

Development and validation of a quantitative method for measuring multiple food intake biomarkers

Background

- Food intake biomarkers (BFIs) are used as objective tools to estimate food intake^{1,2}. However only few BFIs are validated for this purpose and for many important foods, biomarkers are currently lacking.
- We have identified 36 potential BFIs, that have been shown in previous studies to reflect the intake of foods or food groups commonly consumed in western diets. A controlled dietary intervention in humans was performed where combination of the specific foods were provided in single and repeated doses to establish pharmacokinetic parameters including half-life and dose-response. To validate the identified candidate biomarkers as specific biomarkers of the foods tested, a rapid multi-method is needed. The aim of this project is therefore to establish a method and apply it to samples from the intervention study.

Materials and Methods

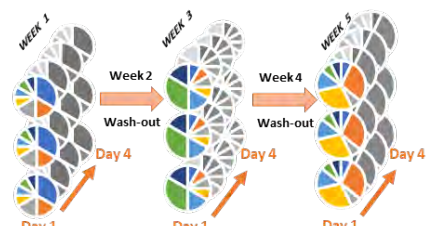


Figure 1: Intervention study in which the current method will be employed. During the intervention weeks 1,3 and 5 the participants consume 3 meals daily for 4 days and the proportion of food changes weekly. Weeks 2 and 4 are the wash-out periods.

Table 1: gradient elution program

Time (min)	MPb (%)	Flow (mL/min)
0.00	0	0.4
1.00	0	0.4
1.50	5	0.4
1.51	5	0.6
4.50	90	0.6
4.51	95	0.8
5.00	95	0.8

- UPLC-MMR method; ExionLC™ coupled with QTRAP 6500+
- Column: ACQUITY UPLC BEH C18, 1.7 µm, 2.1x 100mm
- Solvent A; water, 0.2% acet. acid and solvent B; acetonitrile, 0.2% acet. acid

Results

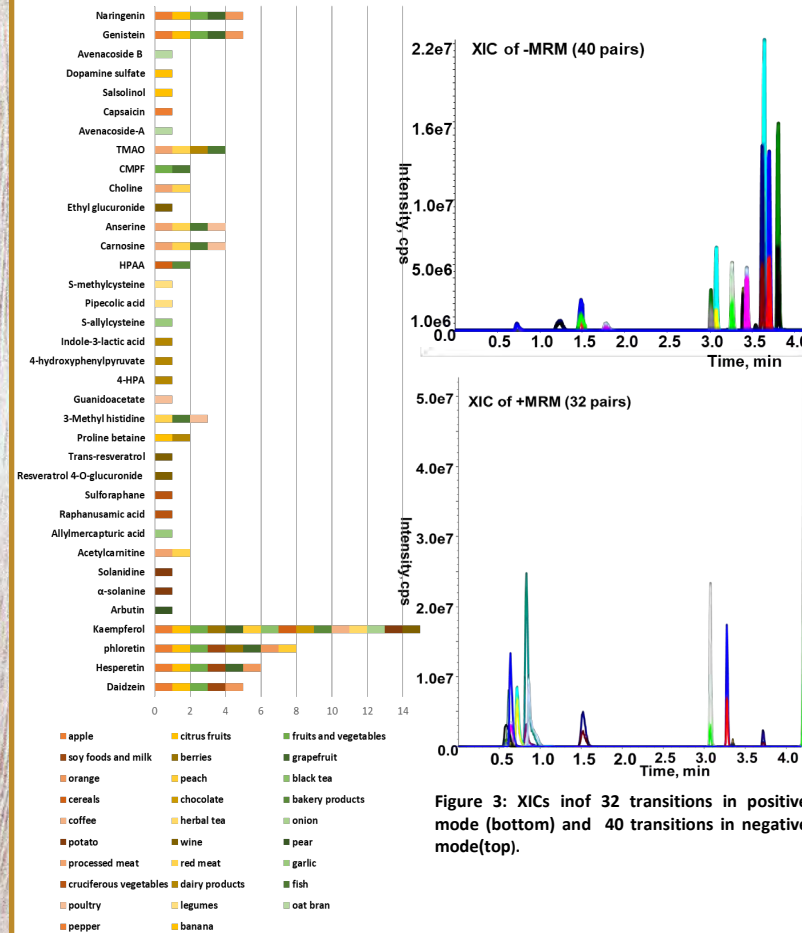


Figure 2: List of the BFIs quantified with the current method and the foods they reflect

Figure 3: XICs inof 32 transitions in positive mode (bottom) and 40 transitions in negative mode(top).

Expected outcomes

- Quantification and validation of 36 BFIs in blood plasma with a single injection and a 5.0 min gradient elution program, including scheduled MRMs in positive and negative ionization mode.
- Method to be applied and validated for human blood plasma samples from intervention study.
- To fill the gap between academic research and the methodological requirements necessary for the developments of clinical and commercial applications for diet assessments.

Reference

- Landberg, R., et al., *Biomarkers of cereal food intake*. Genes & Nutrition, 2019. **14**(1): p. 28.
- Brennan, L. and F.B. Hu, *Metabolomics-Based Dietary Biomarkers in Nutritional Epidemiology-Current Status and Future Opportunities*. Mol Nutr Food Res, 2019. **63**(1): p. e1701064.

Acknowledgements

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Replacement of vegetable oils with the oleaginous yeast *Rhodotorula toruloides* biomass in the diet of Arctic char (*Salvelinus alpinus*), effects on fish growth performance Mathilde Brunel¹, Viktoriia Burkina^{1,2}, Sabine Sampels¹, Anna-Karin Dahlberg³, Volkmar Passoth¹ and Jana Pickova¹.

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Background/introduction/summary

A current and main limitation in fish production is the fish feed formulation as more sustainable ingredients should be included in the fish feed for the long-term perspective of sustainable aquaculture.

The aim of this study was to replace part of the fish feed by the biomass of the oleaginous yeast *Rhodotorula toruloides* in the diet of Arctic char (*Salvelinus alpinus*), to evaluate its safety and to



investigate the fish performance with the feed change.

R. toruloides was used for its capacity to produce considerable amounts of oil as well as for its ability to grow on abundant, non-edible plant biomass such as lignocellulosic hydrolysate (Brandenburg et al., 2021).

Materials and Methods

A feeding trial was performed at an aquaculture center with fish divided into two groups: a control group and a yeast group of fish fed with yeast biomass from *R. toruloides*.



Aquaculture Center

Formulation of both feeds was strictly controlled to remain iso-nitrogenous and iso-energetic. Yeast biomass and its hydrolysate were investigated for heavy metals and organic pollutants.

Several fish growth parameters were measured in addition to the enzyme activity of ethoxyresorufin-O-deethylase (EROD) in fish livers.

Lastly, a sensory analysis was conducted to evaluate potential differentiated fish taste, smell or texture, as a result of feeding with *R. toruloides* biomass.

Results

Table 1: Composition of control and treatment feeds (%).

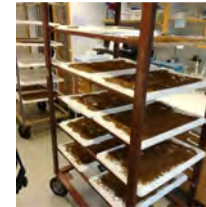
Feed ingredients	Control feed (%)	Yeast biomass feed (%)
Fish meal	52.8	53.5
Fish oil	12.5	12.6
Vegetable oil	5.80	-
Mineral mix	0.48	0.49
Vitamin mix	0.96	0.97
Red mineral mix	0.14	0.15
Gelatine	0.48	0.49
Wheat meal	18.7	14.1
Casein	5.76	-
Ca ₂ SO ₄	2.40	2.43
Yeast	-	15.3 (5.8% oil)
Total	100	100

Table 3: Concentrations of organic pollutants in hydrolysate and yeast samples (mean \pm SD, n = 3).

	Σ PAH ₁₇	Σ PCB ₂₀
Hydrolysate, ng.g ⁻¹	<LOQ or n.d	n.d
Yeast, ng.g ⁻¹ lipid weight	200 \pm 12	n.d

Table 2: Analysis of heavy metal concentrations in yeast biomass and its hydrolysate (mg.kg⁻¹ or mg.l⁻¹). ALS Scandinavia, Sweden (Commission Regulation (EC) No 1881/2006 and No 835/2011).

Element	EU legislation mg.kg ⁻¹	Hydrolysate mg.l ⁻¹	Yeast mg.kg ⁻¹
Al	1	0.3360	0.5390
As	0.01	0.0053	<LOQ
Cd	0.05	0.0058	0.0196
Hg	0.50	<LOQ	<LOQ
Pb	0.30	0.0164	0.0343



Fish feed formulation



Arctic char (*Salvelinus alpinus*)

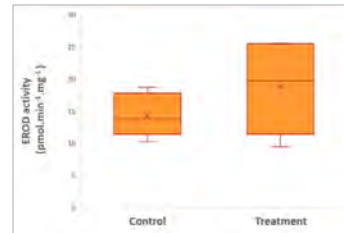


Figure 1: EROD activity in hepatic microsomes of Arctic char fed with two different diets for 53 days (n=12), pmol.min⁻¹.mg⁻¹.

Table 4: Fish performance in both feed groups (mean \pm SD, n=96).

Growth parameters	Control group	Yeast group	p-value
Initial weight (g)	209 \pm 65.4	200 \pm 62.9	0.7360
Final length (cm)	29.4 \pm 2.20	29.2 \pm 2.54	0.7417
Final weight (g)	314 \pm 99.1	303 \pm 94.3	0.5882
Liver weight (g)	3.75 \pm 2.07	4.61 \pm 1.91	0.0365

Conclusions

Heavy metals and organic pollutants analyses showed no toxic levels of fish feed with yeast biomass as levels were below European legislation and no significant effects were observed in enzyme activity of EROD in fish liver between the two groups of fish.

Fish from both feed performed similar in their growth except for the liver weight. No significant difference in the sensory evaluation was detected.

Additional studies at a bigger scale should to be conducted to confirm the results observed.



Sensory evaluation

Reference

Brandenburg J, Blomqvist J, Shapaval V, Kohler A, Sampels S, Sandgren M, Passoth V (2021). Oleaginous yeasts respond differently to carbon sources present in lignocellulose hydrolysate. *Biotechnol Biofuels* 14:24 <https://doi.org/10.1186/s13068-021-01974-2>
Commission Regulation (EC) No 1881/2006. (2006). Setting maximum levels for certain contaminants in foodstuffs. <http://data.europa.eu/eli/reg/2006/1881/oj>
Commission Regulation (EC) No 835/2011. (2011). Regulation (EC) No 1881/2006 as regards maximum levels for polycyclic aromatic hydrocarbons in foodstuffs.

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Protein Extraction from Cold-Pressed Hempseed Press Cake – from Laboratory to Pilot Scale

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Background/introduction/summary

Industrial hempseed (containing less than 0.3 % THC) contains mainly two storage proteins, edestin and albumin, which are easily digested and have a good amino acid profile (1).

From 1 kg cold-pressed industrial hempseed 350 g hempseed oil and 650 g hempseed press cake (HPC) is generated.

HPC contains high amounts of protein (30-50 %) (2), which can be extracted.

Phytic acid, which is a potent inhibitor of iron absorption, is present in HPC (3). The phytic acid levels were therefore measured in the produced hemp protein precipitates.

Objective: to optimize a protein extraction on HPC with no pre-treatment (e.g. defatting step or enzyme treatment), suitable for future larger scale production of hempseed protein with reduced levels of phytic acid.

Materials and Methods

- 50 g HPC was milled and dispersed in tap water (1:10).
- Alkali extraction, tested parameters:

pH	9.0, 10.0, 10.5, 11.0, 12.0
Temperature	Room temperature (approx. 20 °C), 30 °C, 50 °C
Monitoring of pH	Non-constant pH, constant pH
Time	1 h, 2 h, 3 h, 4 h

- Centrifugation
- Precipitation, tested pH values: 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5
- Centrifugation

Pilot trial: 2 kg HPC was alkali extracted at a constant pH 10.5 in room temperature for 4 h. The first separation step was performed with a decanter. Precipitation pH 5.5.

Results

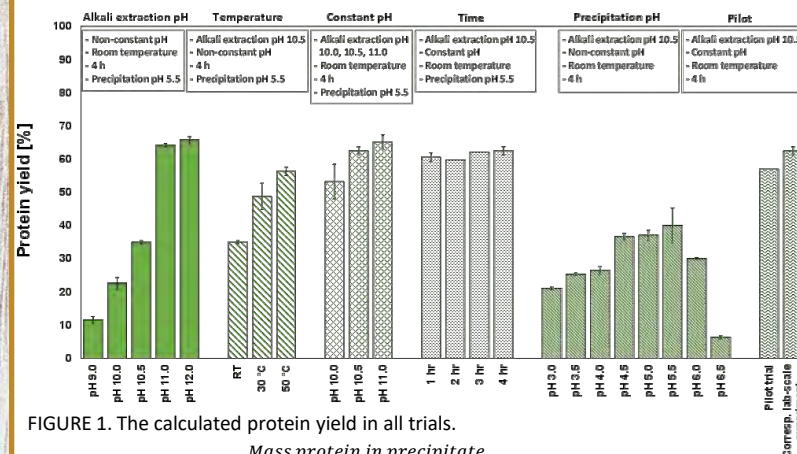


FIGURE 1. The calculated protein yield in all trials.

$$\text{Protein yield (\%)} = \frac{\text{Mass protein in precipitate}}{\text{Mass protein in HPC}}$$

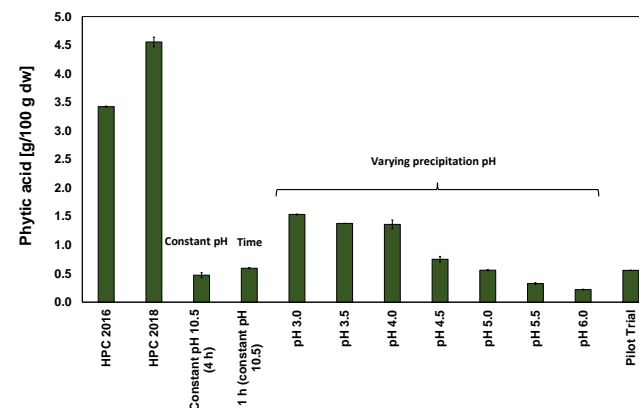


FIGURE 2. Phytic acid content in HPC from two different harvest years and precipitates from different trials. Higher precipitation pH reduced the level of phytic acid.

Conclusions

The optimal process parameters were concluded to be:

- ✓ Alkali extraction pH 10.5
- ✓ Room temperature
- ✓ Constant pH
- ✓ Alkali extraction time 1 h
- ✓ Precipitation pH 5.5

The phytic acid content was significantly reduced by the protein extraction process.



FIGURE 3. Precipitates from time trials, 1 h (top), 2 h (middle), 3 h (below).

Reference

- Callaway, J. C., (2004a). Hempseed as a nutritional resource: An overview. *Euphytica*, 140(1-2), 65-72.
- House, J. D., J. Neufeld & G. Leson, (2010). Evaluating the Quality of Protein from Hemp Seed (*Cannabis sativa* L.) Products Through the use of the Protein Digestibility-Corrected Amino Acid Score Method. *Journal of Agricultural and Food Chemistry*, 58(22), 11801-11807.
- Pojic, M., A. Misan, M. Sakac, T. Dapcevic Hadnadev, B. Saric, I. Milovanovic & M. Hadnadev, (2014). Characterization of byproducts originating from hemp oil processing. *J Agric Food Chem*, 62(51), 12436-12442.

Acknowledgements

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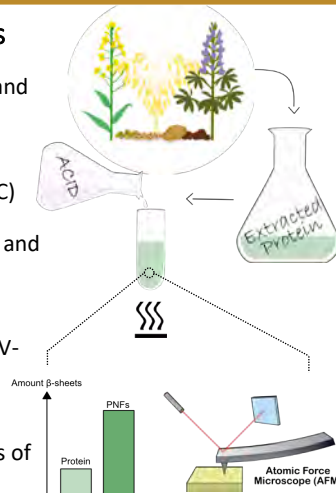
Background/introduction/summary

- There is a great need to develop more sustainable food
- Texture makes the food appetizing
- **Protein nanofibrils (PNFs)** have demonstrated many useful applications within the material sciences due to their positive impact on the strength and stiffness of the material
- PNFs are characterized by a high content of β -sheets, packed in a cross- β structure and linked together with hydrogen bonds
- **Aim:** Generate new sustainable texturized food application from plant-based protein nanofibrils



Materials and Methods

- Plant protein extraction and purification
- Plant protein characterization (SDS, SEC)
- Generating PNFs (low pH and high temperature)
- Characterizing secondary structure of PNFs (ThT, UV-CD, FTIR)
- Determination of morphological alterations of PNFs (AFM)

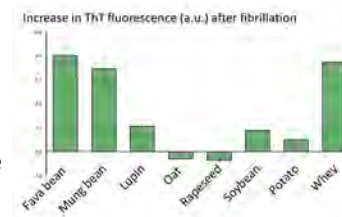


Results

We were able to extract protein and generate PNFs from fava bean, mung bean, lupin, oat and rapeseed, potato, soybean. This was compared with protein and PNFs from whey.

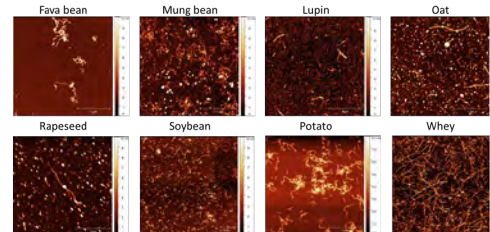
Secondary structure analysis

ThT is a fluorescent dye that binds to PNFs. ThT assay showed an increase in fluorescent after fibrillation for all proteins except oat and rapeseed. However, the presence of PNFs in the fibrillated sample from oat and rapeseed was confirmed with UV-CD, FTIR and AFM.



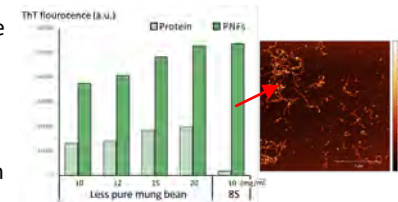
Morphology of PNFs

The PNFs differed in length and morphology (curly/straight). The reason that whey is dominant in forming many and long PNFs are probably due to that the major protein is small and the protein isolate is pure.



Purity and size of protein affect the ability to form PNFs

We proved this hypothesis by generating a pure isolate from the major protein in mung bean 8S. PNFs from 8S generated a higher ThT response at lower concentrations and longer PNFs compared to the less pure protein from mung bean.



Conclusions

- ThT assay has limitations as detection method of PNFs
- We were able to characterize PNFs from 7 different plant-based proteins
- AFM confirmed different morphologies among these PNFs
- Size and purity of protein affect the ability to form PNFs
- One step closer to understand how to use plant-based PNFs in a food application

Reference

Herneke et al. 2021
<https://doi.org/10.1021/acsfoodscitech.1c00034>



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Differential Glycemic Effects of Low- versus High-Glycemic Index Mediterranean-Style Eating Patterns in Adults at Risk for Type 2 Diabetes: The MEDGI-Carb Randomized Controlled Trial

Background/introduction/summary

A Mediterranean-style healthy eating pattern (MED-HEP) supports metabolic health, but the utility of including low-glycemic index (GI) foods to minimize postprandial glucose excursions remain unclear. Therefore, we investigated the relative contribution of GI towards improvements in postprandial glycemia and glycemic variability after adopting a MED-HEP

Materials and Methods

We conducted a randomized, controlled dietary intervention, comparing high- versus low-GI diets in a multi-national (Italy, Sweden, and the United States) sample of adults at risk for type 2 diabetes. For 12 weeks, participants consumed either a low-GI or high-GI MED-HEP. We assessed postprandial plasma glucose and insulin responses to high- or low-GI meals, and daily glycemic variability via continuous glucose monitoring at baseline and post-intervention

Results

One hundred sixty adults (86 females, 74 males; aged 55 ± 11 y, BMI 31 ± 3 kg/m², mean \pm SD) with \geq two metabolic syndrome traits completed the intervention.

Postprandial insulin concentrations were greater after the high-GI versus the low-GI test meals at baseline ($p = 0.004$), but not post-intervention ($p = 0.17$).

Postprandial glucose after the high-GI test meal increased post-intervention, being significantly higher than that after the low-GI test meal (35%, $p < 0.001$).

Average daily glucose concentrations decreased in both groups post-intervention.

Indices of 24-h glycemic variability were reduced in the low-GI group as compared to baseline and the high-GI intervention group

Conclusions

The acute superiority in the indices of postprandial glucose control of participants who emphasized low-GI foods relative to those who emphasized high-GI foods is sustained and was further amplified over time in the context of a background MED-HEP.

Since low-GI foods are an inherent element of a traditional Mediterranean diet, our findings suggest that low-GI foods may contribute to the health benefits seen from the MED-HEP

Reference

<https://www.mdpi.com/2072-6643/14/3/706>

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The Effect of Plant-Based Proteins on Markers of Gut and Metabolic Health

Background/introduction/summary

Plant-based proteins were shown to have a lower impact on the climate in comparison to animal proteins which launched a transition from a diet based on animal protein to a plant-based diet¹. However, detailed scientific knowledge about related health effects is still lacking.

This pilot study focuses on colonic protein fermentation and its effect on microbiota composition, gut markers and metabolites with the aim to determine influencing factors of protein digestibility, to investigate nutrient interactions regarding fermentation processes in the colon and to understand metabolic mechanisms.

The study is part of the PhD project within PAN Sweden Research Centre. With the newly gained knowledge the long-term goal is to create "sustainable produced products with health benefits for everyone".

Materials and Methods

After a 4-week baseline period, participants are asked to supplement their diet with a plant protein. The protein amount is calculated individually in regards to the body weight.

During the whole course of the study weekly faecal samples are collected as well as questionnaires to evaluate bowel habits, gastrointestinal symptoms, physical activity and individual food habits.

After the start of the dietary intervention, 24h urine samples and fasting blood samples are additionally collected once a week. Furthermore, the body composition is measured weekly during the intervention.

Results

The pilot study started in November 2021 and the intervention is still ongoing. First results are expected during summer 2022. In total, 32 healthy male and female participants have been included in the present study (1 drop out as of now).

The screening consisted of an 1-hour meeting during which study details – such as the schedule, the participant's tasks and the intervention – were explained. Additionally, a case report form was filled in for each interested person to evaluate e.g. medical background and to assess if any of the exclusion criteria apply.

The exclusion criteria included: age <18 or >45 years; BMI <18.5 or >30 kg/m²; acute chronic disease, inflammatory or functional gastrointestinal diseases; eating disorder; vegan diet; use of antibiotic medication, laxatives or anti-diarrhoeal medication during the last 3 months prior the first visit; regular consumption of probiotic or prebiotic products for the past 6 weeks before the first visit; more than 5 h of moderate-vigorous exercise per week; use of dietary protein or fibre supplementation; pregnancy or breastfeeding; smoking or usage of snus; unstable body weight during the last 3 months before the first visit.

Furthermore, people were asked to hand in three food diaries after the screening which comprised two weekdays and one weekend day. These diaries were assessed regarding protein and dietary fibre intake and people were excluded if their diet was too low in protein and/or dietary fibre.

After advertising the study, 306 people reported interest and 93 could be booked for a first meeting. Eventually, 78 people were screened either at Campus USÖ (Örebro University) or via Zoom. After analysing all documents, 37 people were considered eligible to participate in the study.

The findings of this pilot study shall help to design future studies, also considering protein amount and duration of dietary interventions.

Conclusions

With an increasing intake of protein, we expect to observe an increase in metabolites which are related to and deriving from proteolytic fermentation in the colon in faecal as well as blood samples.

Furthermore, we hypothesised that a 4-week dietary intervention will result in microbiota composition changes also in regard to protein-fermenting bacteria.

We expect that even at higher doses participants will be compliant with the protein supplementation.

Reference

1. Poore, J. & Nemecek, T. (2018): Reducing food's environmental impacts through producers and consumers. *Science* 360 (6392): 987–992.

Acknowledgements

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Innovation Management in Food System Transitions

Background/introduction/summary

In order to safeguard long-term food production, the world's food systems need to radically transform, and transition towards sustainability. My project seeks to understand how such a transformation could take place in a specific food value chain: studying farmers, food processors and retailers to understand the role of the firm in the transition process, in relation to innovation management.

My project is nested within the Center for Food Innovation for Sustainable System Transition, FINEST:
<https://www.ri.se/en/finest>,

FINEST is a collaboration between RISE, Chalmers, Uppsala University, and 16 other industry partners from the food sector.

Materials and Methods

Results

My research project commenced during the fall of 2021, when I initiated my first pre-study focusing on innovation management in food retail, and intra-firm collaborations. The purpose of the pre-study is to inform future studies in our chosen topic area, which at this point remains relatively unexplored, or largely overlooked.

To better understand how my research could contribute to the overall goals of our center, the pre-study is still ongoing, currently moving along with new actors across the value chain, both in primary production, and in food processing. Our ambition is to specify a clear direction in the coming months, but thus far, no results have yet become available.

While it is still very premature, we expect our research to contribute with new knowledge related to innovation, business- and collaboration models, with hopes of testing these together with stakeholders in and outside of the center.

I am interested in studying various forms of collaborative innovation, i.e., open innovation, co-creation processes between stakeholders in the food value chain (for example between farmers and food processors, farmer x retailers, or between processors and food retail).

If my research sounds interesting to you, or if you have any ideas concerning potential research problems or questions, please feel free to research out. I welcome any form of input. If you know of any researchers I should definitely meet, please do get in touch!

Conclusions

Reference

Acknowledgements

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FODMAPs, but not gluten, elicit modest symptoms of irritable bowel syndrome: a double-blind, placebo-controlled, randomized three-way crossover trial

Background/introduction/summary

Irritable bowel syndrome (IBS) is a chronic common functional bowel disorder¹. Symptoms have been associated with foods, such as FODMAPs (easily fermentable dietary fiber containing Fermentable Oligosaccharides, Disaccharides, Monosaccharides, and Polyols) and gluten. Previous studies suffer from a suboptimal study design due to small sample size and for being unblinded or single-blinded. Furthermore, studies have focused on the elimination of FODMAPs from the diet, not as a provocation².

Therefore, **the aim of this study** was to investigate the effects of week-long intervention with FODMAPs, gluten or non-fermentable placebo on the IBS symptom severity score (IBS-SSS) in a double-blind, randomized, placebo-controlled cross-over study design.

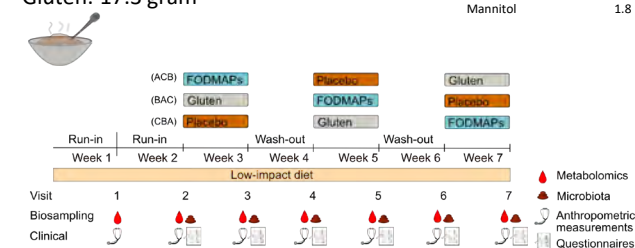
Materials and Methods

Medium to severe IBS
n=110
Women and men

Daily doses (1.5 times a daily intake)

FODMAPs: 50 gram
Gluten: 17.3 gram

Fructose 19.5
Lactose 15.2
Galacto-oligosaccharides 1.5
Fructo-oligosaccharides 7.0
Sorbitol 4.5
Mannitol 1.8



Results

In subjects with moderate to severe IBS (n=103), FODMAPs caused higher total IBS-SSS (mean [SE] 240 [9]) than placebo (208 [9]; p=0.00056) or gluten (198 [9]; p=0.013), but with no difference between gluten and placebo (p=1.0) (Figure 1). In order for clinical significance a change of 50 points is needed, the difference between FODMAPs and placebo was 42 points. Proportion of participants increasing with 50 or 100 points did not differ between the interventions (Figure 2). Also, there were large interindividual differences in response to the interventions (Figure 3).

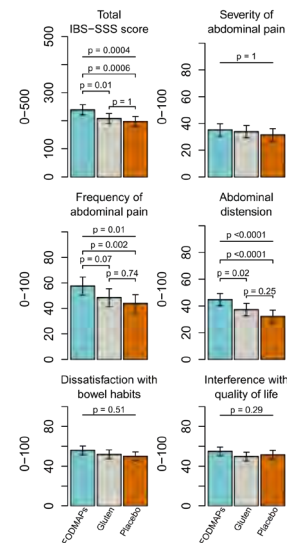


Figure 1. IBS-SSS score after intervention with FODMAPs, gluten, or placebo. Higher scores indicate more severe symptoms

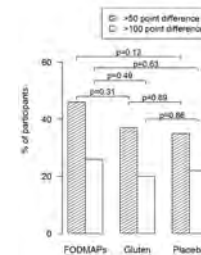


Figure 2. Percentage of participants with an increase in total IBS-SSS score of >50 points, or >100 points

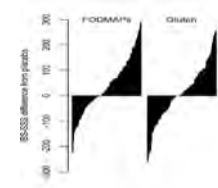


Figure 3. Total IBS-SSS for the interventions for each individual as a difference to placebo

Conclusions

FODMAPs, but not gluten, caused modest gastrointestinal symptoms in people with IBS, compared to placebo. There was a considerable interindividual variability in response to the interventions which warrants further detailed studies to identify underlying causes and enable prediction of responses.

Ongoing work in this project is to study the effect of the interventions on the metabolome and the gut microbiota in order to gain mechanistic insights. In addition, the possibility to predict outcome in relation to the interventions is under investigation.

Reference

¹. Functional Gastrointestinal Disorders: History, Pathophysiology, Clinical Features, and Rome IV. *Gastroenterology* 2016;150:1262–1279

² Dionne et al. A Systematic Review and Meta-Analysis Evaluating the Efficacy of a Gluten-Free Diet and a Low FODMAPs Diet in Treating Symptoms of Irritable Bowel Syndrome. *Am J Gastroenterology* 2018;11(9):1290-1300

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Diet during pregnancy and lactation in relation to offspring allergy

Background

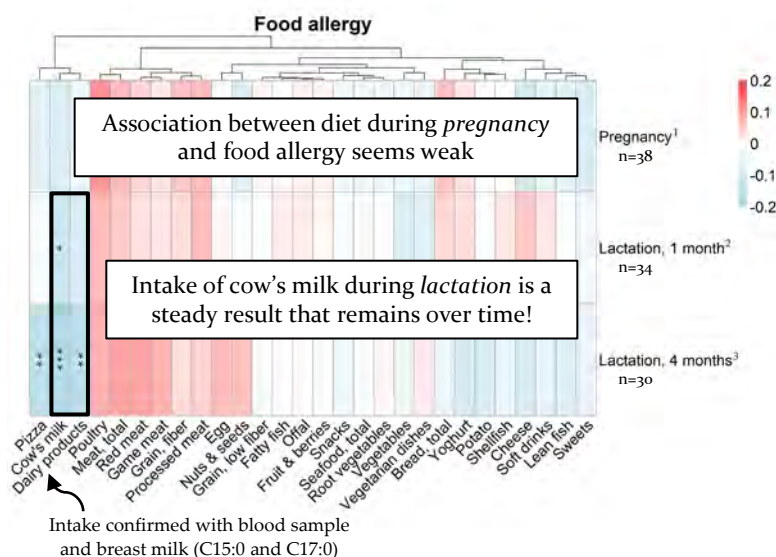
- Allergy is one of the most common chronic diseases in childhood, affecting up to 30% of children in industrialized countries.
- While the etiology of allergies is not yet completely understood, it appears to reflect complex interactions of genetic and various environmental and lifestyle factors.
- Maternal diet during pregnancy and lactation have been discussed as potential lifestyle factors that can modify the risk of allergy in the offspring.
- *The aim* was to assess and compare the dietary intake of pregnant and lactating women using questionnaires, validate it with dietary biomarkers in erythrocytes and breast milk, and relate these data to doctor diagnosed allergy in the offspring at 12 months of age.

Materials and Methods

- Data from the Swedish birth cohort NICE
- Repeated semi-quantitative food frequency questionnaire *Gestational week 34, 1 month and 4 months postpartum*
- Doctor's diagnosed allergy at 12 months
- Analysis of fatty acids in erythrocytes (GC-FID) and in breast milk (GC-MS)
- Partial Spearman correlation with diet and allergy *Adjusted for heredity, siblings, birth season and total energy intake*
- Unsupervised hierarchical cluster analysis

Results

- 508 mother-child couples included in the statistical analyses.
- The prevalence of allergy at 12 months of age were 7.7% with food allergy, 6.5% with atopic eczema and 6.5% with asthma.
- A higher maternal consumption of cow's milk during lactation was significantly associated with lower prevalence of food allergy in the offspring.
- Higher maternal consumption of fruit and berries during lactation was significantly associated with increased prevalence of atopic eczema in the offspring.
- Intake of cow's milk correlated with the proportions of pentadecanoic acid (15:0) and heptadecanoic acid (17:0) in breast milk and pentadecanoic acid in breast milk was in turn associated with lower prevalence of offspring food allergy.



Conclusions

- Maternal intake of cow's milk during lactation, as confirmed by measurements of dietary biomarkers in maternal blood and breast milk samples, is associated with lower prevalence of physician-diagnosed food allergy by 12 months of age.
- Our results suggest that maternal diet modulate the infant's immune system, affecting subsequent allergy development.

Reference

Stråvik M, Barman M, Hesselmar B, Sandin A, Wold AE, Sandberg AS. *Maternal intake of cow's milk during lactation is associated with lower prevalence of food allergy in offspring.* Nutrients. 2020 Dec;12(12):3680.

Acknowledgements

We thank all participating families, and everyone involved in the work leading up to this publication. For more detailed information see the original article (listed above).

Contact

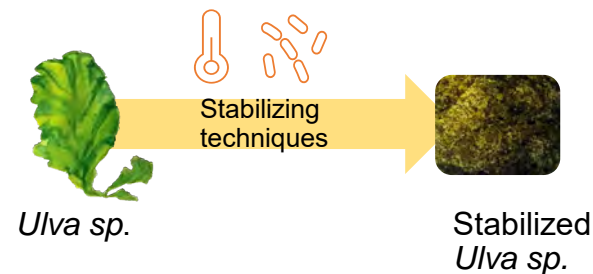
PhD student Mia Stråvik: mia.stravik@chalmers.se
<https://www.chalmers.se/en/Staff/Pages/mia-stravik.aspx>

Stabilizing *Ulva sp.* biomass for its future application in food products

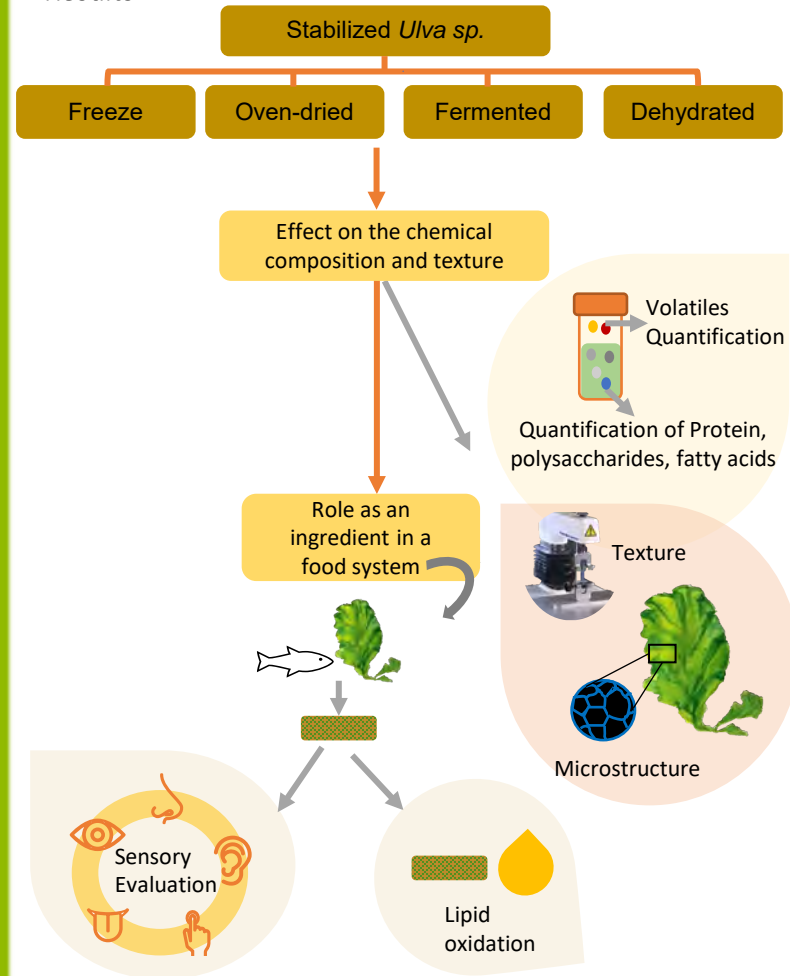
Background/introduction/summary

Seaweed is perishable after harvest due to its high moisture content and sensitive compounds, making its use in the food industry challenging¹. Efficient methods to preserve the quality of seaweed will facilitate its usage as a sustainable food ingredient^{1,2}. The aim is to design tailor-made methods for stabilizing *Ulva sp.* and determine how these affect the suitability of *Ulva sp.* as a food ingredient in terms of chemical composition, microstructure, techno functionality & nutritional properties.

Materials and Methods



Results



Conclusions

- Tailor-made post-harvest methods for stabilizing *Ulva sp.*
- Knowledge of specific stabilization effects on chemical, nutritional, microbial and physical features of *Ulva sp.*
- Possible applications of *Ulva sp.* as a food ingredient.

Reference

- ¹ Albers, E. *et al.* Influence of preservation methods on biochemical composition and downstream processing of cultivated *Saccharina latissima* biomass. *Algal Res.* **55**, 102261 (2021).
² Wong, K. & Chikung Cheung, P. Influence of drying treatment on three *Sargassum* species: Protein extractability, in vitro protein digestibility and amino acid profile of protein concentrates. *J. Appl. Phycol.* **13**, 51–58 (2001).

Acknowledgements

FORMAS

Blå mat
- centrum for framtidens sjomat



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Food Science Sweden

Chalmers | LTH | RISE | SLU | OrU

Maximizing protein yield during pH-shift processing of herring co-products combined with antioxidant-rich materials

Introduction

The pH-shift process is a promising tool to **recover functional proteins** from fish co-products, but lipid oxidation is a problem.

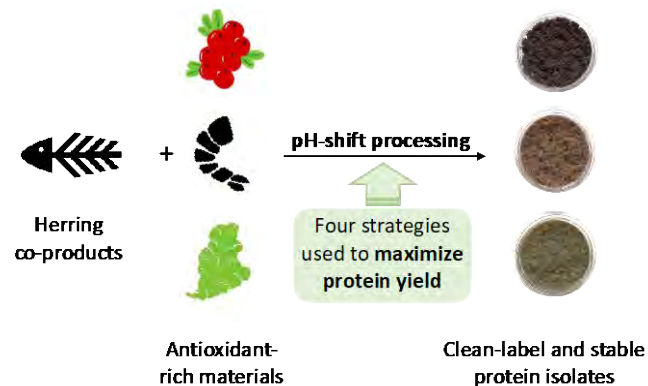
We have developed a **clean label** processing concept, “**Cross-processing**”, which combines fish co-products with antioxidant-rich materials during the pH-shift processing to produce **stable protein isolates**. However, protein yield was reduced.

The present study was aimed to counteract this yield-reduction during the cross-processing of herring co-products with lingonberry press-cake, shrimp shells and green seaweed by four strategies.

Cross-processing papers:

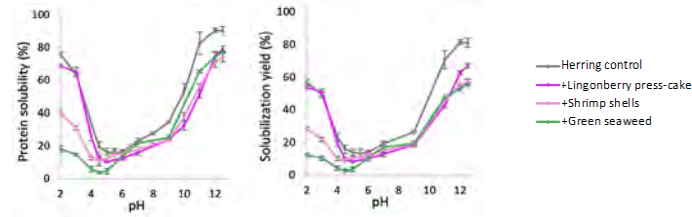


Materials and Methods



Results

Optimization of solubilization and precipitation pH



For all three helpers, the solubilization pH should be increased from the previously used 11.5 to 12, while the precipitation pH should be decreased from previously used 5.5 to 5.0/4.5 during alkali-aided solubilization to compensate for the loss of protein solubility and yield caused by the helpers.

↑water addition: increased total protein yield for all three helpers.

High shear mechanical homogenization (HSMH): replace SST-HSMH by RD-HSMH



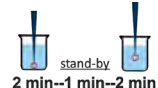
VS.



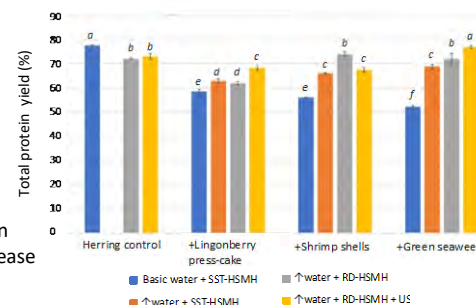
For +Shrimp, +Green seaweed: total protein yield was improved to the same levels as for herring controls.

Ultrasonication (US)

- with US probe.
- stand on ice.



For +Lingonberry, +Green seaweed: significant increase of total protein yield.



Conclusions

- ❖ This study confirmed earlier findings that cross-processing hampered protein solubility and solubilization yields.
- ❖ With shrimp shells and green seaweeds, reductions in solubilization yield were larger for acid- than alkaline solubilization, therefore using the former principle, shrimp shells or green seaweed cannot be recommended as helpers.
- ❖ It is possible to compensate for the loss in protein yield induced by cross-processing if optimizing the solubilization and precipitation pH's, slightly increasing the ratio of water to raw material, and by using RD-HSMH +/- US.
- ❖ Besides the effects on protein yield, the impacts of the process conditions on the structural and functional properties of the recovered protein isolates will be also investigated.

Reference

Zhang J., Ström A., Bordes R., Alming M., Undeland I. & Abdollahi M. (2022). High shear homogenization and ultrasound assisted cross-processing of herring co-products for maximum protein yield and functionality. *Submitted*.

Acknowledgements

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Chalmers | LTH | RISE | SLU | OrU

Evaluation of appetite measure visual analogue scales in home-setting: VASA-home

Introduction/Background

Dietary trials aiming to measure appetite and satiety have certain methodological challenges with resource-intensive assessments and large individual variation (1). Commonly used methods for appetite assessment include extended periods of time in a clinic, where participants fill in ratings on a visual analogue scale (VAS) and consume all their meals. This method is highly resource demanding regarding study personnel and facilities and challenging for study participants. This is problematic as appetite and satiety is identified as one of the most predominant factors for weight gain (2)(3). In this trial we aim to validate VAS in appetite assessment in the home setting.

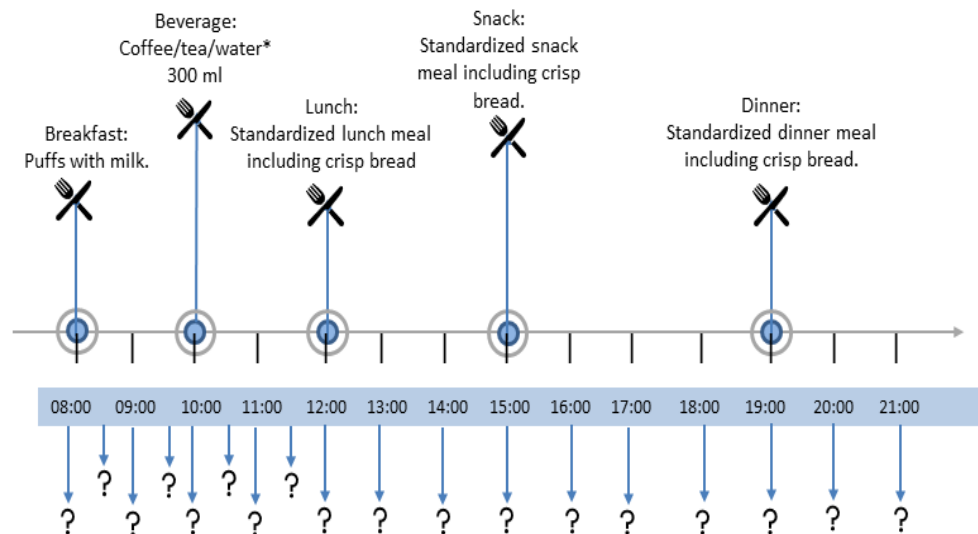
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Expected outcomes

- Additions outcomes
- Investigate differences in appetite response between rye- and wheat-based diets.
- Compare the postprandial response of glucose, insulin and selected appetite regulating hormones, following rye-based diet.
- Investigate if subjective appetite is affected by venous blood collecting done in parallel with the appetite assessment

Participants continuously answered questions about their appetite every 30 minutes from 8:00 to 12:00 and every 60 minutes from 13:00 to 21:00.



Acknowledgements

FORMAS, Barilla and Lantmännen for funding of the trial

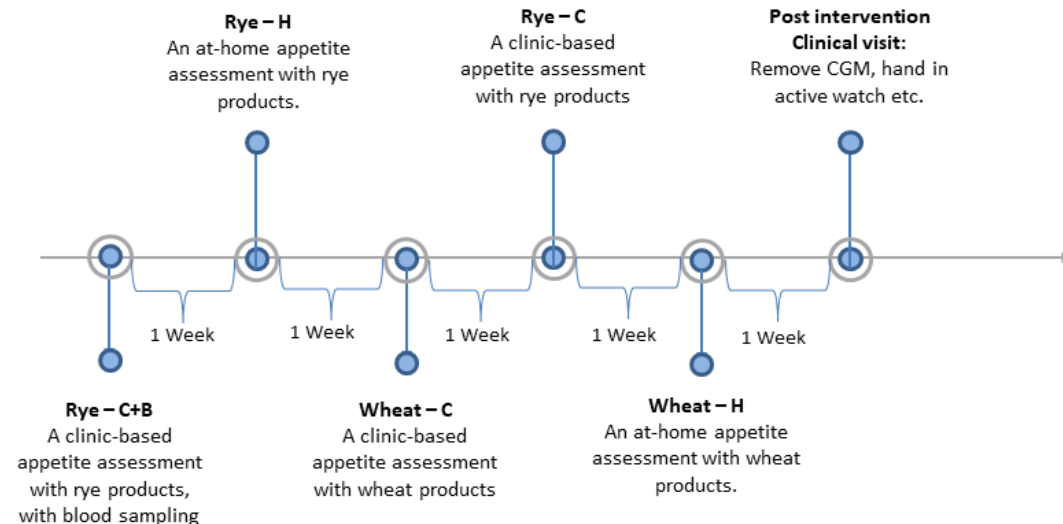
References

1. Gibbons C. 2019
2. Forde CG. 2015
3. Dalton M. 2013

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In the figure below the flow of participants is shown and on the left 5 different intervention days illustrated, where both location and diet is different for every occasion.



Introduction

The traditional western diet is characterised by high meat consumption. This has negative effects on human health and the environment. Therefore, a transition towards a more plant-based diet is needed^{1,2}. However, there is little known about the impact of this shift on various health domains^{3,4}. In addition, most plant proteins show limited functional properties due to their poor solubility^{5,6}. Furthermore, plant proteins often contain antinutritional factors (ANF) such as phytic acid, tannins or oligosaccharides which reduce their bioavailability^{4,7}. This makes a detailed evaluation of plant protein in terms of their quality and functional properties essential.



Project overview

Different methods will be used to characterize the (micro) structure and bioavailability of the different model proteins coming from oat, faba bean, soy and pea.

(MICRO) STRUCTURE

Microscopy
Texture analysis
Rheology



BIOAVAILABILITY

Amino Acids
Nutrients
Antinutrients



EFFECT OF PROCESSING ON STRUCTURE & BIOAVAILABILITY

Emulsifying, Extrusion, Fermentation, Enzymatic Hydrolysis

Outlook

(MICRO) STRUCTURE -> Information on functional properties

The solubility as one key factor is essential for the gelation, emulsification and foaming ability of proteins^{8,9}.

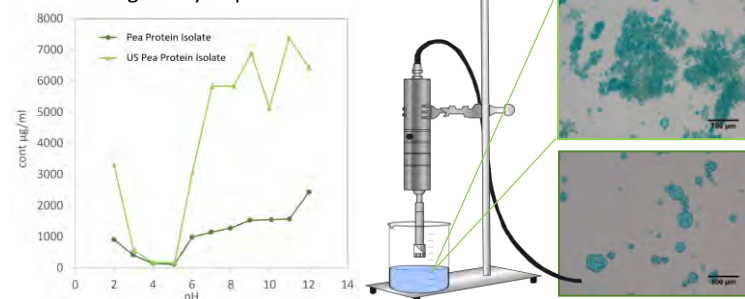


Figure 1. Solubility of pea protein isolate at different pH (left) before and after ultrasound pre-treatment (right)

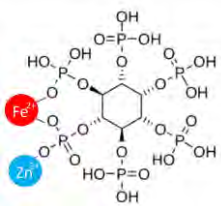


Figure 2. Phytate-mineral complex

BIOAVAILABILITY -> Information on health aspects

Phytic acid influences the functional properties of proteins⁹. However, by forming an insoluble and indigestible phytate-mineral complex, it negatively affects the bioavailability of zinc and iron^{7, 10}. Characterizing the nutrients and antinutrients can give an estimation on the bioavailability of minerals.

EFFECT OF PROCESSING -> Structure & Bioavailability

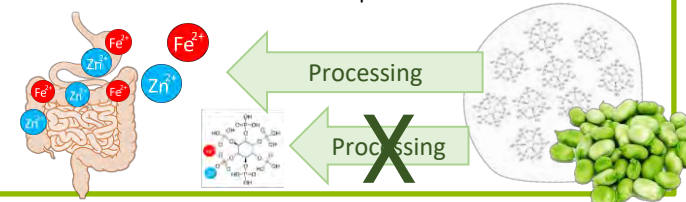
Extrusion, fermentation, gelation, emulsification or enzymatic hydrolysis determine the texture of the final product⁶. In addition, some of these processes show potential to lower the number of antinutrients and can therefore improve the bioavailability^{11,12, 13}.



Figure 3. Extruded Soy

Summary & Conclusions

The characterization of plant-based proteins is essential for a shift towards a more plant-based diet. This includes the functional properties as well as the bioavailability of the raw materials. Most research has focussed on the risk of nutritional deficiencies (vitamins, minerals), especially in children, pregnant women and the elderly^{3, 4}. However, processing methods like fermentation, germination, enzymatic treatments and extrusion have the potential to reduce this ANF and therefore improve their notional value⁸.



References

Scan the QR Code to see all references



Acknowledgement

This work is in collaboration with **PAN Sweden**
Main supervisor: Maud Langton
Co supervisors: Galia Zamaratskaia, Marie Alminger, Anders Högborg



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Multifunctional membrane vesicles produced by *L. reuteri* DSM 17938 and their potential link to relief of infantile colic

Ludwig Lundberg^{*1,2}, Yanhong Pang^{*1}, Manuel Forsberg³, Eva Sverremark Ekström³, Gianfranco Grompone², Helena Bysell² and Stefan Roos^{1,2}

^{*}The authors contributed equally to this work

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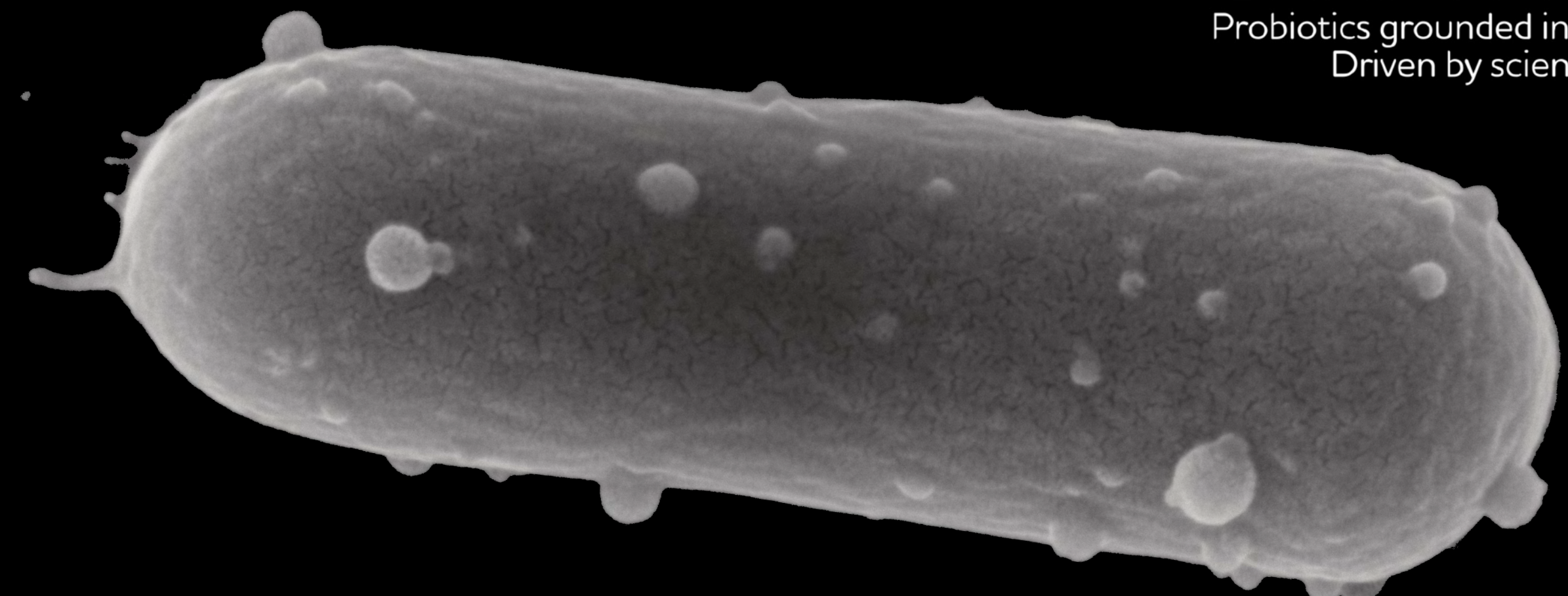
3. Department of Molecular Biosciences, The Wenner-Gren Institute, Stockholm University, Stockholm, Sweden.



BioGaia
Probiotics grounded in evolution
Driven by science

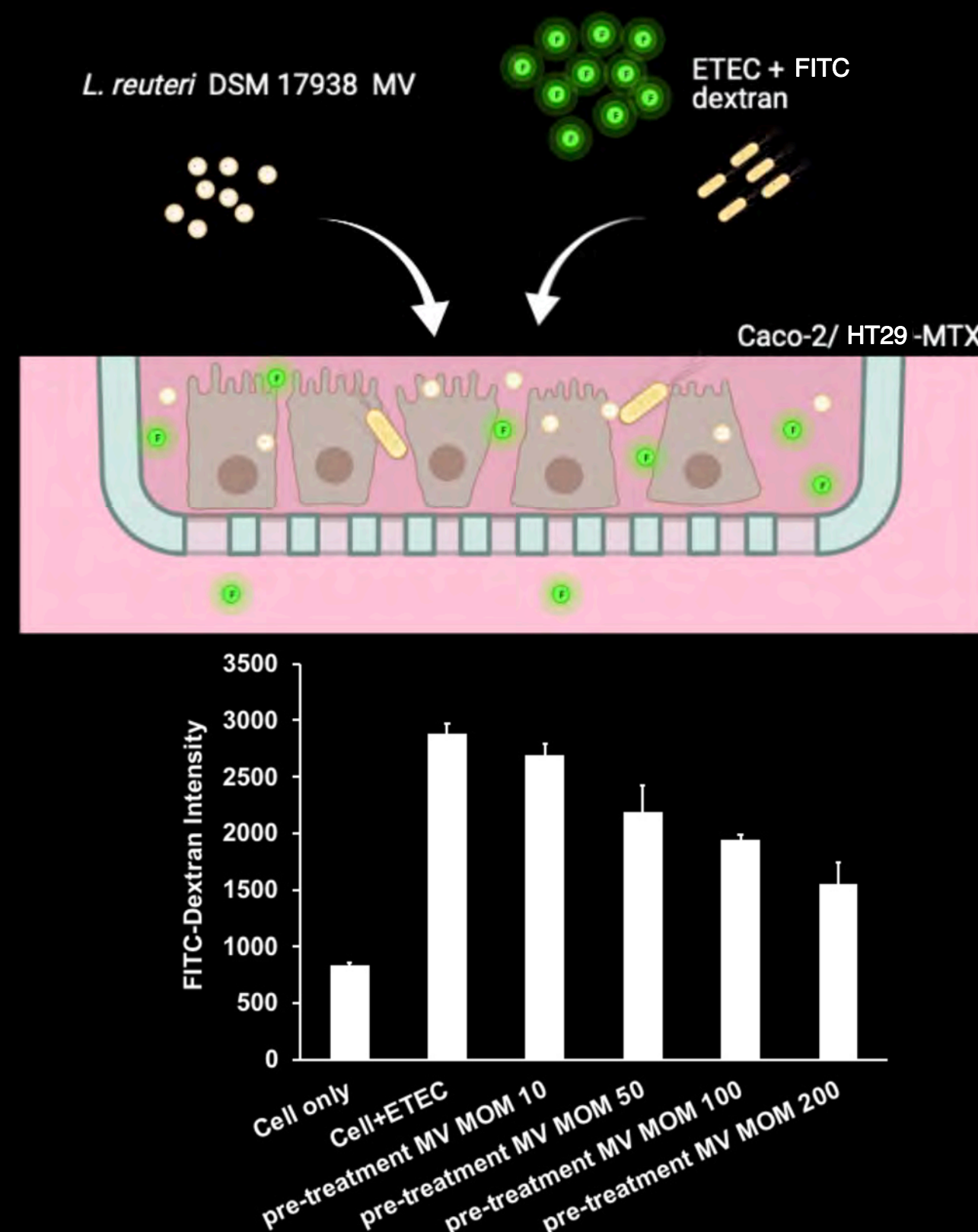
Introduction

Bacterial extracellular membrane vesicles (MV) are potent mediators of microbe-host interactions, and not only important in host-pathogen interactions but also for the interactions between mutualistic bacteria and their hosts. *Limosilactobacillus reuteri* DSM 17938 is a well-studied probiotic bacterium and have among other been proven to ameliorate infantile colic. MV from DSM 17938 have recently been shown to modulate gut motility in an *ex vivo* mouse model (1) and dampen pro-inflammatory cytokine responses in stimulated PBMC (2). Here we wanted to investigate the mode of action of DSM 17938 derived MV.

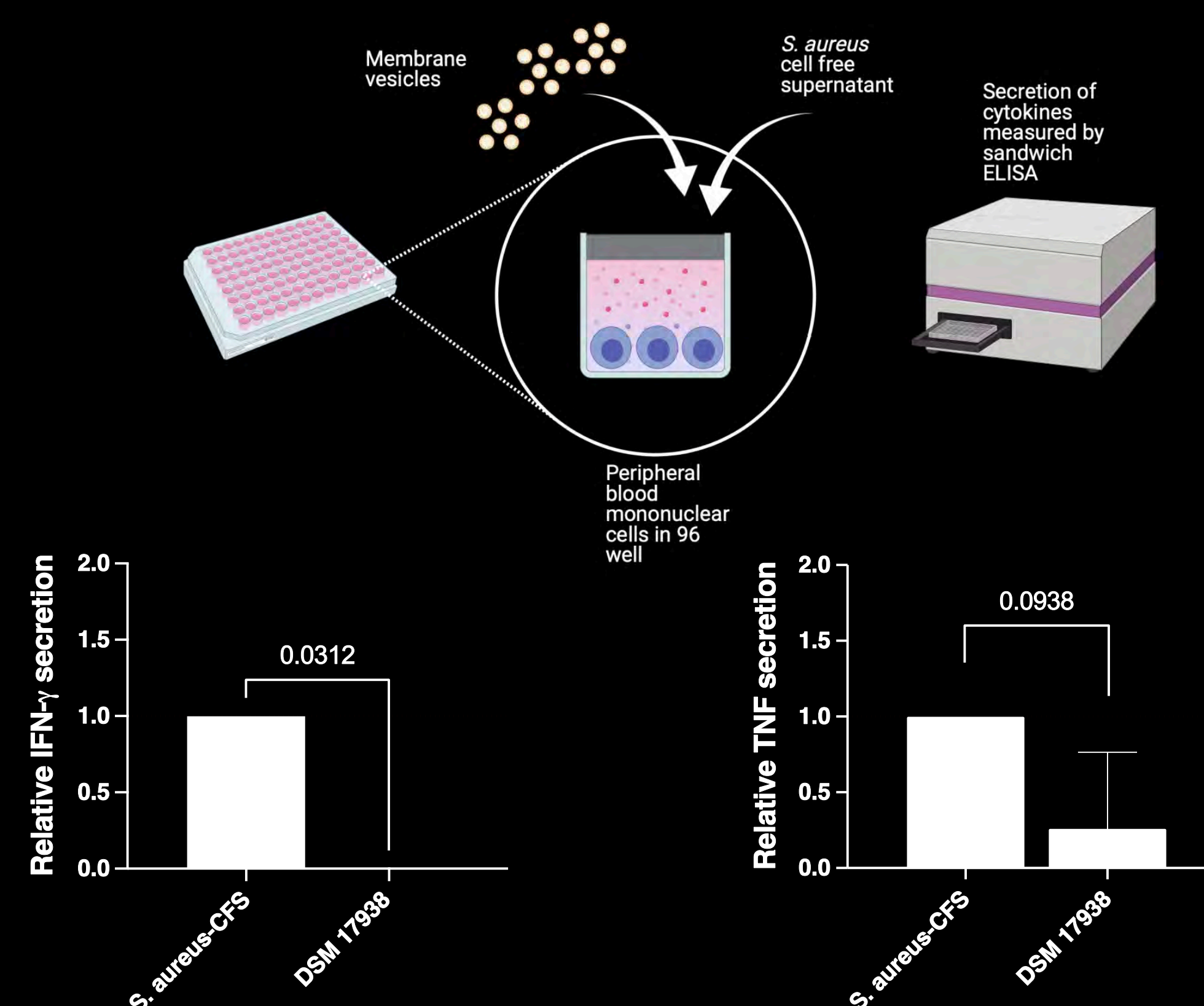


Host interactions

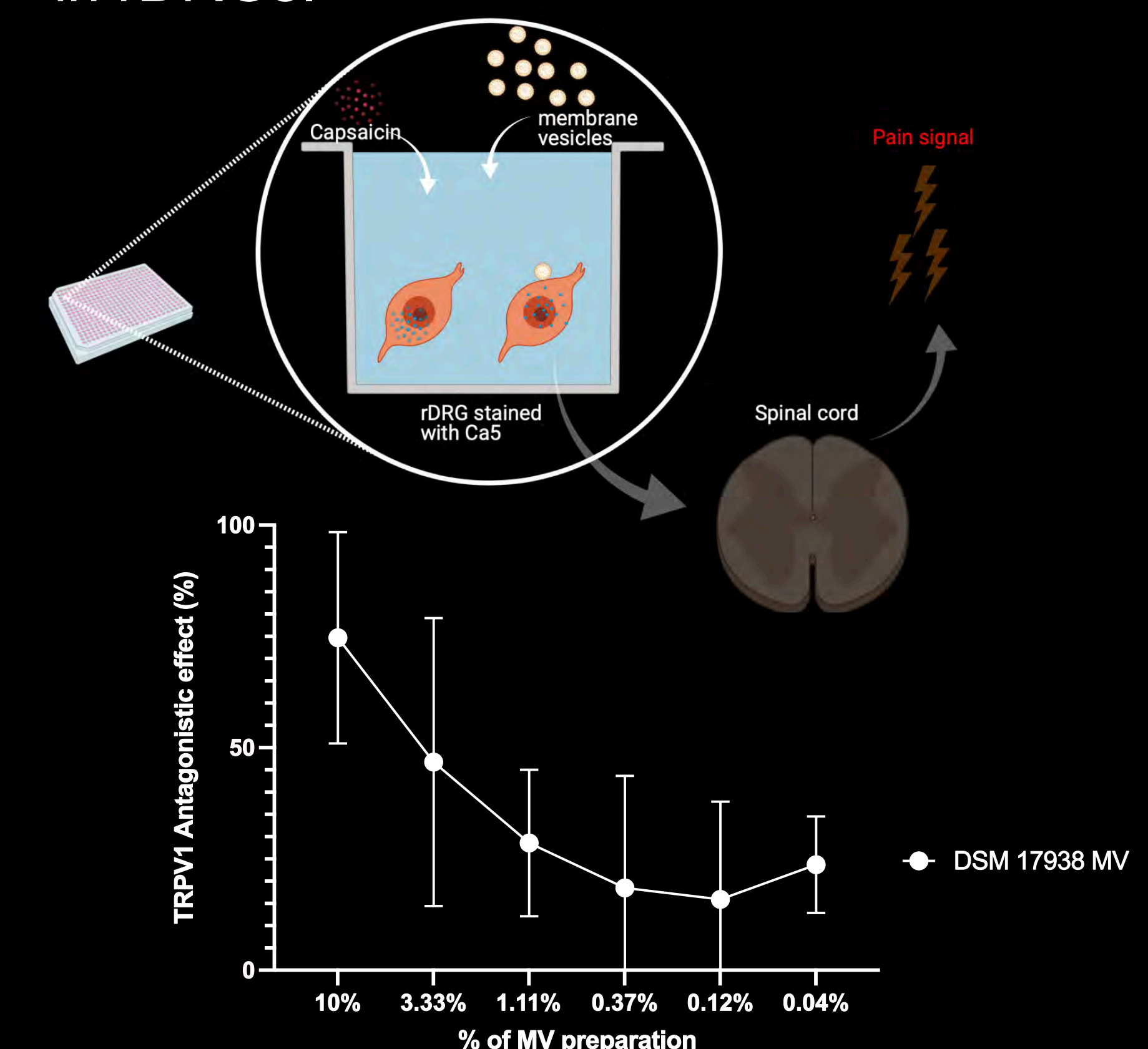
MV dose-dependently reduce leakage induced by ETEC in a Caco-2/HT29-MTX model.



MV dampen IFN- γ and TNF- α secretion induced by *S. aureus* cell free supernatant in a peripheral blood mononuclear cells model.



MV antagonize the pain receptor TRPV1 in a dose-dependent manner in rDRGs.



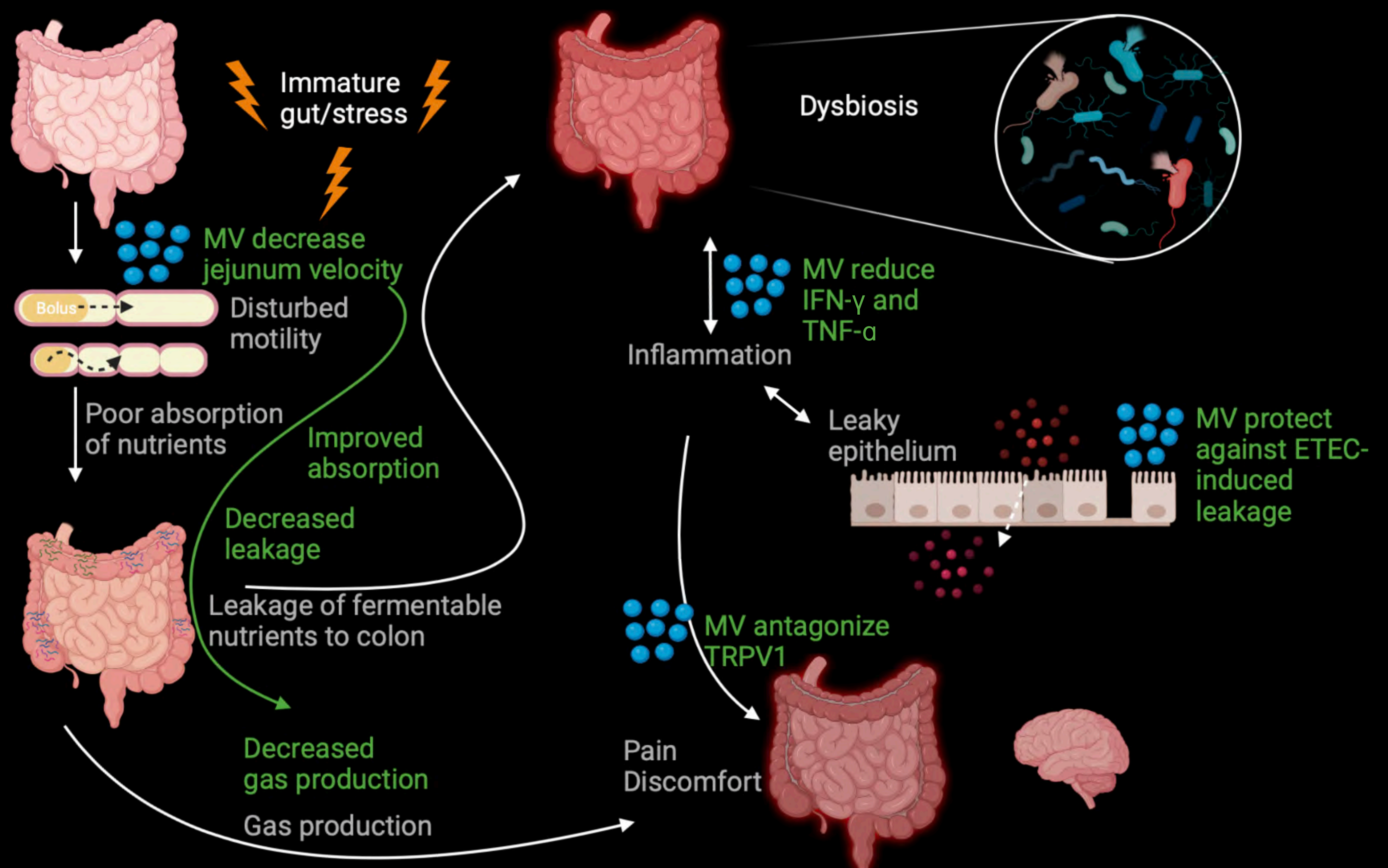
Summary

Here we describe further multifunctionality of *L. reuteri* DSM 17938 derived MV:

- MV Contain DNA, RNA and carry both lipoteichoic acid and a 5'-nucleotidase. This enzyme is an analogue to CD73 present on e.g. Treg cells, and catalyze the production of the potent signal molecule adenosine (data not shown).
- MV display additional effects in host interaction models:
- Dampen capsaicin activation of the pain receptor TRPV1 in a model with primary dorsal root ganglion cells from rat.
- Decrease epithelial cell leakage caused by enterotoxigenic *E. coli* (ETEC) in Caco-2/HT29-MTX monolayers.
- Induce upregulation of IL-1 β and IL-6 in naïve PBMC, and dampened IFN- γ and TNF- α responses in *Staphylococcus aureus* challenged PBMC.



We believe that the demonstrated effects of the MV reproduce the mechanistic actions by which strain DSM 17938 is thought to ameliorate infantile colic, providing key information for development of new, innovative products.



Conclusion

The demonstrated effects of the *L. reuteri* derived MV reproduce the mechanistic actions by which strain DSM 17938 is thought to ameliorate infantile colic. MV from *L. reuteri* are potent, bioactive nanoparticles that demonstrate a novel type of multifunctionality of MV from a mutualistic bacterium.

References

- (1) West, C.L. et al., 2020. *PloS one*, 15(1), p.e0225481.
- (2) Forsberg, M.M. et al., 2019. *Scientific Reports*, 9(1), pp.1–13.

Acknowledgements



Nanoxis Consulting AB

Faecal microbiota composition affects the *in vitro* fermentation of rye, oat and wheat bread

Introduction

- Fermentation of dietary fibre by gut microbes produces short chain fatty acids (SCFA), most importantly acetate, propionate and butyrate.
- Recent *in vitro* studies [1,2] have shown differences in fermentation between microbiota community compositions, with respect to time, SCFA production, and preference to substrate.
- The aim of this study was to investigate how faecal microbiota composition influences the fermentation of oat, rye and wheat breads with differing dietary fibre amount and composition.

Materials and Methods

- Two faecal donors with different microbial community compositions were recruited.
- Whole grain rye bread, whole grain oat bread and refined wheat bread samples were digested chemically and enzymatically and chemical composition of bread and derived fermentation substrate were analysed.
- *In vitro* fermentation model was used to study SCFA and gas production, degradation of dietary fibre, pH, and changes in microbiota composition at 8h and after 24-hour fermentation experiments.

Results

- Higher acetate ($p=0.003$) and butyrate ($p<0.0001$) levels at 24h were seen in donor II with high relative abundance of *Prevotella* and *Subdoligranulum*, whereas propionate levels were higher in donor I ($p=0.02$) with high relative abundance of *Bacteroides* and *Escherichia/Shigella*.
- Total gas production was higher in donor II ($p<0.0001$).
- Gas and SCFA levels followed the substrate fibre amount with rye contributing to highest and wheat to lowest levels.
- Some differences in fibre degradation, for example in water-insoluble arabinoxylan, were observed between the donors and substrates.
- Shifts in microbiota composition were observed during fermentation, and were driven by different substrates.

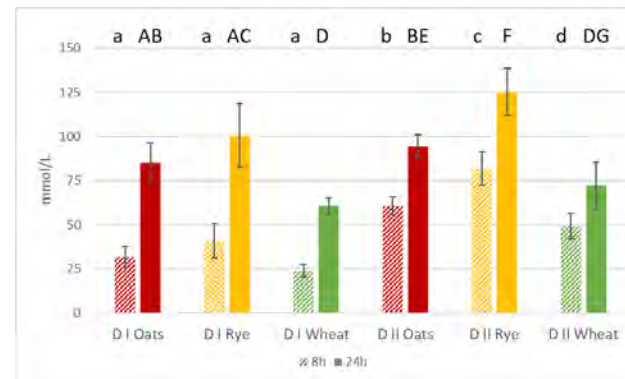


Figure 1. Total short chain fatty acid levels at 8h and 24 h. Different letters indicate significant difference between samples; lowercase 8h, uppercase 24h. D, Donor.

Conclusions

- The results indicate contrasting fermentation capacity and substrate utilisation potential between different microbiota profiles in the human gut.
- Differences in gut microbiota composition could in part explain intra-individual differences in diet-related health outcomes.
- Findings can lead to personalised dietary recommendations on fibre intake, or products containing special fibre composition for different microbiota profiles, but human clinical trials are needed.

References

1. Chen, T., et al., *Fiber-utilizing capacity varies in Prevotella- versus Bacteroides-dominated gut microbiota*. Sci Rep, 2017. 7(1): p. 2594.
2. Wu, Q., et al., *Fermentation properties of isomaltooligosaccharides are affected by human fecal enterotypes*. Anaerobe, 2017. 48: p. 206-214.

Acknowledgements

Roger Andersson & Johan Dicksved, SLU
Study was funded by LivsID industry doctor programme and Fazer.



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Lifetime net GHG emissions and contribution to the food system from dairy cows fed best practice diets

Background

Animal production affects the environment, both negatively and positively. It can e.g. contribute to eutrophication and increased global warming, but at the same time, it can contribute to ecosystem services as well as biodiversity and be an efficient and sustainable way of producing high-quality protein from non-human edible resources

Project aim:

- Investigate lifetime greenhouse gas emissions from high-producing dairy cows and replacement heifers fed diets based on feeds that are associated with low negative environmental impact.
- Estimate net food production and emissions intensity

Materials and Methods

Experiment 1: Lantmännen's experimental dairy farm "Nötcenter Viken". Spring 2022.

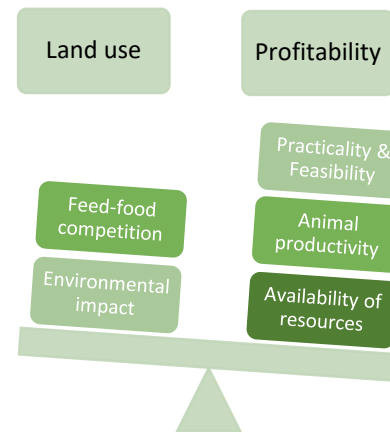
48 dairy cows in peak lactation will be fed best practice diets for 8 weeks.

Measurements:

- Feed intake & digestibility
- Milk yield
- Enteric methane emissions measurements (GreenFeed, C-Lock)
- Estimations of the environmental impact of feed production

"Best practice diets"

Selecting feed ingredients and formulating dairy rations that are in line with the concept of Sustainability is a complex problem that requires trade-offs.



Experimental diets:

1. Control diet
 - A commonly used diet aiming to maximize milk production
2. By-products based diet
 - Limit feed-food competition
 - Prioritize resources with low environmental impact
3. Home-grown diet
 - Locally grown feeds on a regional level

Conclusions

Feed intake, milk production and methane emission will be used to calculate the net food contribution and the emission intensity from the system.

The results from this project will allow for:

- the comparison of different production options
- investigate and quantify the role and contribution of animal production in the food system.

Supervisors

Professor Sigrid Agenäs, SLU
Dr. Mikaela Lindberg, SLU
Associate Professor Ulf Sonesson, RISE
Cecilia Lindahl, Lantmännen

Acknowledgements

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Background/introduction/summary

Faba bean is a promising raw material for the production of protein-rich plant-based foods. This study aimed to investigate faba bean protein gels and the effect of substituting part of the protein for starch and fibre on gel texture and microstructure. Increased knowledge could facilitate the development of novel locally produced plant-based foods based on faba bean.



Materials and Methods

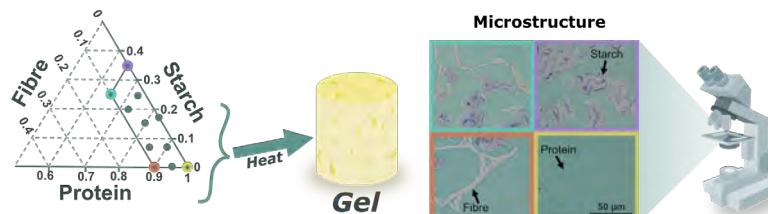
Protein, starch and fibre was extracted from Swedish Faba beans. Gelation was induced by heating to create gels with different composition.

- Oscillatory rheology was used to monitor the gel formation and gel stiffness (G')
- Textural properties was analysed by compression tests giving the gel strength and brittleness
- The microstructure was characterized using light and electron microscopy

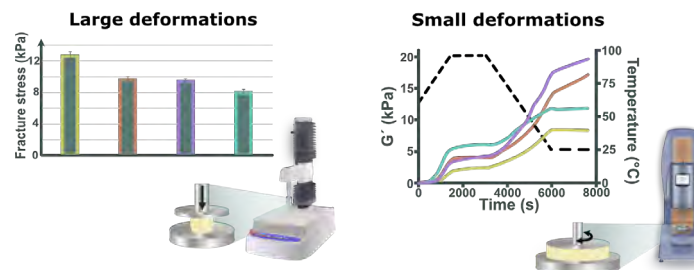


Results

Microstructure: Protein was the continuous phase for all gels. Starch was present as swollen and deformed granules as well as leaked amylose. The amylose was found as small aggregates throughout the protein network and on the granule surfaces. The fibre fraction was visible mainly as cell wall fragments.



Rheology and Texture: Substituting part of the protein for starch and/or fibre decreased the fracture stress and fracture strain, likely related to the creation of inhomogeneities acting as stress concentrators. Simultaneously, an increase in G' of the gels was observed, hypothesised to result from water adsorption by the starch/fibre resulting in a higher effective protein concentration in the surroundings.



Conclusions

Substituting protein for starch and/or fibre:

- Reduced the fracture stress and fracture strain
- Increased the Young's and storage modulus
- Introduced changes in the microstructure which were correlated to textural changes

In a broader perspective, our results indicate that the purity of the faba bean protein fraction can significantly affect the textural properties of gels.

Reference

Johansson et al. *Effect of Starch and Fibre on Faba Bean Protein Gel Characteristics*; SLU, Uppsala, Sweden, 2022.

Acknowledgements

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Supervisors
Maud Langton
Anna Ström
Corine Sandström

Effect of pH-shift processing on *in vitro* digestibility and Caco-2 cell bioavailability of sea lettuce proteins

Background/introduction/summary

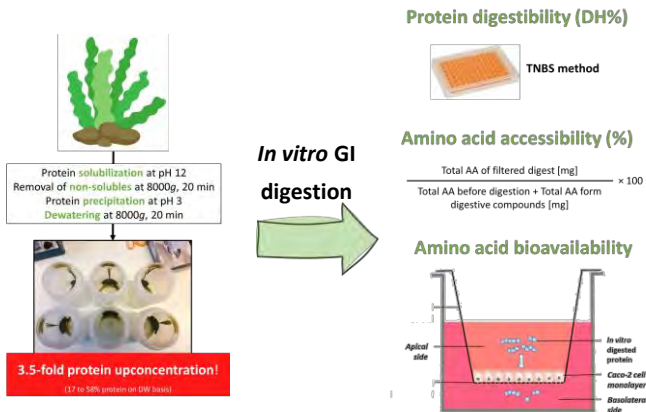
Consumption of **alternative protein sources** is forecasted to grow by an annual rate of 9 % until 2054! [1]

Seaweed is a promising protein source, but natural **protein level still relatively low**, calling for protein concentrating techniques...also, the **nutritional quality** of seaweed proteins can be influenced by the presence of **antinutrients** e.g. fibers and phenols [2-3]



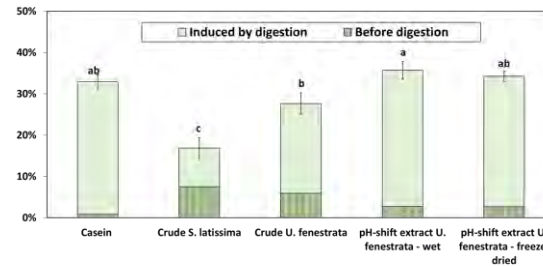
Hypotheses: Structural disintegration and partial removal of antinutritional factors during the pH-shift processing will increase the digestibility, accessibility, and bioavailability of seaweed proteins

Materials and Methods



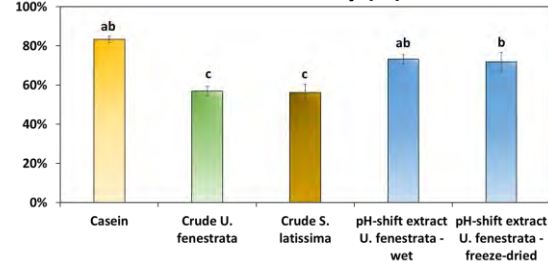
Results

Digestibility (DH%)



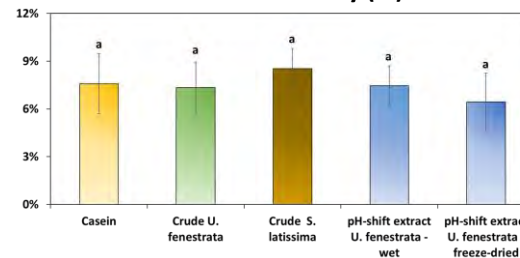
pH-shift processing improved the digestibility of *U. fenestrata* proteins ($p < 0.05$)

Accessibility (%)



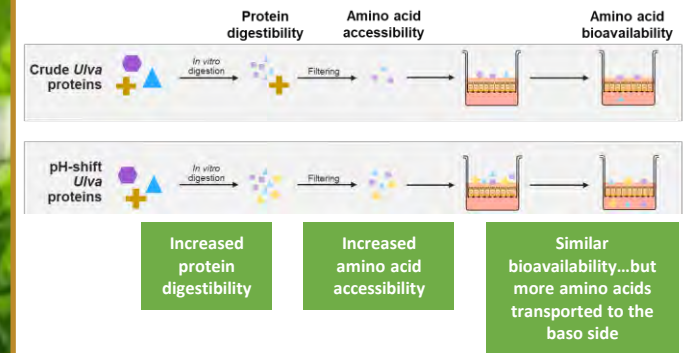
pH-shift protein extracts presented higher amino acid accessibility than crude *U. fenestrata* ($p < 0.05$)

Bioavailability (%)



The accessible fraction of crude seaweeds and pH-shift extracts was as bioavailable as casein

Conclusions



Reference

- [1] Probst, L., Frideres, L., Pedersen, B., & Amato, F. (2015)
- [2] S. M. Tibbetts, J. E. Milley, and S. P. Lall (2016)
- [3] J. Fleurence, M. Morançais, and J. Dumay (2017)

Acknowledgements



SWEAWEED project funded by the Swedish Foundation for Strategic Research, Project number: RBP14-0045

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Novel Arabinoxylanase for Processing of Oat Carbohydrates into Prebiotics

S. Norlander¹, A. Jasilionis¹, Z. Gulshan Kazi¹, C. Grey¹, P. Adlercreutz¹, E. Nordberg Karlsson¹. ¹Division of Biotechnology, Lund University, Sweden

Introduction

- Dietary fiber consumption needs to be increased globally to prevent diet related diseases
- Fibers with prebiotic potential can be solubilized from the hemicellulose arabinoxylan (AX) in cereal side-streams using different carbohydrate active enzymes ^[1]
- Food industry needs specific arabinoxylanases, with limited side activity, for production of tailored fibers
- We have identified, produced and characterized a novel GH5_34 arabinoxylanase, *HhXyn*, for intended use in oat processing to increase soluble prebiotic fiber content
- Commercially available homologue *CtXyn5A* (nzytech) was used for comparison^[2]

Materials and Methods

- Standard *E. coli* expression system
- Affinity chromatography purification using ÄKTA
- DNS reducing end assay to evaluate enzymatic activity
- MODDE software to design experiment and create model
- HPAEC-PAD for identification of enzymatic products

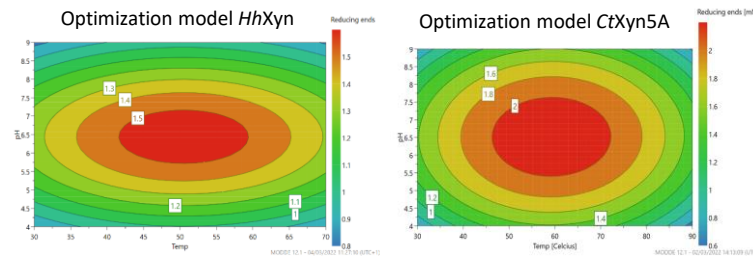
Substrates used

- Commercial AX from various biomass
- Industrial oat bran fraction
- In-house alkali extracted oat AX fiber products

Results

- Substrate preference determined using DNS assay show *HhXyn* activity on commercial rye and wheat AX as well as on extracted oat bran fibers, without showing cleavage of β -glucan
- Optimal temperature and pH conditions for a 10 min reaction on wheat AX was determined to 50 °C and pH 6.5 for *HhXyn*. The enzyme reaction rate was stable at these conditions for at least 36 h
- Maximal reactions rates obtained using optimized reaction conditions were determined to 0.21 mM/min for *HhXyn* (50 °C) and 0.32 mM/min for *CtXyn5A* (60 °C) at 20 mg/L enzyme concentration

Substrate	<i>HhXyn</i>	<i>CtXyn5A</i>
Rye AX	✓✓	✓✓
Wheat AX	✓✓	✓✓
Beechwood xylan	✗	✗
Oat β -glucan	✗	✗
Insoluble oat bran fibers	✗	✗
Soluble oat bran fibers	✓	✓
Desalted soluble oat bran fibers	✓✓	✓✓

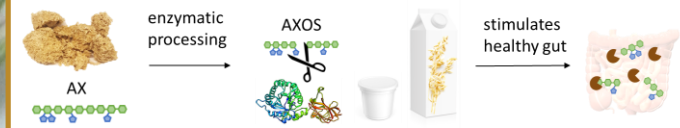


Conclusions

- Our findings show the great potential of using *HhXyn* for fiber solubilization and modification in oat grain processing, without compromising the beneficial β -glucan content in novel oat products

Future studies and experiments

- Product profile analysis using HPAEC-PAD-MS
- Docking simulations
- Domain organization influence on activity and stability
- Optimization for prebiotic and high-fiber oat products



References

- [1] <https://doi.org/10.1016/j.biortech.2021.126114>
[2] <https://doi.org/10.1107/S1744309111020823>

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Differences between Arterial and Venous Umbilical Cord Plasma Metabolome and Association with Parity

Background/introduction/summary

Analysis of umbilical cord blood is important for assessing neonatal health. Sampling is normally performed by squeezing out blood after severing the cord, which leads to mixing of arterial and venous blood. Furthermore, additional variance may also be induced by traits not related to the present study question. In order to reduce variance in studies of umbilical cord blood we aimed to:

- Identify key differences between arterial and venous cord blood to determine the potential impact of sampling on the observed metabolic profile.
- Find associations between the maternal and infant traits gestational length, parity, birth weight, sex, maternal age and maternal BMI and the venous and arterial umbilical cord metabolomes.

Materials and Methods

48 paired venous and arterial cord plasma from the NICE-cohort [1] were analysed using a combination of targeted and untargeted GC-QqQ-MS. Multilevel random forest analysis with unbiased variable selection and repeated double cross-validation [2] was used as a discriminant analysis for differentiating venous and arterial umbilical cord. Random forest regression analyses were performed for the continuous variables; gestational length, birth weight, maternal age and maternal BMI while random forest classification was used for the dichotomous outcome variables sex and parity. Variables selected by the algorithms were further processed using the Mann-Whitney U-test

Results

A classification rate of 79% was achieved for arteriovenous differences ($p = 0.004$). Several monosaccharides had higher concentrations in the arterial cord plasma while amino acids were higher in venous plasma, suggesting that the main differences in the measured arterial and venous plasma metabolomes are related to amino acid and energy metabolism.

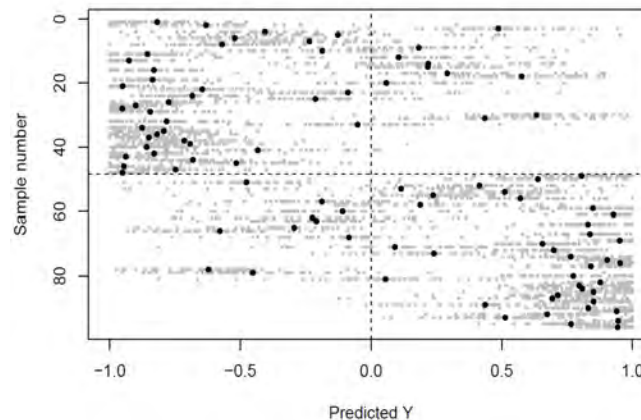


Fig. 1. Prediction results from multilevel RF analysis of metabolome differences of venous and arterial umbilical cord plasma. Black dots in top right and top left corners indicating correctly classified samples.

Venous cord plasma metabolites related to energy metabolism were positively associated with parity (77% classification rate, $p = 0.004$) while arterial cord plasma metabolites were not. Differences mainly driven by organic acids involved in energy metabolism.

No further associations between infant and maternal traits and the metabolomes were found

Conclusions

This study underlines the importance of selecting the appropriate sample matrix depending on study question. Moreover, the use of mixed, arterial, or venous cord blood could contribute to difficulties when trying to compare studies, especially given the potential for differing proportions of arterial and venous blood in mixed cord blood samples. We further found that parity associated with metabolites in the venous umbilical cord plasma related to energy metabolism, meaning that whether the mother has undergone previous deliveries affects the umbilical cord plasma metabolome. This may be an important factor to account for when matching case-control pairs and for outcomes that may be related to energy metabolism

Reference

- [1] Barman M, et al. "Nutritional impact on Immunological maturation during Childhood in relation to the Environment (NICE): a prospective birth cohort in northern Sweden." *BMJ open* 8.10 (2018): e022013.
[2] Shi L, et al. "Variable selection and validation in multivariate modelling." *Bioinformatics* 35.6 (2018): 972-980.

Acknowledgements

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Consumer perception and political consumerism about food containing plant-based proteins

Background/introduction/summary

It has been suggested that meat consumption should be reduced for the sake of both environmental and human health. Plant-based meat substitutes could be a good option to meet the claim. However, boosting the use of plant-based meat substitutes will be successful when the products are attractive enough to consumers. To understand the various drivers and barriers to reducing meat consumption and adopting plant-based meat substitutes, researchers have investigated consumer attitudes, acceptability, and sensory properties of plant-based meat substitutes. The aim of the PhD project is to identify determinants and drivers of sustainable and healthy food consumption, in particular, of food containing plant-based protein from an individual and group perspective.

Materials and Methods

Study1. Sensory perception on products that contain plant-based protein.

Study 2. How sensory perception interacts with psychological, social, and biological determinants in relation to plant-based food.

Study 3. How emotion and stress affect food perception.

Study 4. Elucidating the role of social reinforcement in sustainable food

Results

Study1.

The range of products was selected from commercially available products. The sensory perception of plant-based food products was examined among consumers with different degrees of meat attachment using Rate-All-That-Apply (RATA) and the hedonic scale.

- The preference on plant-based food products in terms of sensory perception
- Identifying the sensory attributes of the ideal product.

Study2.

The previous study (1) extends to the meal perspective to examine sensory perceptions in relation to previous experiences, beliefs, current diets, and drivers for sustainable food choice. The questionnaire will be including questions for CATA, liking, JAR, previous experience, beliefs, current diets, and drivers for sustainability.

Study3.

How and whether certain emotions affect food perception by studying brain areas, involved in emotional activities. The study will focus on the results from the fMRI together with earlier research on emotions and sensory perceptions.

Study4.

How the effects of social reinforcement versus information on food selection in social networks. Participants are randomized into one of two networks, one exposed to information about the environmental effects of meat consumption and the other is exposed to social reinforcement.

Conclusions

I am broadly interested in the role of food in modern society, with particular emphasis on the individual and social factors affecting food choices and, consequently, contributing ways to improve public health and sustainable lifestyle.

Reference

Main supervisor: Åsa Öström (Örebro University)
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Lower iron absorption from texturized fava bean protein meals compared to meat and cod protein meals



Test meals containing texturized fava bean protein, beef protein and cod protein

WHAT DID WE DO?

- Two single meal studies using double radioisotopes of iron (^{55}Fe and ^{59}Fe)
- Subjects: 30 women of fertile ages
- Test meals were served two times each in the order BBAA
- Each subject served as her own control
- Iron absorption was measured by whole body counting and liquid scintillator (erythrocyte incorporation)

Study was performed in collaboration with Sahlgrenska Academy

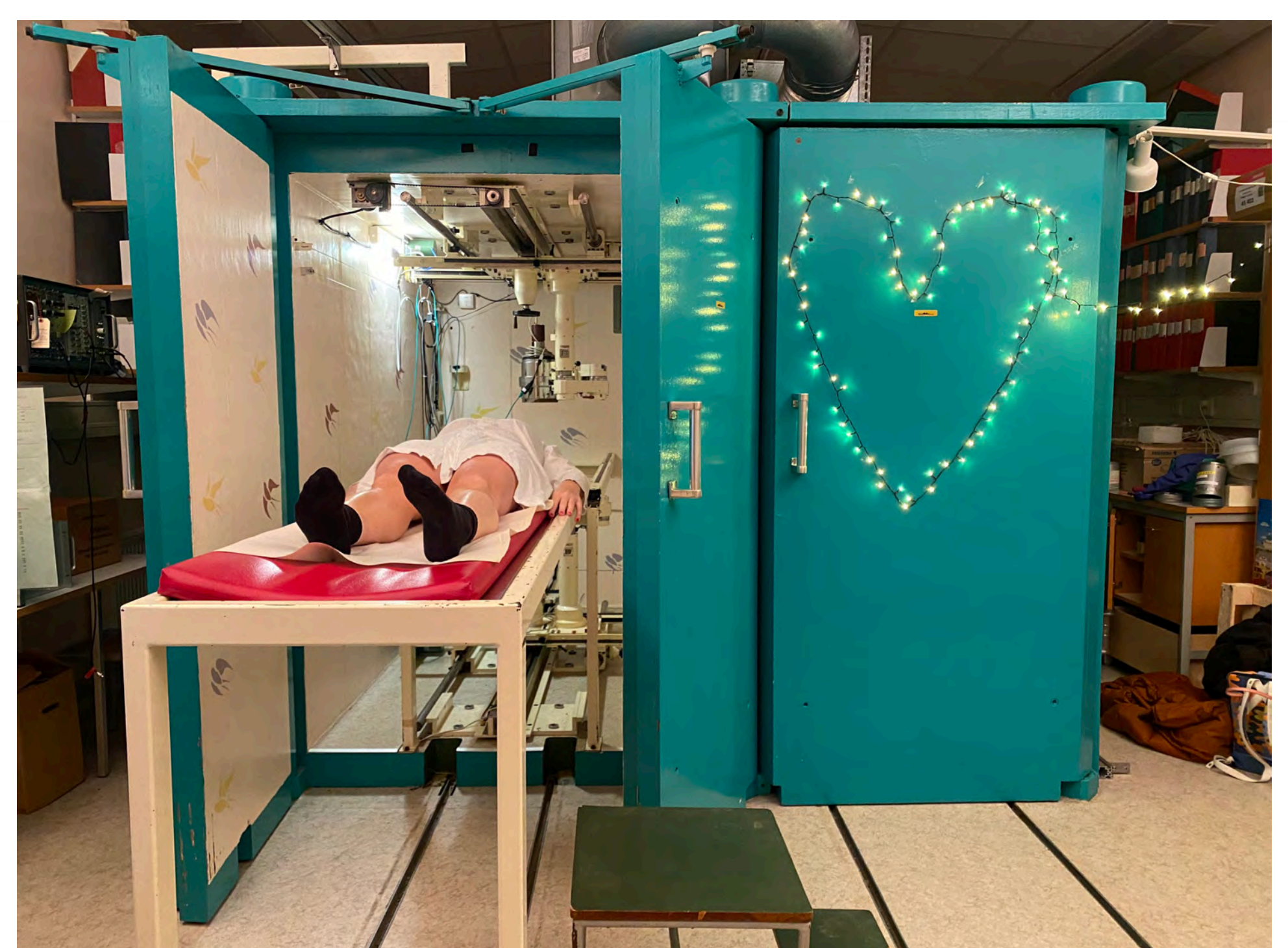
WHAT DID WE FIND?

Preliminary data:

- Iron absorption was **4 times higher** from meals with beef protein compared to fava bean protein
- Iron absorption was **3 times higher** from meals with cod protein compared to fava bean protein

WHY IS THIS RELEVANT?

The prevalence of iron deficiency among fertile women in western civilizations is around 25%. Plant based diets have a low bioavailability of iron and adds on to the vulnerability of developing iron deficiency. Iron deficiency negatively affects mental and physical stamina, and can cause lasting cognitive impairment in children. Including nutrition and bioavailability into the protein shift is essential in order to avoid negative health effects and nutritional deficiencies.



Whole body counter

Faba Bean Fractions for 3D Printing of Protein-, Starch- and Fibre-Rich Foods

Mathias Johansson, Klara Nilsson, Fanny Knab & Maud Langton



Background/introduction/summary

3D printing is a technique that can be used to create personalised foods.

By combining different ingredients novel textures, such as plant-based steaks with textural properties resembling those of meat can be created.

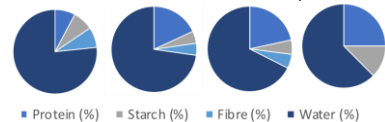
By creating new shapes and textures, 3D printing can make different foods more appealing.

In this study, the following two current trends—3D printing and plant-based foods—are combined. The objective was to produce 100% faba bean-based 3D-printed food prototypes and investigate how ink composition and object structure influence printability and texture.

Materials and Methods

FB fraction extracted and combined to make inks:

Fibre rich, Starch rich, Protein rich, Protein & starch rich



Influence of: ink composition, direction of compression & infill pattern

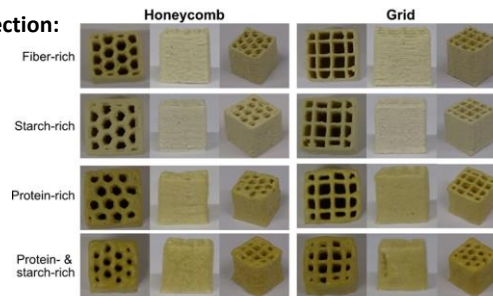


Results

Ink rheology : All inks showed elasticity-dominating behaviour. The starch rich inks had the highest storage modulus along with yield stress indicating that this ink was the most "solid" like.

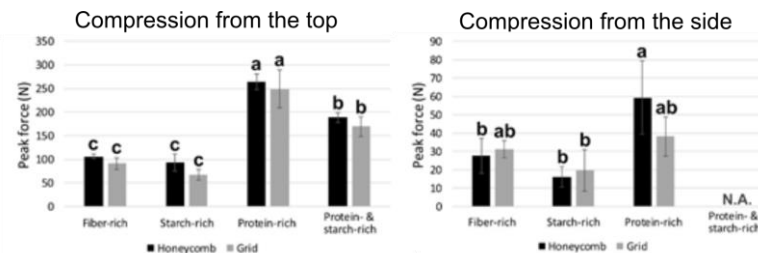
Printability & visual inspection:

The protein & starch-rich cubes were the most troublesome to print. Fibre- and starch rich cubes created more stable cubes with straighter walls and more defined infill patterns



Compression testing : when cubes were compressed from the top ~5-10 times larger force was required compared to when cubes were compressed from the side. In general the protein rich samples required more force to be compressed and would therefore be perceived as harder. No significant difference between infill patterns.

The higher force required for compression was negatively correlated with particle size ($r = -0.623$; $p = 0.002$) and positively correlated with the number of particles ($r = 0.716$; $p < 0.001$) produced during compression.



Conclusions

- Protein, starch and fibre rich fractions extracted from faba beans can be successfully combined to create nutritious printable inks for extrusion based 3D printing.
- Inks with a lower loss tangent showed a higher shape stability.
- The ink composition had a clear effect on textural properties of freeze dried 3D printed objects while the infill pattern did not.
- An increased heterogeneity of the microstructure seemed related to the decreased peak force during compression.

Reference

<https://doi.org/10.3390/pr10030466>



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