| Tuesday 25 October 2022 | | |
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| | **PCH-North** | **PCH-South** |
| | **Session Chair: Douglas Goff** | |
| 8:30-9:10 | P3 Prof. Dr. .Mike Gidley, Australia, factors affecting in vitro gut fermentation outcomes from hydrocolloids and their assemblies | |
| 9;10-9:45 | K3 Prof. Dr. Vassilis Kontogiorgos, Australia, Adsorption kinetics and dilatational rheology of plant proteins at the air- and oil-water interfaces | |
| 9:45-10:20 | K4 Prof. Dr. Youling Xiong, USA, Nonthermal bond disruption to unlock the functionality of structurally complex proteins. | |
| 10:20-10:50 | **Break** | |
| | **Session Chair: Katsuyoshi Nishinari** | **Session Chair: Yong-Cheng Shi** |
| 10:50-11:10 | C25 - Synergistic gelation between yellow mustard gum and κ-carrageenan Go to abstract | C28 - Stabilization of air-water interfaces with oat prolamin nanoparticles Go to abstract |
| 11:10-11:30 | C26 - Textural and rheological properties of glucono-delta-lactone induced set plant-based youghurts Go to abstract | C29 - Modulation of the viscosity of guar-based fracking fluids using salts Go to abstract |
| 11:30-11:50 | C27 - Assessing protein solubility of commercial pea protein for application in food systems Go to abstract | C30 - Physical properties of mixed gels of fish and mammalian gelatins. Go to abstract |
| 11:50-12:30 | **Lunch / Poster** | |
| | **Session Chair: Steve Cui** | |
| 12:30-1:30 | Industrial Applications - Industrial hydrocolloids challenges: from raw material to market Plus Round-Table Discussion | |
| 1:30-2:10 | P4 Prof. Dr Aiqian Ye, New Zealand, Gastric colloidal behaviour of milk protein as a tool for manipulating nutrient digestion | |
| 2:10-2:45 | K5 Prof. Dr. Qi Wang, Canada, Application of Food Hydrocolloids in Microencapsulation of Antibiotic Alternatives in Food and Agriculture Production | |
| 2:45-3:10 | **Break** | |
| | **Session Chair: Youling Xiong** | **Session Chair: Qi Wang** |
| 3:10-3:30 | C31 - Molecular interactions and in-depth dynamic simulations on ß-casein and phenolic acid complexes under ultra-high temperature conditions Go to abstract | C38 - Nanoencapsulation and Bioavailability Enhancement Study of Microalga Phaeodactylum tricornutum Extract Containing Fucoxanthin Go to abstract |
| 3:30-3:50 | C32 - Revealing the characteristics of Enzymatic Cross-linked Micellar Casein powders by Asymmetrical Flow Field-Flow Fractionation Go to abstract | C39 - Effect of the mechanical and calorimetric glass transition temperatures in regulating the molecular transport of bioactive compounds in high-solid hydrocolloid systems Go to abstract |
| 3:50-4:10 | C33 – Microstructural evolution during acid induced gelation of cow, goat, and sheep milk probed by time-resolved (ultra)-small angle neutron scattering Go to abstract | C40 - Visualizing the microscopic structures of non-destructive starch hydrogels using synchrotron-based X-ray computed tomography Go to abstract |
| 4:10-4:30 | C34 - The interaction of milk proteins and digestive enzyme (pepsin) Go to abstract | C41 - Starch structure and exchangeable protons contribute to reduced aging of high-amylose wheat bread Go to abstract |
| 4:30-4:50 | C35 - Identification and control of malodourous compounds in UHT beverages incorporating fava bean protein and soy protein Go to abstract | C42 - Influence of nanocellulose with different particle size on pasting and rheological properties of wheat starch Go to abstract |
| 4:50-5:10 | C36(r) – Characterization of the mixed gel from whey protein isolate and sodium caseinate in the presence of gluconic delta lactone with or without heat-treatment Go to abstract | C43 - Gelation of cereal ß-glucan after solubilization at the physiological temperature: effect of molecular structure Go to abstract |
| 5:10-5:30 | C37(r) - Supramolecular self-assembly of sodium caseinate with calix[4]resorcinol Go to abstract | C44(r) - Molecular characterization of interactions between Lectin - a protein from the common edible mushroom (Agaricus bisporus) - with dietary carbohydrates Go to abstract |
| 6:00 | Conference Banquet | |

C25- **Synergistic gelation between yellow mustard gum and κ-carrageenan**

Xinya Wang[1, 2], H. Douglas Goff[2], Steve W. Cui[1]

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Yellow mustard gum (YMG) has been included in the newest version of the Handbook of Hydrocolloids (2021) as emerging gums that "have commercial potential and can be considered to have credentials as natural gums for clean labeling". In addition to its functionality (thickening, emulsifying and gelling) as hydrocolloids, YMG has been found to synergistically interact with κ-carrageenan to form a firm and elastic gel. Our recent study described an overall synergistic gelation process (heating, cooling, and curing) of YMG-κ-carrageenan mixtures by a rheological approach. Based on the gel characteristics and gelling process, a primary interaction mechanism was proposed as a combination of polymer interactions (both association and segregation) and ion migration.

However, the contributions of the above two factors have not been demonstrated with direct evidence at a molecular level. A further investigation of the interaction mechanism is needed to validate the proposed mechanism using more techniques.

In this study, a differential scanning calorimeter (DSC) and stress relaxation tests were used to illustrate the synergistic gelation mechanism of YMG- κ-carrageenan. DSC evaluated the thermal properties of the gels that indicate the changes in polymer conformation in the synergistic gel system during gelling and melting. The shifts of exotherm/endotherm peaks were observed in the synergistic binary gel compared with the pure κ-carrageenan gel suggesting new polymers formed through an association between YMG and κ-carrageenan. Stress relaxation tests were applied to the YMG-C mixtures of different blending ratios at different temperatures (10°C to 60°C). A concept of entanglement network numbers was applied to provide a quantitative measurement for the viscoelastic characteristics of the binary gels. The effects of the blending ratio on the synergistic gelation were concluded based on the quantitative determination.

The results confirmed the early proposed gelation mechanism. YMG-C (3:7) mixture formed a single-phase gel on cooling. The gelation was ascribed to the conformational transitions of the "new" polymers developed by YMG and κ-carrageenan. The new polymer could be a complex of linear β-glucan chain and κ-carrageenan polymer chain. Double helical chains were bound on the smooth regions of the linear glucan chain on mixing at a high temperature. The new complex then went through the "coil to helix" and the helix aggregation to form a gel network

on cooling, which resulted in the gel network with thicker strands than the double helix chain alone, thus leading to higher gel strength.

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# C26 - Textural and rheological properties of glucono-delta-lactone induced set plant-based youghurts

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This research presents a novel method of inducing the formation of protein-structured vegan youghurts as an alternative to their traditional polysaccharide-structured counterparts. As a slow acidifying agent, glucono-delta-lactone (GDL) was evaluated for its potential to form cold-set, youghurt-like gels from soy and lentil milks. Soy (5.3% protein) and lentil (6.1% protein) milks were coagulated using GDL concentrations of 1%, 2%, and 3% (w/w), and stored for 120 minutes at 25°C. The structure and behaviour of these gels were evaluated and compared to a control (dairy-derived Greek youghurt) using texture analysis and rheological tests. Puncture tests were performed using a 13mm diameter acrylic probe (TA-10) at a speed of 1mm/sec to a penetration depth of 10mm. Results showed that soy milk formed the strongest protein gel structures across all GDL concentrations, demonstrated by the significantly greater mean firmness and initial resistance to deformation. The 1% GDL (w/w) soy youghurt was found to have the most similar firmness to the control (36g vs. 28g). Though, a greater brittleness of the soy gels was observed due to the many fracture points in the profile. Strain sweeps (1Hz, 20°C) and subsequent frequency sweeps (0.1% shear strain, 20°C) were used for rheological analysis. All samples possessed greater initial elastic storage moduli than viscous storage moduli, demonstrating a higher proportion of solid-like behaviour which also increased with greater GDL concentrations. The soy youghurts had the largest moduli for both the strain and frequency sweeps thereby possessing the largest amount of solid-like behaviour of all samples. Overall, both the soy and lentil youghurts with 1% GDL were the most similar to the Greek yoghurt control. This optimization of plant-protein type and GDL concentrations to mimic dairy-derived youghurts on a textural and rheological basis can allow for improved consumer acceptance of these products, and a more rapid alternative to traditional youghurt coagulation methods.

Keywords: Glucono-delta-lactone, youghurt, plant-based, vegan, high-protein

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# C27- Assessing protein solubility of commercial pea protein for application in food systems

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With growing interest in plant-based foods there is an increased importance in understanding the functional properties of proteins and how they behave in food systems. Plant-based alternatives to dairy, in particular, coffee creamers and cheese rely on stability at low pH. Pea protein is a promising plant protein source as it is gluten free, has low allergenicity, and diverse functionality. However, there are many commercial pea proteins available with the same label claim but differ in functionality, indicating there is still a need to further understand how the protein behave at various pH's present in food systems. Five commercial pea proteins with minimum 80% protein content were assessed for their functional properties. For the intended investigation of plant-based dairy systems, the solubility at pH ranges 4.2, 5, and 5.5 were compared. The solubilities were classifies by high (30-20%), medium (19-10%), and low ( <10%). Four trends were identified, two of the pea proteins demonstrated high solubility at pH 5.5 followed by a 20% decrease reaching low solubility. Two proteins had medium solubility at pH 5.5, one dropped instantly to low solubility at pH 5 while one was able to maintain medium solubility and then drop to low solubility at pH 4.2. The last trend observed was consistent low solubility from pH 5.5 to 4.2. The identified trends provide useful insight into how the pea protein would behave in food systems. The results enable us to correlate the required protein functionality to the solubility behaviour at different pH's.

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# C28- Stabilization of air-water interfaces with oat prolamin nanoparticles.

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Prolamins are a storage protein found in cereal grains which are insoluble in water, but soluble in 70% aqueous ethanol. The insolubility of prolamins in water can be exploited to produce monodisperse colloidal nanoparticles through an antisolvent precipitation method. Nanoparticles made from the prolamins of wheat (gliadin), corn (zein), and sorghum (kafirin) have been widely studied and have shown potential for use as emulsifying and foaming agents. The interface-stabilizing abilities of nanoparticles made from avenin, the prolamin in oats, have yet to be explored. The objective of this study is to relate the physicochemical properties of avenin nanoparticles (ANPs) to their air-water interfacial and foaming properties. The properties of avenin nanoparticles are herein compared to those made from gliadin, as past studies have shown gliadin nanoparticles (GNPs) to be effective stabilizers of air-water interfaces.

Avenin and gliadin proteins were extracted from oat protein isolate and gluten flour, respectively, using 70 v/v% aqueous ethanol. ANPs and GNPs were then prepared using an antisolvent precipitation method, followed by rotary evaporation to remove the ethanol from the nanoparticle dispersions and dilution to a final protein content of 0.5 w/w% with DI water. The zeta-potential, particle size distribution and polydispersity index of particles as a function of pH (3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0) was measured to determine their pH stability. The air-water interfacial tension of the ANP and GNP dispersions was determined using drop shape tensiometry. ANP- and GNP-stabilized foams were prepared by vigorous overhead stirring and the foamability and foam stability over time was measured.

Zeta-potential values measured as a function of pH revealed that ANPs had an isoelectric point of pH 4.8, while GNPs had an isoelectric point of pH 7.0. Particle size and polydispersity measurements showed an increase in particle size and polydispersity close to each protein particle's respective isoelectric point, indicating colloidal instability. Furthermore, zeta-potential measurements indicated that ANPs had a greater absolute value of surface charge than GNPs at all measured pH values with the exception of pH 5.0, close to the isoelectric point of the ANPs. Air-water tensiometry revealed that the surface tension of the ANP dispersions (39 mN/m) was slightly lower than that of GNPs (43 mN/m) after 10 minutes of steady-state measurement at pH 6.0. Foamability was assessed based on the initial liquid volume (25 mL) and the foam volume after 2 minutes of stirring. ANPs had a higher foamability than GNPs at pH 6.0, producing foams with volumes that were 260% of the initial liquid particle dispersion volume, compared to 220% for the foams made with GNPs. The stability of the ANP- and GNP-stabilized foams was comparable, however, with all foams retaining approximately 60% of the initial foam volume after 60 minutes.

These results indicate that these novel ANPs have potential for use as foaming agents in food systems, particularly in applications close to neutral pH where they show greater colloidal stability and foamability than GNPs

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# C29- Modulation of the viscosity of guar-based fracking fluids using salts

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Fracking is an enhanced oil recovery technology for the extraction of oil and gas from reservoirs with low permeability. This technology uses viscoelastic fluids (fracking fluids) to fracture oil reservoirs and to transport sand within the fractures, to prop them open. Saline water (called produced water) is released from fractured formations during oil production. The salinity of produced water renders challenging its reuse to formulate fracking fluids, because it can decrease fracking fluid viscosity. This is the case for guar-based fluids, which are the most common fracking fluids. As a result, produced water is often discarded. Since fracking uses from 500 to 100,000 m3 of water to frack a single oil well, reusing produced water would be highly beneficial to reduce freshwater consumption. Our study investigates the effect of chloride salts (CaCl2, MgCl2 and Fe(III)Cl) and of sulfate salts (MgSO4 and FeSO4) at different concentrations (0.05-1 M) on the viscosity of aqueous guar solutions. All chloride salts tested increase the viscosity of guar solutions in the concentration range analyzed, and promote the formation of small guar aggregates. At 0.05 M concentrations, the effect of MgSO4 is similar to chloride salts. In contrast, 1 M MgSO4 decreases the viscosity of guar solutions. Similarly, 0.05 M and 1 M FeSO4 decreases the viscosity of aqueous guar solutions. This decrease is ascribed to large guar aggregate formation, as opposed to a cohesive network. Sodium cocoyl glutamate (SGC) increases the viscosity of non-crosslinked guar solutions and the shear viscoelastic moduli of guar solutions crosslinked with sodium tetraborate. Specifically, it restores the viscosity of guar solutions with MgSO4, and increases it above values measured in DI water in the presence of MgCl2. Attenuated Total Reflectance – Fourier Transform Infrared (ATR-FTIR) spectroscopy shows that hydrogen bonding (H-bonding) is more significant in guar + SCG + 0.7 M MgCl2 samples than in guar + SCG + 0.7 M MgSO4. This result indicates that the formation of a H-bonded network is correlated to high viscosity. ATR-FTIR also indicates that MgSO4 weakens H-bonding of water clusters, whereas SCG restores it, to enable guar hydration even in the presence of MgSO4. Our study highlights which salts are most problematic (e.g., FeSO4), and proposes a potential additive (SCG) to increase the viscosity of guar in the presence of selected salts (e.g., magnesium salts), by promoting H-bonding.

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# C30- Physical properties of mixed gels of fish and mammalian gelatins

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Dynamic viscoelasticities of mixed solutions of fish and mammalian gelatins with different gelling temperature and gel hardness have been measured. Increases of elasticities of mixed solution on cooling became gradual in comprise ways of each of fish and mammalian solution suggesting the interaction between the fish and mammalian gelatins. On reheating, on the other hand, two step melting behaviors were observed showing the individual disaggregation of each gelatin chain in the mixture. The change of CD intensity indicated the formation and dissociation of the aggregation of each gelatin. The mechanism of gelling and melting and network structure are discussed.

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# C31- Molecular interactions and in-depth dynamic simulations on β-casein and phenolic acid complexes under ultra-high temperature conditions

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The inclusion of insoluble plant fibres into functional beverage formulations remains a challenge due to the adverse effect on organoleptic properties particularly post ultra-high temperature (UHT) processing. Successfully incorporating insoluble fibres into these formulations would increase both the intake of fibre and the consumption of microconstituents such as phenolic acids that have antioxidant properties and other health benefits. Current literature maintains that the phenolic compounds, present in insoluble dietary fibres, do not irreversibly react with proteins unless in highly basic conditions or in the presence of appropriate enzymes. However, the effect of elevated processing temperatures on the type of interactions taking place has not been thoroughly investigated.

The outcome of MALDI-TOF-MS analysis shows that phenolic acids interact chemically rather than physically with β-casein at elevated (140°C) temperatures, permanently altering the protein. Molecular docking demonstrates that the structure of the phenolic acid appears to have a significant effect on the binding site of the protein, with the main bond forming between different amino acid residues depending on ligand structure [1]. A further molecular dynamics analysis illustrates that the permanent addition of 4-hydroxybenzoic acid to the lys32 residue of the β-casein molecule has a significant impact on protein density, solvent accessibility, and hydrogen bond formation, reducing the overall stability of the protein.

Interestingly, the diffusion of phenolic acids from a beta casein containing solution into water is significantly altered by prior heat treatment, with changes to the structural properties and association behaviour of the covalently modified protein likely being behind the altered diffusion kinetics of the phenolic compound [2]. These outcomes demonstrate that both protein and phenolic compound are significantly affected by UHT treatment, likely causing a change in their functionality and bio-availability. Therefore, greater knowledge of these molecular interactions is vital for successful formulation of fibre fortified beverages.

*References:*

1. Condict, L., Hung, A., Ashton, J., & Kasapis, S. (2021). High-temperature binding parameters and molecular dynamics of 4-hydroxybenzoic acid and β-casein complexes, determined via the method of continuous variation and fluorescence spectroscopy. Food Hydrocolloids, 114, 106567. https://doi.org/10.1016/j.foodhyd.2020.106567
2. Condict, L., Kaur, J., Hung, A., Ashton, J., & Kasapis, S. (2019). Combined spectroscopic, molecular docking and quantum mechanics study of β-casein and ferulic acid interactions following UHT-like treatment. Food Hydrocolloids, 89, 351-359. https://doi.org/10.1016/j.foodhyd.2018.10.055

# C32- Revealing the characteristics of Enzymatic Cross-linked Micellar Casein powders by Asymmetrical Flow Field-Flow Fractionation

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Enzymatically cross-linking milk proteins by microbial transglutaminase is a promising strategy for developing functional properties in dairy products such as reinforced gel strength, reduction of syneresis, and increased heat thermal resistance. Even though the study of enzymatically modified milk powders is attractive since the enzymatic treatment of caseins followed by spray drying would reduce the cost related to the enzyme incubation and the thermal treatment for the enzyme inactivation for food companies, little research has addressed this subject. Therefore, we evaluated the microstructural characteristics of four spray-dried micellar casein powders (SMCP) with different cross-linking (CL) extents in dry conditions and after solubilization to study the impact of the SMCP modification on the casein micelle.

- Cross-linked casein micellar powders (CL-MCP) showed particle size increase measured by Laser Diffraction. No differences on the powder surface were detected by Scanning Electron Microscopy (SEM). Both, SEM and CLSM observations confirmed the CL-MCP have a well-defined sphere shape, whereas non-cross-linked SMCP were smaller and amorphous.
- A higher concentration of amino acids was detected by Time-of-Flight Secondary Ion Mass Spectrometry for CL-MCP which could indicate a formation of an outer layer of the powders.
- The ultrasound relaxation test showed that more time is needed for the water to diffuse towards the core of the extensively CL-MCP in comparison to control MCP. Also, it was found that the solubility of the CL-MCP, determined by the protein content of the supernatant by HPLC, is lower than that of the non-cross-linked powders.
- Once completely hydrated, the Multi-Angle Light Scattering (MALS) results of the separated fractions by Field-Flow-Fractionation analysis showed that extensively CL-MCP depicts smaller casein micelles size whereas the non-cross-linked casein micelle leads to the formation of aggregates, probably due to the destabilization of the caseins during the spray-drying.
- The cross-linking also leads to the formation of small particles (Radius of gyration (Rg) < 50 nm) with a high apparent density. The Rg over the hydrodynamic radius (Rh) (Rg/Rh ratio), a qualitative measurement of the conformational shape of aggregates, indicates that these cross-linked particles are rather spherical.
- The apparent viscosity of the CL-MCP is reduced as a function of the cross-linking extent.

To conclude, this study demonstrates the structural differences between the CL-MCP at different polymerization extents. Cross-linking of the powders changes the macrostructure of the powders and influences the wetting time and solubility of the micellar casein powders. The modification of the micellar casein by the cross-linking leads to a decrease in the micelle size, which indicates that cross-linking leads to the compaction of the micelle due to the formation of intra-micellar cross-linking. Further studies are required to determine the applications of CL-MCP in the dairy industry.

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# C33- Microstructural evolution during acid induced gelation of cow, goat, and sheep milk probed by time-resolved (ultra)-small angle neutron scattering

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Milks from small ruminant animals, such as goat and sheep, have gained increasing interest from the industry for the manufacture of various dairy products such as yoghurts. Heat treatment of milk is typically applied to improve the yoghurt texture. Here, time-resolved ultra-small angle neutron scattering (USANS) and small-angle neutron scattering (SANS) were employed to probe in situ the microstructural evolution of cow, goat, and sheep milks in D2O during acidification as affected by the heat treatment. Milk gelation can be envisaged as the progressive aggregation of the building blocks (casein micelles) in a fractal manner, which leads to the formation of micron scaled (~ 3-10 μm) protein agglomerates. The heat treatment considerably enhanced the gelation of all milks, which is reflected by a faster increase in the fractal dimensions and aggregate sizes. For all three types of milks, similar final plateau fractal dimensions were observed for unheated (~2.2-2.4) and heated milks (~2.4-2.5), suggesting similar mass fractal microstructures in the size range probed by USANS. The final storage modulus after 10 h (G′ final) follow the order of heated sheep milk ≈ sheep milk ≈ heated cow milk > cow milk > heated goat milk > goat milk. The colloidal calcium phosphate (CCP) dissolution kinetics tracked by SANS followed a similar trend as the evolution of the sample acidity (pD-value) and are not significantly affected by the types of milk or the heat treatment. This study shows a great potential of using time resolved USANS and SANS to investigate the microstructural evolution of protein aggregation and gelation.

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# C36(r) - Characterization of the mixed gel from whey protein isolate and sodium caseinate in the presence of gluconic delta lactone with or without heat-treatment

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The interactions between different proteins in mixed-protein gel systems are interesting because they are able to produce novel physicochemical properties of gels. However, some details remain unknown—for example, how an individual protein contributes to the final gel network.

We investigated on the characteristics of the mixed protein gel made from whey protein isolate (WPI) and sodium caseinate (SC) using gluconic delta lactone (GDL) with or without heat-treatment. Ultrasound spectroscopy, rheological measurement, confocal laser scanning microscopy (CLSM) and SEM observation were performed,

The dynamic modulus of the sole SC system increased most rapidly among the three gel formulations, and it implied that the SC leads the gel formation in the mixed protein system..

The decrease of the ultrasonic velocity of sole SC system was higher than those of sole WPI system or the mixed system. It suggested that SC is the primary cause of the velocity reduction, namely sol-gel transition.

The CLSM images which has been fluorescent labeled separately for each protein revealed that the pore sizes of gel network in the mixed protein are larger than those of sole SC gel. Furthermore, the rate of coexistence of WPI and SC increased by heat-treatment.

Based on our results, it appears that the inclusion of WPI in a SC-based gel modifies the texture and three-dimensional network of the resulting gel

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# C37(r)- Supramolecular self-assembly of sodium caseinate with calix[4]resorcinol

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Of particular interest among the variety of self-assembling molecules can be caused by three-dimensional macrocycles, namely calixarenes. Calix[n]arenes are synthetic cyclooligomers with a variable number of phenol units (n) linked by methylene bridges in ortho position. These macrocycles have the shape of a chalice with wide upper rim and narrow bottom rim. In the calixarene family, calix[4]resorcinols are distinguished, since they can improve solubility, stability and bioavailability of different molecules. Low cytotoxicity and high biocompatibility of calix[4]resorcinols gives the prospect of their application in the modification of natural hydrocolloids. Moreover, calix[4]resorcinols are easily functionalized along the upper and lower rims, after which they can bind a certain molecule, self-aggregate, enter into joint aggregation with a bound molecule and have stimulus-sensitive properties. Chemical modification of calix[4]resorcinols can also be implemented by specific fragments to improved functionalities of hydrocolloids.

In this work, the mixed self-assembly of sodium caseinate and calix[4]resorcinol with covalently linked viologen groups were investigated. A set of physicochemical methods (UV-visible absorption and fluorescence spectrophotometry, potentiometry, transmission electron microscopy, dynamic and electrophoretic light scattering) was used to study the aggregation and encapsulating properties of the supramolecular system based on these components. Supramolecular interactions between sodium caseinate and calix[4]resorcinol led to the spontaneous formation of spherical nanoparticles, avoiding lengthy synthetic procedures for modifying biopolymer. The effectiveness of the mixed caseinate–calix[4]resorcinol compositions as nanocontainers for both hydrophobic antioxidant quercetin and hydrophilic antitumor drug doxorubicin was evaluated. This study demonstrates features of such supramolecular structures, highlighting their potential applications in drug delivery.

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# C34- The interaction of milk proteins and digestive enzyme (pepsin)

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In milk and dairy product digestion, coagulation of casein micelles occurs and plays a key role in the gastric transit of proteins. This coagulation is induced by specific hydrolysis of the Phe105-Met106 bond of κ-casein catalyzed by pepsin at pH > 6, and which results in the destruction of the casein micelles. When pH further decreases to < 4 in the gastric environment, both caseins and whey proteins are progressively hydrolyzed into peptides by pepsin. In this study, the kinetics of pepsin-induced hydrolysis and coagulation of casein micelles in bovine skim milk, as well as the relationship between the clot structure and the gastric transit of proteins was investigated using reverse-phase HPLC, rheological determination, confocal laser scanning microscopy (CLSM), and small angle scattering techniques. The effects of important variables, such as pH, temperature and divalent cations are given and discussed. By quantitative determination of the released para-κ-casein using reverse-phase HPLC, the hydrolysis of κ-casein was found to follow a combined kinetic model of first-order hydrolysis and pepsin deactivation. The hydrolysis rate of κ-casein highly depends on the pepsin concentration, milk pH and temperature, while independent with the calcium concentration. The milk coagulated faster at lower pH, higher temperature, and higher calcium concentration with a lower requirement of κ-casein hydrolysis extent (Hct, %). E.g., the Hct are ~73, 68, 57, 33% for the samples at pH 6.3, 6.0, 5.7, 5.3, respectively (at 37°C), and ~ 83, 75, 71% for the samples at 31, 37, 43°C, respectively (at pH 6.0). The progressive hydrolysis of milk proteins in the later stage of digestion was impacted by the clot structure. For example, when 200 mL of cold (4°C), control (37°C) and warm (50°C) milk were ingested in a human gastric simulator (HGS), the coagulation of cold milk was slower than control and warm milk. A soft clot with a much looser microstructure obtained from cold milk, in turn facilitated the breakdown and hydrolysis of milk proteins by pepsin. In addition, time-resolved (ultra) small angle neutron scattering (U)SANS and small angle X-ray scattering (SAXS) were employed to probe in situ the microstructural evolutions of milk during the pepsin-induced coagulation and progressive hydrolysis of milk proteins. The scattering intensity in USANS and SANS increased at the initial stage and decreased at the later stage. To describe the hierarchical structure of milk gels, a fractal model was used to fit the USANS data, where the fractal dimensions and aggregate sizes were calculated. The knowledge obtained from this study provides further understanding on the mechanisms of milk coagulation under gastric conditions, and its relationship with the progressive hydrolysis of proteins and gastric emptying of milk. It also shows a great potential of using time-resolved USANS and SAXS to investigate the microstructural evolution of protein coagulation and hydrolysis during digestion.

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# C35- Identification and control of malodourous compounds in UHT beverages incorporating fava bean protein and soy protein

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Legume proteins have represented a growth area in recent years, with a decline of dairy milk consumption linked with the rising popularity in health consciousness and vegan/vegetarian diets. IBISworld expects that milk alternatives are projected to grow 8.3% annually over the next five years beyond 2019-2020. Legume proteins contain significant amounts of antioxidative vitamins, minerals and unsaturated fats, assisting in lowering the risk of cardiovascular disease, high blood pressure and high cholesterol. However, consumer acceptance has been one of the biggest challenges for legume protein formulations as legume-based systems are linked with producing undesirable flavour and mouthfeel (‘chalky’, ‘grity', ‘earthy', ‘pasty’ etc.) [1]. As it currently stands, UHT treated, animal-based protein isolates are deemed the 'gold standard' in terms of desirable flavour and mouthfeel.

It is theorized that the main cause of the malodorous flavour in legume protein isolates is due to the presence of the highly unstable phospholipids. These remain bound to legume protein and oleosins, the proteins that form a monolayer membrane to surround and stabilise oil bodies in legumes, during the manufacture of legume protein isolate using the isoelectric precipitation process. Linoleic and oleic acids can react to form undesirable compounds such as 2-pentylfuran and hexanal during processing and storage [2] Removing these fatty acids may result in a more neutral flavour profile that mimics closely the animal-based protein isolates which consumers are familiar with.

In this study, fava protein isolate (FPI) and soy protein isolate (SPI) were defatted via a membrane ultrafiltration process for comparison with their control counterparts and animal-based protein isolates. Model systems were heat treated using ultra high temperature processing (UHT) at a temperature of 140˚C and packaged aseptically for a subsequent shelf-life study at 22˚C. Instrumental analysis was conducted on a gas chromatography-mass spectrometry (GC-MS) device, with compounds being identified using the Agilent software library (NIST Library). Compounds of interest (malodourous and low detection threshold) were then confirmed using analytical standards. It was found that 40 volatile compounds were present in defatted and control protein isolate samples, 16 of which contributed substantially to odour production.

Findings indicated that the samples which underwent membrane ultrafiltration (defatted FPI and SPI) had developed a more neutral flavour profile, which can be comparable to animal-based protein isolates. Therefore, the present work confirms that the flavour profile of FPI and SPI

based beverages, over a long shelf life, can be improved with the removal of bound phospholipids.

*References:*


1. Fischer E., Cachon R., & Cayot N. (2020). Pisum sativum vs Glycine max, a comparative review of nutritional, physicochemical, and sensory properties for food uses. Trends in Food Science and Technology, 95, pp. 196 - 204, https://doi.org/10.1016/j.tifs.2019.11.021
2. Alqahtani, N. K., Ashton, J., Katopo, L., Gorczyca, E., & Kasapis, S. (2018). Shelf-life studies of flavour characteristics in model UHT liquid systems enriched with wholegrain oat. Heliyon, 4(3), e00566. https://doi.org/10.1016/j.heliyon.2018.e00566


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# C38- Nanoencapsulation and Bioavailability Enhancement Study of Microalga Phaeodactylum tricornutum Extract Containing Fucoxanthin

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This study aims to develop two nanoparticles encapsulated by Phaeodactylum tricornutum extract (PE) containing fucoxanthin (FX) with alginate and casein (A-C-PE) and A-C-PE coated with chitosan (Cs-A-C-PE) and systemically evaluate their stability and bioavailability by in vitro digestion, intestinal cell permeability and in vivo pharmacokinetic (PK) studies. In the simulated gastrointestinal condition, two types of nanoparticles (A-C-PE, Cs-A-C-PE) showed the controlled release of FX from the encapsulating materials compared to PE. In Caco-2 cell permeability study, A-C-PE and Cs-A-C-PE showed higher cell permeability than PE, based on the value of apparent permeability coefficient. In vivo PK study, two metabolites of FX (fucoxanthinol and amarouciaxanthin A) were analyzed in plasma of mouse administrated A-C-PE, Cs-A-C-PE and PE. PK parameters of two metabolites exhibited that two nanoparticles have higher bioavailability than PE. In conclusion, two types of PE-loaded nanoparticles containing FX significantly promote the bioavailability of FX through the overall delivery aspect.

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# C39- Effect of the mechanical and calorimetric glass transition temperatures in regulating the molecular transport of bioactive compounds in high-solid hydrocolloid systems

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The glass transition temperature (Tg) indicates a reversible transformation from the rubbery plateau to a glassy consistency in materials science. In high-solid food systems, the concept of glass transition temperature is considered as an index of convenience in controlling the rate of physicochemical, enzymatic and biological processes.[1,2] At temperatures below Tg (i.e. in the glassy state), dense packing and reduction in segmental mobility of polymer chains diminishes the hole-free volume in the matrix.3,4] Whether the mechanical or calorimetric Tg is the most relevant index to follow the diffusion of bioactive compounds in high-solid amorphous foods is an interesting question that merits examination.

In doing so, the three-dimensional structure of distinct molecular weights of gelatine/glucose syrup systems and κ-carrageenan/polydextrose systems with increased potassium ions were formulated to entrap bioactive compounds. The physiochemical characteristics of the systems were determined using differential scanning calorimetry (DSC), small deformation dynamic oscillation, Fourier-transform infrared spectroscopy (FTIR), wide-angle X-ray diffraction (WAXD) and scanning electron microscopy (SEM). The molecular theory of diffusion, combined with the concept of free volume, was utilised to model the release mechanism of various bioactive compounds as affected by changes in the structural relaxation of the polymer/co-solute systems.

The investigation of the molecular transport of nicotinic acid from bovine and fish gelatin networks demonstrated the importance of mechanical glass transition temperature in controlling the diffusion of this bioactive. The molecular weight of polymers affects the ability to form a network, and the diffusion of nicotinic acid is governed by the polymeric network's structural relaxation (α-transition). In accordance with this study, work on the release mechanism of caffeine in κ-carrageenan matrices showed that potassium counterion stabilisation of the polysaccharide helices increases the decoupling between polymeric matrix and bioactive compound diffusion. In conclusion, results demonstrated the prominent effect of the mechanical over the calorimetric glass transition temperature on the release kinetics of bioactive compounds and bode well for designing delivery vehicles with added bio-functionality.

*References*

1. Roudaut, G., Simatos, D., Champion, D., Contreras-Lopez, E., & Le Meste, M. (2004). Molecular mobility around the glass transition temperature: A mini review. Innovative Food Science & Emerging Technologies, 5(2), 127–134.
2. Gray, D. A., Bowen, S. E., Farhat, I., & Hill, S. E. (2008). Lipid oxidation in glassy and rubbery-state starch extrudates. Food Chemistry, 106, 227–234
3. Hoare, T. R., & Kohane, D. S. (2008). Hydrogels in drug delivery: Progress and challenges. Polymer, 49(8), 1993–2007. <

4. Panyonyai, N., Bannikova, A., Small, D. M., & Kasapis, S. (2015). Controlled release of thiamine in a glassy κ-carrageenan/glucose syrup matrix. Carbohydrate Polymers, 115, 723-731.

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# C40- Visualizing the microscopic structures of non-destructive starch hydrogels using synchrotron-based X-ray computed tomography

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Starch hydrogel plays vital roles in the quality and performance of food products, bioplastics, pharmaceutical products, and biomedical materials. Recent research has clearly demonstrated that starches of various botanical origins show different gelation behaviors over the cooking temperatures of 95-140°C (Liu et al., Food Hydrocolloids, 2019, 94:217-228). However, important research questions remain regarding the structure-function relationships of starch hydrogels prepared under different conditions. This presentation will focus on the use of synchrotron-based X-ray computed tomography (SXCT) as an advanced and non-destructive method to visualize the microscopic structures of pea, high-amylose, waxy maize, and tapioca starch hydrogels/pastes from cooking at 95 and 140°C. The captured structural features revealed that the existence of swollen starch granules/remnants with good integrity was crucial for developing a strong, true gel from pea starch after 95°C cooking and that the re-association and alignment of amylose chains to establish stable junction zones was vital for forming a strong, true gel from high-amylose maize starch after 140°C cooking. The images of the non-destructive starch hydrogels as captured by SXCT will also be compared and discussed with those of freeze-dried starch gels as depicted by scanning electron microscopy (SEM). The gelation mechanisms of different native starches are elucidated by SXCT and SEM will be meaningful for utilizing this versatile and economical hydrocolloid as an effective gelling agent in diverse industrial applications.

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# C41- Starch structure and exchangeable protons contribute to reduced aging of high-amylose wheat bread

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Incorporation of high amylose wheat flour (HAWF), as a functional ingredient, could reduce both rate and degree of starch digestion in foods (e.g. Bread, tortillas and noodles), and elevate nutritionally-beneficial resistant starch levels. In addition, high amylose wheat bread (HAWB) prepared from part or all HAWF with amylose content (AM) 71% and 84% has limited storage-induced changes, including firmness and starch retrogradation. Melting enthalpy of recrystallized amylopectin (ΔHAP) increased significantly on storage for wild-type (WT), slightly for 71% AM but not at all for bread with 84% AM. Firmness of bread was positively related to AM content and ΔHAP. Exchangeable proton populations and mobility in HAWB crumb were higher than WT bread measured by 1H T2 NMR, consistent with the higher water content needed to make doughs from HAWF leading to the crumb network being more plasticized and hindering crumb aging. The resistant starch content of bread was elevated significantly with the increase of AM content but was not enhanced during storage. Although HAWB has a harder crumb than wild-type, it has greater shelf-life stability and higher nutritional value.

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# C42- Influence of nanocellulose with different particle size on pasting and rheological properties of wheat starch

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Tailored design of novel materials based on starch-nanocellulose requires a huge understanding about structural properties, and how these structures define the composite's functionality. Cellulose nanofibrils (CNF) and cellulose nanocrystals (CNC) have been described as biomaterials with wide applications in polymer science. However, their use in food science and nutrition, specifically designing food structures with functionality is gaining interest. The goal of this work was to investigate how CNF and CNC modify macrostructural features of wheat starch specially those related with pasting and rheological properties.

Bacterial CNF (Vuelo Pharma, Brazil) and cotton CNC (UPC-UMaine, USA) were blended with wheat starch (Sigma-Aldrich, Germany). CNF and CNC were added at concentrations up to 10%w/w. Starch-CNF and starch-CNC blends were processed by Rapid-Visco-Analysis (RVA, 90°C/3min) and cooled to 25°C. Pasting parameters (peak temperature and peak, hot-paste, final and setback viscosity) were assessed. After RVA, starch-nanocellulose pastes were characterized in terms of rheological properties at 25°C: dynamic frequency sweep (0.1-600rad/s), dynamic time sweep (4h) and in-shear recovery (100 1/s, 60s).

Previous analysis by Atomic-Force-Microscopy and Dynamic-Light-Scattering allowed to assess the particle size (120nm for CNC, 4000nm for CNF) and charge (-49mV in CNC, 1.3mV in CNF). Our results showed that addition of nanocellulose significantly modified the pasting properties of starch, but strongly influenced by the particle size of nanocellulose. Thus, CNF significantly increased all pasting parameters of wheat paste, whereas CNC only slightly increased the same parameters (e.g. final viscosity of 1700cP, 2000cP and 4700cP in control starch, 10%CNC-starch and 10%CNF-starch, respectively). Changes in final and setback viscosities could suggest changes during the self-association of amylose in presence of nanocellulose. Those changes can be understood from the rheology characterization. Our results showed that both CNC and CNF produced a significant increase in G' at 25°C, which was also proportional to the nanocellulose concentration. However, values of loss factor (G''/G') suggest big structural differences presumably addressed by the particle size of nanocellulose. Loss factor values were lower in pastes CNC-starch than in CNF-starch, over the whole frequency range tested. The latter was confirmed by dynamic time sweep, which showed that CNC promoted the self-association of amylose detected from the faster increase in G' and faster decrease in loss factor, which in turn approaches rapidly to values lower than 0.1 depicting the behavior as strong gels. The opposite was observed in CNF-starch, where G' were lower than control in those samples containing CNF. Indeed, loss factor of gels containing CNF reached values higher than 0.1 depicting the behavior of these as weak gels. Interestingly, in-

shear recovery data showed that strong gels promoted by CNC has lower capacity of recovery with values around 57-62%, whilst weak gels containing CNF showed values of 80-67%.

Our study concluded that particle size of nanocellulose provoked big structural changes in wheat starch, which would be associated with how the amylose self-associates in presence of nanocellulose. This knowledge could be useful for the tailored design of starch-nanocellulose composites to be used in different industrial applications (foods, pharma, biomedicine, etc).

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# C43- Influence of nanocellulose with different particle size on pasting and rheological properties of wheat starch

ade CRIQUET[1]; Francisco MELO[2]; Javier ENRIONE[3,4] and Paulo DÍAZ-CALDERÓN[3,4]

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[2]*Department of Physics, Faculty of Sciences, Universidad de Santiago de Chile, CHILE.*
[3]*Biopolymer Research and Engineering Laboratory, School of Nutrition and Dietetics, Faculty of Medicine, Universidad de los Andes, CHILE.*
[4]*Center for Biomedical Research and Innovation (CIIB), Faculty of Medicine, Universidad de los Andes, CHILE.*

Tailored design of novel materials based on starch-nanocellulose requires a huge understanding about structural properties, and how these structures define the composite's functionality. Cellulose nanofibrils (CNF) and cellulose nanocrystals (CNC) have been described as biomaterials with wide applications in polymer science. However, their use in food science and nutrition, specifically designing food structures with functionality is gaining interest. The goal of this work was to investigate how CNF and CNC modify macrostructural features of wheat starch specially those related with pasting and rheological properties.

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Our study concluded that particle size of nanocellulose provoked big structural changes in wheat starch, which would be associated with how the amylose self-associates in presence of nanocellulose. This knowledge could be useful for the tailored design of starch-nanocellulose composites to be used in different industrial applications (foods, pharma, biomedicine, etc).

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# C43- Gelation of cereal β-glucan after solubilization at the physiological temperature: effect of molecular structure

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Introduction: Cereal β-glucan is well-known for its health benefits, such as lowering blood cholesterol, which are directly related to its rheological properties. Although typically forming viscous solutions, β-glucan was previously shown to form gels at low concentration after partial dissolution at the physiological temperature of 37°C. However, this was not seen in all β-glucans, suggesting an influence of structural variation. This study aimed to elucidate the effect of the molecular structure of β-glucan on its gelation behavior after solubilization at 37°C.

Methods: β-Glucans from 12 barley and 11 oat cultivars were extracted and screened for the relative abundance of DP3 and DP4 structural units (DP3:DP4 ratio) by quantifying the oligosaccharides released by lichenase enzyme using high-performance anion-exchange chromatography with pulsed amperometric detection. Two barley and two oat cultivars with differing DP3:DP4 ratios were selected for further experiments. The isolated β-glucans were dissolved at 1% concentration at 37°C and the gel properties were determined with a rheometer after 2 h and 24 h of storage using dynamic oscillatory measurements.

Results: The DP3:DP4 ratios were higher in barley than in oat although variation among cultivars was relatively small. Large differences were observed in the gel properties of the four selected cultivars. After 2 h of storage, all samples behaved as viscous solutions, while in 24 h, the oat β-glucans had formed a weak gel structure. The barley samples, in contrast, showed little to no structure development.

Discussion: The results show that the molecular characteristics of β-glucan determine its ability to gel after incomplete dissolution. It is suggested that this gelation is driven by an interplay between the DP3:DP4 ratio and the molecular weight. This study contributes to the understanding of the rheological behavior of β-glucan under physiologically relevant conditions.

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# C44- Molecular characterization of interactions between Lectin - a protein from the common edible mushroom (Agaricus bisporus) - with dietary carbohydrates

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Lectins can be widely found in living organisms such as animals, fungi, plants, bacteria and viruses. Most lectins in plants are storage proteins and play a critical role in the defense of external threats. Lectins are either univalent or polyvalent proteins of nonimmune origin that bind reversibly and noncovalently to specific sugars on the opposing cell. Their activity originates from the ability to recognize and reversibly bind carbohydrates and glycoconjugates. The molecular mechanism of ligand binding and the binding stoichiometry between Agaricus bisporus lectin (ABL) and dietary carbohydrates are yet to be studied[1,2,3].

In the present work, we applied circular dichroism (CD), Fourier-transform infrared spectroscopy (FTIR), intrinsic fluorescence spectroscopy and molecular docking techniques to evaluate the interactions between ABL and dietary carbohydrates/antigen recognition agents (galactose, glucose, N-acetyl-D-galactosamine and N-acetyl-D-glucosamine).

Intrinsic fluorescence measurements with increasing concentrations of dietary carbohydrates/antigen recognition agents resulted in a considerable quenching of fluorescence intensity of the ABL solutions. This indicates that binding of the ligand has occurred and nonlinear fitting of quenching data shows that the binding strength of interactions is intermediate to strong, with galactose exhibiting the strongest molecular interactions. Circular dichroism and Fourier transform infrared analyses record alteration in the protein secondary structure with ligand binding. Molecular docking highlights the likely binding positions of each ligand to the ABL molecule further arguing for the presence of stable interactions between the protein and the ligands, which differ in the conformation of a single epimeric hydroxyl group at position four of the sugar ring. These findings give a deeper understanding of the molecular interactions between lectin from Agaricus bisporus and dietary carbohydrates providing a theoretical basis for its functionality as a nutraceutical with hypoglycemic capability.

*References*

1. Tirta Ismaya, W., Tjandrawinata, R. R., & Rachmawati, H. (2020). Lectins from the edible mushroom agaricus bisporus and their therapeutic potentials. Molecules, 25(10), 2368
2. Singh, R. S., Bhari, R., & Kaur, H. P. (2010). Mushroom lectins: Current status and future perspectives. Critical Reviews in Biotechnology, 30(2), 99–126.
3. Condict, L., Hung, A., Ashton, J., & Kasapis, S. (2021). High-temperature binding parameters and molecular dynamics of 4-hydroxybenzoic acid and β-casein complexes, determined via the method of continuous variation and fluorescence spectroscopy. Food Hydrocolloids, 114, 106567.

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# Industrial hydrocolloids challenges: from raw material to market.

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Natural polysaccharides are part of the hydrocolloids mainly used in the food industry as additives. They represent an important market that is still growing but faces some threats.

Nowadays, the supply of raw materials is crucial to guarantee a high quality of products and has simultaneously to comply with sustainability approach. The production of polysaccharides also faces challenges on technological aspects. The processes, to produce them into the form of powders, implement relatively similar operations regardless of the nature and origin of the polysaccharides. However, process operations and polysaccharide powders represent areas of study which are under explored or exploited.

*Keywords* Polysaccharides, Industry, Processes, Market, Challenges.

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