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AGROHUB
III Andalucía IBVF - Sevilla 2026
III Andalucía Agro-Hub PhD students meeting
Instituto de Bioquímica Vegetal y Fotosíntesis (IBVF) (CSIC-US)
Sevilla, 12-13th March 2026
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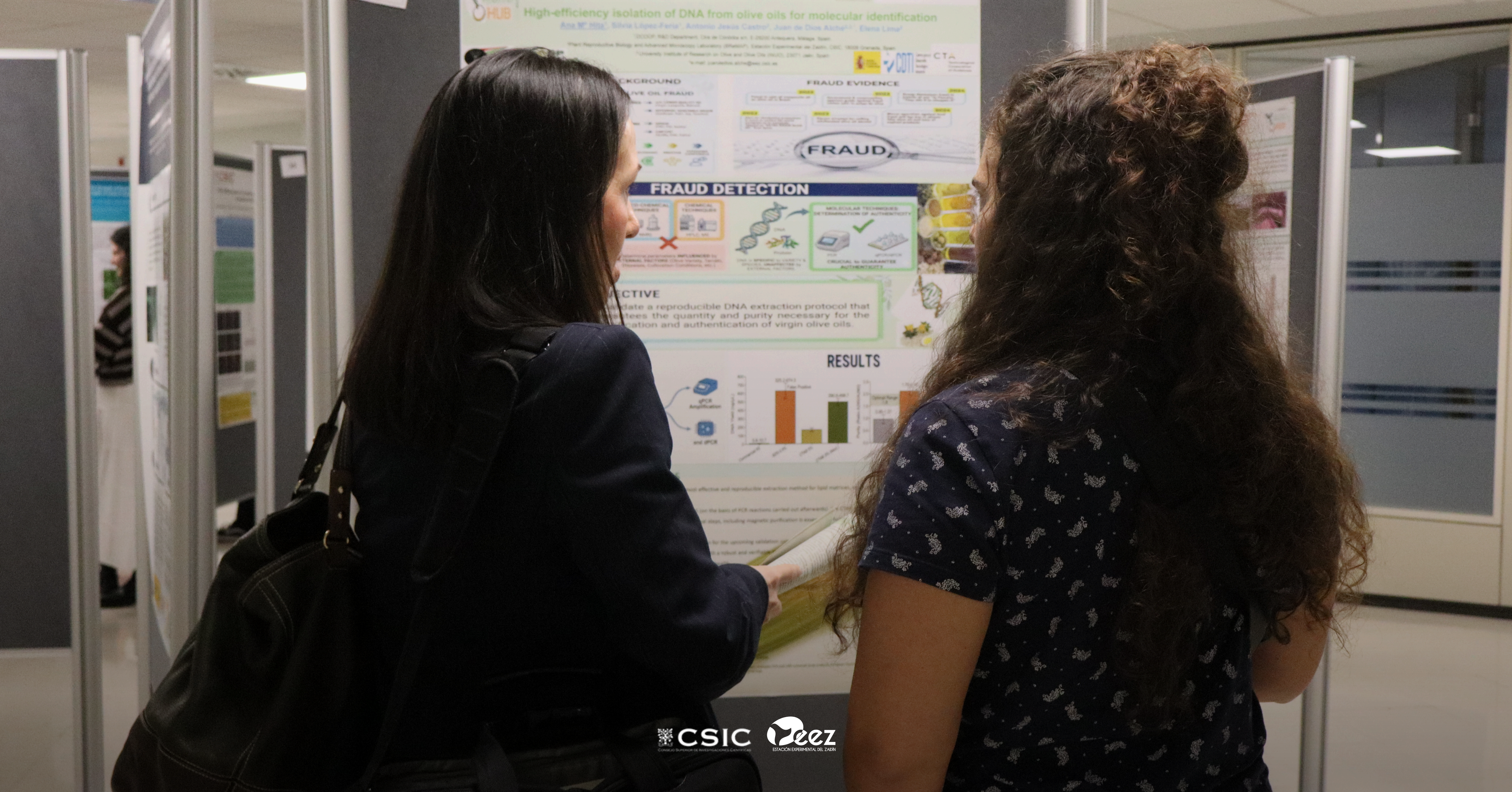
High-efficiency isolation of DNA from olive oils for molecular identification
FRAUD EVIDENCE
FRAUD
FRAUD DETECTION
RESULTS
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2 SYT1 Ca2+-related interactors
eca1/4 mutant generation
eca1/4 x Col0
crossing
MAGENTA
Ca2+ cytosol
YELLOW
wt
syt1
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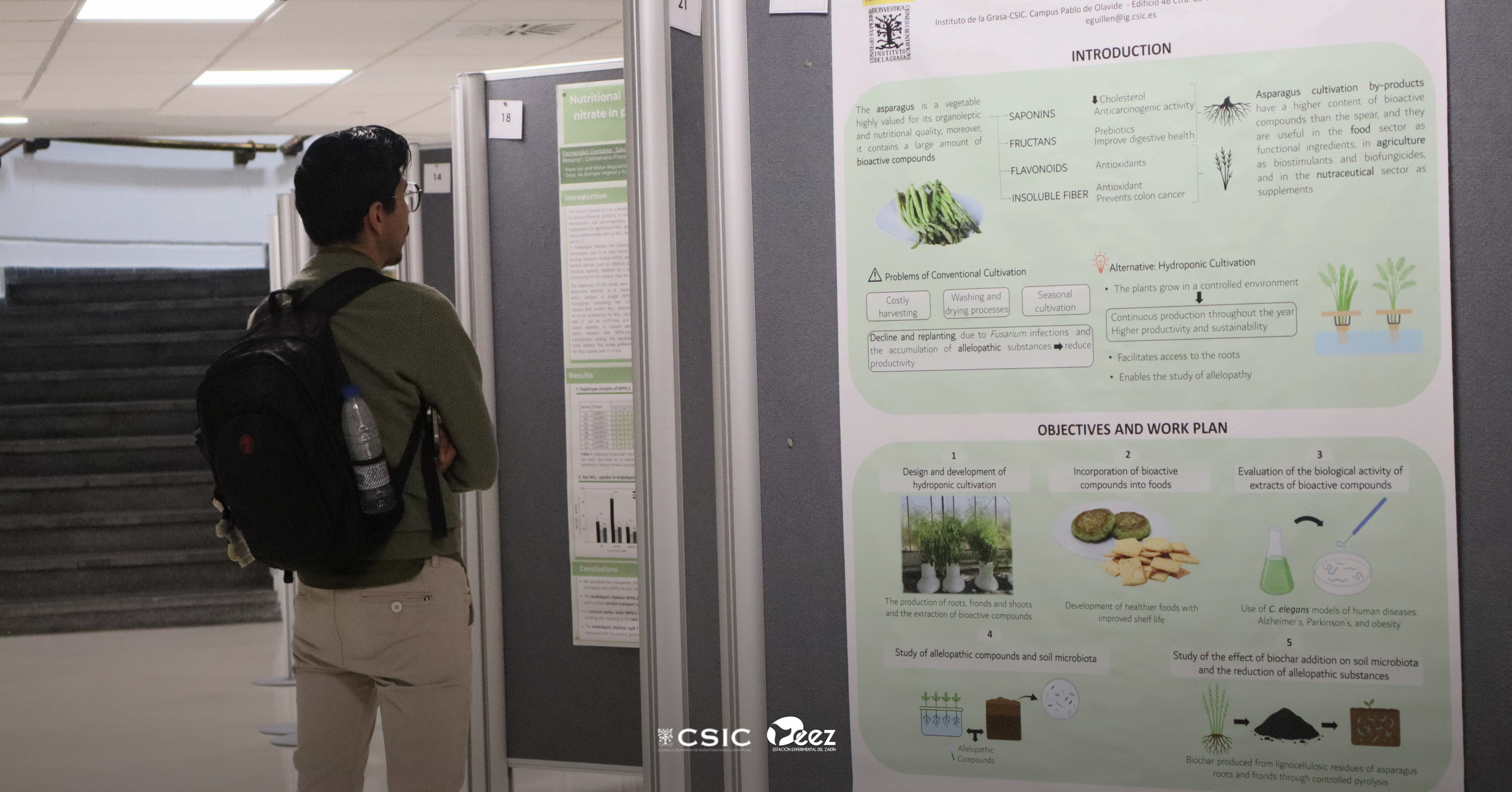
Instituto de la Grasa-CSIC. Campus Pablo de Olavide - Edificio 46
eguillen@ig.csic.es
INTRODUCTION
The asparagus is a vegetable highly valued for its organoleptic and nutritional quality; moreover, it contains a large amount of bioactive compounds
SAPONINS
FRUCTANS
FLAVONOIDS
INSOLUBLE FIBER
Cholesterol
Anticarcinogenic activity
Prebiotics
Improve digestive health
Antioxidants
Antioxidant
Prevents colon cancer
Asparagus cultivation by-products have a higher content of bioactive compounds than the spear, and they are useful in the food sector as functional ingredients, in agriculture as biostimulants and biofungicides, and in the nutraceutical sector as supplements
Problems of Conventional Cultivation
Costly harvesting
Washing and drying processes
Seasonal cultivation
Decline and replanting, due to Fusarium infections and the accumulation of allelopathic substances reduce productivity
Alternative: Hydroponic Cultivation
The plants grow in a controlled environment
Continuous production throughout the year
Higher productivity and sustainability
Facilitates access to the roots
Enables the study of allelopathy
OBJECTIVES AND WORK PLAN
1
Design and development of hydroponic cultivation
The production of roots, fronds and shoots and the extraction of bioactive compounds
2
Incorporation of bioactive compounds into foods
Development of healthier foods with improved shelf life
3
Evaluation of the biological activity of extracts of bioactive compounds
Use of C. elegans models of human diseases: Alzheimer's, Parkinson's, and obesity
4
Study of allelopathic compounds and soil microbiota
Allelopathic Compounds
5
Study of the effect of biochar addition on soil microbiota and the reduction of allelopathic substances
Biochar produced from lignocellulosic residues of asparagus roots and fronds through controlled pyrolysis
18
14
Nutritional
nitrate in p
Introduction
Results
Conclusions
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12/03/26
Agro-Hub PhD Student
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ANTI-INFLAMMAT.
EFFECT
type II phyllobilins
DFCC
EPIGENETIC
REGULATION
Tejo Internacional
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21
Dynamics of the clover endophytic microbiome during phenanthrene rhizoremediation:
implications of the LuxR874 regulator of Novosphingobium resinovorum HR1a
González-Pagán, L., Molina, L. & Segura, A.
Department of Environmental Protection, Estación Experimental del Zaidín, CSIC, Granada.
INTRODUCTION
Figure 3. A. PCoA Bray Curtis Distance of Bacteria.
B. PCoA Bray Curtis Distance of Fungi.
Figure 5. In vitro antifungal activity.
CONCLUSION
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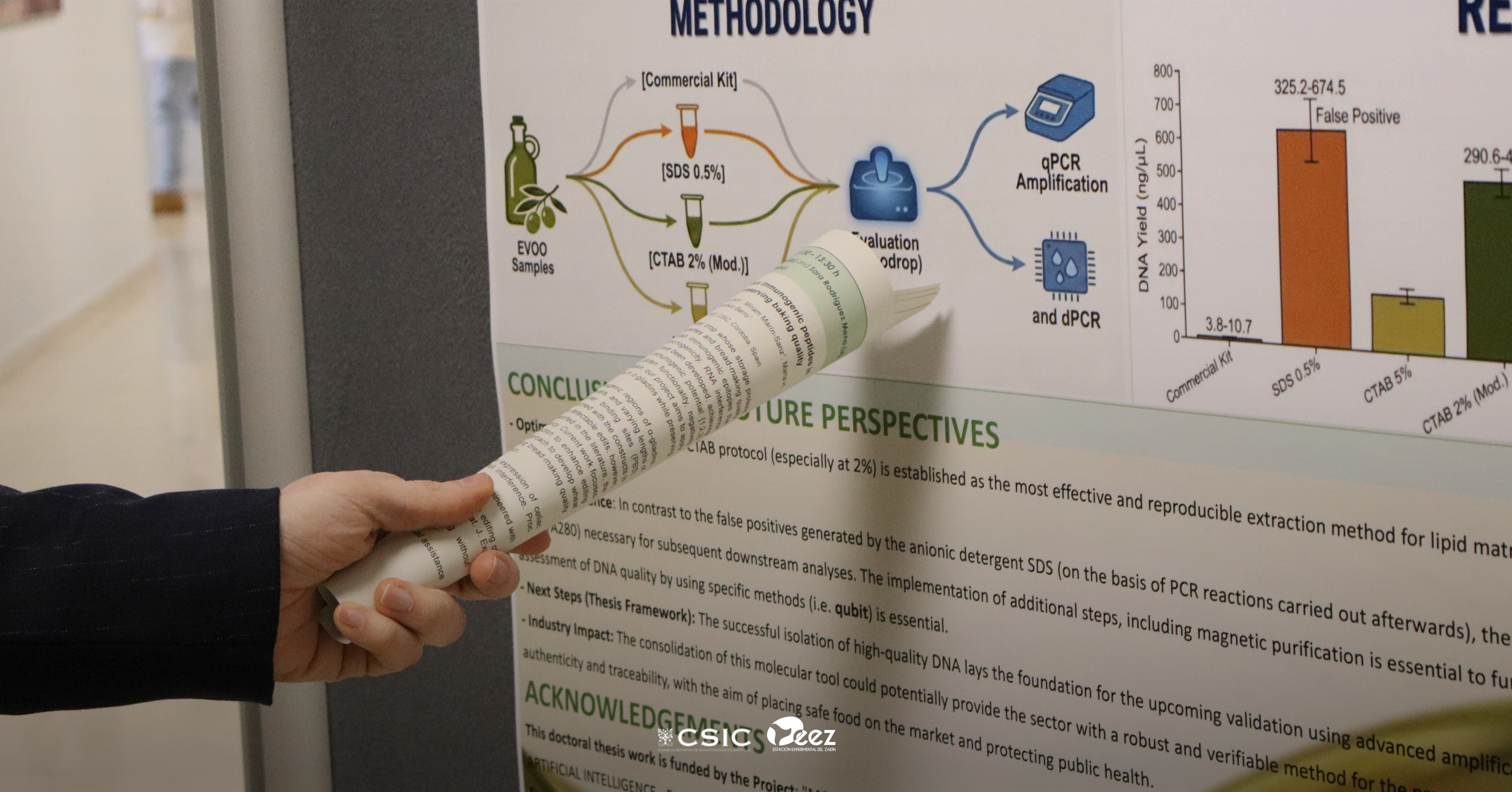
METHODOLOGY
[Commercial Kit]
[SDS 0.5%]
[CTAB 2% (Mod.)]
EVOO
Samples
qPCR
Amplification
and dPCR
DNA Yield (ng/µL)
800
700
600
500
400
300
200
100
0
325.2-674.5
False Positive
3.8-10.7
Commercial Kit
SDS 0.5%
CTAB 5%
CTAB 2% (Mod.)
TURE PERSPECTIVES
CTAB protocol (especially at 2%) is established as the most effective and reproducible extraction method for lipid matr
In contrast to the false positives generated by the anionic detergent SDS (on the basis of PCR reactions carried out afterwards), the
A280) necessary for subsequent downstream analyses. The implementation of additional steps, including magnetic purification is essential to fu
assessment of DNA quality by using specific methods (i.e. qubit) is essential.
- Next Steps (Thesis Framework): The successful isolation of high-quality DNA lays the foundation for the upcoming validation using advanced amplific
- Industry Impact: The consolidation of this molecular tool could potentially provide the sector with a robust and verifiable method for the
authenticity and traceability, with the aim of placing safe food on the market and protecting public health.
ACKNOWLEDGEMENTS
This doctoral thesis work is funded by the Project:
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Extracytoplasmic function sigma factors (σECF) in the regulation of the type III secretion system (T3SS) in Pseudomonas
María Serrano-Morales, Raquel Herrera, Alfonso Lázaro-Payo, and Marian Llamas
Dept. of Biotechnology and Environmental Protection, Estación Experimental del Zaidín-CSIC, Granada
Pathogenic bacteria of the Pseudomonas genus like the phytopathogen Pseudomonas syringae and the human pathogen Pseudomonas aeruginosa use the type III secretion system (T3SS) to inject toxic effectors directly into host cells, promoting virulence and host colonization (Fig. 1). In P. syringae was longer known that production of T3SS requires the function of an extracytoplasmic function σ factor (σECF), which are regulatory proteins that binds to the RNA polymerase promoting transcription of target genes in response to specific signals. By transcriptomic analyses, we recently identified a novel σECF factor of P. aeruginosa, named σRcsI, that controls T3SS production in this pathogen (Table 1). Using green fluorescence protein (gfp) transcriptional fusions of T3SS promoter regions (Fig. 2A) and by Western-blot using an antibody directed to the T3SS protein PcrV (Fig. 2B), we confirmed T3SS induction in response to σRcsI. The σRcsI factor belong to the ECF293 group the activity of which is activated in response to oxidative stress by a signaling cascade that also involves a zinc-containing anti-σ factor encoded by a gene located downstream the rcsI gene (named RcsR) (Fig. 3). By Alphafold, we generated an interaction model of the σRcsI/RcsR complex (Fig. 4A), which was confirmed by BACHT two hybrid analyses (Fig 4B). Besides T3SS genes, our transcriptomic analyses showed that the σRcsI factor promotes production of the methionine sulfoxide reductase MsrP and MsrQ, which have been recently shown to be expressed in response to hypochlorous acid (HOCl), a compound produced by neutrophils in response to pathogens. Using gfp transcriptional fusions to T3SS promoters we demonstrated that the P. aeruginosa T3SS system in induced by HOCl in a σRcsI–dependent manner (Fig 5).
I. Transcriptomic analyses in P. aeruginosa
56 protein coding genes > 5-fold up-regulated in response to σRcsI
III. Genetic context of the σRcsI and RcsR
Figure 3. Schematic representation of the rcsI-rcsR gene cluster
IV. Interaction between the σRcsI and RcsR proteins
Table 1. Result of transcriptomic analysis showing the genes that are induced in response to the σRcsI factor
II. gfp transcriptional fusions to T3SS genes and Western blot
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syt1
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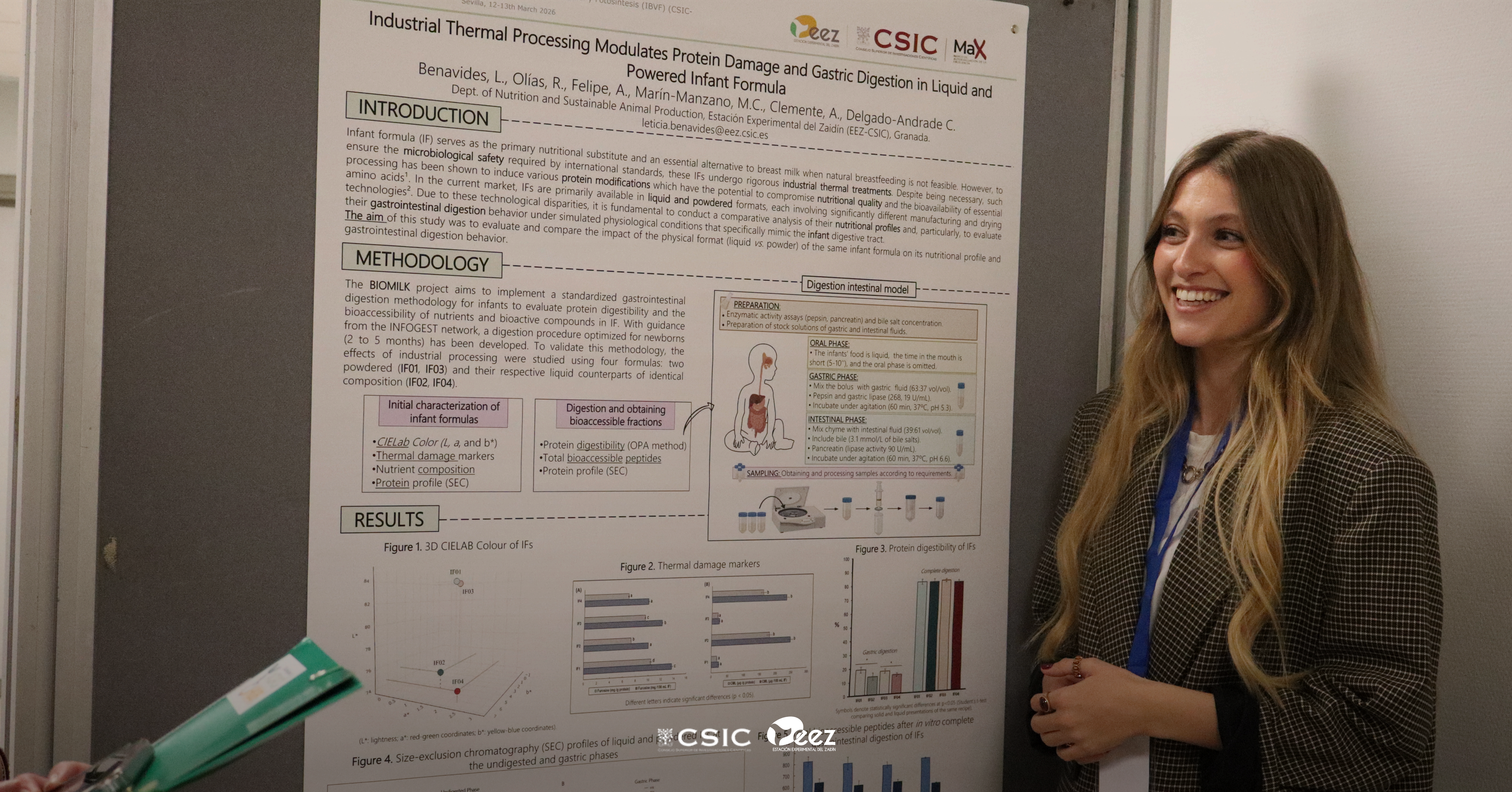
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Industrial Thermal Processing Modulates Protein Damage and Gastric Digestion in Liquid and Powered Infant Formula
Benavides, L., Olías, R., Felipe, A., Marín-Manzano, M.C., Clemente, A., Delgado-Andrade C.
Dept. of Nutrition and Sustainable Animal Production, Estación Experimental del Zaidín (EEZ-CSIC), Granada.
leticia.benavides@eez.csic.es
INTRODUCTION
Infant formula (IF) serves as the primary nutritional substitute and an essential alternative to breast milk when natural breastfeeding is not feasible. However, to ensure the microbiological safety required by international standards, these IFs undergo rigorous industrial thermal treatments. Despite being necessary, such processing has been shown to induce various protein modifications which have the potential to compromise nutritional quality and the bioavailability of essential amino acids1. In the current market, IFs are primarily available in liquid and powdered formats, each involving significantly different manufacturing and drying technologies2. Due to these technological disparities, it is fundamental to conduct a comparative analysis of their nutritional profiles and, particularly, to evaluate their gastrointestinal digestion behavior under simulated physiological conditions that specifically mimic the infant digestive tract.
The aim of this study was to evaluate and compare the impact of the physical format (liquid vs. powder) of the same infant formula on its nutritional profile and gastrointestinal digestion behavior.
METHODOLOGY
The BIOMILK project aims to implement a standardized gastrointestinal digestion methodology for infants to evaluate protein digestibility and the bioaccessibility of nutrients and bioactive compounds in IF. With guidance from the INFOGEST network, a digestion procedure optimized for newborns (2 to 5 months) has been developed. To validate this methodology, the effects of industrial processing were studied using four formulas: two powdered (IF01, IF03) and their respective liquid counterparts of identical composition (IF02, IF04).
Initial characterization of infant formulas
•CIELab Color (L, a, and b*)
•Thermal damage markers
•Nutrient composition
•Protein profile (SEC)
Digestion and obtaining bioaccessible fractions
•Protein digestibility (OPA method)
•Total bioaccessible peptides
•Protein profile (SEC)
Digestion intestinal model
PREPARATION:
• Enzymatic activity assays (pepsin, pancreatin) and bile salt concentration.
• Preparation of stock solutions of gastric and intestinal fluids.
ORAL PHASE:
• The infants' food is liquid, the time in the mouth is short (5-10"), and the oral phase is omitted.
GASTRIC PHASE:
• Mix the bolus with gastric fluid (63:37 vol/vol).
• Pepsin and gastric lipase (268, 19 U/mL).
• Incubate under agitation (60 min, 37ºC, pH 5.3).
INTESTINAL PHASE:
• Mix chyme with intestinal fluid (39:61 vol/vol).
• Include bile (3.1 mmol/L of bile salts).
• Pancreatin (lipase activity 90 U/mL).
• Incubate under agitation (60 min, 37ºC, pH 6.6).
SAMPLING: Obtaining and processing samples according to requirements.
RESULTS
Figure 1. 3D CIELAB Colour of IFs
IF01
IF03
IF02
IF04
(L*: lightness; a*: red-green coordinates; b*: yellow-blue coordinates)
Figure 2. Thermal damage markers
Different letters indicate significant differences (p < 0.05)
Figure 3. Protein digestibility of IFs
Complete digestion
Gastric digestion
Figure 4. Size-exclusion chromatography (SEC) profiles of liquid and powdered the undigested and gastric phases
ccessible peptides after in vitro complete intestinal digestion of IFs
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