybersecurity Engineering" Specialized Master's at IMT Nord Europe.

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Dr. Imen MEGDICHE

**ISIS ENGINEERING SCHOOL - INU CHAMPOLLION
TOULOUSE INSTITUTE OF COMPUTER SCIENCE
RESEARCH, FRANCE**

Imen Megdiche is a Senior Lecturer and director of research at the ISIS Engineering School in Castres, part of University Jean-François Champollion, and a researcher at the Toulouse Institute of Computer Science Research (IRIT). Her research focuses on digital health, addressing key challenges across the patient life journey—from well-being and diagnosis to long-term monitoring.

She specializes in big data storage and integration, leveraging advanced AI techniques such as federated learning, bias mitigation, and anomaly detection to improve healthcare outcomes. Her interdisciplinary approach combines data-driven methodologies with cutting-edge AI solutions to enhance patient care and health system efficiency.

Session 4:

IA & One Health Concept

Abstracts for Oral Communications

XAI-Pulmonet: AN Explainable AI Framework for Multi-Class Lung Disease Classification

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Abstract

Although traditional deep learning models have demonstrated strong performance in classification tasks, their limited interpretability often renders them as 'black boxes', hindering their adoption in therapeutic applications. This study proposes a novel method to enhance interpretability in classifying X-ray images as COVID-19, pneumonia, or normal by combining handcrafted features with deep features extracted using Convolutional Neural Networks. To enhance the transparency of the model's decision-making process, we applied several Explainable Artificial Intelligence methods, such as SHAP, LIME, Grad-CAM, and Grad-CAM++. We evaluated the effectiveness of our model against other transfer learning-based architectures, including EfficientNetB0, InceptionV3, and ResNet, using a range of performance metrics. The model augmented with data enhancement techniques outperformed the others, achieving an accuracy of 95%. Furthermore, Grad-CAM and Grad-CAM++ visually identified the key regions and features that guided classification decisions, contributing to greater interpretability and confidence in AI-driven diagnostic support.

Keywords: Explainable Artificial Intelligence, Chest X-ray Classification, Handcrafted and Deep Features Fusion, Data Augmentation.

A Real Time Multimodal System for Elderly Human Activity Recognition: Case of Fall Detection

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Background and Aim:

With the global increase in the elderly population, ensuring the safety of seniors living independently has become a pressing societal concern. In particular, continuous monitoring of older adults residing alone is vital, as falls represent one of the most critical risks they face within the home environment. These incidents occur suddenly and involuntarily and can result in severe health complications, including fractures of the hip, forearm, and humerus, and, in some cases, may even be fatal. According to reports from the World Health Organization (WHO), approximately 28–35% of older adults experience at least one fall annually, with a significant number of cases leading to death. Research also indicates that timely intervention can reduce mortality rates by up to 80% and decrease the duration of hospitalization by approximately 26%. Various commercial fall detection solutions have been developed and are typically categorized as either wearable or non-wearable devices. While wearable technologies were originally designed to support elderly monitoring, they present several limitations, such as discomfort, forgetfulness in usage, susceptibility to damage, and the necessity for frequent recharging. In light of these challenges, the research community has shifted its focus toward non-wearable alternatives, particularly those based on vision sensors. Among these, RGB camera-based systems have emerged as a promising approach due to their reliability and compatibility with the needs of elderly users. This thesis aims to design and develop a real-time fall detection framework that utilizes deep learning-based feature representations derived from visual data. The proposed system seeks to enhance the monitoring of elderly individuals by providing an accurate, non-intrusive, and responsive solution for fall detection.

Title: Sequence 2 Sequence (Seq2Seq) Models for Breast Cancer Images Deblurring, Segmentation and Classification

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Supervised by: Pr. Omar NAIFAR

Co-supervised by: Dr. Wael OUARDA

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Background and Aim:

Breast cancer is the most commonly diagnosed cancer among women and a leading cause of cancer-related deaths, accounting for 15.52% of female cancer mortality. Imaging modalities like mammography, ultrasound, MRI, and CT play a vital role in diagnosis, yet challenges remain due to image quality, noise, and variability.

This research aims to improve diagnosis through:

- Image deblurring,

- Accurate segmentation of tumor regions,

- Robust classification into malignant, benign, and normal classes.

Methods:

-Utilization of Sequence-to-Sequence (Seq2Seq) models tailored for:

- ✓ Image Deblurring to enhance clarity.
- ✓ Segmentation using advanced models like the Segment Anything Model (SAM),
- ✓ Classification into three categories (malignant, benign, normal).

- Incorporation of data augmentation techniques to improve model performance.

- Analysis of breast cancer imaging modalities and review of recent literature.

Results from state of the art:

- SAM-based Seq2Seq models show adaptability and strong potential for precise breast region segmentation.

- GAN-based augmentation improves mass classification performance in ultrasound and mammograms.

- The combination of deblurring, segmentation, and classification using Seq2Seq provides a comprehensive pipeline for improving breast cancer image analysis.

Conclusion:

The integration of Seq2Seq models for deblurring, segmentation, and classification can significantly enhance the interpretability and diagnostic accuracy of breast cancer imaging. The approach holds promise for clinical application by automating and improving the reliability of diagnosis through advanced deep learning techniques.

Keywords: Breast Cancer, Seq2Seq, Segmentation, Deblurring, Classification

Abstract Core:

Breast cancer remains a leading cause of mortality among women globally, underscoring the need for accurate and early diagnosis. Medical imaging plays a critical role in breast cancer detection; however, challenges such as image blur, poor segmentation, and variability in tumor appearance hinder diagnosis. This work proposes the use of Sequence-to-Sequence (Seq2Seq) models to address three core challenges in breast cancer imaging: deblurring, segmentation, and classification. Deblurring enhances image clarity to aid precise tumor visualization. Segmentation involves delineating tumor regions, crucial for treatment planning and monitoring. Classification assigns labels to tissue types malignant, benign, or normal supporting effective clinical decisions.

A comprehensive literature review identifies the potential of integrating advanced deep learning techniques, especially the Segment Anything Model (SAM), adapted for breast region segmentation. Data augmentation techniques, particularly GAN-based approaches, further improve model generalization. By combining these elements, the proposed framework aims to deliver high-quality, interpretable outputs for breast cancer analysis. Preliminary results indicate promising performance of the SAM-based segmentation pipeline and enhanced classification accuracy following augmentation.

This study contributes to the advancement of automated diagnostic tools for breast cancer and demonstrates the power of Seq2Seq architectures in transforming medical imaging workflows.

Methods:

We propose a fall detection system based on RGB video input, utilizing a spatio-temporal deep neural network architecture. The model is designed to effectively capture both spatial features and temporal dynamics associated with fall events, enabling accurate and real-time detection.

Artificial Intelligence: A transformative tool for predicting Endocrine-Disrupting Chemicals potential in the one health concept?

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,
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Endocrine Disrupting Chemicals (EDCs) are a global problem for environmental and human health. It is estimated that there are about 1000 chemicals with endocrine-acting properties. EDCs comprise pesticides, fungicides, industrial chemicals, plasticizers etc. For example, increasing concern over bisphenol A (BPA) as an EDC and its possible adverse effects on human health have prompted the removal of BPA from consumer products, often labeled "BPA-free." Some of the chemical replacements, however, are also bisphenols and may have similar physiopathological risks for organisms. EDC-associated diseases and disabilities extend well beyond bisphenols to a wide range of emerging synthetic chemicals, with effects including adverse neurodevelopmental outcomes, diabetes, cardiovascular disease, and reproductive disorders. The costs of EDC exposures are estimated to be 163 billion € in the European Union and 340 billion $ in the USA (Attina, et al. 2016). In this context, it is important to highlight the need for two key AI-powered strategies:

-AI-enhanced screening of new chemicals for endocrine-disrupting properties before market approval, preventing the replacement of regulated bisphenols (e.g., BPA) with regrettable alternatives.

-AI-driven biomonitoring to track EDC exposure in Humans, wildlife, and ecosystems. Advanced data analytics (e.g., sensor networks, omics-based biomarkers) can identify contamination, assess cumulative risks, and guide remediation efforts.

In conclusion, a multidisciplinary approach combining expertise from endocrinology, physiology, chemistry, and computer science will be essential to effectively address these challenges for optimum one health.

Keywords : Endocrine Disrupting Chemicals, One health, AI screening

Ref: Attina TM et al., 2016 Exposure to endocrine-disrupting chemicals in the USA: a population-based disease burden and cost analysis. Lancet Diabetes Endocrinol 4 996-1003.

Session 4:

IA & One Health Concept

Abstracts for Poster Presentation

Artificial intelligence for sperm morphology analysis

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Background and Aim:

Sperm morphology assessment is a crucial parameter in semen analysis but remains highly subjective, leading to significant inter- and intra-laboratory variability. Manual analysis is time-consuming and operator-dependent. Computer-Assisted Sperm Analysis (CASA) systems have attempted to automate this process, but their accuracy remains controversial, particularly due to limited publicly available datasets that mostly focus on sperm head morphology. The aim of this study was to develop an automated sperm morphology assessment method using the KNIME Analytics Platform and compare its performance to manual evaluation following WHO guidelines.

Material and Methods:

This study included 37 semen samples collected over one year from patients attending our laboratory for infertility investigation. Semen smears were stained with the Spermoscan® kit. A total of 1000 individual spermatozoa images were obtained using the MMC® CASA system. Three experts classified these images according to the modified David classification. The images were processed using a convolutional neural network (CNN)-based algorithm developed in the KNIME Analytics Platform. The dataset was divided into a training set (80%) and a test set (20%) to evaluate classification performance.

Results:

Among the 1000 analyzed images, 116 spermatozoa were classified as normal, while 884 exhibited abnormalities .The highest classification accuracy was observed for post-acrosomal abnormalities (97% true positive rate), whereas multiple tail abnormalities had the lowest accuracy (69% true positive rate). The overall accuracy of the model reached 99.5%, with an analysis time of less than 10 seconds per sample.

Conclusions:

Our results highlight the potential of artificial intelligence in improving the standardization and efficiency of sperm morphology assessment. Despite the promising performance of our model, an expansion of the dataset, particularly for rare abnormalities, is necessary to enhance classification accuracy further. This approach may contribute to reducing variability in sperm analysis and optimizing fertility evaluations.

Keywords:

Sperm morphology, Artificial intelligence, KNIME, Deep learning, CASA system

Session 5 :

One Health Concept for environment

ADRIC

جمعية تنمية البحث والتجديد وادماج الكفاءات

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Prof. Sonia KHOUFI

CENTRE OF BIOTECHNOLOGY OF SFAX, TUNSIA

Prof. Sonia KHOUFI holds a Ph.D. in Biological Sciences from the Faculty of Sciences of Sfax (FSS) and a Habilitation to Supervise Research (HDR) in Biological Engineering from ENIS. Since joining CBS in 2008, she has been a senior researcher at the Laboratory of Environmental Bioprocesses (LBPE), focusing on bioprocess development for waste and wastewater treatment and valorization.

A recognized expert in methanisation, she has led numerous national and international projects, including CEOMED (ENI CBC MED) and BIOGASMENA (ERANETMED). She has coordinated the LBPE-CBS biogas program since 2015 and contributed to projects such as SAFWA, PHC UTIQUE, and Pyrodigest. From 2017 to 2025, she served as an external examiner at Vaal University of Technology in South Africa. Her work bridges academic research with applied environmental and energy solutions.

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Prof. Asma SAKKA HLAILI

FACULTY OF SCIENCE AT BIZERTE, TUNISIA

Asma SAKKA HLAILI is professor at Univ. of Carthage, Faculty of Science at Bizerte (Tunisia). She obtained a PhD in Biology from Univ. Laval in 1999. She has more than 25 years of experience in research on the eco-biology and diversity of plankton, the toxic and harmful algal blooms, the marine eco-toxicology and bio-remediation, the planktonic food webs and the ecosystem health indicators.

She has participated in several national and international projects concerning the ecology, the pollution and the sustainable development of coastal and marine waters. She is a member of international and Mediterranean networks of experts in harmful microalgae (GlobalHAB-IOC-SCOR), aquatic ecotoxicology (ECOBIM) and Environmental Climate Change (ECC). She has more than Sixty international publication.

Session 5:

One Health Concept for Environment

Abstracts for Oral Communication

Olive Mill waste water (OMW):recovery of high added value compounds used in public health and biomethane potential

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Background and Aim: Olive mill wastewater (OMW), a by-product of the olive oil extraction process, possess significant environmental challenges due to its high organic load and phenolic content. In fact, this high added value molecules, possess various biological activities beneficial to public health. In this study, we investigate the effect of OMW bioactive compounds on inflammation as well as on enzyme inhibition in hepatic cells. Moreover, the biomethanepotential of OMW was also explored before and after treatment.

Results: Our findings demonstrated that the treatment and the recovery high added values compounds was successfully reached using a pilot developed in the framework of the INNOVA project.The anti-inflammatory activity testshowed that various compounds present in OMW reduced ROS formation and nitric oxide level in hepG2 cells with hydrowytyrosol exhibiting the strongest effect. Similarly, PTP1B of inhibition by these compounds revealed that hydroxytysol and oleuropein inhibited efficiently this enzyme suggesting their potential as promising antidiabetic molecules. Furthermore, BMP batches showed the highest biomethane potential yields were achieved by mixing the OMW with a slurry of organic market waste and by depolyphenolized OMW mixed with retentate from an ultrafiltration pretreatment. Both mixtures reaching up to 350 NL methane per kg of organic dry matter. Germination test demonstrated that the digestate can be safely used for irrigation after appropriate dilution.

Conclusion: The promising results open several avenues for future research and development within the food and cosmeceutical sectors. Additionally, the energetic valorization of OMW in biodigesters is a feasible economic approach

Keywords: phytochemicals; olive mill waste water; inflammation;enzyme inhibition, biomethane potential

Wound healing potential of *Pistacia lentiscus* distilled leaf extract, quercetin-3-*O*-rhamnoside, and myricetin-3-*O*-rhamnoside in a Rat model.

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Abstract

The development of bioproducts able to accelerate wound healing is an important topic in biomedicine. The present work was performed to investigate the phenolic composition of the waste of *Pistacia lentiscus* L. leaf (PDL) result of the distillation step, determine the extract molecules that may transmit the cutaneous barrier, isolate molecules from the extract, and evaluate their wound healing activity.

HPLC-MS analysis showed the presence of a high amount of flavonol glycosides in the PDL extract. A transdermal diffusion study was carried out using a Franz diffusion cell and start-M membrane to determine the molecules that may transmit the cutaneous barrier. Myricetin-3-*O*-rhamnoside (MM) transmits the membrane barrier with a high amount of 52.102 ± 0.001 µg/g of cream followed by quercetin-3-*O*-rhamnoside (QM). Therefore, QM and MM, which were present in the PDL extract with high quantities of 10.47 ± 0.26 and 12.17 ± 0.74 mg/ g dry weight, respectively, were isolated using various chromatographic techniques.

The wound healing study on rats using PDL extract and its isolated molecules showed that the topical application of PDL (at a concentration of 20 mg/ml) (PDL 20), MM, and QM accelerated wound healing and reduced inflammatory cell infiltration compared to the control group of rats. Moreover, the cutaneous wound tissues treated with PDL 20, MM, and QM exhibited significantly higher hydroxyproline content than the control group of rats, which means a high collagen biosynthesis in wound tissues.

Therefore, PDL extract, MM, and QM could be used as effective cutaneous wound healing agents.

Keywords: *Pistacia lentiscus* distilled leaves, myricetin-3-*O*-rhamnoside, quercetin-3-*O*-rhamnoside, transdermal diffusion, wound healing.

L'approche « One Health » en Tunisie: état des lieux

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Rectorat de Jendouba

1-TITRE DE L'INTERVENTION :

L'approche « One Health » en Tunisie: état des lieux

2-INTERET DU SUJET :

Les interactions entre la santé humaine, animale, végétale et environnementale est d'un grand intérêt au 21 ^{e} siècle vue la dégradation de l'environnement et les risques liés à la transmission des maladies entre différentes espèces (humains, animaux végétaux) menaçant. La Tunisie essaye à travers sa législation à coordonner dans différents domaines afin d'améliorer la santé globale. Malgré les efforts accrus, l'application de cette approche devient pertinente face aux limites et défis sanitaires croissants que connait la Tunisie en ce siècle à l'instar des autres Etats.

3-PROBLEMATIQUE

Quelles sont les mesures de mises en œuvres tunisiennes prisent dans le cadre de l'approche c'est ses limites ?

4-APPROCHES :

Juridique et analyse des textes instaurant l'approche « One Health » en Tunisie et ses limites et défis.

5-CONCLUSION GENERALE ET RECOMMANDATION

6-PRESENTATION POWER POINT (15 minutes)

7-PLAN DE L'INTERVENTION

I. Les initiatives tunisiennes de mise en œuvre de l'approche « One Health »

A. Les mécanismes utilisés

1. La création de comités intersectoriels
2. La coopération interinstitutionnelle

B. L'instauration de systèmes de surveillance et gestion des risques sanitaires

1. Les réseaux de surveillance vétérinaire pour la détection et le contrôle contre les menaces pour la santé publique et animale.

2. La surveillance des impacts environnementaux sur la santé publique

II. Les limites de l'application de l'approche en Tunisie et ses défis

A. Les problèmes dus aux manques de coordinations et de gouvernance

1. Une fragmentation des structures institutionnelles

2. Une politique publique incohérente

B. Des contraintes techniques et financières diverses

1. Une insuffisance des ressources financières et humaines significatives

2. Une capacité technique limitée assortie d'infrastructures de surveillance réduites.

Conclusion générale

Recommandations

RESUME

L'interconnexion de la santé humaine, végétale, animale ainsi qu'environnementale est un nouveau concept global qui aide à mieux comprendre la santé des vivants sur notre planète. Cette approche « One Health » ou « une seule santé », repose à la fois sur l'idée que la santé des vivants tous confondus (humains, animaux, plantes et environnement) forme un tout indivisible, dépendant l'un de l'autre. L'approche a permis en Tunisie d'effectuer des progrès significatifs consistant à la création de mécanismes de coordination intersectoriels en vue de l'amélioration des systèmes de surveillance des zoonoses ainsi que des risques environnementaux. Cependant, des limites et des défis demeurent face aux manques de coordination entre les différentes institutions étatiques aggravés par des insuffisances financières, humaines et techniques. La Tunisie pour y faire face est confrontée à plusieurs défis à relever afin que l'approche « One Health » soit plus efficace.

Session 5:

One Health Concept for Environment

Abstracts for Poster Presentation

Extraction, characterization and upgrading of natural unconventional oils

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Background and Aim:

The objectives of working, first, is to extract unconventional oils, then to characterize them physico-chemical, in addition, to follow the digestibility in vitro by lipolytic enzymes and finally, to make a biotechnological valorization.

Methods:

- Oil extraction by organic solvent (hexane) and determination of the yield extraction.
- Lipase activity essay using emultion with the extracted oil and gum arabic (2ml+18ml).
- Digestibility studies using gastric and pancreatic enzymes (to mime the human physiological conditions)

Results:

Preliminary results found meet standards to consider the selected plant as a major source of unconventional oils.

Rhamnus cathartica oil is characterized by the abundance of long-chain TAG, DAG and F.F.A.

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Conclusion:

The potential use of unconventional oil is diversifying for example use a multifunctional lipid excipient for the development of new lipid formulations.

Keywords (max 5 words): non conventionnal plant, oil extraction, digectibility, biological activity

Abstract

World consumption of vegetable oils increased by 15% in millions of metric tonnes in 2021/2022 compared to 2017/2018. This increase is explained by the primordial role of vegetable oils in the living world, either as a basis in the diet, in pharmacology and in oleochemicals such as transformation into biodiesel. In Tunisia, in particular, consumption and demand are increasing significantly. This alternative lies in the production of unconventional oils of natural origin, while respecting the three pillars of sustainable development. These objectives of working, first, is to extract unconventional oils, then to characterize them physico-

chemical, in addition, to follow the digestibility in vitro by lipolytic enzymes and finally, to make a biotechnological valorization.

Pilot-scale Anaerobic Digestion of Biowaste: A Holistic Strategy for Environmental and Health Co-benefits

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Background and Aim Organic waste, particularly fruit and vegetable wastes (FVWs), represents a significant fraction of municipal biowaste and poses environmental and public health risks if not properly managed. Landfilling contributes to greenhouse gas emissions, soil and water contamination, and poses significant health risks, impacting human, animal, and plant health through air and water pollution, and disease transmission. In the context of the One Health approach which recognizes the interconnectedness of human, animal, and environmental health, anaerobic digestion (AD) offers a sustainable and integrated solution. This biological process converts organic matter into biogas, a renewable energy source, and digestate, a nutrient-rich biofertilizer. Implementing AD can significantly reduce landfill waste, mitigate methane emissions, and decrease reliance on fossil fuels. Furthermore, the digestate can enhance soil health, reduce the need for synthetic fertilizers, and improve crop yields, thus positively affecting plant and potentially animal health through a healthier food chain.

Methods This study presents the results of a pilot-scale AD process applied to FVWs, aiming to reduce environmental pollution, recover bioenergy, and produce a nutrient-rich digestate suitable for agricultural reuse. The operating parameters as organic load and hydraulic retention time were optimized.

Results Nutrient-rich digestate and biogas containing up to 62.6% methane were generated by the developed anaerobic system. This process has the capacity to treat 20 kg of FVWs per m^3 of reactor per day with a methane yield of 54 m^3 per ton of FVWs.

Conclusion The findings highlight the potential of AD as a key component in circular waste management strategies that align with both environmental protection and health security objectives.

Keywords: Organic wastes, environmental and health risks, anaerobic digestion, bioenergy, fertilizer.

Neurobehavioral deficits and brain oxidative stress induced by aluminum exposure in the adult male rat: the preventive effect of *Cheatomorpha gracilis* polysaccharide compounds

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Abstract

Aluminum has been considered as a major risk factor linked to several physiological disturbances, especially neurodegenerative disease. On the other hand, it has been claimed that seaweed polysaccharides (PSs) exhibit biological activities that may have therapeutic significance and that they control several central nervous system physiological processes. The current study aims to investigate the neuroprotective and antioxidant effect of PS extracted from ***Cheatomorpha** gracilis* against aluminum-induced toxicity. Our research showed that aluminum significantly reduced Mg^{2+} and Ca^{2+}-ATPase activities while also causing severe behavioral changes, hematological issues, and histological changes in the brain. Additionally, while vitamin C and glutathione (GSH) levels, superoxide dismutase (SOD), and glutathione peroxidase (GPx) activities were significantly decreased in the brain of aluminum-treated rats, malondialdehyde (MDA) and the advanced oxidation of protein products (AOPP) were significantly elevated. It's interesting to note that PS lessened the neurotoxicity caused by aluminum and decreased oxidative stress damage, behavioral changes, and brain histology abnormalities.

Keywords Aluminum toxicity, Polysaccharide, *C.gracilis*, Brain.

Harmful phytoplankton in the Bizerte Lagoon and related environmental and health risks

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The occurrence of harmful phytoplankton has increased in coastal waters worldwide during the last decades, especially in shellfish culture areas. Proliferation of harmful species were often associated with detrimental environmental and economic impacts. They can also have health threat, when they produce potent toxic. So, studies on their ecology, diversity and toxicity have received considerable attention. Our study investigated the dynamics of harmful phytoplankton in the Bizerte Lagoon, the most important shellfish area in Tunisia. The sampling was carried out during two seasons (autumn and spring) in six stations characterized by environmental variability and different nutrient richness. In each season, harmful phytoplankton showed spatial variation, with cellular density ranging from 2.3×10^3 to 7.8×10^4 cells L^{-1}. The highest abundances were recorded at stations highly rich with nutrients. Harmful phytoplankton has also displayed a clear seasonal shift in their community structure. Autmn was a favorable season for the proliferation of dinoflagellates, which contributed 62-95% of total harmful phytoplankton in most stations. These included the potential producers of paralytic shellfish poisoning (*Alexandrium*), diarrheic shellfish poisoning (*Prorocentrum*), ichthyotoxins (*Karenia mikimotoi* and *Gyrodinium*), and the discolouration of seawater *(Neoceratium*). In the opposite, harmful diatoms, which were composed of the potentially neurotoxic species (*Pseudo-nitzschia*) and species responsible of discoloration and degradation of seawater quality (*Chaetoceros* and *Cylindrotecha closterium*), developed mainly during spring in several stations (52-71% of total harmful phytoplankton). Canonical correspondence analyses revealed significant relationships between the harmful species and the physico-chemical and nutritive conditions. The widespread distribution of harmful phytoplankton in the Bizerte Lagoon, with the presence of several toxic diatoms and dinoflagellates, suggests a potential risk to the shellfish farming sector and human health.