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Division of Science for Food, Bioproducts and Waste TRANSFORM

Michael O'Donohue, Laurence Fournaison, Mélanie Delclos, Rachel Boutrou

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INRAE

Research and Innovation 2020 For Food, Bioproducts & Waste

Division of Science for Food, Bioproducts and Waste
TRANSFORM

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LEGAL MENTIONS

Editor: *Michael O'Donohue, Head of division*

Editorial committee: *Cécile Barron, Rachel Boutrou, Sylvie Clerjon, Paul-Henri Ducrot, Pascale Manchado-Sarni, Carole Tournier, Gabriel Paës, Laurence Prévosto, Olivier Tranquet, Olivier Vitrac, Catherine Garnier, Laurence Fournaison*

Design: *Mélanie Delclos*

INRAE
Division of Science for Food, Bioproducts and Waste TRANSFORM
3 impasse Yvette Cauchois
CS 71627 44316 Nantes Cedex 03
Tél. +33 (0)2 40 67 51 45
transform@inrae.fr

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Foreword

A new community, new ambitions

This report is unlike any other, because it is the first from the brand-new TRANSFORM division. The merger of INRA and IRSTEA led to the creation of TRANSFORM, an INRAE division entirely devoted to science for the food, non-food and bioproduct and waste engineering. This new division, of which we are very proud, contains all the ingredients necessary to allow INRAE to become a major provider of technology innovations for the circular bioeconomy.

Sustainability is a recurrent theme throughout this report. Whether it is a matter of sustainable food, codesigned processes, for example that use less energy, or biobased products, the work of my staff members is driven by a common will to contribute to the circular bioeconomy transition. When reading this report you will notice that sustainability is not just about environmental impact. On the contrary, to confer sustainability to processes, products and associated functions one must take on board a wide range of considerations, finding the right balance between environmental impact, social acceptability and economic viability. This is why our research addresses fundamental and applied scientific questions related to the quality of products and the efficiency of processes, and also applied mathematics and data science, methods that allow us to better visualize our results, organize and exploit our knowledge and predict the quality and impact of our research products.

While wishing you a very pleasant read of this inaugural annual report of the TRANSFORM division, I would like to take the opportunity to thank my staff members for their engagement and enthusiasm in the service of science.

Michael O'Donohue

Head of division

TRANSFORM - Division of Science for Food, Bioproducts and Waste Engineering

Technical Processes

TRANSFORM has a large range of advanced equipment located within institutional research infrastructures. This year, several research infrastructures have been awarded by INRAE, such as the European platform IBISBA, the distributed research infrastructure PROBE and seven other collaborative scientific infrastructures. You will also find two examples of scientific advances achieved with the BIBS platform equipment.

RECOGNISED INFRASTRUCTURES

PROBE

Autumn 2019 marked a landmark for the distributed research infrastructure called PROBE–Platform for profiling properties of food and biobased products–as it secured the official INRAE contract-network stamp.

Food and non-food agricultural crops share a complex yet versatile array of structures and compositions that shape and dictate their properties in use. The sensory attributes of raw and processed foods, for example, depend on the ability of key molecules like aroma compounds to diffuse in the food-material matrix. The success of the bioeconomy also hinges on our ability to characterize bioresources and bioproducts and predictively map out how agricultural raw materials could be repurposed to make innovative materials with specific functional properties. This means that regardless of whether the purpose targeted is food or non-food use, we need to develop methods and concepts to (i) analyze a diverse array of complex heterogeneous crop resources and (ii) capture the structural changes occurring through processing trajectories that shape the functionalities of the end-products.

The PROBE distributed research infrastructure is setting out to acquire and integrate advanced science on the structure, properties, and functionalities (including sensoriality) of the input materials, in-process products, and end-product outputs. The strategy is to deploy a battery of physical-chemical methods at a range of scales in order to pinpoint the impact of pivotal structural parameters on product quality, properties, and functionality–whether for food or non-food use. PROBE leverages advanced competences across 4 platforms articulating highly complementary competences in terms of molecules studied and approaches mobilized: (i) BIBS (Nantes), for structural characterization and localization of biopolymers like polysaccharides and lipids; (ii) ChemoSens (Dijon), for physical-chemical and organoleptic characterization of foods and lipid profiling in foods and neurosensory tissue; (iii) Polyphenols, for characterization of plant-source polyphenols, foods and processables; and (iv) AgroResonance, for coordinated deployment of NMR and MRI methods to advance food–farming, plant science, nutrition, and health.

TRANSFORM at the heart of IBISBA

EU-IBISBA

IBISBA (Industrial Biotechnology Innovation and Synthetic Biology Acceleration) is a distributed European infrastructure project that is present since September 2018 on the ESFRI roadmap (www.ibisba.eu). Currently IBISBA is supported by European H2020 funding (H2020 projects IBISBA 1.0 and PREP-IBISBA). On the 1st January 2020, EU-IBISBA entered into preparatory phase, meaning that the project is moving forward towards future implementation of the research infrastructure in the form of a new European legal entity. The preparatory phase provides the time and funds to study the business case and model for this entity, and also to prepare its legal statutes.

IBISBA-FR

As a distributed European infrastructure, EU-IBISBA is built upon existing infrastructure in different member states. IBISBA's French node is supported by INRAE, the CEA and the CNRS. Currently, the INRAE components involved are Toulouse White Biotechnology and ICEO, a core facility that offers enzyme screening and engineering services. The INRAE contingent of IBISBA-FR is completed by the contribution of third party services from other INRAE infrastructure (METATOUL, a component of IR METABOHUB and GeT-Biopuces, a component of GenoToul) and from the MICALIS laboratory.

What does IBISBA aim to do ?

IBISBA federates and coordinates research infrastructure across Europe, building the capacity to operate end-to-end bioprocess development, translating promising early research results into innovation and piloted tested process. To achieve this, IBISBA is building a community of infrastructure trained to work together and thus achieve operational interoperability. Currently, funding available in the framework of IBISBA 1.0 is providing subsidized infrastructure access to researchers across Europe and from third countries.

Harmonization and FAIRization of knowledge assets

As a European research infrastructure, IBISBA is conducting cutting edge work on FAIR data and is promoting harmonization of practices, in favour of research reproductibility. Currently, IBISBA operates a data repositry (IBISBAhub - hub.ibisba.eu) that can be used by anyone (IBISBA members and non-members alike can create an account) to FAIRize data and knowledge assets. IBISBAhub can do lots of things, including minting of DOIs. The idea behind IBISBAhub is to create a knowledge commons that will provide a means to share standardized protocols, experimental and automated workflows, as well as other research items that are of interest to the wider industrial biotechnology community.

TRANSFORM collective scientific facilities

AGRORESONANCE - UR QUAPA

Nuclear Magnetic Resonance (NMR) phenomena captured in spectra or images (MRI) are exploited for a broad panel of analytical methods that make it possible to determine the structural chemistry of organic compounds, quantify the dynamics of small molecules, and characterize the organization of matter at different scales. NMR thus gives access to precious information on the composition and structure of tissues and materials and the workings of the living world.

The AgroResonance platform is part of the INRAE Clermont-Auvergne-Rhône-Alpes research campus. It hosts top-flight competences and cutting-edge facilities to propose analysis and development work and resolve key questions in food–farming, plant science, nutrition, and health.

AgroResonance is certified to ISO 9001 and carries the sponsored 'infrastructural science facility' seal. As founder member of the IBiSA-sponsored regional multimodal imaging platform In Vivo Imaging in Auvergne (IVIA), it also enjoys access to the vast majority of Clermont-Ferrand-community in vivo imaging facilities for animals and humans.

Contact: jean-marie.bonny@inrae.fr

BIOPOLYMERS, STRUCTURAL BIOLOGY - UR BIA

Physical-chemical characterization of natural bioresources and bioproducts from millimetre-scale down to nanometre-scale. BIBS articulates bespoke equipment purpose-engineered for studying biopolymers (polysaccharides, proteins, lipids). This hardware is used to characterize their structures (identification, modifications) and how they interact, organize and localize in biological systems (like plant tissues/organs, algae, or bacterial media) and synthetic systems (typically foods, food matrices, biofilms, and composite materials). The BIBS campus is also geared to tackle dynamic parameters (diffusion, water mobility), track degradative or transformative processes at work, and screen large sample libraries on chemical and structural criteria.

Contact: contact-bibs@inrae.fr

ENVIRONMENTAL BIOTECHNOLOGY AND BIOEFINERY PLATFORM - BIO2E - UR LBE

Bio2E–the Environmental Biotechnology and Biorefinery platform–transfers and translates technologies developed through research led at LBE–the Environmental Biotechnology Laboratory. Bio2E connects the INRAE Transfert business unit's portfolio of contract-service activities with LBE's R&D partnerships offer. This articulation enables the top-flight competences developed at LBE to reach out to industry. The Bio2E platform tailors its offer to fit partner needs: collaborative R&D, contract-service analytics, feasibility studies, training and education, expertise, hosting, industrial facility commissioning and diagnostics.

Contact: diana.garcia-bernet@inrae.fr

CHEMOSENS- UMR CSGA

ChemoSens is the research and methods engineering platform serving INRAE's Centre for Taste & Food Science (CSGA) in Dijon. It breaks new science ground by combining chemistry with sensory analysis to develop novel approaches for characterizing foods and foodways.
ChemoSens mobilizes techniques borrowed from physical-chemical analysis to characterize the flavour compounds in a food and profile the tastant molecules that get released as we eat it. It possesses advanced scientific expertise in lipid profiling in foods and neurosensory tissue.
ChemoSens is also internationally reputed as a lead authority in the sensometrics arena, and some of its flagship methods–like 'temporal dominance of sensations'–have gained currency across the globe. ChemoSens has compiled vast databases and developed the TimeSens® online software bundling sensory data acquisition with statistical analysis.
Contact: geraldine.Lucchi@inrae.fr

MILK SCIENCE PLATFORM (PFL) - UMR STLO

PFL is an 'experimental facility' (https://www6.rennes.inrae.fr/plateforme_lait) equipped to co-host a suite of dairy technology processes at different scales and through flexible yet firmly controlled routes including fractionation of milk compounds, fashioning dairy matrices to a gradient of concentrations with or without fermentation (fresh produce, cheeses or condensed milk), and matrix dry-out. The 800m² facility was entirely refitted in 2013 and has been ISO 9001-certified since 2009. The platform is open to university and industry partnerships. It mobilizes in-house expertise (technology, process engineering, biochemistry, microbiology, nutrition, and eco-design) that is put to work on university or private-sector research projects and advanced training programmes delivered to the next generation of food-industry leaders.

Contact: gilles.garric@inrae.fr

PLANET PLATFORM - UMR IATE

PLANET is an experimental platform developed and run by the IATE joint research unit that boasts around 700 m² of research space–including 150 m² dedicated to food science–housing around a hundred instrumented equipment systems working from lab scale (with a few grammes) up to pilot scale (10-or-so kg) alongside prototypes developed in tandem with the unit's research engineers. These equipment systems are tasked with scaling unit-operation process routes for transforming plant biomass streams into commodity feedstocks to support food, energy, material or green chemistry applications. The platform tackles focal challenges ranging from cereal commodity fractionation and structure science to dry refinery of lignocellulosic biomass and agrimaterial formwork, and back to characterization of crude feedstocks, process powders, and end-products. A core team of 6 dedicated FTEs runs the unit and leads its technology and methodology development effort.

Contact: adrien.reau@inrae.fr

TOULOUSE WHITE BIOTECHNOLOGY (TWB)

TWB delivers expert project engineering to support the development of sustainable bio-driven process pathways by leveraging alternative economically-compelling industrial biotechnology solutions. With that vision, TWB federates collective intelligence by creating new research–industry–investor intersections and connects this community to its science and technology resource platforms that offer cutting-edge strain engineering and culture and fermentation processes.

TWB was created in 2012 via a three-way INRAE–INA–CNRS stewardship and support agreement (with INRAE as lead administrator) and by 2020 it had built up a consortium of 52 public-/private-sector partners. In this time, TWB has helped to launch 184 collaborative R&D research projects and helped to grow a hive of start-ups that in total have attracted nearly €100M in seed capital.

Contact: paquet@insa-toulouse.fr

X-ray micro-computed tomography (µCT) tracks wheat grain morphology through its development

Read more

Le DQT, Alvarado C, Girousse C, Legland D, Chateigner-Boutin AL

Use of X-ray micro computed tomography imaging to analyze the morphology of wheat grain through its development, Plant Methods . 2019

Contacts

David Legland and Anne-Laure Chateigner-Boutin

BIA (UR 1268)

david.legland@inrae.fr

anne-laure.chateigner-boutin@inrae.fr

Context

Wheat is one of the most important cereal crops farmed, used in staple foods that feed much of Europe and the world. Declining crop yields and the impact of grain shape on flour milling yields make it paramount to better map out and quantify morphology changes in the developing wheat grain. Microscopy imaging–the standard approach for plant tissues–is held back here, as the field-of-view is limited and the sample has to be sliced to get a mountable section. Our objective was to put together a methodology for quantifying developmental changes in morphology through wheat grain growth from 3D µCT images.

Results

3D µCT images of whole wheat grains were acquired at various developmental stages at a spatial resolution of just a few microns. We developed methods to identify inner and outer wheat grain tissues (endosperm, germ, and pericarp) and an image processing pipeline to semi-automatically segment these different compartments of the grain–all in 3D. A morphometric analysis added to the workflow then brought quantitative description of the variations in wheat grain morphology through developmental growth–from changes in tissue sizes and relative volumes to variations in crease shape, which is a key trait for the flour milling processes.

Future Outlook

We anticipate this research to better identify the focal regions involved in wheat grain growth and shape changes. We are now working on applying a statistical shape modelling protocol to identify the representative grain shapes for each developmental stage and, ultimately, to build a 4D model (3D+time dimension) of wheat grain growth. Merging grain anatomy data captured by tomography with information from other modalities (such as compositional clues captured by microscopy) should provide a clearer picture of how wheat grain growth processes work at tissue scale.

@Le DQT, Legland D. et Chateigner-Boutin AL

Imaging of the developing grain: macroscopic imaging, reconstruction by X-ray micro-tomography, and segmentation of the different compartments. On the left an early stage of development (100 degree days after flowering) and on the right the grain filling stage (300 degree days after flowering).

@INRAE - David Ropartz

High-resolution ion mobility to probe biomolecular structures

Read more

Ujma J; Ropartz D; Giles K; Richardson K; Langridge D; Wildgoose J; Green M; Pringle S. *Cyclic Ion Mobility Mass Spectrometry Distinguishes Anomers and Open-Ring Forms of Pentasaccharides.*

Journal of the American Society for Mass Spectrometry . 2019

Ropartz, D; Fanuel, M; Ujma, J; Palmer, M; Giles, K; Rogniaux, H
Structure Determination of Large Isomeric Oligosaccharides of Natural Origin through Multipass and Multistage Cyclic Traveling-Wave Ion Mobility.

Mass Spectrometry Analytical Chemistry . 2019

Contacts

David Ropartz and Hélène Rogniaux
BIA (UR 1268)
david.ropartz@inrae.fr
helene.rogniaux@inrae.fr

Context

The structural determination of polysaccharides and oligosaccharides is crucial for understanding their biological function and usability in industry. Degree of polymerization, nature of the sugar monomers, bonding between building blocks, and chemical substituents are all key structural features. However, characterizing polysaccharides remains a challenge for analytical chemists due to the complexity and heterogeneity of the structures involved.

Mass spectrometry (MS) is ideally placed as a method for addressing these issues, but MS analysis cannot differentiate between identical-mass conformational isomers. Coupling MS with ion mobility (IM) spectrometry to separate gas-phase ions based on their conformation is an attractive approach to unlock the power of MS for structural glycoscience. However, the separation resolution currently achievable in IM is still too underpowered to characterize subtle differences when carbohydrates have a high degree of polymerization.

Results

Since 2015 we have been working hand in hand with Waters to develop a new, applied-research-ready, high-resolution ion mobility technology. This disruptive technology has introduced a multi-pass cyclic ion mobility separator that allows ions to travel theoretically unlimited drift lengths.
We showed that it makes an appropriate technology for separating isomers in mixtures, and we demonstrated that it can separate **α**-ring, **β**-ring and open-ring anomeric configurations for each given isomer. Working on a complex mixture, we also evidenced the different conformers released by a degradative enzyme on a polysaccharide, which made it possible to define the specific activity of the enzyme by providing–for the first time–quantitative information on the different species formed.

Future Outlook

The new levels of knowledge unlocked with this approach mark a big stride forward in glycoscience research. The instrument was installed at the BIBS platform in November 2019, making it only the second of its kind in Europe and the first to be used to decipher carbohydrate structure. The technology will be coupled with high-performance liquid chromatography to further extend the possibilities for investigating complex mixtures and further expand its analytical dynamic range.

Catalyze through sustainable routes

Enzymes are produced naturally by microorganisms. They are put to work as 'organic' catalysts to sustainably drive the conversion of plant biomass under 'green' process conditions.

This write-up illustrates how TRANSFORM scientists have learned to work with enzymes to debottleneck the recalcitrance of plant biomass to enzymatic hydrolysis. We also study how enzymes work deep inside plant cells–in the cell wall where they are involved in reshaping the polymer-linked architecture, and in the seeds where oil stores accumulate.

Discovery of a new fungal family of metalloproteins

Read more

Labourel A, Frandsen KEH, Zhang F, Brouilly N, Grisel S, Haon M, Ciano L, Ropartz D, Fanuel M, Martin F, Navarro D, Rosso MN, Tandrup T, Bissaro B, Johansen KS, Zerva A, Walton PH, Henrissat B, Leggio LL, Berrin JG
A fungal family of lytic polysaccharide monooxygenase-like copper proteins. Nature Chemical Biology. 2020

Filiatrault-Chastel C, Navarro D, Haon M, Grisel S, Herpoël-Gimbert I, Chevret D, Fanuel M, Henrissat B, Heiss-Blanquet S, Margeot A, Berrin JG.
AA16, a new lytic polysaccharide monooxygenase family identified in fungal secretomes. Biotechnology for Biofuels. 2019

Research collaborations

- INRAE, Biodiversité et Biotechnologie Fongiques (BBF), UMR1163, Aix Marseille Université, Marseille, France
- Biological Chemistry Section, Department of Chemistry, University of Copenhagen, Copenhagen, Denmark
- INRAE, UMR1136, Interactions Arbres/Microorganismes, Laboratoire d'Excellence ARBRE, Centre INRAE-Lorraine, Université de Lorraine, Champenoux, France
- Department of Chemistry, University of York, York, UK
- INRAE, UR 1268 Biopolymères Interactions Assemblages (BIA) Nantes, France
- INRAE, CNRS, USC1408 Architecture et Fonction des Macromolécules Biologiques (AFMB), Marseille, France

Contact

Jean-Guy Berrin
BBF (UMR 1163)
jean-guy.berrin@inrae.fr

Context

Lytic polysaccharide monooxygenases (LPMO) are copper enzymes found in filamentous fungi and bacteria. These enzymes were discovered over a decade ago, but they have already revolutionized the way we see lignocellulose degradation. LPMOs are specialized in the enzymatic degradation of plant biomass through oxidative degradation of recalcitrant polysaccharides. Industry employs LPMOs in the enzyme cocktails used to process plant biomass feedstock into energy (second-generation biofuels). These same enzymes can also be constructively exploited to produce cellulose-based materials.

Results

While hunting for new LPMOs in wood-decaying fungi, we discovered a whole new family of proteins of unknown function in various fungal lineages that shared different lifestyles (symbionts to saprotrophs to pathogens). 3D structure and sequence analysis showed that these new proteins share huge overlaps with LPMOs. Although they can bind copper just like LPMOs, they otherwise form a distinct family of proteins that are devoid of enzymatic activity, which suggests they evolutionarily diverged to alternative functions. Investigation into the biological role of these LPMO-like proteins in the ectomycorrhizal symbiont fungus *Laccaria bicolor* found that the proteins localize to the interface between fungal hyphae and tree rootlet cells. One member is also found in *Cryptococcus neoformans*–the pathogenic agent that causes fungal meningitis. The American team went on to show that suppressing the gene encoding this protein neutralized much of its pathogenicity. This new protein family is evolutionarily tied to LPMOs.

Future Outlook

This research opens up opportunities to investigate vital biological processes.

A whole new look at lignin recalcitrance

Read more

Lambert E, Aguié-Béghin V, Dessaint D, Foulon L, Chabbert B, Paës G, Molinari M

Real time and quantitative imaging of lignocellulosic films hydrolysis by Atomic Force Microscopy reveals lignin recalcitrance at nanoscale.

Biomacromolecules . 2019

Mobilization and Impact

- PhD thesis defended in December 2018 by Eléonore Lambert
- Two ANR-funded projects (Lignoprog et Funlock)

Contact

Gabriel Paës

UMR FARE

gabriel.paes@inrae.fr

Context

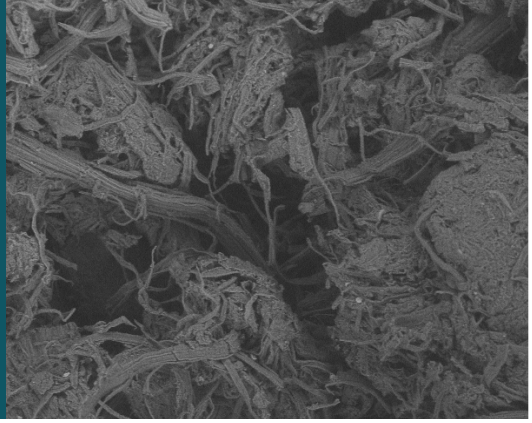
To optimize the processing of lignocellulosic biomass, the way forward hinges on imaging, which gathers approaches drilling down on a gradient of scales–from mm to nm–via photon, electron and atomic force microscopy techniques. These are powerful tools for understanding the recalcitrance of the biomass and the role played by lignin which is widely recognized as a bottleneck to more efficient bioprocesses. Atomic force microscopy (AFM) images have so far provided essentially qualitative characterization but have failed to capture nanoscale structure changes.

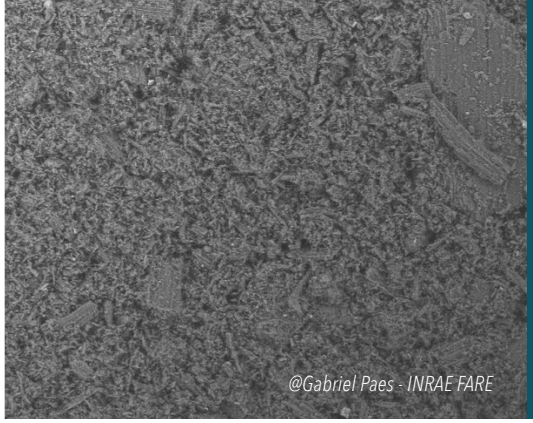
Results

Here, to devise a working protocol for dynamic AFM-enabled observation of lignocellulolytic enzymes at work, we prepared polymer films containing cellulose and varying amounts of lignin. The lignin content translates into less-efficient enzymatic hydrolysis. To study the impact of lignin at nanometre-scale, we developed an in-situ time-lapse AFM imaging system to visualize the hydrolysis process over a time-window of several hours. We were able to observe differences in lignin node and plaque arrangements with different lignin concentrations and to see how these structures changed patterns over the course of hydrolysis. The real breakthrough was that we managed to quantify the structural time–course change in film surface by developing a new marker–our 'relative deconstruction index'–that proves sharper than conventional topographic imaging measurements. This index helped us to learn that recalcitrance to hydrolysis is explained not just by net lignin content but also by lignin distribution down at polymer scale. This pivotal finding enabled us to establish, for the first time with quantitative nanometre-scale AFM-enabled evidence, the barrier effect of lignin-packed structures against enzymatic action.

Future Outlook

The next step is a quantitative dynamic deconstruction study on samples of the far more structurally complex and challenging wood lignocellulose. As this approach is already firmly methodized at cellular scale, we will ultimately be equipped to perform dynamic multi-scale observations (along the cellular-scale to polymer-scale gradient) of enzymatic action at work.





Fungal enzymes: the key to unlock hydrolysis of plant biomass

Read more

Paës G, Navarro D, Benoit Y, Blanquet S, Chabbert B, Chaussepied B, Coutinho PM, Durand S, Grigoriev IV, Haon M, Heux L, Launay C, Margeot A, Nishiyama Y, Raouche S, Rosso MN, Bonnin E, Berrin JG

Tracking of enzymatic biomass deconstruction by fungal secretomes highlights markers of lignocellulose recalcitrance.

Biotechnology for Biofuels . 2019

Contacts

Jean-Guy Berrin, Gabriel Paës, Estelle Bonnin

UMR BBF, UMR FARE, UR BIA

jean-guy.berrin@inrae.fr

gabriel.paes@inrae.fr

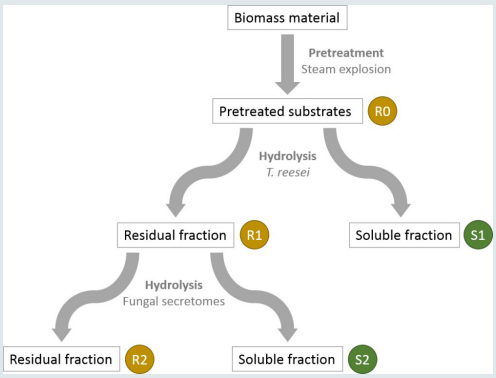
estelle.bonnin@inrae.fr

Context

The recalcitrance of plant biomass to enzymatic hydrolysis is a multifactorial problem for industry. The funded FUNLOCK project set out to identify novel enzymes to unlock the enzymatic deconstruction of plant biomass. This enzymatic hydrolysis step is one of the limiting factors strangling the current process for producing second-generation biofuels from lignocellulosic biomass. One of the first challenges set for the project was to identify markers of recalcitrance.

Results

The approach adopted was to perform structural and chemical analyses of the recalcitrant fraction before and after enzymatic treatment of various substrates in order to pinpoint and overcome the hurdles to efficient hydrolysis. The project team studied a large panel of markers in order to track and trend progress of the enzymatic reactions. They evaluated the effect of cocktails of fungal enzymes secreted by three species of basidiomycete fungi put to work on several lignocellulosic residues. Structural modifications to soluble and insoluble fractions were analyzed using spectroscopic methods and cutting-edge biophysical techniques. The fungal secretomes applied to highly-recalcitrant biomass samples expanded the window of release of remaining sugars. The correlations between these markers essentially reveal how nanometre-scale properties (polymer content and organization) influence macro-scale properties (particle size). This sharp approach has identified relevant markers of deconstruction (water sorption) to guide target-enzyme selection using multivariate analysis.



Sequential steps in fungal enzyme-driven hydrolysis of lignocellulosic biomass samples

Future Outlook

We have found these fungi but not yet uncovered all their secrets, so we need to push ahead with further investigation into their enzymatic machinery. An even deeper systematic time–course evaluation of these markers through the process of enzymatic digestion-driven deconstruction of lignocellulosic biomass will serve to develop novel enzyme cocktails for biorefineries. Tracking these markers will inform a finer-grained study into the enzymatic hydrolysis step in order to improve the second-generation biofuel production process using lignocellulosic biomass feedstocks.

Enzyme mobility through structured media

Read more

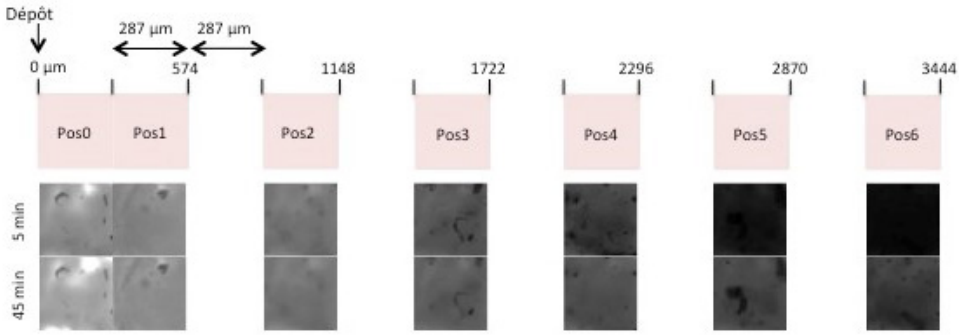
Bonnin E, Alvarado C, Bouchet B, Garnier C, Jamme F, Devaux, M-F

Mobility of pectin methylesterase in pectin/cellulose gels is enhanced by the presence of cellulose and by its catalytic capacity.

Scientific Reports . 2019

Context

Out in nature, enzymes are often at work in environments where material density and structural barriers can cut short their activity. A case in point comes from the enzymes acting on the plant cell wall, which is a complex network of polysaccharides and polymer assemblies that envelopes each cell. The aim of this research is to mimic the cell wall by preparing complex substrates structured with cell wall polysaccharides, then use this model to investigate the behaviour of cell wall-degrading enzymes.



Enzyme diffusion through a pectin/cellulose gel between spot deposition (at left) and 3.5 mm into the gel.
Line at top: Positions of the images / Line at middle: Images of the enzyme inside the gel 5 minutes after deposition.
Line at bottom: Images of the enzyme inside the gel 45 minutes after deposition

Results

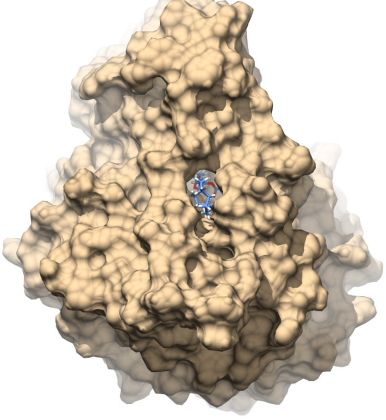
We studied the diffusion of native-active or heat-inactivated pectin methylesterase in pectin/cellulose gels. Its time–course movement through these gels was tracked using its deep-UV autofluorescence signal at the SOLEIL synchrotron facility, and a bespoke image processing protocol was developed to quantify the time–course signal intensity of its diffusion kinetics at micrometric scale. Our results show that enzyme diffusion is dictated by at least two criteria: i) only the active enzyme was able to diffuse, which shows that enzyme mobility hinges on catalytic ability– enzyme motion is likely driven by the heat released during catalysis; ii) enzyme migration was improved by the presence of cellulose in the gel, which suggests that the mixture of the two polysaccharides allows pores to form and facilitate diffusion of the enzyme.

Future Outlook

Here we showed that the enzymes involved in reshaping the polymer-linked plant cell wall architecture over the cell's life are able to effectuate through-cell-wall movement over a distance of µm up to a few mm once they get activated. The next step is to get a step closer to *in vivo* by working on systems with a higher solid content and studying the behaviour of several enzymes operating in synergy.

Contact

Estelle Bonnin
UR BIA
estelle.bonnin@inrae.fr



@Eric Dubreucq

How do flavonols inhibit a lipase without occupying the catalytic site?

Read more

Nasri R, Bidel L PR, Rugani N, Perrier V, Carriere F, Dubreucq E, Jay-Allemand C

Inhibition of CpLIP2 Lipase Hydrolytic Activity by Four Flavonols (Galangin, Kaempferol, Quercetin, Myricetin) Compared to Orlistat and Their Binding Mechanisms Studied by Quenching of Fluorescence.

Molecules . 2019

Contacts

Luc Bidel, Eric Dubreucq and Christian Jay-Allemand

UMR IATE and AGAP

luc.bidel@inrae.fr

eric.dubreucq@supagro.fr

christian.jay-allemand@umontpellier.fr

Context

Inhibition of CpLIP2–a recombinant lipase from *Candida parapsilosis*–is a model in antifungal drug discovery. The CpLIP2 enzyme is inhibited by four flavonols: galangin, kaempferol, quercitin, and myricetin. The mechanisms of CpLIP2 inhibition by flavonols can be probed by using intrinsic tryptophan fluorescence quenching through flavonol–lipase interactions and comparing the variations against the effects of a brand-name pharmaceutical lipase inhibitor–in this case, orlistat (tetrahydrolipstatin).

Results

After a 60-second pre-incubation with CpLIP2, kaempferol (14 µM) strongly inhibited its hydrolytic activity by an estimated 80% using ethyl oleate as model substrate. We established a relationship between accessible surface area per tryptophan and number of binding sites per enzyme for all the flavonols tested.
The CpLIP2 lipase contains 7 tryptophan residues that vary in fluorescence with degree of hydrophobicity of their microenvironment: fluorescence decreased by a static quenching mechanism as lipase–flavonol complexes formed. The quenching constant correlated strongly to lipase activity in the presence of inhibitors, which raises prospects for developing a fluorescence-based screening method to discover potent new inhibitors of enzymes involved in infection mechanisms.
The study exposed the crucial role of number of hydroxyl groups on the flavonol B-ring. Furthermore, we identified a potentially potent combination (galangin + myricetin) for securing synergistic effects that mobilize noncovalent binding forces. Based on our theoretical calculations, the 4 flavonols tested here preferentially occupy the hydrophobic microenvironment surrounding one of the 7 tryptophans in the protein lid, including in the presence of orlistat binding to the active-site pocket.
These new but early insights suggest that the flavonols were able to inhibit the activity of the enzyme–without occupying the catalytic site–by tightly limiting access to substrates. This process could arise from changes in the physical-chemical properties of the substrates access channel, but also from conformational changes in the domain regulating enzymatic activity.

Future Outlook

We now aim to validate the mechanisms of CpLIP2 inhibition by kaempferol and further explore the role played by aromatic amino acids like tryptophan in these mechanisms.

Iron—a new cofactor in seed oil synthesis

Read more

Aymé L, Arragain S, Canonge M, Baud S, Touati N, Bimai O, Jagic F, Louis-Mondesir C, Briozzo P, Fontecave M, Chardot T

Arabidopsis thaliana DGAT3 is a [2Fe-2S] protein involved in TAG biosynthesis.

Scientific Reports . 2018

Mobilization and impact

DGAT3 is a new target for green and blue biotechnologies (lipid production,biofuels, heathfood).

Contacts

Thierry Chardot and Pierre Briozzo

UMR IJPB

thierry.chardot@inrae.fr

pierre.briozzo@inrae.fr

Context

The Kennedy pathway, which orchestrates de novo seed oil synthesis, was discovered back in 1956, but it was not until 1990 that the enzymes catalyzing the final committed step were uncovered and their genes cloned. In plants, type-1 diglyceride acyltransferases (DGAT1) mostly express in seeds that yield edible seed oils, whereas type-2 (DGAT2) expresses in non-food seed oils. Type-3 DGATs, unlike the other DGATs which are membrane-bound, are cytosolic. They possess ferredoxin motifs, which points to possible metal cofactor binding. Our research on the model-organism plant *A. thaliana* finds evidence that DGAT3 is involved in unsaturated fatty acid metabolism. The demonstration that DGAT3 carries a metal cofactor would point the way to a novel plant-lipid synthesis pathway.

Results

We showed that the DGAT3 protein in *A. thaliana* (AtDGAT3; At1g48300) is expressed in germinating seeds, which puts it on a whole other trajectory to the other DGATs which are involved in oil accumulation in the maturing seed. The recombinant protein from *E. coli* proves active. Its rusty brown colour points to an associated cofactor. Using a battery of approaches (trace-element assays and UV–visible and electron paramagnetic resonance spectroscopies), we demonstrated that the metal cofactor was a [2Fe-2S] centre cluster that is manifestly redox-active but seemingly disconnected from lipid metabolism. Metalloproteins already carry out a number of functions–now we can add a DGAT role to the list.

Future Outlook

We now need to determine the prevalence of the enzyme in plants, its expression template during plant development, its subcellular localization, its substrates and metabolites, and the role played by the [2Fe-2S] centre. If we manage to identify the enzyme's metabolic pathway, then we could potentially co-engineer the pathway with DGAT3 to produce novel lipids for green and blue biotechnology applications (functional lipids for foods, green chemistry).

Design-engineering for sustainable foodways

At the TRANSFORM division, we remodel food processing routes to make them water- and energy-efficient, and therefore suitably adapted to local production and population needs in emerging economies.

Digital tools developed upstream capture and collate our process and product knowledge in a shareable format and enable us to consolidate and capitalize the knowledge and craft expertise of our agents.

Comté cheese pre-ripening cellar (Tourment cheesemakers, Jura, France))

A numerical tool to consolidate the craft of cheesemaking

Read more

Buche P, Cuq B, Fortin J, Sipieter C

Expertise-based decision support for managing food quality in agri-food companies.

Computers and Electronics in Agriculture 163 (Article 104843) . 2019

Mobilization and impact

The CASDAR-programme [special research credits] DOCaMEx project coordinated by the *Centre Technique de Franche Comté* (CTFC) served as the framework for testing the expertise-based decision support tool on several PDO cheese value chains (Comté, Reblochon, Salers, Emmental de Savoie, Cantal). The method and software are purpose-designed to support these value chains, and the genericity of the process makes it valuably transposable to other commodity chains (durum wheat, vines and wines, and more).

Contact

Patrice Buche

UMR IATE

patrice.buche@inrae.fr

Context

Cheese value chains that carry Geographical Indication (PDO/PGI) status ground their product differentiation strategy in the outside marketplace on upvaluing their local home-terroir resources and experiential know-how in production and processing craft. Inside the protected-designation value chains, they are struggling to protect and pass on this know-how, chiefly in terms of finding and training apprentices. The development of 'numerical' methods that can serve expert-system knowledge bases raises new prospects for mobilizing collective expertise within a value chain.

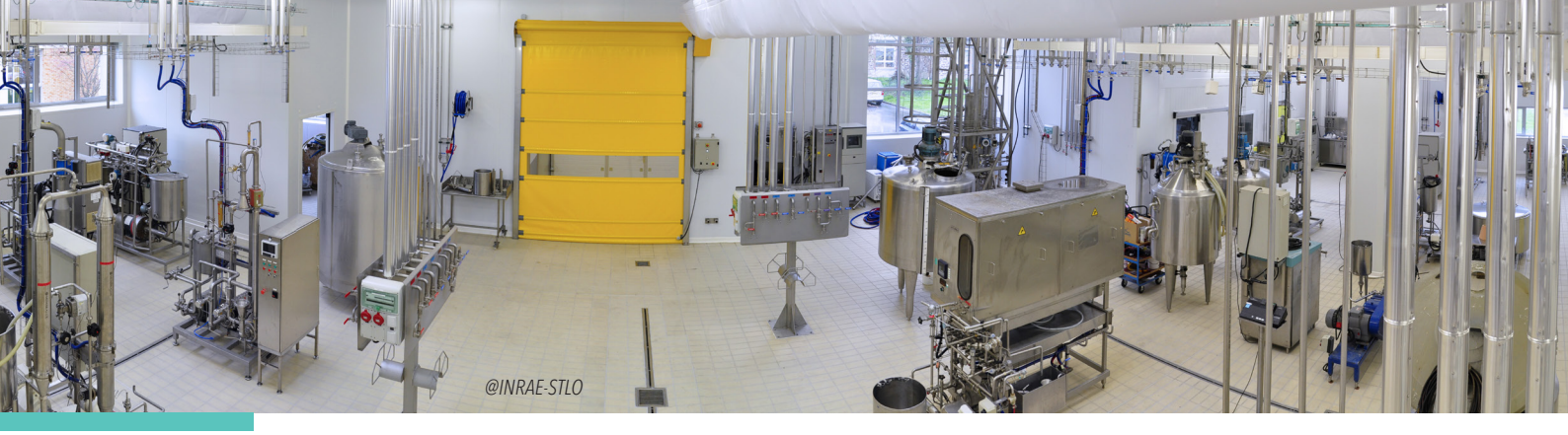
Results

Based on experiential feedback, we developed a novel method for capturing knowledge assets and making them actionable as decision support for technical actions. We put together a complete methodology with an allied software package to produce a 4-step process: (1) capturing the formal and informal knowledge assets of process-line operatives and process experts, (2) validating this knowledge together as a team community, and (3) encoding it into a knowledge representation and reasoning language based on a core ontology enabling (4) semi-automated decision support for recommended actions. The recommendations are based on graphing causal relationships between product defects/attributes and the allied technical actions grounded in explanatory mechanisms. The tool can also map out the potential knock-on impacts of a recommended action on other product defects/attributes, which makes it equally useful for learning and training purposes. It is designed with a convenient user-friendly interface that makes it easy to use in daily practice and to integrate experiential feedback to populate and update the knowledge base.

Future Outlook

The genericity of the ontology used here for structuring knowledge makes it valuably transposable to any kind of food commodity chain and processing route.

The next step is to internalize the uncertainty tied to <focal situation (defect/attribute), explanatory situation, technical action> tuples. This uncertainty will be measured based on experiential feedback from cheesemakers and cheese technologists, factoring in the frequency of the situation-events and the efficiency of action taken in these events.



Cheesemaking technology made water and energy-efficient, revisited for emerging markets

Read more

Chamberland J, Benoit S, Harel-Oger M, Pouliot Y, Jeantet R, Garric G

Comparing economic and environmental performance of three industrial cheesemaking processes through a predictive analysis.

Journal of Cleaner Production . 2019

Mobilization and impact

* predictive analysis on the From'Innov process model published in the *Journal of Cleaner Production* (impact factor of 6.395 in 2018) [3]

* the From'Innov process is licensed under 3 option agreements (Laïta, Lactalis, Quescrem) with two more option agreements in the pipeline (the milk collection EIG MODALA and the start-up Breizh Cheddar).

Contacts

Gilles Garric, Marielle Harel-Oger

UMR STLO

gilles.garric@inrae.fr

marielle.harel-oger@inrae.fr

Context

Cheese consumption is expanding fast in emerging economies. This new-market consumer demand revolves around taste, non-cold storability, and functionality (stringy for pizzas or spreadable for sandwiches). Back in France, market demand is for smaller-scale production (local food, organic produce) but bigger exports through solutions that are cheaper to make and ship.

Results

We have invented a whole new cheesemaking process that meets these divergent demands. Its core principle is grounded in simplifying key traditional cheesemaking steps: ripening is replaced by producing aroma on a small segment of the cheese in under five days, and draining is done on filters. This simplified process enables smallholders to make all kinds of cheese varieties, getting their taste and texture and even adding fruit, plants or herbs produced on-farm to differentiate in the marketplace. The process was compared against the traditional cheesemaking process and the membrane ultrafiltration process (named MMV after its inventors Maubois, Mocquot & Vassal) by modelling virtual cheese plants processing 100 tonnes of per day into Camembert-type cheese. Yield records found that the From'Innov process was the most efficient, generating the highest margins while using at least 25% less process water and energy compared to the traditional processes. Bigger facilities can dry this new kind of cheese into a cheaper-to-export powder. End-users would then just have to rehydrate the powder and retexturize the product–or even just let consumers decide how to use it once back at home.

Future Outlook

This new process is patent-protected, whether working directly from milk (From'Innov) or working up from cheese powder (Valo'From).

The technology not only improves profitability and simplifies the cheesemaking process–it will also help improve the cheesemaking industry's environmental footprint. The next step is to benchmark the eco-efficiency of the Valo'From process against other pre-cheese powder-based approaches on the market.

@Jocelyn De Souza

How does tumbling affect mass transfers in the dried meat production process? Applied research on Biltong

Read more

Mirade P-S, Portanguen S, Sicard J, De Souza J, Musavu Ndob A, Hoffman L-C, Goli T, Collignan A

Impact of tumbling operating parameters on salt, water and acetic acid transfers during biltong-type meat processing.

Journal of Food Engineering . 2020

Research collaborations

This work materialized through PhD research led by INRAE–CIRAD under the wider GloFoodS metaprogramme, leading out from a research collaboration between INRAE–QuaPA, the CIRAD, the QualiSud joint research unit in Montpellier, and Stellenbosch University in South Africa.

Contact

Pierre-Sylvain Mirade

UR QUAPA

pierre-sylvain.mirade@inrae.fr

Context

Biltong is a dry-cured meat product from Southern Africa, typically made from beef or antelope. It is prepared through a series of steps: first making the cut, then salting, acidifying, spicing, massaging and, finally, drying. Rising demand and changing foodways (for biltong that is softer, not as dry, and contains less salt) are now moving production practice towards a more industrial method that employs a tumbling process. However, these industrially-processed products have a shorter shelf-life than traditional biltong and require better control to stabilize the microbial load of the end-product.

Our research sets out to investigate the tumbling process and its impacts on the mass transfer mechanisms (salt, water and acetic acid) in small beef meat pieces.

Results

Here we profiled salt, water and acetic acid transfers 25 mm deep into meat samples. The results showed that tumbling increases salt and acid diffusion deeper into the meat. The driving process factor was the mechanical action tied to size of the tumbler, followed by tumbling time and, to lesser extent, whether vacuum was used.

This study also showed that tumbling conditions did not significantly impact water content profiles but did significantly impact salt and acetic acid concentration profiles. The most intensive tumbling conditions produced high concentration gradients with a high salt concentration and low pH at the meat surface, which may help keep the meat safe at the later drying step.

Future Outlook

The next step is to study how the drying step shapes the food safety and sensory properties of the biltong so as to secure the best post-drying trade-off between good meat hygiene and a sufficiently tender and organoleptically acceptable end-product.

Learning to craft wine aroma by adding nitrogen mid-fermentation ?

Read more

Mouret J-R, Farines V, Sablayrolles J-M, Trelea IC

Prediction of the production kinetics of the main fermentative aromas in winemaking fermentations.

Bioechemical Engineering Journal . 2015

Seguinot P, Rollero S, Sanchez I, Sablayrolles J-M, Ortiz-Julien A, Camarasa C, Mouret J-R

Impact of the timing and the nature of nitrogen additions on the production kinetics of fermentative aromas by Saccharomyces cerevisiae during winemaking fermentation in synthetic media.

Food Microbiology . 2018

Research collaborations

* INRAE–SPO, in a collaborative venture with private partner Lallemand, the INRAE–Pech Rouge station, and INRAE–Mistea.

* ANR-sponsored StarWine project (2019–2022), coordinated by INRAE–SPO

* FUI-funded [one-time cross-ministry funding package] NV2 project (2017–2021)

Contact

Jean-Roch Mouret

UMR SPO

jean-roch.mouret@inrae.fr

Context

The past few years have seen consumer tastes shifting increasingly towards more fruit-forward wines.

Fermentative aroma compounds–led by esters–enhance the fruit-forward flavour. We identified initial nitrogen content as the key factor driving production of these compounds. Given that the nitrogen can be added not just pre-process but also mid-process, and in either mineral form (as ammonium) or organic form (as a mixture of amino acids), we sought to test these variables in an effort to find actionable ways to tune the amount of fruit-forward aromas produced in the wines.

Results

We were able to determine the exact kinetics of fermentative aroma compound synthesis using a high-throughput on-line volatile compound profiling system, which enabled us to time–course key kinetic parameters such as production rates and yields.

Adding nitrogen, at the doses studied here, very significantly increased the production of acetate esters, especially when the nitrogen source was organic. We also learned that the nitrogen was more efficient when added mid-fermentation than at the beginning.

We found that nitrogen added mid-fermentation leads to overexpression of the genes encoding the enzymatic activity that converts alcohols to acetate esters, which ultimately results in more efficient conversion of alcohol precursors into esters. We demonstrated that it is possible to de-correlate the production of certain aroma compounds (esters) in relation to others (higher alcohols) and thereby guide the taste of the wine towards different profiles.

Future Outlook

These findings raise prospects for learning how to methodize the production of fermentative aroma compounds during alcohol fermentation.
We are working to round off the mathematical model in order to develop equations enabling real-time control of alcohol fermentation. We will also be mobilizing the data through an integrated vine-to-cellar approach designed to help winegrowers and winemakers confidently fit their wine nitrogen to target-wine profile.

BaGaTel connects food quality to composition and processing

Read more

Allard T, Guichard E, Perret B, Guillemin H, Pénicaud C

Mise en relation de données relatives aux procédés de fabrication, écoconception, composition et qualité des produits laitiers à l'aide d'une base de données guidée par une ontologie.

Cahiers techniques de l'INRA . 2018

Pénicaud C, *et al.*

Relating transformation process, eco-design, composition and sensory quality in cheeses using PO2 ontology.

International Dairy Journal . 2019

Mobilization and impact

BaGaTel database: registered as IDDN.FR.001.500004.000.R.P.2016.00010300, 2016

Contacts

Elisabeth Guichard, Caroline Pénicaud, Bruno Perret, Hervé Guillemin

UMR CSGA, UMR SayFood, Plateforme PLASTIC, URTAL

elisabeth.guichard@inrae.fr

caroline.penicaud@inrae.fr

bruno.perret@inrae.fr

herve.guillemin@inrae.fr

Context

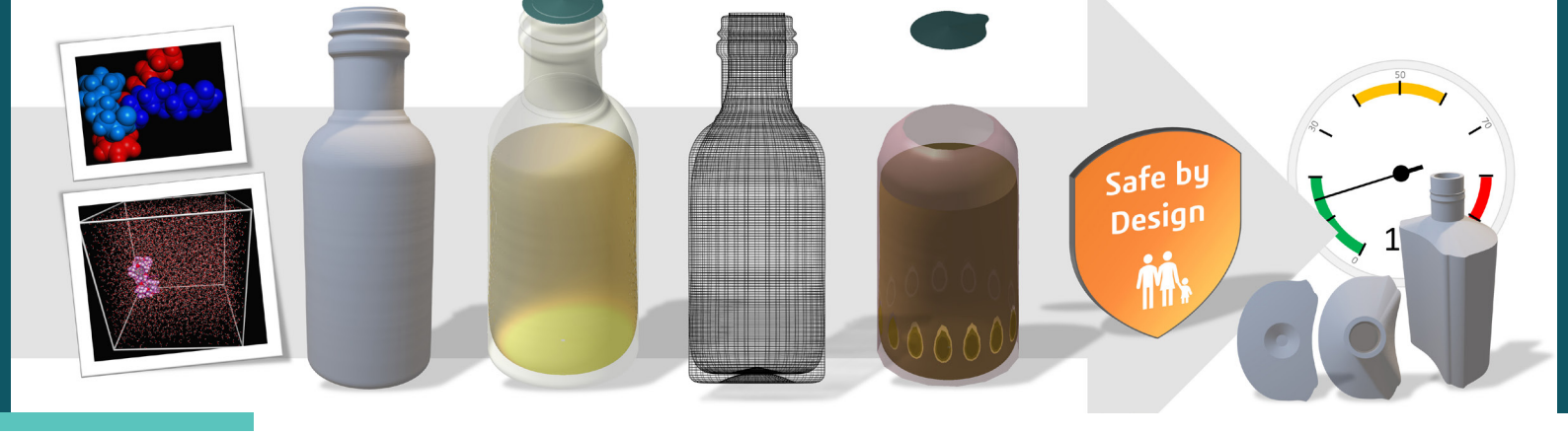
New food formulation and existing food reformulation are a critical part of the new societal demands equation. However, there is not a single scientific study cross-connecting a product's nutritional value with its sensory attributes and environmental footprint. To address this gap, we developed the BaGaTel database to structure data from over 40 projects to fit food-science 'process and observation ontology' (PO²) with input from experts in various fields of dairy-product research from upstream production to downstream consumption.
Dairy products were the chosen model as they cover a broad panel of processing, compositional and structure/microstructure diversity.
Project summaries, a glossary of key terms, and a tutorial (video) on the BaGaTel data capture interface can be found online via the NutriSensAI portal (http://plasticnet.grignon.inrae.fr/portailbagatel).

Results

The BaGaTel database helps find answers to key science questions. The data can be queried and connected to gauge missing data in certain projects or to run multicriteria analyses. We have shown in both real and model cheeses that the relationship between intensity of salt perception and effective salt content is modulated by the interplays between water, lipid and protein contents.
We have mobilized the manufacturing-process data to quantify the energy and raw material inputs needed for the life cycle inventory. Environmental impacts were calculated using SimaPro LCA software and the results were imported into BaGaTel. We are now in development work to secure interoperability between BaGaTel and the MEANS platform in order to facilitate early-upstream project integration of the environmental dimension.

Future Outlook

We are now working on importing data output from four TRANSFORM platforms on grape winemaking to make it actionable for multiway statistical analysis.
In execution of the French national plan for open science, our plan (ANR DataSusFood 2020–2022) is to open all non-confidential BaGaTel-hosted data via the INRA data repository (https://data.inrae.fr/) and assign DOIs. Our objective is to progressively climb through the different levels of the FAIR principles (Findable, Accessible, Interoperable, Reusable).



Materials can cross-contaminate—some risks warrant better control

Read more

Nguyen P-M, Julien J-M, Breysse C, Lyathaud C, Thébault J, Vitrac O

Project SafeFoodPack Design: case study on indirect migration from paper and boards.

Food Additives and Contaminants . 2017

Nguyen P-M, Dorey S, Vitrac O

The Ubiquitous Issue of Cross-Mass Transfer: Applications to Single-Use Systems.

Molecules . 2019

Mobilization and impact

Migration-specific training is now on offer through the FITNess ('Food packaging open courseware for higher education and staff of companies') e-learning platform, featuring courses, case studies, online simulations, and preventive measures for action. It is funded by the ERASMUS+ programme and hosted on INRAE servers.

Contact

Olivier Vitrac

UMR SayFood

olivier.vitrac@inrae.fr

Context

Food contact materials are almost paradoxically the main source of chemical contaminants in food. Substances of unknown origin are termed NIAS, for 'non-intentionally-added substances'. Research shows that these NIAS contaminants are not newly-formed but essentially come from cross-transfers between packaging materials, where substances in no-containment-function material A (e.g. overwrap, secondary packaging) are found in container material B. Even with material A removed, material B will still be a source of A plus B substances. This contaminant vector, which does not require perfect A-to-B contacts, was demonstrated in biopharmaceuticals applications, but the issue is ubiquitous and also concerns food-sector applications.

Results

The entire end-to-end supply chain was coded into the INRA's FMECAengine open-source software platform to pinpoint the critical steps and substances. Validation tests were carried out with bags and contact reactants (multilayer material B) folded up and packed into an overwrap (multilayer material A). Cross-transfers between A and B were then tracked and traced over a period of months, right through to the final step where B cross-migrates into the simulated culture media. We achieved reasonably good predictions of migration kinetics for all the substances in A and B by accounting for the effects of temperature and mean A-to-B gap distance. We also found that, counterintuitively, the main source of NIAS was not gamma-irradiation sterilization but the overwrap material (A) used to conserve sterility.

FMECAengine has now been re-edited to integrate non-permanent contacts (like folding, removal of overwraps).

Future Outlook

This research points to potential risks that stem–indirectly–from the new French 'anti-waste law for a circular economy' just voted in, as it aims to mainstream the repeated reuse and recycling of materials, which increases the risk of cross-migration contamination. This is where delayed contamination of recycled-carton overwrap by mineral oil is a concern, because it carries a significant fraction of carcinogenic or reprotoxic substances.

Food fortification to improve childhood malnutrition in the Global South

Read more

Moustiés C, Bourlieu-Lacanal C, Barea B, Servent A, Hemery YM, Avallone S

Qualité nutritionnelle, microbiologique et stabilité à l'oxydation de formules infantiles fortifiées ou aliments thérapeutiques dans les pays du sud.

JFN - Journées Francophones de la Nutrition, Nantes, 13 au 15 décembre . 2017

Moustiés C, Bourlieu-Lacanal C, Servent A, Barea B, Hemery Y, Avallone S

Lipid composition and state of oxidation of fortified infant flours in low income countries are not optimal and strongly affected by the time of storage.

EJLST . 2019

Contacts

Sylvie Avallone and Claire Bourlieu

UMR QUALISUD CIRAD et UMR IATE

sylvie.avallone@supagro.fr

claire.bourlieu@inrae.fr

Context

Globally, 200 million children under five are malnourished–an unacceptably high figure in this day and age. Fortified food staples enriched with vital vitamins and other macro/micronutrients are proposed as part of the solution to malnutrition. Fortified foods are complex dispersed systems that follow long supply-chain channels and deliver a gradient of nutritional quality shaped by multiple interplaying factors. A key strategic challenge is to stably control the nutritional quality of these products so that they do not lose effective biological value. This research set out to assess the nutritional quality of infant formulas and ready-to-eat therapeutic foods field-sampled in Africa and Asia and to pinpoint the determinants (intrinsic factors, environment factors, packaging factors, and more) dictating their stability. We assessed lipid composition and oxidation state as well as product formulation and packaging along a series of post-production timepoints.

Results

The 'field-up' results surfaced a comparatively lower nutritional quality and nutrient stability in formulas than in ready-to-eat therapeutic foods. Certain fortified infant formulas contained over-high proportions of omega-6 fatty acids. We also observed high overages in vitamins A, D, and E at early timepoints whereas formulas in storage for more than a year showed vitamin shortages. Six out of the 13 formulas tested showed peroxide values above the internationally-guidelined thresholds. Even formulas packaged with an oxygen-impermeable multilayer aluminium/polyethylene barrier suffered oxidation after a year in storage. We proposed a global rethink on curbing the practice of vitamin overages, supporting local-made products, and reformulating to get better omega-6/omega-3 ratios. We have also developed a predictive model of vitamin A oxidation kinetics in infant formulas, which is a limiting factor for nutritional quality, and we have issued a set of advocacy recommendations on formulation and packaging.

Future Outlook

Our time–course model of vitamin A oxidation kinetics in a standard infant cereal could be validated to work for other formulations and made to integrate predictive oxidation patterns for other lipid nutrients. Upcoming projects are set to work through a multicriteria infant formula optimization strategy factoring in our findings along with on-the-ground production–distribution constraints.

@INRAE

An ultrasound sensor for on-line quantification of food-industry clean-in-place process equipment

Read more

Chen B, Callens D, Campistron P, Moulin E, Debreyne P, Delaplace G

Monitoring cleaning cycles of fouled ducts using ultrasonic Coda Wave Interferometry (CWI).

Ultrasonics . 2019

Déclaration d'invention INRA-IEMN

Moulin E, Delaplace G, Campistron P, Chen B, Debreyne P, Chihib N-E, Abdallah M, Khelissa O

Methode non invasive visant au suivi l'attachement et/ou detachement de dépots sur une paroi solide par traitements de coda ultrasonores, DI-RV-18-0065 . Juin 2018

Mobilization and impact

The latest results will be unveiled in June 6-11, 2021 at the XIVth Heat Exchanger Fouling and Cleaning conference in Wagrain, Austria.

Contact

Guillaume Delaplace

UR UMET

guillaume.delaplace@inrae.fr

Context

Most food processing industries regularly run into process-stream fouling problems. Hot process-stream surfaces in contact with food material experience the same progressive fouling as kitchenware at home (like pots and pans), so they too require regular cleaning. The problem is compounded by the fact that the surfaces of industrial process equipment are inaccessible, which means cleaning gets done 'blind', following a prescribed protocol that is often disproportionately aggressive for the actual amount of foulant to clean. This overcompensation generates a substantial economic and environmental burden, as it overconsumes water, detergent, and energy. A sensible route to minimizing these impacts is to develop non-intrusive sensors that give an accurate 'inside' picture of apparent fouling.

Results

With that vision, we applied a non-invasive ultrasound-based method called Coda Wave Interferometry (CWI) to quantify the on-surface fouling factor of use/clean process cycles. We artificially created layers of various deposits (waxes, biofilms, milk deposits) on process-equipment surfaces and then tested how the method performed at detecting the formation and/or cleandown of these deposits.

The results showed that the CWI method capably monitored the fouling rate of food-fouled solid surfaces and could workably be deployed on-line as a non-invasive solution.

Future Outlook

Further trials are underway to work on the robustness of the method. A prototype sensor sleeve was developed to move the invention up the technology readiness level scale, and it already points to an array of potential industry applications. Development projects have been tabled with food-industry partners but also with industry partners operating in salt-water environments and studying corrosion (namely in the frame of the European Interreg 2 Seas project SOCORRO2) to test out surface fouling by marine sediments.

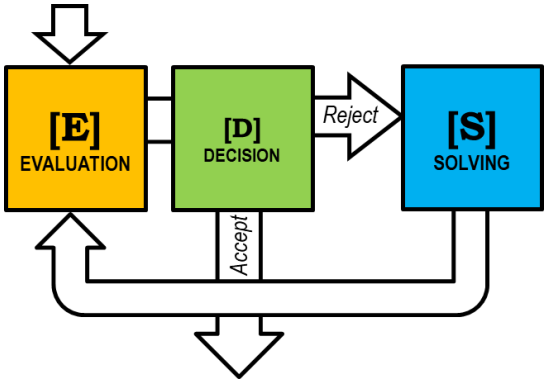
Sensor-measured in-pipe milk fouling.

Food packaging design, re-innovated

Read more

Nguyen P-M, Goujon A, Sauvegrain P, Vitrac O
A Computer-Aided Methodology to Design Safe Food Packaging and Related Systems.
AIChE Journal . 2013

Zhu Y, Guillemat B, Vitrac O
Rational Design of Packaging: Toward Safer and Ecodesigned Food Packaging Systems.
Frontiers in Chemistry . 2019



Contact

Olivier Vitrac
UMR SayFood
olivier.vitrac@inrae.fr

Context

Regulatory pressure is undeniably converging with societal pressure for safer and greener food and food supply chains. Revising the existing technical solutions requires new degrees of freedom. In the food packaging sphere, the strategy of replacing a thermoplastic composite matrix with a biodegradable biobased matrix is reductive and possibly even unworkable. There are so many other variables to factor in—the material's food compatibility, design life and distribution channels, the recyclability of the packaging materials, and the chemical risks associated with using novel materials or integrating recycled polymers.

Results

The new food packaging eco-design and safety-by-design methodology slots in between the life cycle analysis step which serves to choose the polymer resin, and the 3D printing or augmented reality step which serves to acceptability-test the new packaging. The '[E][D][S]' methodology wraps three iterative steps into the same integrated tool: 1) multiscale [E]valuation of cross-coupled transfers (from molecular thermodynamics up to 3D bottle-scale); [D]ecision on the baseline-minimum criteria for design life, food health–hygiene, and mechanical strength; re[S]olution of the geometric constraints to accommodate the competing goals of minimal package mass with maximal packaged shelf life.

With high-throughput implementation, the approach can explore hundreds of alternatives (concepts, formats, use-case conditions) and gain up to 50% in weight on PET bottles used for alcoholic beverages and up to 70% in environmental performance by incorporating recycled PET. The 3D data generated is compatible with all the industry-standard design and deployment packages.

Future Outlook

Packaged-food shelf life is conditioned exclusively by mass-transfer processes (loss of weight, sorptive and permeative loss of ethanol and aroma compounds, desorptive migration of packaging components). As we possess a powerfully predictive model of oxidative reactions through research on deep frying, we now propose to integrate an oxidative-process module.

The developments harness and articulate an array of INRAE-developed open-source tools. The new 3D solver will be integrated into an open-source project dubbed FMECAengine3D. Note that the 1D/2D version of FMECAengine is already employed by technical and industrial development centres.

Good Food feeds good health

TRANSFORM scientists study the natural components of fruit and vegetables–to learn what they do and how they can be purposed to enhance nutritional value. We also factor in sensory properties of foods to understand consumer food preferences and design food products formulated especially for seniors and other target populations.

Predicting the technological quality of cooked ham right from the farm

Read more

Théron L, Sayd T, Chambon C, Vénien A, Viala D, Astruc T, Vautier A, Santé-Lhoutellier V

Deciphering PSE-like muscle defect in cooked hams: A signature from the tissue to the molecular scale.

Food Chemistry . 2019

Contact

Laetitia Théron

UR QUAPA

laetitia.theron@inrae.fr

Context

Good-quality cooked ham is a proud mainstay of French charcuterie. However, predicting the quality of cooked ham is a major challenge for the industry, as the main in-processing defect of ham muscle is a PSE-like destructuration that can only be picked up after deboning, which means big economic losses at the slicer. We are steadily deciphering the mechanisms that trigger the defect, but detection upstream of process lines–or even from the farm gate–remains a challenge for the commodity chain. Spectral fingerprints of blood plasma are part of a battery of approaches widely used in medicine for biomarker discovery. These suitably practicable non-invasive approaches were used here to define markers that point to the PSE-like destructuration defect.

Results

We developed a method for predicting the PSE-like defect in cooked ham based a combination of chemometrics and spectral fingerprinting of pig plasma. Blood samples were taken *in vivo* on 120 pigs. At 24h *post mortem*, the hams were screened against a reference read-off scale then split into two groups on the basis of whether or not they showed signs of the destructuration defect. Spectral fingerprints were acquired by MALDI-TOF (Matrix-Assisted Laser Desorption/Ionization–Time-Of-Flight) mass spectrometry and ATR-FTIR (Attenuated Total Reflectance–Fourier Transform InfraRed) spectroscopy on pig plasma samples, then analyzed using neural networks. The coupled methods proved to offer complementary predictive capabilities–combining the two spectral fingerprints by selecting the 30 most discriminatory peaks in the two approaches correctly predicted 100% of the data.

Future Outlook

Full-scale deployment of this approach in real industry conditions would make it possible to run a predictive test of cooked ham quality without losing valuable carcass, as it is based on a simple blood sample. Ultimately, it would become possible to manage product technological quality upstream of slaughter, adapt products to technological processing routes based on the quality of the raw material, or even to select animals based on their fingerprinted traits. This research opens up new prospects for methodizing food quality and new applications surrounding food-animal selection.

Design of an optimized-nutritional-value tomato, onion and olive oil sauce

Read more

Yu J, Gleize B, Zhang L, Caris-Veyrat C, Renard CMGC

Heating tomato puree in the presence of lipids and onion: The impact of onion on lycopene isomerization.

Food Chemistry . 2019

Yu J, Gleize B, Zhang L, Caris-Veyrat C, Renard CMGC

Microwave heating of tomato puree in the presence of onion and EVOO: The effect on lycopene isomerization and transfer into oil.

LWT – Food Science and Technology . 2019

Collaboration

* Béatrice Gleize & Catherine Renard. UMR408 SQPOV (Sécurité et Qualité des Produits d'Origine Végétale), INRAE, Université d'Avignon, F-84000 Avignon, France.

* Yu Jiahao & Zhang Lianfu. State Key Laboratory of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu, China

Contacts

Béatrice Gleize and Catherine Renard

UMR SQPOV

beatrice.gleize@inrae.fr

catherine.renard@inrae.fr

Context

Part of the healthfulness of eating fruit and vegetables comes from fat-soluble micronutrients called carotenoids. The major carotenoid found in tomatoes is lycopene, but dietary lycopene from fruit and vegetables offers little bioaccessibility. The lycopene we eat and digest has to get released from the food-plant matrix, taken up in the mixed micelles formed by dietary lipids, and then absorbed into the intestinal cells before it can finally start having healthful effect.

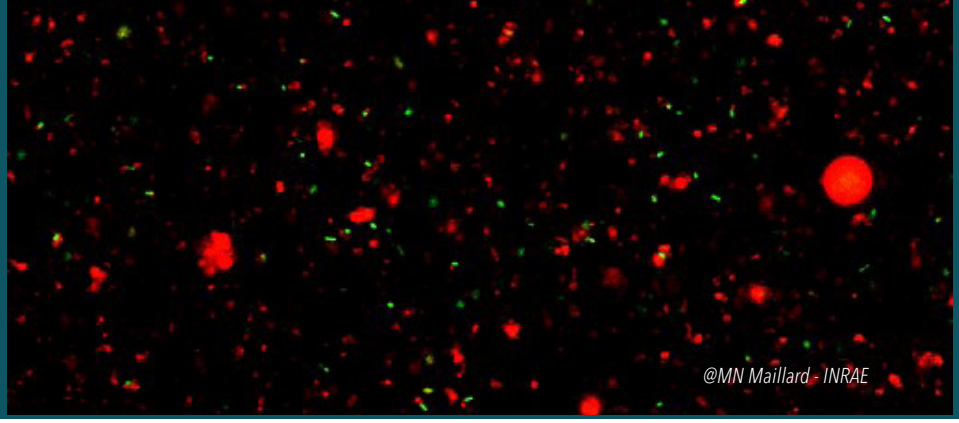
With a vision to design a multi-ingredient high-nutritional-value tomato sauce, we worked on optimizing product composition and processing routes to improve the bioavailability of the lycopene component.

Results

In both cooking protocols studied (90°C for 2 hours and microwaving at 250W for 20 minutes), adding olive oil and raw onion to tomato purée doubled or even tripled the proportion of *cis*-isomers of lycopene. The increase was linearly correlated to amount of added raw onion (0%–50%) in the sauce. We proposed a mechanism of lycopene isomerization via diallyl disulfide (DADS), which is formed by alliinase-catalyzed breakdown of the alliin naturally found in onion.
The tomato-based sauces enriched with cis-isomers of lycopene showed higher all-lycopene transfer into the olive oil (+60%) and dramatically better bioaccessibility (i.e. a 4–8-fold improvement, as measured on an *in vitro* digestion model). The *cis*-isomerization of lycopene induced by presence of raw onion during cooking is therefore a key step for improving the bioavailability of lycopene in tomato-based processed foods.

Future Outlook

Processing can be leveraged to improve the nutritional quality of food through recipe and process-route optimization. Approaches like this could be envisioned for other food products based on fruit and vegetable vectors of healthful carotenoids like lutein and beta-carotene. Our findings also reach out to a wider general-public audience, where they can help home cooks prepare 'home-made' tomato sauces in a way that brings out more valuable micronutrients.



Natural phenolic compounds pair up activities for better food

Read more

Pernin A, Dubois-Brissonnet F, Roux S, Masson M, Bosc V, Maillard M-N

Phenolic compounds can delay the oxidation of polyunsaturated fatty acids and the growth of Listeria monocytogenes: structure-activity relationships.

Journal of the Science of Food and Agriculture . 2018

Pernin A, Bosc V, Soto P, Le Roux E, Maillard M-N

Lipid oxidation in oil-in-water emulsions rich in omega-3: effect of aqueous phase viscosity, emulsifiers, and antioxidants.

European Journal of Lipid Science and Technology . 2019

Collaboration

* Micalis Institute (University of Paris-Saclay, INRAE, AgroParisTech)–Biofilms and Spatially-organized communities (B3D) team, Pr. Florence Dubois-Brissonnet.

* Contract: PhD thesis by Aurélia Pernin defended on 20 December 2018. Funding from the French Ministry of Higher Education, Research & Innovation–ABIES Doctoral School

Contact

Marie-Noëlle Maillard

UMR SayFood

marie-noelle.maillard@agroparistech.fr

Context

Dietary omega-3 polyunsaturated fatty acids (PUFA), especially EPA and DHA, are recommended for their many health benefits. However, in foods exposed to air, they are vulnerable to oxidation, which can result in off-tastes. Furthermore, fridge-temperature exposure to exogenous PUFA accelerates the growth of *Listeria monocytogenes*, which can shorten the time-window to maximum tolerable thresholds and unsafe food health–hygiene. We posited that natural phenolic compounds would make good candidates in the effort to combat these processes without recourse to synthetic additives. Several natural phenolics found abundantly in various plant ingredients show a dual antioxidant–antimicrobial activity, but this valuable activity has gone practically unresearched in complex food media.

Results

Our study used tests in model media to select a set of dual-activity phenolics and put them to work in emulsion systems that we tailor-made to control their composition and structure. The two activities are very strongly modulated by the concentration and physical-chemical properties of the compounds and their localization in either of the phases or at the phase–phase interface. Eugenol, for example, is an efficient antioxidant but loses its antimicrobial activity in emulsion, whereas ferulic acid remains localized to the aqueous phase where it preferentially exerts an antimicrobial activity that is partly dependent on its degree of dissociation.

Future Outlook

These results can find applications in the protection of ready-to-eat foods rich in omega-3 PUFA by prolonging their shelf life. Thoughtfully selecting combinations of phenolic compounds to deliver complementary antioxidant–antimicrobial effects offers a natural way to reduce the use of food additives–and an opportunity to upcycle food–farming industry coproducts as phenolics-rich ingredients.

Natural food colourings with a bright future

Read more

Trouillas P, Sancho-Garcia J-C, De Freitas V, Gierschner J, Otyepka M, Dangles O

Stabilizing and modulating color by copigmentation: insights from theory and experiment.

Chemical Reviews . 2016

Dangles O, Fenger J-A

The chemical reactivity of anthocyanins and its consequences in food science and nutrition.

Molecules . 2018

Collaboration

Our research is integral to an international colour research programme coordinated by Mars Wrigley (USA) with input from 4 other academic partners (USA, Japan, Italy).

Contacts

Olivier Dangles and Julie-Anne Fenger

UMR SQPOV

olivier.dangles@univ-avignon.fr

julie-anne.fenger@inrae.fr

Context

Artificial food colourings have a tainted image that turns consumers away. Replacing them with plant-based colorants would have a huge net-positive socio-economic impact. Anthocyanidins are natural pigments abundantly found in fruit and vegetables, where they express as deep reds, purples and even blues depending on pH. However, they tend to lose colour stability once extracted from their natural sources, which makes it a priority to find more sophisticated anthocyanidins that can confer attractive time-stable colours. Red cabbage and purple sweet potato are naturally rich in anthocyanidins monoacylated or diacylated with p-hydroxycinnamic acid (HCA) residues, and they make good candidates.

Results

Diacylation makes anthocyanidins far more colour-stable than monoacylation. To illustrate, the time lag to 50% colour loss at pH7 at 50°C is around 2½ hours for a diacylated red-cabbage anthocyanidin vs 10–15 minutes for its monoacylated homologue and just a few minutes for the non-acylated reference compound. This is because diacylated anthocyanidins can 'sandwich-stack' into conformations where both faces of the chromophore interact with the HCA residues. However, the effectiveness of the protection conferred by an acyl residue is heavily dependent on the positions of the acylated sugar on the chromophore and the acyl residue on the sugar.

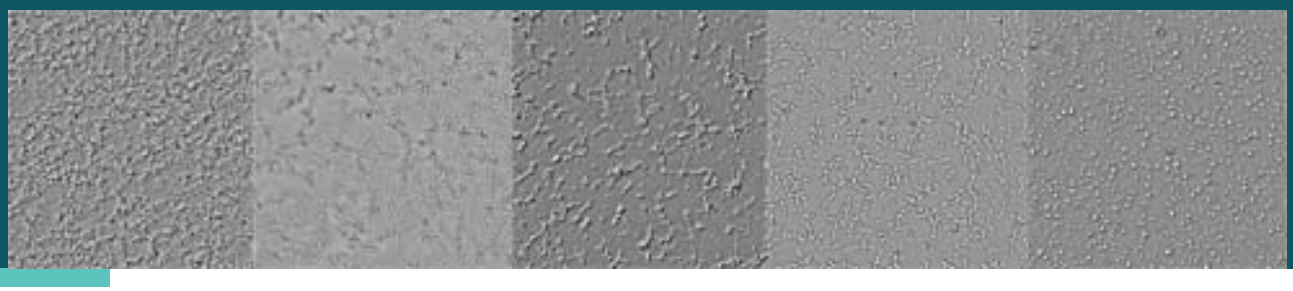
For colour pigments to 'wash out' during extended heating, there has to be not only added water, which is reversible, but also irreversible autoxidation and hydrolysis processes involved. These processes are also inhibited with diacylated anthocyanidins, although protection against water addition is still the most efficient counter-strategy.

Strong chromophore–acyl residue interactions enable diacylated anthocyanidins to fold (or even self-associate), but they also promote binding into stable iron complexes. These iron complexes are valuable on two fronts: they express attractive blues, and they are more heat-stable. Iron complexes with the monoacylated or non-acylated homologues show less stability, and the progressive leach-out of iron ions triggers water addition on the released chromophore and also accelerates the autoxidation process.

Future Outlook

Even though acylated anthocyanidins are efficiently protected against water addition by HCA residue–chromophore interactions, they remain relatively exposed to autoxidation, especially in pH-neutral media. The discovery of efficient antioxidants and formulations (typically in biopolymer matrices, i.e. food proteins, pectins, and other polysaccharides) offers bright prospects.

@ INRAE - Adeline Boire



Understanding the role of surface charge distribution in protein–protein associations

Read more

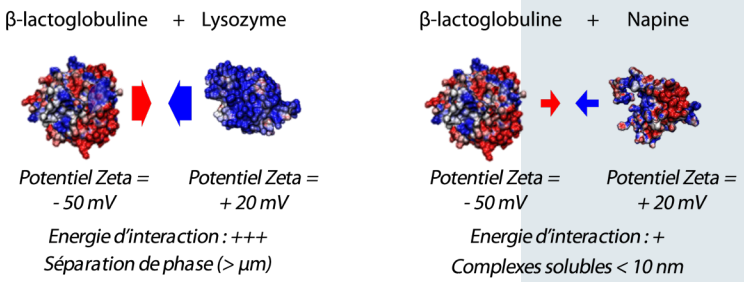
Ainis W-N, Boire A, Solé-Jamault V, Nicolas A, Bouhallab S, Ipsen R

Contrasting assemblies of oppositely charged proteins.

Langmuir . 2019

Collaboration

* William Nicholas Ainis & Richard Ipsen (Copenhagen University, Danemark)



Assemblies of different oppositely-charged proteins show contrasting positive-charge distributions (in blue) and negative-charge distributions (in red).

Contacts

Adeline Boire and Saïd Bouhallab

UR BIA, UMR STLO

adeline.boire@inrae.fr

said.bouhallab@inrae.fr

Context

Oppositely-charged proteins can form soluble assemblies that, under specific physical-chemical conditions, lead to liquid–liquid phase separation–a process also dubbed 'heteroprotein complex coacervation'. The phase behaviour of globular proteins is generally confidently described by colloidal theory and global parameters including net charge, virial coefficient and surface hydrophobicity. However, this oversimplistic vision of protein–protein interactions fails to capture a number of phenomena at work–including the heterogeneous distribution of protein surface charges, which may play a major role in protein–protein interaction and assembly. We recently set out to understand how surface charge distribution shapes patterns of coacervation between oppositely-charged proteins.

Results

We studied the complexation of a negatively-charged protein, β-lactoglobulin, with two positively-charged proteins, lysozyme and napine, chosen because they share a similar net charge and molecular weight but a different surface charge distribution. By articulating an experimental approach with numerical simulations, we showed that β-lactoglobulin had more affinity for lysozyme than napine–even though they shared a similar charge number. We also showed that β-lactoglobulin and lysozyme form heteroprotein assemblies that lead to phase separation at microscopic scale whereas, surprisingly, β-lactoglobulin and lysozyme complexed into smaller soluble assemblies that stayed in the nanometer-size range. Based on the evidence, these findings stem from the heterogeneous surface charge distribution of the proteins and their intrinsic structure.

Future Outlook

The structure and dynamics of soluble complexes warrants further investigation to better understand the determinism underpinning stucturational protein pathways. We anticipate this research as a starting point to innovate the use of controlled food-protein assemblies to encapsulate bioactive compounds or to texturize food products.

@Kaboompics-Pixabay

The continued trend towards pale rosé wines—explained

Read more

Le marché des vins rosés.

OIV Focus . 2015

Gil M, Avila-Salas F, Santos L-S, Iturmendi N, Moine V, Cheynier V, Saucier C

Rosé Wine Fining Using Polyvinylpolypyrrolidone: Colorimetry, Targeted Polyphenomics, and Molecular Dynamics Simulations.

Journal of Agricultural and Food Chemistry . 2017

Contact

Cedric Saucier
UMR SPO
cedric.saucier@umontpellier.fr

Context

Rosé wine is increasing in popularity and the consumption of rosé wines has increased by 20% globally since 2002 (OIV, 2015). Over the past ten years, rosés from Provence and from the South of France in general have noticeably paler over the years. It looks like this trend is here to stay, as lighter-coloured rosé wine resonates with consumers, and has prompted winemakers to produce increasingly pale-coloured wines. This is typically involves using polyvinylpolypyrrolidone (PVPP) as a fining agent during the winemaking process. Our study looks at the question of colour and beyond that to investigate the effect of PVPP fining on thiol aromas.

Results

The PVPP fining used in rosé winemaking can adjust the intensity and hue of their pink colour and prevent certain organoleptic taints. Here we investigated the effect of PVPP fining treatments during fermentation by measuring colour, polyphenol content and thiol aromas. This study revealed certain key findings:

- PVPP fining had an impact on colour, phenolic composition and thiol content of rosé wines.
- PVPP treatment had a strong effect on coumaroylated anthocyanins, flavonols and flavanols.
- PVPP-treated rosés showed a substantial gain in thiols aromas compared to control. This was a dose-dependent phenomenon with increase in thiol molecule such as 3-sulfanylhexyl acetate (3SHA) and 3-sulfanylhexan-1-ol (3SH).

This concomitant effect on thiol aroma content was demonstrated here for the first time, and may ultimately explain why consumers are drawn to paler rosés.

Future Outlook

Our research is now shifting focus to gain a clearer understanding of this dose–response effect of PVPP on colour and aroma of rosé wine.

Digestion of apple polyphenols by the gut microbiota

Read more

Le Bourvellec C, Bagano Vilas Boas P, Lepercq P, Comtet-Marre S, Auffret P, Ruiz P, Bott R, Renard C, Dufour C, Chatel JM, Mosoni P

Procyanidin-Cell Wall Interactions within Apple Matrices Decrease the Metabolization of Procyanidins by the Human Gut Microbiota and the Anti-Inflammatory Effect of the Resulting Microbial Metabolome In Vitro.

Nutrients . 2019

Contact

Carine Le Bouvellec

UMR SQPOV

carine.le-bourvellec@inrae.fr

Context

Polyphenol and fibre-rich foods are recommended as part of a healthy diet, but the mechanisms behind their biological effects on the body are sketchy at best.

The bulk of the polyphenols found in apples are B-type procyanidins. Not only do we know little about the microbial metabolization of procyanidins during the digestive process, we also need to factor in the pre-ingestion treatments undergone by the fruit, i.e. chewing the fresh apple or crush–cook–sterilize processing to make compotes, for instance. Procyanidins are known to form complexes with dietary fibre.

We designed this *in vitro* study to investigate the extent to which these procyanidin–apple complexes modulate the production of microbial metabolites and whether these metabolites have an anti-inflammatory effect on intestinal cells. We also assessed the pre-biotic effect of specifically-developed 'procyanidin–apple fibre' matrices.

Results

The study focused on *in vitro* batch fermentation of three model apple matrices with gut microbiota from four healthy donors. The three matrices were compositionally identical but had different procyanidin-to-fibre linkaging (weak bonds vs covalent bonds vs no bonds).

Our *in vitro* results suggest that the procyanidins metabolized by the gut microbiota produce bioactive metabolites with potentially promising anti-inflammatory effects. Paradoxically, complexation with fibre may partially inhibit this metabolic activity, as the results also showed that non-fibre-bound procyanidins underwent more microbiota-driven degradation (84% degradation) than procyanidins complexed with fibre (<68% degradation). Furthermore, non-fibre-bound procyanidins significantly increased the abundance of bacterial *Adlercreutzia* and *Gordonibacter* genera but inhibited fibre fermentation–especially butyrate production.

Future Outlook

Prospects leading out of this work include immediately isolating the microorganisms involved in the metabolism of B-type procyanidins and identifying the microbial metabolites involved in their anti-inflammatory effects. We will then need to study the prevalence of the microorganisms involved in procyanidin metabolism in humans and correlate that prevalence to the presence of bioactive metabolites of interest. From there, we could see the extent to which diet has an effect on these two markers, and move forward to test out nutritional strategies in human subjects.

Learning how seniors chew protein-rich soft-crumb foods

Read more

Assad-Bustillos M, Tournier C, Septier C, Della Valle G, Feron G

Relationships of oral comfort perception and bolus properties in the elderly with salivary flow rate and oral health status for two soft cereal foods.

Food Research International . 2019

Assad-Bustillos M, Tournier C, Feron G, Guessasma S, Reguerre AL, Della Valle G

Fragmentation of two soft cereal products chewed by elderly with different oral health status.

Food Hydrocolloids . 2019

Mobilization and impact

This research framed under the ANR [French national research agency]-funded ALIMASSENS project (ANR-14-CE20-0003) led to a PhD thesis by Mélissa Assad-Bustillos via a CIFRE [industrial research placement training] agreement arranged with Cerelab.

Contacts

Gilles Feron and Guy Della Valle

UMR CSGA, UR BIA

gilles.feron@inrae.fr

guy.della-valle@inrae.fr

Context

To fashion a food offer that caters to the elderly (aged 65 and over), we need to first understand the impacts of age-related changes in oral–dental health on chewing and the consequences for meal enjoyment. With that vision, we chose two classic widely-retailed cereal products known to offer a soft-textured tender crumb: brioche and sponge cake. After groundwork to detail the mechanics and pore structure of these foods, we determined the destructuration mechanisms surrounding how foods are broken down in the mouth and transformed into a ready-to-swallow bolus in 20 elderly volunteers. The 20 subjects presented varying stimulated salivary flow rates and either poor or satisfactory oral–dental health status in terms of posterior functional tooth units.

Results

Size of the food bolus particles was determined by image analysis across three mastication cycles, and the resulting particle-size distribution curves were modelled to determine the polydispersity and median size of the particles. Analysis showed a progressive decrease in particle size for the sponge cake, which points to a pure fragmentation process, whereas for the brioche, chewing mobilized a complex interplay of fragmentation and agglomeration processes, with better oral–dental health status tipping the equation towards fragmentation for both foods. Furthermore, rheological analysis of the boli showed that their viscosity is governed by amount of saliva and directly connected to perception of oral comfort. Finally, adding pulse proteins to back up the 'protein-rich' nutritional claim has little impact on destructuration and perceived in-mouth comfort, and yet the proteins remain readily digestible.

Future Outlook

Inquiry into the chewing process thus informs the design of new foods for seniors. Note too that these results served to validate a numerical model of chewing and design new cereal-based foods high in added plant protein, and work has moved forward into bioavailability and bioaccessibility studies.

Clean processes and biobased products

TRANSFORM scientists are helping to lift the circular economy. We forge ways to upcycle food–farming industry coproducts into high-added-value compounds for use in an array of applications, through fungal-driven enzymatic hydrolysis, cascading extraction, or supramolecular assembly. We also study how plant fibres can lend structure to innovative biobased materials and support purpose-adapted properties.

TRANSFORM is also working on solutions to reduce the carbon footprint of the food supply chain–starting with less energy-demanding retail display cases for the cold chain.

Bringing green biotech solutions to the health – cosmetics – nutraceuticals sector

Read more

Lomascolo A, Fine F, Peyronnet C, Sigoillot J-C, Navarro D, Odinot E

Process for preparing a vinylphenolic compound from a precursor hydroxycinnamic acid derived from an oilseed cake.

Patent WO 2017/072450 A1

Odinot E, et *al.*

A two-step bioconversion process for canolol production from rapeseed meal combining an Aspergillus niger *feruloyl esterase and the fungus* Neolentinus lepideus.

Microorganisms . 2017

Collaboration

To tackle this challenge, UMR 1163 BBF joined forces with Terres Inovia and Terres Univia to research whether wood-decaying and biomass-degrading fungi have the lignocellulolytic machinery needed to make oilseed meal bioconversion practicable.

Contact

Anne Lomascolo

UMR BBF

anne.lomascolo@univ-amu.fr

Context

Rapeseed is the leading oilseed crop in France in terms of hectarage and volumes farmed. The process of crushing oilseeds creates solid coproducts called meals. These coproducts contain value-streamable compounds, typically polysaccharides and phenolics that make precious substrates for developing biotech processes, especially processes that recruit lignocellulolytic fungi or their lignocellulolytic enzymes. It is essential to enhance the value of these agricultural coproducts through biotechnology by producing high added value compounds, while meeting the challenges of the circular economy in the sector. To tackle this challenge, UMR 1163 BBF joined forces with Terres Inovia and Terres Univia to explore whether wood-decaying and biomass-degrading fungi have the lignocellulolytic machinery to make oilseed meal bioconversion practicable.

Results

Two innovative fungal bioconversion and upcycling processes were developed. The first process yields a versatile industrially-valuable fungal biocatalyst, and the second produces biobased phenolic platform molecules for process applications in pharmaceuticals, cosmetics, nutraceuticals, and novel biomaterials. Leading out of the project, the partners set up OléoInnov, a biotech start-up missioned with delivering clean, green, inherently non-toxic process solutions.

This research-backed start-up will set out to leverage the powerful broad-spectrum enzymatic potential of fungi to produce biobased molecules ready for use in high-added-value industries like health–molecules which are currently absent from markets because they are difficult to produce by classical chemical synthesis. The first example is canolol (2,6-dimethoxy-4-vinylphenol) yielded by fungal conversion of the sinapic acid in rapeseed meal. Canolol is a potent antioxidant and anti-inflammatory, as well as a platform molecule for the synthesis of biobased polymers.

Future Outlook

The short-term goal for OléoInnov is to complete the scaling up needed for operable process industrialization, but the start-up also aims to continue its promising R&D activity in order to develop new oilcrop biomass bioconversion processes and expand its market reach in the next five years.

@INRAE

Upcycling food–farming industry coproducts to aid crop protection

Read more

Fameau A-L, Gaillard C, Marion D, Bakan B

Interfacial properties of functionalized assemblies of hydroxy-fatty acid salts isolated from fruit tomato peels.

Green Chemistry . 2013

Bakan B, Marion D, Ernenwein C, Keller C

Utilisation d'une composition formulée d'acides gras hydroxylés pour la défense des plantes contre des agents pathogènes.

Dépôt INRA/société SDP – Réf. 18/72017 . 2018

Collaboration

UMR IRHS (Institut de Recherche en Horticulture et Semences)

UE Horti (Angers)

Contact

Bénédicte Bakan

UR BIA

benedicte.bakan@inrae.fr

Context

Pomace is a fruit processing industry coproduct–essentially the skins and seeds of the fruit–that is still a largely undervalued resource. However, the skins are an abundant source of cutin, a polyester composed of hydroxy fatty acids that is also a source of novel natural chemicals with outstanding surfactant properties.

In parallel, the crop protection industry is facing strong demand for new biocontrol solutions to debottleneck today's product offer. However, cutin is the front-line barrier against plant pathogens that produce cutinases. In-lab trials on cells have often considered the substances released by these hydrolases as signal molecules. This gave rise to the idea of developing a new biocontrol strategy by (i) exploiting an industrially practicable source of cutin monomers, (ii) exploiting the emulsifying properties of these molecules to formulate them, and (iii) exploiting their biological action to elicit plant defences.

Results

Working up from tomato canning industry pomaces (sourced through UNIPROLEDI) and in partnership with agricultural supplies business SDP, the INRAE developed a biorefinery process to extract hydroxy fatty acids from tomato cutin at industry-practicable yields and purity. After a successful formulation effort, these extracts showed practical potential for crop protection against biological pests.

Using this proof-of-concept allowed the PEEL project to developed a pre-industrial trial aimed at scaling processes for the extraction of new molecules. Several INRAE units are engaged in PEEL, where the project brief is:

i) to realize industrial scale-up of the biorefinery process by creating a circular economy based on upcycling food–farming industry coproducts,

ii) to assess the performances of these process-extracted molecules for eliciting plant defences and protecting a range of crops (rapeseed, corn, wheat, apple trees, vines) and identify the molecular mechanisms elicited in field-crop conditions.

Future Outlook

This process holds unrivalled potential for the development of novel plant defence elicitors.

@NickyPe- Pixabay

Flax as structural reinforcement for innovative ecomaterials: the secret is in milling !

Read more

Mayer-Laigle C, Bourmaud A, Shah D-U, Follain N, Beaugrand J

Unravelling the consequences of ultra-fine milling on physical and chemical characteristics of flax fibres.

Powder Technology . 2019

Badouard C, Traon F, Denoual C, Mayer-Laigle C, Paës G, Bourmaud A

Exploring mechanical properties of fully compostable flax reinforced composite filaments for 3D printing applications.

Industrial Crops and Products . 2019

Collaboration

This research created the opportunity to launch new 3D printing-driven collaborations between INRAE and the IRDL in France and SCION Institute in New Zealand.

Contacts

Claire Mayer, Gabriel Paës, Johnny Beaugrand

UMR IATE, UMR FARE, UR BIA

claire.mayer@inrae.fr

gabriel.paes@inrae.fr

johnny.beaugrand@inrae.fr

Context

Plant fibre and agricultural bioproducts and coproducts are increasingly being employed as reinforcement additives in agro-based composites to minimize their environmental footprint. This is where 3D printing opens up a vast array of new architecture opportunities with a minimum of start-material feedstock.
Whatever the shaping process used, plant-based reinforcements need to be prepped either by cutting the long fibres or by milling, and both processes affect their subsequent workability. Our research sets out to get a clear picture of the relationship between the starting properties of plant particles and the functional properties of the end-materials in which they are incorporated.

Results

Our efforts have focused on the processability of powder-form plant particles and on the mechanical properties of 3D-printed and injection-moulded materials, and accommodating the specific constraints tied to each of these processes.
Our work revealed that processed flax-powder particle sizes influenced the properties of the thermoplastic polymer. Sizes greater than 200 µm were found to maximize the elongation ratio (length-to-diameter) and are amenable to injection processes. Sizes less than 100 µm were found to prove better for fused deposition modelling 3D printing processes, as they help resolve process issues like (i) nozzle clogging, (ii) fault zones in the manufactured object, and (iii) in-printing filament breaks.
Advanced comminution processes developed at the IATE joint research unit's PLANET platform ('PLANt Processing with Emergent Technologies') served to yield these target sizes.
Advanced developments in the extrusion and 3D printing processes then managed to incorporate up to 30% flax plant biomass into the composite matrix.

Future Outlook

This research articulating the potential of 3D printing with the responsiveness of ultrafine flax powders now paves the way to creating smart materials that are able to self-sense or responsively adapt to changing environmental conditions (temperature, humidity, pH, and so on), thus heralding '4D materials'. We are now looking at extending this research to encompass other plant-biomass feedstocks.

@Ana Villares - ACS Omega

Supramolecular assembly of cellulose nanocrystals

Read more

Villares A, Moreau C, Cathala B

Star-like supramolecular complexes of reducing-end-functionalized cellulose nanocrystals.

ACS Omega . 2018

Chemin M, Moreau C, Cathala B, Villares A

Adsorption behavior of reducing end-modified cellulose nanocrystals: a kinetic study using quartz crystal microbalance.

Journal of Renewable Materials . 2020

Contact

Ana Villares

UR BIA

ana.villares@inrae.fr

Context

Cellulose is the most abundant renewable polymer on Earth– photosynthetic processes alone produce around 200 billion tonnes a year. Acid hydrolysis of cellulosic fibres can isolate cellulose nanocrystals, which are 3–7 nm-thick 100–2000 nm-long rod-shaped crystalline fibrils. These nanocelluloses have a reducing end (C1=O, hemiacetal) and a nonreducing end (C4-OH). The selective reactivity of the C1=O chain makes it possible to functionalize the (more reactive) reducing end, creating monofunctional nano-building-blocks with chemically differentiated ends.

A big challenge for nanocellulose development is to control intermolecular and intramolecular interactions in order to tune their functionalities. One potential but under-researched strategy is to exploit the reactivity of the carbonyl groups on the reducing ends, where their nanometre-scale anisotropy can serve to scaffold novel supramolecular architectures and design innovative self-assembled materials.

Results

We developed a strategy to fabricate novel nano-objects scaffolded by biotin–streptavidin interaction. Streptavidin is a protein with such remarkable affinity for biotin that it can noncovalently bond up to four biotin ligands into a very stable complex. This controlled assembly of cellulose nanocrystals is characterized by the increase in hydrodynamic radius after the streptavidin is added. Atomic force microscopy observations show end-linked nanocrystal complexes, thus confirming specific reducing-end linkage. These encouraging findings provide evidence that a single biotin molecule is capable of facilitating the association of several nanometre-sized nano-objects.

Furthermore, the biotin-functionalized nanocrystals are adsorbed onto streptavidin-coated substrate surfaces. Adsorption studies using quartz crystal microbalance with dissipation monitoring on the nanocrystals showed a perpendicular orientation, which is clear evidence of the interaction between the biotin-functionalized reducing end and the streptavidin surface.

Future Outlook

Prospects leading out of this work include developing clean and sustainable processes for modifying nanocellulose surfaces to drive different types of supramolecular-scale self-assembly. We aim to deposit end-anchored nanocrystal layers and add stucturational groups (for functional responsiveness, hydrophobicity, conductivity, etc.) to create nanoparticles with clearly differentiated ends or to couple several nanocrystals together into nanoarchitectures.

Re-engineering plant-fibre morphology to improve biobased composite performances

Read more

Padovani J, Legland D, Pernes M, Gallos A, Thomachot-Schneider C, Shah D-U, Bourmaud A, Beaugrand J

Beating of hemp bast fibres: an examination of a hydro-mechanical treatment on chemical, structural, and nanomechanical property evolutions.

Cellulose . 2019

Contacts

Johnny Beaugrand and David Legland

UMR FARE, UR BIA

johnny.beaugrand@inrae.fr

david.legland@inrae.fr

Context

Lignocellulosic fibres like hemp and flax make excellent feedstocks to support the bioeconomy and the wider transition for green growth. Both have already found use in the automotive industry, largely because their mechanical properties enhance the quality of biobased materials. However, this argument is no longer enough to create new markets where these renewable fibres can prove dependable industry alternatives. We need to discover and disentangle a host of interdependent factors (initial fibre quality–process-induced properties) that can either speed or slow market adoption of low-carbon ecomaterials. The goal of our research was to purpose-develop a novel image-driven analysis protocol to find out how features of fibre morphology shape the mechanical properties of composite materials.

Results

Fibre morphology was quantified using automated on-line image analysis systems at each step in the material processing route, where we applied a combined wet–mechanical refining treatment on the hemp bast fibre. We learned that fibre branching increased with intensity of hydro-mechanical treatment. These ramifications create microfibrils that are thought to help the fibres physically embed in a polymer matrix, which lends tensile strength to the biobased composite. We also tested our experimental morphometric statistics against other more conventional analytical methods for describing plant-fibre microstructure. We found co-correlation between increased fibre-branching and decreased fibre stiffness with the hydro-mechanical treatment. This in-depth investigation into intrinsic features of plant fibres brought key insight into how hydro-mechanical treatments affect the structural integrity of the fibres, and the need to find trade-offs between improved fibre morphology and damaged fibre skeleton architecture.

Future Outlook

These findings ultimately offer a blueprint towards attuning hydro-mechanical process parameters (on the refinery mill side) to get the optimal sweet spot that creates fibrillation yet keeps the fibres long. There are both economic and environmental stakes to this effort, but it also poses us more fundamental challenges surrounding composition–structure–property intersections.

@INRAE - Visualisation du rideau d'air dans un meuble de vente ouvert

Innovative retail display cabinets for energy management and temperature fluctuations damping

Read more

Ben-Abdallah R, Leducq D, Hoang H-M, Pateau O, Ballot-Miguet B, Delahaye A, Fournaison L

Modeling and experimental investigation for load temperature prediction at transient conditions of open refrigerated display cabinet using Modelica environment.

International Journal of Refrigeration . 2018

Ben-Abdallah R, Leducq D, Hoang H-M, Fournaison L, Pateau O, Ballot-Miguet B, Delahaye A

Experimental investigation of the use of PCM in an open display cabinet for energy management purposes.

Energy Conversion and Management . 2019

Collaboration

EDF- industrial and commercial refrigeration team

Contact

Hong – Minh Hoang

UMR FRISE

hong-minh.hoang@inrae.fr

Context

Refrigeration accounts for 17% of energy use in industrialized countries, and 35% in the food sector. Retail display cabinets are a ubiquitous yet energy-demanding feature of the supermarket landscape. These cases could integrate Phase-Change Materials (PCM) as thermal energy storage device to become more energy-efficient and reduce their environmental footprint. The integrated PCM can release its latent energy as useful cooling over a given time-window, which will depend on the volume of the PCM and its energy storage capacity. This solution brings flexibility for store energy management, helps damp the intermittency effects of renewable energy sources, and can harness energy-sustainable photovoltaic or wind power. However, deployment and integration of this kind of energy storage solution hinges on optimizing key decisions to choose the right PCM in the right amount and in the right position inside the cabinets to not upset its thermal equilibrium.

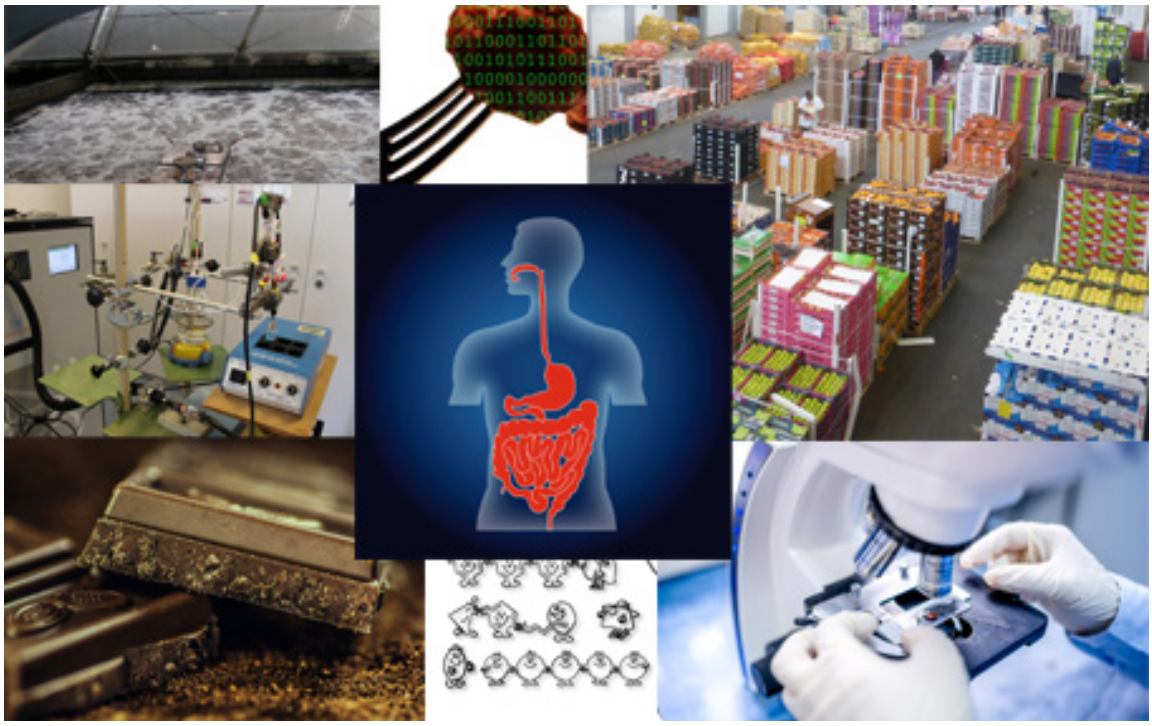
Results

We studied the behaviour of the PCM and its effect on the thermal and energy efficiency performances of the display cabinet. The novelty of this work was that we introduced the PCM (7 kg of water), contained in a heat exchanger, into the rear duct of a display cabinet. The PCM-equipped display cabinet has proven capable of storing and releasing useful energy. PCM charging takes four hours and is twice as long as the PCM discharging time. In a 16°C ambient temperature, built-in PCM storage limits product temperature rise to just 1°C when the cold machine was turned off for two hours, against 2°C without PCM storage. These results clearly demonstrate that a thermal energy storage holds potential for applying in-store energy management strategies.

Future Outlook

The presence of the PCM in the retail display cabinet alters its thermal and hydraulic behaviour. To optimize its thermal and energy performances, it is important to reconfigure the display-cabinet architecture and appropriately adjust the airflows. Reconfigurability with one or composite PCMs in various positions (under the shelves, inside the refrigeration system, etc.) opens up a catalogue of options. Wider expansion of this elegant technology will need to be thought through by a multicriteria analysis covering thermal–energy–environmental–economic benefit objectives.

Understand, model, predict



At TRANSFORM, we pursue research to understand and model the key steps in food digestion by developing increasingly sharp research models adapted to specific products and populations.

An emerging opportunity lies in developing predictive models to stage process properties or functionalities. Ongoing predictive modelling research is tackling how to put chocolate into sensory classes, meat digestion, polymer migration in food-packaging materials, microbial community metabolism, and biofiltration-process greenhouse gas emissions.

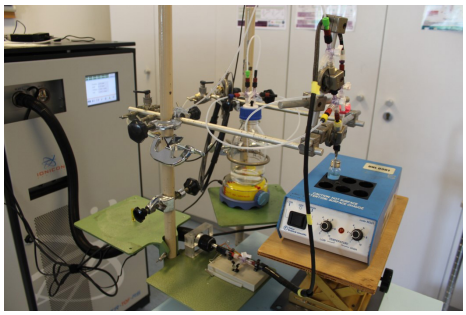
A predictive model that puts chocolate into sensory classes

Read more

Deuscher Z, Andriot I, Sémon E, Repoux M, Preys S, Roger J-M, Boulanger R, Labouré H, Le Quéré J-L

Volatile compounds profiling by using Proton Transfer Reaction – Time of Flight – Mass Spectrometry (PTR-ToF-MS). The case study of dark chocolates organoleptic differences..

Journal of Mass Spectrometry . 2019



@ Zoe Deuscher
Instrument (PTR-ToF-MS) and setup allowing direct injection of VOCs.

Contact

Jean-Luc Le Quéré
UMR CSGA
jean-luc.le-quere@inrae.fr

Context

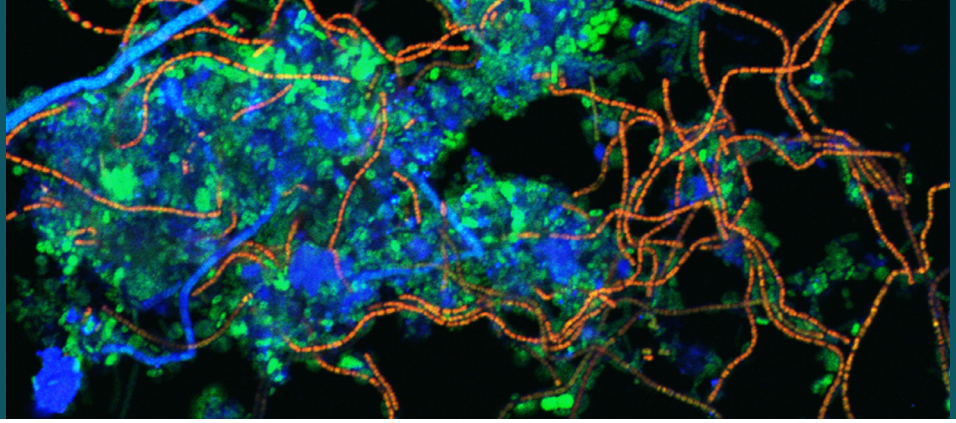
Consumer preference for a food like chocolate is largely due to its aromatic composition. Perception of this component is closely tied to the aroma compounds that are released as we eat the food. Premium chocolate makers Valrhona run systematic sensory analysis as part of an in-house programme to qualify their pure-origin dark chocolate, which is made to the same standard process recipe from different cocoa cultivar batches. This analysis produces sensory profiles that class the chocolates into four big sensory clusters called poles. The challenge was to come up with a rapid method of analysis to emulate and then model this sensory classification. The objective here was to mobilize a rapid all-in-one technique for characterizing the volatile organic compounds (VOCs) that make up chocolate aroma, in order to produce a predictive model of this sensory classification. Direct-injection proton-transfer reaction-mass spectrometry (PTR-MS) met our project criteria.

Results

Global VOC profiles of a set of 206 representative chocolate samples classified in the four sensory poles were obtained by direct-injection mass spectrometry using proton-transfer-reaction as ionization process coupled to a time-of-flight mass analyzer for high-resolution detection (PTR-ToF-MS). Multivariate data analysis including PLS-type discriminant analysis on the release of 143 significant ions in the 206 samples enabled us to construct a predictive model that puts chocolate into sensory classes based on aggregate VOC composition profile. Variable selection using purpose-dedicated methods uncovered a compact set of VOCs that can discriminate chocolate samples into the four sensory clusters. The covariate selection (CovSel) method in particular, used here for the first time on a mass spectrometry dataset, made it possible to correctly model the initial sensory classification using ten times fewer target ions.

Future Outlook

The next step is to develop a transferable chocolate volatilome analysis method that can serve to operationalize predictive sensory classification of cocoa for the chocolate industry.



@Durban Nadège, INRAE, UR PROSE

Simple models to predict complex microbial community metabolism—with applications for environmental biotechnology

Read more

Desmond-Le Quemener E, Bouchez T

A thermodynamic theory of microbial growth.

ISME Journal . 2014

Delattre H, Desmond-Le Quemener E, Duquennoi C, Filali A, Bouchez T

Consistent microbial dynamics and functional community patterns derived from first principles.

ISME Journal . 2019

Collaboration

Development of the microbial transition state theory and assessment of the potential power of microbial thermodynamics models is the focus of an ongoing ANR-sponsored project (ANR THERMOMIC 2016–2020) that is coordinated by INRAE–PROSE with LBE and TBI on board.

Contact

Théodore Bouchez

UR PROSE

theodore.bouchez@inrae.fr

Context

Microorganisms are not just the most abundant forms of life on Earth–microbial communities are key engines that drive Earth's biogeochemical cycles. They essentially cycle chemical elements across the entire planet, and the TRANSFORM division harnesses their extraordinary biocatalytic capacities in a catalogue of biotech processes. Successful development of the bioeconomy needs solid foundations to understand and methodize the use of microbial communities for biotransformation purposes.

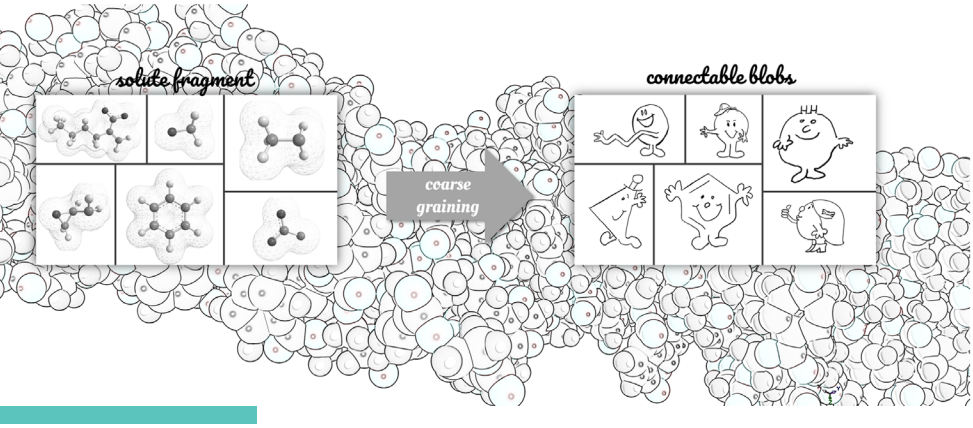
Results

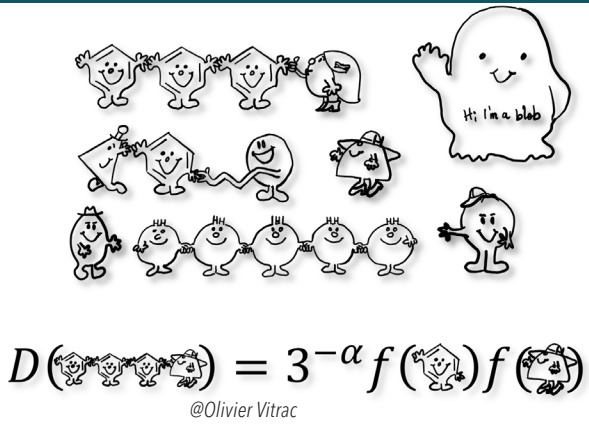
Models of microbial dynamics are grounded in phenomenological equations, and foremost the seminal equation proposed by Jacques Monod in the 1940s. However, these models cannot be used without first calibrating parameters against population-specific experimental data. Attempts to explore complex microbial communities dominated by uncultured microorganisms quickly run up against this constraint, which limits use of these models and bottlenecks their predictive abilities. That said, in a given set of physical-chemical conditions, whether in nature or in unconfined biotechnology processes, biotransformation will generally repeat the same functional patterns of metabolism, which suggests that there are generic deterministic processes at work to assemble functional microbial communities. We contend that energy balances play a major role in lending structure to microbial functions within ecosystems.

We propose a theory framework grounded in a manageably small set of simple physical concepts to capture, through generic first principles and mathematically explicit expression, the influence of energy on rate of growth in microbial populations. The overarching objective is to use known physical-chemical conditions to emerge the metabolic functions of microbial ecosystems. We have brought illustration of the predictive abilities of our new approach by modelling an increasingly complex gradient of microbial ecosystems using a compact number of parameters. We showed that an activated sludge process community can be modelled with three times fewer parameters than conventional approaches.

Future Outlook

We anticipate this approach as a starting point towards a whole new class of microbial ecosystem models potentially demonstrating more powerful predictive capabilities. To take this pure research into applied practice, we have started work on translating the new kinetics equations from our theory into simulation software to support environmental biotechnology process engineering.





Predicting diffusion coefficients to support thermoplastic polymer recycling and repeated use

Read more

Fang X, Domenek S, Ducruet V, Refregiers M, Vitrac O

Diffusion of Aromatic Solutes in Aliphatic Polymers above Glass Transition Temperature.

Macromolecules . 2013

Zhu Y, Welle F, Vitrac O

A blob model to parameterize polymer hole free volumes and solute diffusion.

Soft-Matter . 2019

Mobilization and impact

As our partner in the joint technology unit called SAFEMAT or 'Safety of food contact materials and packaging', LNE, the French national reference metrology laboratory for food contact materials, is already using the results presented here to evaluate the safety of food packaging on the EU market.

Contact

Olivier Vitrac

UMR SayFood

olivier.vitrac@agroparistech.fr

Context

The eminent laws of diffusion fail to accommodate the diffusion of molecules that are bigger than the voids entangled between segments of a solid thermoplastic polymer. The US EPA, then the US FDA and the European Commission have each put forward more or less empirical models to purpose-overestimate the diffusion coefficients based solely on the molecular mass of the solute. These models are incomplete, incoherent, and unreliable, and it is even advised against using them to assess the performances of mechanical polymer recycling processes, since they underestimate the levels of residual migrant contaminants in the recycled thermoplastics.

Results

The new more unified theory developed here borrows advancements made in two big condensed-phase diffusion theories: coupled-mode theory and Vrentas–Duda free-volume theory. It offers an elegant final formulation, as it is analytical and makes it possible to hand-build diffusion coefficients by combining solid bricks, which we dub 'blobs', and even reproduce the articulated behaviour of the molecule under study. Note that it also provides an experimental paradigm for evaluating the theoretical concept of 'hole-free volume', a special type of free volume that redistributes without any energy barriers, even in the glassy state. As it stands, the approach covers 11 (rubbery-state and glassy-state) polymers, i.e. over 95% of all plastic food packaging materials, as well as the vast majority of substances (whether rigid, linear or low-branched chains, spanning solvents, oligomers and processing aids) with or without polymer interactions.

LNE, the French national reference metrology laboratory for food contact materials, is already using our model output to evaluate the safety of food packaging on the EU market. The model has been used to validate an acceptable recycled polyethylene terephthalate (rPET) incorporation rate for all Pernod-Ricard-group PET bottles.

Future Outlook

The approach could well be generalized to cover crosslinked polymers like elastomers and varnishes–provided it first gets validated and then, very probably, reparameterized–and we anticipate it could determine the set of acceptable conditions needed to clear recycled thermoplastics as safe for use in food-contact materials, both for ready-authorized polymers like PET and as-yet-unauthorized polymers like polyolefins and polyamides. This new data and the underpinning theories are compiled and curated by the EU task-force TF-MathMod which is mandated to re-update the state of the art in predictive models for migration testing.

@J. Sicard - Modelling meat digestion processes for adults and the elderly

Computing harnessed to predict in-stomach meat digestion

Read more

Sicard J, Mirade PS, Portanguen S, Clerjon S, Kondjoyan A

Simulation of the gastric digestion of proteins of meat bolus using a reaction-diffusion model.

Food & Function . 2018

Contact

Jason Sicard

UR QUAPA

jason.sicard@inrae.fr

Context

Protein digestion rate is the main factor influencing uptake in the body. Speeding up protein digestion rate can help ensure adequate absorption of the essential amino acids found in meat, making it a supportive nutritional strategy geared to older people struggling with declining muscle capacity and who are reluctant to increase their intake.

However, protein digestion rate depends on a cluster of factors, particularly in the stomach where it depends on ability to quickly regain the optimal acidic pH after ingesting the food bolus, on the rate and viscosity of the gastric fluid getting mixed and churned by stomach muscle contractions, on pepsin secretion, on type of food, and on the size of the chewed-down bolus particles. Every one of these factors except type of food can decline with age and/or age-related diseases.

Results

We developed a model to predict meat digestion as it transits through the stomach. The mathematical modelling is grounded in *in vitro* results, which means it can yield long-run predictions or information that may otherwise be impossible to obtain experimentally. The model combines the kinetics of pepsin-driven protein degradation with laws governing pepsin diffusion and proton diffusion in food-bolus particles, all while accounting for the buffering capacity of the meat that slows the drop in pH.

The results unsurprisingly show that the normally highly efficient digestion of meat proteins in the young adult stomach can rapidly collapse when they start to lose masticatory capacity or when gastric acid secretion and gastric motor function start to decline.

The real benefit of this model is that it can quantify the in-stomach effect of the many factors that speed or slow protein digestion rate, and thus inform efforts to adapt foods to target populations–like the elderly.

Future Outlook

The model could be expanded to factor in the effect of food–food interactions and then compared against *in vivo* measurements by nutritionists and physiologists on human subjects. It could also be transposed to other protein-rich food matrices, such as fish and dairy or plant-based protein foods.

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Learning to better predict biofiltration-process greenhouse gas emissions

Read more

Bollon J, Filali A, Fayolle Y, Guerin S, Rocher V, Gillot S

N_2O emissions from full-scale nitrifying biofilters.

Water Research . 2016

Fiat J, Filali A, Fayolle Y, Bernier J, Rocher V, Spérandio M, Gillot S

Considering the plug-flow behavior of the gas phase in nitrifying BAF models significantly improves the prediction of N_2O emissions.

Water Research . 2019

Collaboration

This research was carried out as part of the ANR-sponsored 'N2Otrack' project (ANR-15-CE040014-02) and the 'Mocopée' research programme, in tight collaboration with SIAAP–the Greater Paris sanitation authority, TBI–Toulouse Biotechnology Institute, Bio & Chemical Engineering and the research unit REVERSAAL.

Contact

Ahlem Filali

UR PROSE

ahlem.filali@inrae.fr

Context

Biofiltration is an intensive wastewater treatment process based on a biofilm grown over a bed media filter. However, nitrifying biofilters are significant emitters of nitrous oxide (N_2O)–a greenhouse gas with potent global warming potential that also contributes to ozone layer depletion. Reducing the carbon footprint of biofiltration facilities thus revolves entirely around learning to control these N_2O emissions.

To gain deeper insight into the mechanisms underpinning N_2O production, we extended a biofiltration model to take in equations describing the main microbially-driven N_2O pathways.

Results

The current crop of biofiltration models make heavy simplifications on the description of gas–liquid exchanges, chiefly by ignoring the change in gas composition through the depth of the biofilter. To integrate this change factor, we proposed to make some structure modifications to the model, such as considering gas hold-up in the biofilter and adding a mass balance for gas-phase reactions.

Our results find that integrating the mass balance for gas-phase reactions has relatively little impact on oxygen mass transfer (little change in oxygen concentration). However, it proves essential to describe the substantial N_2O fluxing into the gas phase (1000-fold change in N_2O from bottom to top of the biofilter bed) and equally essential to properly model N_2O gas–liquid flux partitioning.

The model developed successfully predicts the nitrification performances and seasonal variability in N_2O emissions of the nitrifying biofilters of Seine Aval, Europe's biggest wastewater treatment facility.

Future Outlook

Research is now turning to assess how well the model can describe N_2O emissions from other big industrial facilities, and to employ it to propose operationalizable emissions reduction strategies. Our hope is that this tool will ultimately serve to refocus operational biofilter scale-up and practice onto environmental criteria including global warming.

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Multicriteria cold-chain assessment

Read more

Duret S, Hoang H, Derens-Bertheau E, Delahaye A, Laguerre O, Guillier L

Combining Quantitative Risk Assessment of Human Health, Food Waste, and Energy Consumption: The Next Step in the Development of the Food Cold Chain?

Risk Analysis . 2019

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Contact

Steven Duret
UR FRISE
steven.duret@inrae.fr

Context

The cold chain is a refrigeration-cooled supply chain designed to keep perishables safe and minimize food waste. However, energy consumption by refrigeration processes adds up substantial economic costs and environmental impacts. One strategy to reduce refrigeration-energy consumption is to increase process temperature, but this shortens shelf-life, which increases food waste and consequently costs, making the action inefficient, as well as potentially pushing the food safety risk unacceptably high. The purpose of this research is to develop a multicriteria decision support tool to optimize cold-chain management.

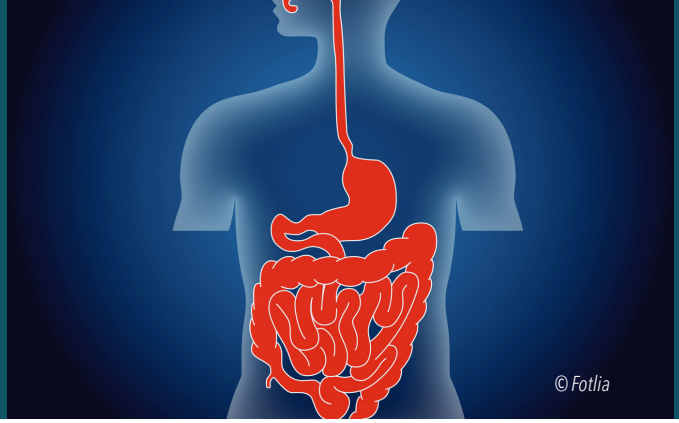
Results

Results show that different sets of equipment require different sets of actions to put into place to guarantee food safety while cutting energy consumption. Increasing the temperature of a home refrigerator has a huge impact on food-safety risk and wastage but little impact on energy bills. To illustrate, increasing in-home refrigerator temperature to 7°C instead of 6°C increases risk by 70% and waste by 30%, all for a meagre 2% gain in energy consumption. In contrast, the in-store retail display case is a link in the cold chain that is more amenable to making energy efficiencies. Provided the food is held at a steady temperature to ensure food shelf-life and food safety, energy consumption can be reduced by optimizing the airflow and temperature stability of the retail-case air curtain. It is possible to cut energy consumption by up to 15% with very little trade-off cost to pay in terms of increasing food safety risk and wastage (<1%).

Here we propose a multicriteria decision analysis method to rank these scenarios. Our method enables stakeholders to prioritize selected decisional criteria by reweighting or by capping key thresholds, which may prove a useful way forward when there is little wiggle room on a criterion like food safety risk. The focus of the tool applied so far has been the cooked-ham cold chain.

Future Outlook

Our approach makes it easy to accommodate new cold chain steps (platforms, manufacturing facilities, and so on) or cold chain breaks where products are transferred between equipment nodes. It is also ready to integrate new criteria such as CO_2 emissions, other quality-change criteria (typically vitamin content or colour gradients) or socio-economic criteria.



Internationally-harmonized digestion models geared to specific population groups

Read more

Brodkorb A *et Al.*

INFOGEST in vitro *simulation of gastrointestinal food digestion.*

Nature Protocols . 2019

Egger L, Ménard O, Baumann C, Duerr D, Schlegel P, Stoll P, Vergères G, Dupont D, Portmann R

Digestion of milk proteins: comparing static and dynamic in vitro *digestion systems with in vivo data.*

Food Research International . 2019

INFOGEST

Contact

Didier Dupont
UMR STLO
didier.dupont@inrae.fr

Context

Over the past 30–40 years, the prevalence of diet-related diseases (obesity, type-II diabetes, heart disease) has been on an upward spiral in practically all developed and developing countries across the globe. It is becoming increasingly urgent to work on the prevention side of the equation. When we eat a food, its first interface with the body is the gastrointestinal tract. The digestion process releases dietary nutrients and bioactive compounds that the body can use, which makes it a vital factor of human health. We need a firmer grasp of food breakdown mechanisms at work in the digestive tract in order to develop mechanistic understanding of food–health intersections.

Results

A vast number of *in vitro* food models have been developed to study food digestion. Unfortunately, though, none of them share the same sets of parameters, making it impossible to meaningfully compare results across studies, and none–or nearly none–have been validated against in vivo (human or animal) physiological data.

One of the missions set for the INFOGEST international research network, for which INRAE is lead coordinator, was to propose an *in vitro* model simulating digestion in healthy adults that uses parameters taken from clinical trials in human subjects. This model was validated for protein digestion against data obtained in pigs and human subjects. It was published in Nature Protocols, which only accepts original protocols that have been used and proven to work by the scientific community–which goes some way to explaining how the original article describing the model got over 1000 citations in the space of 5 years. A YouTube channel has been created to deliver video tutorials teaching new users how to take the model into their lab, calibrate the digestive enzymes and quantify the bile salts, and three researcher workshops have been held in Europe to train up sixty-odd model users. A similar model–this time mimicking newborn digestion–has also been developed.

Future Outlook

The protocol is on track to be made an ISO/FIL standard, and the EFSA is assessing the relevance of using the model as added predictive input to allergenicity assessments of novel proteins.

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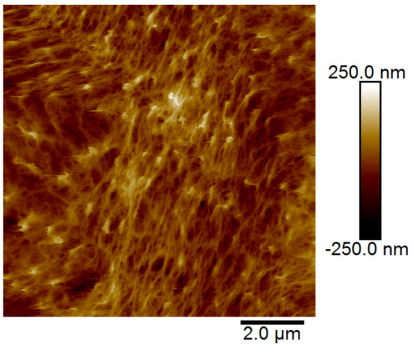
Characterization of a novel model of oral mucosa

Read more

Aybeke EN, Ployon S, Brulé M, De Fonseca B, Bourillot E, Morzel M, Lesniewska, E Canon, F

Nanoscale Mapping of the Physical Surface Properties of Human Buccal Cells and Changes Induced by Saliva.

Langmuir . 2019



Contact

Francis Canon
UMR CSGA
francis.canon@inrae.fr

Context

Flavour is a major driver of food intake. The oral mucosa may play a key role in capturing certain elements of flavour perception, like astringency and aroma persistence. When we eat a food, its flavour compounds interact with the oral mucosa in different ways depending on their nature and mucosa surface properties. However, very few studies have attempted to characterize these interactions. We developed an innovative model of oral mucosa cells expressing MUC1–a key oral epithelium mucin involved in mucosal pellicle formation–and then characterized its surface properties using innovative atomic force microscopy techniques.

Results

Chemical Force Microscopy (CFM) was used to characterize the surface hydrophobicity of the epithelial cells, and scanning microwave microscopy (SMM) was used to characterize the dielectric properties of the cell surface. These properties were recorded in four different conditions: native TR146 epithelial cells with and without mucosal pellicle, and transmembrane MUC1-expressing TR146 epithelial cells with or without mucosal pellicle.
The results find that MUC1 expression by epithelial cells modifies their surface hydrophobicity and charge properties without substantially modifying their surface morphology. The results also suggest that salivary proteins bind to MUC1 at the most hydrophobic and heavily-charged surface areas. This study brings foundational insight into the surface properties of oral mucosa and the interplays that shape non-covalent interactions between oral mucosa and flavour compounds.

Future Outlook

The methods developed through this research offer new solutions for mapping the physical-chemical properties of biological surfaces. Note too that a new oral mucosa model is already in the development pipeline.

COLLECTIVE PUBLICATIONS

Controlling and designing protein assembly in food: what lessons can we learn from soft matter physics?

Innovative conceptualization and new approaches can help envision new food process routes and new food functionalities. The TRANSFORM division counts several scientists who mobilize concepts borrowed from soft matter physics to gain a better grasp of the processes that give structure to matter. They have joined forces to formalize these soft matter-led approaches and their insights into the physics underpinning protein structure in foods. Their work demonstrates how concepts from soft matter physics can help to rationalize and coordinate protein–protein interaction and protein assembly, for both plant and animal proteins.

The group's effort to gain unified vision led to a review paper that was published in *Annual Review of Food Science and Technology* in 2019.

The team federates people working across INRAE–BIA (Nantes), INRAE–STLO (Rennes), INRAE–TBI (Toulouse), INRAE–IATE (Montpellier) and INRAE–SayFood (Massy).

Bibliography:

Boire A, *et al.*

Soft-Matter Approaches for Controlling Food Protein Interactions and Assembly.

Annual Review of Food Science and Technology . 2019

Contacts:

Adeline Boire and Paul Menut / **UR BIA and UMR SayFood**

adeline.boire@inrae.fr / paul.menut@inrae.fr

Nuclear magnetic resonance in food science—a look at the latest developments and applications

Nuclear Magnetic Resonance (NMR) and Magnetic Resonance Imaging (MRI) play a pivotal role in food science as methods for characterizing food products and processes and assessing the impacts of processing on the nutritional value and sensory attributes of foods. This work, grouped in a special issue, is part of the understanding of global changes and the need of major adaptations in terms of production, processing, consumption and value-creation of raw materials for human consumption.

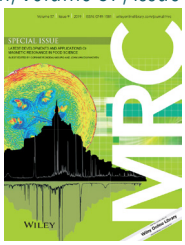
Bibliography:

It was co-edited by the IRMFood team at the INRAE–OPAALE research unit in Rennes in collaboration with Wageningen University and Unilever, and it has its own special issue:

Latest Developments and Applications of Magnetic Resonance in Food Science.

Special Issue of Magnetic Resonance in Chemistry, Guest edited by Corinne Rondeau-Mouro and John van Duynhoven, Volume 57, Issue 9, 2019, ISSN: 0749-1581

https://onlinelibrary.wiley.com/toc/1097458xa/2019/57/9

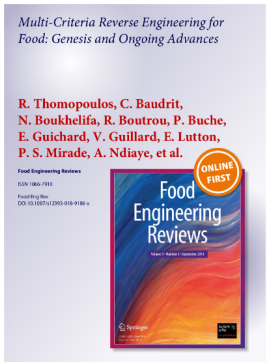


Contact:

Corinne Rondeau-Mouro / **UR OPAALE**

corinne.rondeau@inrae.fr

A Transform collective co-authors a paper on the concept and practice of multi-criteria reverse engineering in the food sector



The paper titled "Multi-criteria reverse engineering for food: Genesis and ongoing advances" maps out the theory and practice of multi-criteria reverse engineering in food packaging and food consumption spheres, both of which are shifting to integrate and deliver new sustainability and personalized food paradigms. The paper discusses advances made with multi-criteria reverse engineering in food-sector spheres (cheese, meat, cereal crops) and non-food sectors like urban planning, and concludes with a set of guidelines on deploying an effective multi-criteria reverse engineering approach in the food sector.

Bibliography:

The group's effort to gain unified vision led to a concept review paper: Thomopoulos R *et al.*, Multi-Criteria Reverse Engineering for Food: Genesis and Ongoing Advances. Food Engineering Reviews, 11 (1), 44-60. (2019)

https://link.springer.com/article/10.1007/s12393-018-9186-x)

Contact:

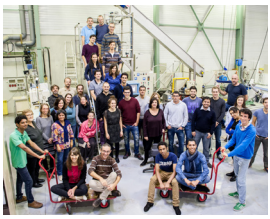
Rallou Thomopoulos rallou.thomopoulos@inrae.fr/ **UMR IATE**

5 units joined CEPIA to form TRANSFORM

UR FRISE

FRISE stands for 'refrigeration process engineering for food safety and environmental performance'–a research unit that leads food refrigeration, cold-chain and shelf-life research. FRISE pursues research into cold-process technologies and cold-chain refrigeration equipment (from tunnel cooler to cold store, refrigerated truck, retail display case, and on to the home fridge).

UR LBE



LBE pursues research to value-stream effluents (mainly from food–farming), biosolids (farm organics, household waste, sewage sludge) and more specific biomasses like microalgae through green biorefinery projects to serve the circular economy. Its value-streaming effort focuses on biomass-to-energy (methane and hydrogen) and biosynthesis of commodity compounds through cleaner safer processes (reducing chemical and microbiological contaminants) offering valuable coproducts like digestates to drive efficient use of farming resources.

UR OPAALE

OPAALE develops methods for the physical, chemical and biological characterization of biomass streams and process routes to support sustainable food systems or to turn agriwaste into energy or resourceful bioeconomic assets. Our impact-driven research also addresses environmental, energy efficiency and health–hygiene challenges across the process-chain via approaches borrowed from fluid mechanics, turbulent flows and microbiology, and spatial optimization of green process technology transitions via an approach integrating the value-chain community to produce decision support tools. Our research mobilizes bespoke science facilities including an NMR spectrometry and imaging systems platform, wind tunnels, experimental prototypes, chemical and microbiological analysis laboratories, and numerical simulation software solutions.

UR PROSE

How do wastewater treatment facilities and waste-to-methane anaerobic digesters work? How can we mobilize this new knowledge to envision next-generation technologies that enable cascading waste-to-value use of wastewater and organic waste? INRAE–PROSE based in Antony just outside Paris is a multidisciplinary community of 30-odd scientists (spanning microbial ecology, biogeochemistry, metrology, process engineering and modelling) that pursues research to resolve these environmental engineering problems that scale from microbial communities up to industrial facilities and articulate today's big sustainability, circular economy and bioeconomy challenges.

UR REVERSAAL

Wastewater is an untapped resource. INRAE–REVERSAAL pursues process engineering research to help reclaim municipal wastewater, urban runoff and sewage sludge as valuable resources. Its mission is to advance knowledge and deliver smart innovative science-backed guidance on wastewater recovery facility design, scaling, operation and optimization. REVERSAAL develops innovative technologies that are transferable to public and private-sector practitioners on the frontline. This research heralds a new generation of water resource recovery facilities seamlessly integrating the network–treatment–river continuum.

Contact our Research Units

Auvergne - Rhône-Alpes

ANIMAL PRODUCT QUALITY (UR QUAPA)
INRAE Site de Theix
63122 SAINT-GENÈS-CHAMPANELLE
+33 (0)4 73 62 41 90
quapa-ara@inrae.fr

REDUCE REUSE RECOVER THE RESSOURCES FROM URBAN WASTEWATERS (UR REVERSAAL)
INRAE Site VILLEURBANNE - LA DOUA
5 rue de la Doua CS 20244
69625 VILLEURBANNE Cedex
+33 (0)4 72 20 89 04
jean-marc.choubert@inrae.fr

Bourgogne - Franche Comté

CENTRE FOR TASTE & FEEDING BEHAVIOUR (UMR CSGA) *
AgroSup Dijon-CNRS-INRAE-Université de Bourgogne
21065 DIJON Cedex
+33 (0)3 80 68 16 23
lionel.Bretillon@inrae.fr

DAIRY TECHNOLOGY & ANALYSIS (UR TAL)
INRAE - 39801 POLIGNY Cedex 1
+33 (0)3 63 57 20 00
eric.Beuvier@inrae.fr

Bretagne - Normandie

OPTIMIZATION OF PROCESSES IN AGRICULTURE, AGRI-FOOD INDUSTRY AND ENVIRONMENT (UR OPAALE)
INRAE RENNES - BEAUREGARD
17 avenue de Cucillé CS 64427 35044 RENNES cedex
+33 (0)2 23 48 21 55
anne.tremier@inrae.fr

SCIENCE & TECHNOLOGY OF MILK & EGG (UMR STLO) *
INRAE – AgroCampus Ouest
35042 RENNES Cedex
+33 (0)2 23 48 53 22
yves.Le-Loir@inrae.fr

Grand-Est

FRACTIONATION OF AGRORESOURCES & ENVIRONMENT (UMR FARE) #
INRAE - Université de Reims Champagne Ardenne - Centre de recherche en environnement et agronomie
51686 REIMS CEDEX 2
33 (0)3 26 77 35 92
bernard.Kurek@inrae.fr

Hauts-De-France

MATERIALS AND TRANSFORMATIONS (UMR UMET)
CNRS – Université de Lille 1 – Ecole nationale supérieure de Chimie – INRAE
59651 VILLENEUVE-D'ASCQ Cedex
33 (0)3 20 43 54 00
patrice.woisel@ensc-lille.fr

Ile-de-France

INSTITUT JEAN-PIERRE BOURGIN (UMR IJPB) #
INRAE – AgroParisTech
78026 VERSAILLES Cedex
+33 (0)1 30 83 30 00
ijpb@inrae.fr

FOOD AND BIOPRODUCT ENGINEERING (UMR SAYFOOD)
AgroParisTech - INRAE
91744 MASSY Cedex
+33 (0)1 69 93 50 26
catherine.Bonazzi@agroparistech.fr

REFRIGERATION PROCESS ENGINEERING FOR FOOD SAFETY AND ENVIRONMENTAL PERFORMANCE (UR FRISE)
INRAE Site ANTONY
1 rue Pierre Gilles de Gennes CS 10030 92761 ANTONY cedex
+33(0)1 40 96 60 21
anthony.delahaye@inrae.fr

ENVIRONMENTAL BIOTECHNOLOGY PROCESSES RESEARCH UNIT (UR PROSE)
INRAE Site ANTONY
1 rue Pierre Gilles de Gennes CS 10030 92761 ANTONY cedex
+33(0)1 40 96 60 40
theodore.bouchez@inrae.fr

Nouvelle Aquitaine

ŒNOLOGY (USC Œ)
INRAE - ISVV
Faculté d'Œnologie
33882 Villenave d'Ornon
+33 (0)5 57 57 58 58
philippe.Darriet@u-bordeaux.fr

INSTITUTE FOR MECHANICS & ENGINEERING (USC I2M)
INRAE – CNRS – Université Bordeaux
Campus Talence, 33405 Talence
+33 (0)5 40 00 28 47
jean-Christophe.Batsale@ensam.eu

Contact our Research Units

Occitanie Pyrénées-Méditerranée

EMERGING TECHNOLOGY
AND POLYMER ENGINEERING (UMR IATE) #
INRAE– Montpellier SupAgro - CIRAD - Université Montpellier
34060 MONTPELLIER Cedex 1
+33 (0)4 99 61 35 43
christian.sanchez@inrae.fr

SCIENCES FOR ŒNOLOGY (UMR SPO)
INRAE - Montpellier SupAgro - Université Montpellier
34060 MONTPELLIER Cedex 1
+33 (0)4 99 61 22 41
jean-Marie.Sablayrolles@inrae.fr

LABORATORY OF ENVIRONMENTAL BIOTECHNOLOGY (UR LBE)
INRAE
avenue des Étangs 11100 NARBONNE
+33 (0)4 68 42 51 51
nicolas.bernet@inrae.fr

PECH ROUGE EXPERIMENTAL UNIT (UE PR)
INRAE – 11430 GRUISSAN
+33 (0)4 68 49 44 00
nicolas.saurin@inrae.fr

AGRO-INDUSTRIAL CHEMISTRY (UMR CAI)
INRAE - INPT - ENSIACET
31030 TOULOUSE Cedex 04
+33 (0)5 34 32 35 00
lca@ensiacet.fr

TOULOUSE BIOTECHNOLOGY INSTITUTE (UMR TBI) #
INRAE - INSA - CNRS
31077 TOULOUSE CEDEX 4
+33 (0)5 61 55 94 01
direction_tbi@insa-toulouse.fr

TOULOUSE WHITE BIOTECHNOLOGY (UMS TWB) #
31520 RAMONVILLE SAINT-AGNE
+33 (0)5 61 28 57 80
twb@toulouse.inra.fr

Pays de la Loire

BIOPOLYMERS, INTERACTIONS, ASSEMBLIES (UR BIA)
INRAE - 44316 NANTES Cedex 03
+33 (0)2 40 67 50 31

PRP Team : INRAE - 35653 LE RHEU Cedex
+33 (0)2 23 48 52 16
biadir-nantes@inrae.fr

STATISTIC, SENSOMETRICS AND CHEMOMETRICS (USC StatSC)
INRAE – Oniris
44322 NANTES Cedex 3
+33 (0)2 51 78 54 50
evelyne.Vigneau@oniris-nantes.fr

Provence - Alpes - Côte d'Azur

FUNGAL BIODIVERSITY AND BIOTECHNOLOGY (UMR BBF) #
INRAE - Aix-Marseille Université - Faculté des Sciences
13288 MARSEILLE Cedex 09
+33 (0)4 91 82 86 00
craig.faulds@univ-amu.fr

SAFETY & QUALITY OF PLANT PRODUCTS (UMR SQPOV) *
INRAE – Université d'Avignon et des Pays
de Vaucluse - Domaine Saint-Paul
84914 AVIGNON Cedex 9
+33 (0)4 32 72 25 00
frederic.carlin@inrae.fr

ARCHITECTURE AND FUNCTION OF BIOLOGICAL MACROMOLECULES (USC AFMB)
INRAE - CNRS - Aix-Marseille Université
13288 MARSEILLE Cedex 09
+33 (0)4 91 82 55 60
secretariat@afmb.univ-mrs.fr

CARNOT 3BCAR

* CARNOT Qualiment Reseau de recherche pour l'innovation alimentaire

Food, bioproducts and waste Division
INRAE - TRANSFORM Division
3 impasse Yvette Cauchois
CS 71627
44316 Nantes Cedex 03
Tél. : +33 1 (0)2 40 67 51 45

Rejoignez-nous sur :

https://www.inrae.fr/en/divisions/transform

Institut national de recherche pour l'agriculture, l'alimentation et l'environnement

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