

HEALTH FOR ALL

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ABSTRACT BOOK

June 4th, 2026

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HEALTH FOR ALL

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Oral presentations: --- Basic science

3D Printing for personalized medicine: comparing content uniformity and dissolution of 3D printed tablets and 3D filled capsules

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Introduction

The increasing popularity of 3D printing in pharmaceuticals enables new approaches for manufacturing in both industrial and community pharmacy fields, supporting precise dosing, customization for extemporaneous preparation, and personalized medicine [1-3]. This study compares the pharmaceutical characteristics of 3D printed tablets (printlets) and 3D filled capsules.

Aim

To investigate content uniformity and *in vitro* dissolution profiles of 3D printed tablets and 3D filled capsules.

Methods

Solid pharmaceuticals were made using FABRX M3DIMAKER 1 printer via semi-solid extrusion (SSE). Printlets were produced at 40 °C (3 mm/s, extrusion width 2 mm, flow rate 5 mm/s) using the gelatin-pectin formulation, while capsule filling was manufactured at 60 °C (127.5 mm/s, vol. flow 0.26 ml/s) using Techa 20 as the excipient. The three APIs that were selected for this study were apigenin, luteolin and cannabidiol. Content uniformity and *in vitro* dissolution testing were performed and the analysis was done with HPLC.

Results

Content uniformity for printlets was 101.0 ± 4.5 % for apigenin, 87.0 ± 4.3 % – luteolin, and 93.0 ± 4.6 % – CBD, whereas 3D-filled capsules achieved 102.0 ± 4.9 %, 98.0 ± 4.5 %, and 96.0 ± 4.8 %, respectively. Dissolution testing showed higher release from printlets (apigenin 85.0 ± 2.5 %, luteolin 85.0 ± 4.2 %, CBD 80.0 ± 3.5 %) compared with 3D-filled capsules (apigenin 75.0 ± 2.6 %, luteolin 70.0 ± 2.9 %, CBD 72.0 ± 3.2 %). These differences are most likely influenced by excipient selection and API interactions affecting solubility, additional excipients may be required to improve the release from capsules.

Conclusions

3D-filled capsules demonstrated superior content uniformity, while printlets provided more pronounced API release. 3D printing shows potential for precise, personalized dosing, however, further formulation development is needed in future research.

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Customizing Idebenone Therapy Using Novel Oral Mucoadhesive Film Technology

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Introduction

Idebenone, a lipophilic antioxidant, shows significant potential in treating mitochondrial and neurodegenerative diseases. However, its therapeutic efficacy is currently hindered by inadequate aqueous solubility and low systemic bioavailability [1]. Buccal drug delivery systems offer a promising route to bypass hepatic first-pass metabolism and significantly improve systemic absorption [2].

Aim

This study aimed to formulate and evaluate Idebenone-loaded mucoadhesive oral films, comparing traditional solvent casting with novel 3D printing technique, to enable personalized antioxidant delivery.

Methods

Films formulated with a polymer matrix of hydroxypropyl methylcellulose, polyvinyl alcohol, gelatin, and PEG-400 were fabricated via solvent casting and semi-solid extrusion (SSE) 3D printing technique. The resulting films were systematically evaluated for their geometrical and morphological properties, mechanical responses, in vitro drug release profiles, and physicochemical characteristics, including Differential Scanning Calorimetry (DSC).

Results

Both fabrication methods produced comparable baseline films. Higher gelatin and PEG-400 concentrations optimized mucoadhesion and mechanical flexibility, achieving a tensile strain of up to 0.68%. Notably, DSC analysis revealed a reduction of over 25% in Idebenone crystallinity within the 3D-printed matrices. This reduced crystallinity directly supported the superior, highly tailored in vitro drug release profile observed in the 3D-printed mesh films

compared to traditional cast equivalents.

Conclusions

The integration of polymeric matrices with 3D semi-solid extrusion presents a highly adaptable platform for Idebenone buccal delivery. This novel technological approach enables precise morphological control for dose and release customization, representing a significant advancement in personalized antioxidant therapies for patients with neurological diseases.

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HUMAN CARDIAC ADIPOSE TISSUE MITOCHONDRIAL RESPIRATION ANALYSIS IN PATIENTS WITH ISCHAEMIC HEART DISEASE

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Introduction

Recent studies suggest that in addition to intravascular atherosclerotic plaque, ischaemic heart disease (IHD) might be characterised by surrounding PVAT pathology. The metabolic profile of other cardiac adipose tissue (AT) sites such as periaortic AT is different and might not be affected in IHD. Mitochondrial function parameters of cardiac AT and their relation to atherosclerotic markers give insight on the processes that occur in advanced atherosclerotic disease.

Aim

This study aims to assess PVAT and periaortic AT mitochondrial respiration parameters and lipoprotein a (lp a) level differences among study groups - patients undergoing heart surgery for advanced IHD or non-IHD.

Methods

This project has received funding from the Research Council of Lithuania (LMTLT), agreement No S-MIP-25-70. Human AT samples were collected at the proximal portion of the CA or the culprit lesion and proximal periaortic site just before the onset of cardiopulmonary bypass, thawed in ice-cold buffer BIOPS solution. AT homogenate oxygen consumption rate (OCR) analysis was performed by Oroboros high-resolution respirometry device: leak respiration measured with complex I substrates pyruvate and malate, oxidative phosphorylation with adenosine diphosphate (ADP), following with complex II substrate succinate addition, completing with uncoupling agent dinitrophenol. Lp a concentration was measured in peripheral blood.

Results

The whole study population exhibited higher oxidative phosphorylation rates with succinate (MDN=384,7, IQR=235,5 fmol/s/mg vs. MDN=322,9, IQR=200,4 fmol/s/mg, Z=1029,0, p=0,014) and dinitrophenol (MDN=405,7, IQR=217 fmol/s/mg vs. MDN=327,8, IQR=223,5 fmol/s/mg, Z=1012,0, p=0,02) in periaortic AT compared to PVAT.

The inter-depot difference between periaortic and pericoronary adipose tissue in complex I-linked LEAK respiration was significantly greater in male ACS and CCS patients compared to male non-IHD patients (Kruskall-Wallis H=9,694, df=2, adj. p=0,008; ACS vs. non-IHD: MDN=12,6, IQR=145 vs. MDN=-34,4, IQR=96,3 fmol/s/mg, Z=2,865, adj. p=0,012; and CCS vs. non-IHD: MDN=-6,2, IQR=59,2 vs. MDN=-34,4, IQR=96,3 fmol/s/mg, Z=2,65, adj. p=0,024, Kruskal-Wallis with Bonferroni correction).

Patients with elevated lp a values had higher periaortic AT OCRs during oxidative phosphorylation with ADP (MDN=253,5, IQR=174,1 vs. MDN=201,8, IQR=125,8 fmol/s/mg, U=480, Z=2,25, p=0,024), succinate (MDN=447,7, IQR=304,3 vs. MDN=364,8, IQR=182,1 fmol/s/mg, U=487, Z=2,38, p=0,017) and dinitrophenol (MDN=462,4, IQR=272,9 vs. MDN=366,3, IQR=159,2 fmol/s/mg, U=507, Z=2,73, p=0,006) compared to patients with normal lp a values.

Conclusions

OCR was higher in periaortic AT compared to PVAT in different respiratory states. The differences might be characteristic to male population and more pronounced in IHD as well as in elevated lp a level setting.

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Factors Associated with Long-Term Post-COVID Cardiovascular Hospitalization in Patients with Pre-Existing Cardiovascular Disease

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Introduction

Despite increasing recognition of post-COVID cardiovascular complications, predictors of long-term cardiovascular hospitalization in patients with pre-existing cardiovascular disease remain unclear.

Aim

We aimed to identify baseline cardiovascular conditions and acute-phase biomarkers associated with long-term post-COVID cardiovascular hospitalization.

Methods

We conducted a retrospective study including 84 adults with confirmed COVID-19 and pre-existing cardiovascular disease. Long-term post-COVID cardiovascular hospitalization was defined as hospitalization for cardiovascular causes occurring within 12 months after the acute phase of COVID-19. Patients were stratified according to the presence or absence of long-term hospitalization. Clinical characteristics and acute-phase laboratory parameters were compared using Mann-Whitney U and chi-square tests.

Results

Most common pre-existing cardiovascular disease was arterial hypertension (77 %), followed by heart failure (41 %), ischemic heart disease (38 %), and rhythm or conduction disorders (35 %). Among hospitalized patients and non-hospitalized patients age did not differ significantly between hospitalized and non-hospitalized patients (median 74.3 [66.5–84.5] vs 73.8 [IQR 67–86]; $p = 0.87$). Pre-existing rhythm or conduction disorders were more common among patients who required long-term hospitalization compared with non-hospitalized patients (64% [16/25] vs 37.5% [12/32]; $\chi^2 = 3.94$, $p = 0.047$).

Acute-phase COVID-19 complications did not differ significantly between patients requiring long-term hospitalization and non-hospitalized patients ($p = 0.26$). Among acute-phase

laboratory parameters, NT-proBNP levels were significantly higher in patients requiring long-term hospitalization compared with non-hospitalized patients (median 2881 [IQR 1783.5–9418.0] vs 1686 [IQR 154–4139] pmol/L; $p = 0.04$). ST2 levels tended to be higher in patients requiring long-term hospitalization compared with non-hospitalized patients (median 39 [IQR 27–89.3] vs 26.3 [IQR 17.4–34.5] $\mu\text{g/L}$); however, the difference did not reach statistical significance ($p = 0.059$). LDH levels were significantly higher in patients requiring long-term hospitalization compared with non-hospitalized patients (median 280.5 [IQR 199.5–381.5] vs 199 [IQR 179–269] U/L; $p = 0.041$). Baseline laboratory parameters, including creatinine, C-reactive protein at disease onset, ferritin, peak D-dimer levels, complete blood count indices, electrolytes, and coagulation markers, did not differ significantly between patients requiring long-term hospitalization and non-hospitalized patients (all $p > 0.05$).

Conclusions

Among patients with pre-existing cardiovascular disease, pre-existing rhythm or conduction disorders, as well as elevated acute-phase NT-proBNP and LDH levels, are associated with long-term post-COVID cardiovascular hospitalization

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Drug metabolism data as secondary findings from genome sequencing for patients with cardiomyopathies

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Introduction

The genomics era enables more robust and sophisticated hereditary disorders diagnostics. High throughput genetic testing generates much more data than clinical situation needs, but this additional information may support patient management by identifying alternative diagnoses, disease risks, and pharmacogenomic variants affecting drug metabolism.

Aim

To evaluate genome wide next generation sequencing (NGS) data usefulness for guiding cardiovascular drug therapy in patients with hypertrophic (HCM) and dilated cardiomyopathies (DCM).

Methods

Patients with HCM and DCM consulted in LSMU Kauno Klinikos (2019–2025) with negative cardiogenetic panel NGS results were selected for genome wide testing. Single nucleotide variants in genes (*VKORC1*, *CYP2C19*, *CYP2C9*, *SLCO1B1*) relevant to cardiovascular drug metabolism were assessed with PharmCAT tool [1]. Clinical recommendations were based on CPIC guidelines [2].

Results

Genome sequencing was performed in 140 patients (91 HCM, 49 DCM; 71.4% male; mean age 54.5 ± 9.6 years). Clinically actionable pharmacogenomic variants for cardiovascular drugs were identified in 111 (79.3%) cases. Detailed analysis showed: 37 patients with intermediate/poor *CYP2C9* metabolism and 74 with increased *VKORC1* sensitivity (suggesting lower warfarin dose at the treatment initiation); 26 of these had atrial

fibrillation who could be treated with such medication. *SLCO1B1* variants, associated with increased atorvastatin, rosuvastatin toxicity risk, were found in 54 patients. Five HCM patients had non-functional *CYP2C19*, indicating reduced clopidogrel activation and increased exposure to mavacamten which is used for obstructive HCM treatment.

Conclusions

Pharmacogenomic data derived from genome-wide NGS may significantly improve drug safety and efficacy in cardiomyopathy patients by enabling personalized therapy and reducing adverse drug reactions.

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Dynamic Cytokine and Coagulation Profiling in Severe COVID-19 Patients Evaluated for Pulmonary Embolism: A Prospective Cohort Study

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Introduction

Coronavirus disease 2019 (COVID-19) is associated with immune dysregulation and an increased risk of thromboembolic complications, including pulmonary embolism (PE) [1-3]. Identification of dynamic immunological predictors of adverse outcomes remains clinically relevant.

Aim

To evaluate associations between coagulation, inflammatory, immunological markers, and in-hospital mortality in patients with severe COVID-19.

Methods

In this prospective observational study, 47 hospitalized adults with severe COVID-19 and suspected PE were enrolled. Serum cytokines, coagulation parameters, and cardiac injury biomarkers were assessed at enrollment and on hospital day 5. PE was confirmed using computed tomography pulmonary angiography. Univariable and multivariable binary logistic regression was used to identify predictors of in-hospital all-cause mortality. Model discrimination was evaluated using the area under the curve (AUC), with internal validation by bootstrap resampling.

Results

PE was diagnosed in 19 patients (40.4%), and 13 patients (27.7%) died during hospitalization. Higher standardized day-5 interleukin (IL)-9 and IL-15 were associated with mortality in univariable analyses, but neither remained significant after Benjamini-Hochberg false discovery rate correction across the 15 day-5 cytokines (IL-9 $q=0.180$; IL-15 $q=0.210$). In an age-adjusted model, day-5 IL-9 remained associated with mortality (adjusted OR per 1

standard deviation increase 3.331, 95% confidence interval [CI] 1.289–8.608, $P=0.013$). Apparent discrimination was moderate (AUC 0.774, 95% CI 0.563–0.984, $P=0.011$), but bootstrap validation showed marked coefficient instability.

Conclusions

Day-5 IL-9 may reflect evolving risk in severe COVID-19, but the association was sensitive to multiple-testing correction and model instability; findings are exploratory and require confirmation in larger, externally validated cohorts.

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Precision Monitoring of Subclinical Hypocalcemia in Dairy Cows Using Blood Biomarkers, In-Line Milk Analysis, and Rumination Data

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Introduction

Subclinical hypocalcemia (SCH) is one of the most common metabolic disorders in early lactation dairy cows and is associated with impaired metabolic adaptation, reduced productivity, and altered behavioral patterns (1). Early identification of SCH using integrated physiological and behavioral indicators may improve herd health management (2).

Aim

The aim of this study was to evaluate subclinical hypocalcemia in dairy cows through an integrated assessment of blood biochemical biomarkers, in-line milk composition parameters, and rumination behavior.

Methods

A prospective observational study was performed on early-lactation dairy cows to evaluate the effects of SCH. Cows were divided into two groups according to blood calcium concentration: SCH ($\text{Ca} < 2.0 \text{ mmol/L}$) and healthy controls ($\text{Ca} \geq 2.0 \text{ mmol/L}$). Blood samples were collected for biochemical analysis, including indicators of mineral status and metabolism. In-line milk composition parameters and rumination behavior data were obtained using automated herd monitoring systems. Data were analyzed using statistical methods to compare differences between groups, and significance was established at $p < 0.05$.

Results

Cows with subclinical hypocalcemia showed significantly lower concentrations of Ca, PHOS, Mg, ALB, TP, GLUC, Fe, and CREA compared with healthy cows. Although milk yield, milk composition, and rumination time did not differ significantly, hypocalcemic cows demonstrated tendencies toward lower milk components and reduced milk temperature, indicating impaired metabolic adaptation during early lactation.

Conclusions

The findings demonstrate that subclinical hypocalcemia is associated with measurable

changes in blood biomarkers, milk composition, and rumination activity in dairy cows. Integrating these indicators may support earlier detection and more effective monitoring of SCH in precision dairy farming systems.

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HEALTH FOR ALL

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Oral presentations: --- Clinical research

Active early rehabilitation compared to traditional acute management in adolescent lateral ankle sprain

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Introduction

Lateral ankle sprain (LAS) is common in adolescents, yet treatment approaches vary [1]. The traditional PRICE (protection, rest, ice, compression, elevation) acute management protocol, combined with NSAIDs, remains widely used despite limited high-quality evidence [2]. The newer PEACE and LOVE (protection, elevation, avoid anti-inflammatories and icing, compression, education, load, optimism, vascularization, exercise) framework addresses both acute care and rehabilitation. It highlights inflammation in tissue repair and suggests that routine NSAIDs and cryotherapy may impair healing [3].

Aim

To compare PRICE + NSAIDs and PEACE and LOVE protocols for adolescent LAS and evaluate functional recovery.

Methods

In this prospective randomized study, 76 adolescents (12-17 years) with first-time LAS were assigned to either PRICE + NSAIDs or PEACE and LOVE. Diagnosis and severity were confirmed clinically and by imaging. Functional outcomes were assessed at 1-2, 5-7, and 12-15 weeks using Biodex isokinetic dynamometry, including ankle inversion/eversion peak torque normalized to body weight, range of motion (ROM), and dynamic balance (Y-Balance Test composite score). Outcomes were expressed as side-to-side deficits. Data were analyzed using two-way mixed ANOVA. 65 participants completed follow-up (PRICE n=32; PEACE and LOVE n=33).

Results

Significant main effects of time were observed for inversion strength at 60°/s ($F = 5.73$, $p = 0.006$) and 120°/s ($F = 10.15$, $p < 0.001$), eversion strength at 120°/s ($F = 6.82$, $p = 0.003$), ankle ROM at 60°/s ($F = 12.79$, $p < 0.001$) and 120°/s ($F = 13.09$, $p < 0.001$), and YBT CS ($F = 6.91$, $p = 0.002$), showing progressive improvement over the 12-15 weeks. No significant

group effects or group $\times$ time interactions were detected for any outcome (all $p > 0.05$), indicating comparable recovery between the PRICE + NSAIDs and PEACE and LOVE protocols.

Conclusions

Both approaches led to progressive recovery after LAS in adolescents, with no between-group differences.

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The effect of short-term dual bronchodilation on segmental bronchi measurements in newly diagnosed COPD patients: real-world study

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Introduction

Evidence suggest that dual bronchodilation in patients with chronic obstructive pulmonary disease (COPD) increases airway inner lumen area (Ai), reduces airway wall thickness and percentage wall area (WA%), as assessed by computed tomography (CT) [1,2]. However, real world data on these effects in treatment-naïve patients remain limited.

Aim

To assess the impact of short-term dual bronchodilation on segmental airway structure and its association with blood eosinophil count in newly diagnosed moderate-to-severe COPD patients.

Methods

This is a prospective observational real-world study. Thirty-four patients performed spirometry and chest CT before and after 12 weeks of dual bronchodilation, segmental bronchi were measured during inspiration in CT. Baseline blood eosinophil count was recorded. Quantitative variables are presented as mean $\pm$ standard deviation or median (interquartile range), as appropriate.

Results

After 12 weeks of treatment, forced expiratory volume in 1 second % predicted increased from $60.6 \pm 13.4\%$ to $68.3 \pm 14.4\%$ ($p < 0.001$). Ai increased in all segmental bronchi (RB1, RB4, RB10, LB1 and LB10, all $p < 0.01$). Accordingly, WA% decreased in all segments (all $p < 0.01$), except RB10. Mean Ai of all segments demonstrated a significant increase ($22.2 \pm 17.3\%$, $p < 0.01$). Mean change in Ai did not differ between patients with eosinophil counts ≥ 300 cells/ μL and those with counts < 300 cells/ μL (4.00 ± 3.19 vs 4.09 ± 3.04 , $p = 0.933$).

Conclusions

Short-term dual bronchodilation significantly improves lung function and segmental airway measurements on CT imaging in newly diagnosed COPD patients. These structural changes were not associated with blood eosinophil count. The findings of our study support the prompt initiation of dual bronchodilation in COPD patients. Further research with larger cohorts are needed to confirm the results.

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Exploring low energy availability and its impact on cardiovascular adaptation in male athletes

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Introduction

Due to the high energy (kilocalories) demands associated with intense physical activity, athletes are often at risk of consuming an insufficient amount of calories. This means that energy is used for physical activity, while the energy left for physiological functions is scarce. Energy availability (EA) is defined as the amount of energy remaining for physiological functions after removing the energy expended during physical activity. Adequate EA for sustaining body weight and physiological functions = ~45 kcal/kg FFM/day, reduced EA 30-45 kcal/kg FFM/day, low EA (LEA) leading to health issues ≤ 30 kcal/kg FFM/day (FFM – fat free mass) (1). In LEA condition, the body has to save energy, and various health issues can occur. Various cardiovascular system abnormalities can occur in LEA including hypotension, orthostatic hypotension, syncope (2). However, information about LEA among male athletes and the impact on cardiovascular adaptation remains scarce

Aim

The aim of this research was to evaluate EA and the impact of calory deficit on cardiovascular system's adaptation to physical exercise in male athletes.

Methods

Using a cross-sectional design, 29 male athletes, age $23,48 \pm 9,64$, underwent bioelectric impedance analysis (fat-free mass and basal metabolic rate were measured); veloergometry (evaluation of cardiovascular adaptation to physical exertion); using 3 day dietary and physical activity analysis, adult and youth compendium (3,4) energy balanced was calculated.

Results

None of the tested male athlete had optimal EA, 72.4% had ≤ 30 kcal/kg FFM/day, while

27.6% had 30-45 kcal/kg FFM/day. It was found that male athletes in a greater calorie deficit require a longer cardiovascular recovery period after exercise ($U=8;p=0.026$).

Conclusions

None of the tested male athletes have optimal EA. Calorie deficit is associated with prolonged cardiovascular recovery after exercise, suggesting impaired cardiovascular adaptation in male.

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Self-reported exposure factors in patients with non-carious cervical lesions: a questionnaire-based analysis

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Introduction

Non-carious cervical lesions (NCCLs) are defects of dental hard tissues in the cervical region with a multifactorial background. Patient-related factors, including dietary habits, oral hygiene practices, parafunctional activity, and general health conditions, may contribute to their development and progression [1,2]. Structured questionnaire assessment may help characterize these exposure patterns [3].

Aim

To characterize self-reported dietary, oral hygiene, parafunctional, and chronic disease-related exposure factors in patients with non-carious cervical lesions.

Methods

A cross-sectional questionnaire-based analysis was performed in 25 patients with clinically diagnosed premolar NCCLs; each patient had at least two defects, 1–2 mm in depth. Participants completed a self-administered questionnaire adapted from Zuza et al. [3]. Selected items were grouped into four binary exposure domains: dietary acid exposure, oral hygiene-related factors, parafunctional habits, and chronic disease-related factors. Data were summarized as percentages with exact binomial 95% confidence intervals. An exploratory exposure-burden score was calculated to describe the number of coexisting domains, and hierarchical cluster analysis was applied to explore patient exposure profiles. Ethical approval was obtained from the Kaunas Regional Biomedical Research Ethics Committee (No. BE-2-59, 18 May 2024).

Results

Dietary acid exposure was the most prominent domain: frequent acidic food intake was reported by 80.0% of participants, and acidic drink intake at least once weekly by 44.0%. A brushing technique with a horizontal component was reported by 72.0%, indicating a possible brushing-related abrasive component. Parafunctional habits were reported by 44.0% of participants, with object chewing being the most frequently recorded habit (20.0%). Chronic disease-related factors were present in 52.0% of patients, including gastrointestinal/reflux-related conditions in 16.0%. The median exposure-burden score was 3 domains (range 1-4), with 60.0% of patients presenting three or more coexisting domains. All four exposure domains were present simultaneously in 20.0% of patients. Hierarchical cluster analysis identified three exploratory exposure profiles: a predominantly dietary acid exposure/oral hygiene-related profile, a profile additionally involving chronic disease-related factors, and a higher-burden profile characterized by the co-occurrence of parafunctional and chronic disease-related factors.

Conclusions

Frequent acidic food intake was the dominant exposure in patients with NCCLs. A brushing technique with a horizontal component and parafunctional habits suggested possible abrasive and biomechanical contributions. Identified exposure profiles may support individualized preventive counselling.

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Changes in young and middle aged women 's psychophysiological state during 6 month yoga intervention

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Introduction

Among many ancient practices, yoga is one of the best-known techniques to manage physical and psychological stress ¹. It is not only important to know how yoga can help women's health ², but also it is a great tool to use for health-related issues ³⁻⁵, with which in turn yoga can help alleviate symptoms caused by mental or physical stress ⁶⁻⁸.

Aim

The purpose of the study was to compare psychophysiological state among young and middle aged women after 2, 4 and 6 months of regular yoga practice.

Methods

The study took place at the Lithuanian University of Health Sciences in Kaunas, Lithuania. Study participants consisted of 63 women (28 young aged and 35 middle aged) who practiced yoga for more than 6 months. Participants had yoga practice for 6 months 2 times per week.

Psychoemotional state was evaluated with the SF-12 questionnaire at the end of every week afterwards yoga practices.

Data analysis was computed using IBM SPSS Statistics 31.0.2.0 (IBM Corp., Chicago, IL, USA) and Microsoft Excel 2026. To analyze the data, Mauchly's sphericity test was used to compare changes between intervention timeline and to validate a repeated measures analysis of variance (ANOVA). Values were presented as means $\pm$ standard deviations with confidence interval 95 % of the mean (mean $\pm$ SDs; CI 95 %) and differences were considered statistically significant when values approached $p < .05$ level.

Results

SF-12 scores after 2, 4 and 6 months of regular yoga practice showed more changes were visible in mental component rather than physical. A significant difference ($p < 0.05$) was observed comparing young aged women's group baseline to 6 months after the intervention, $54,71 \pm 7,05$ to $57,64 \pm 3,69$ ($p = 0,03$; CI -5,53-(-0,33)) respectively.

Mental component was the one that showed a bigger effect during and after 6-month yoga intervention. A significant difference ($p < 0.05$) was observed comparing young aged women's group baseline to 2 months after the intervention, from $41,36 \pm 10,58$ to $46.65 \pm 10,25$ ($p = 0,01$; CI -9,32-(-1,27)) respectively; baseline to 4 months after the intervention, from $41,36 \pm 10,58$ to $45,86 \pm 8,95$ ($p = 0,03$; CI -8,61-(-0,38)) respectively; baseline to 6 months after the intervention, $41,36 \pm 10,58$ to $49,40 \pm 9,27$ ($p = 0,00$; CI -12,12-(-3,96)).

Conclusions

This study revealed that yoga practices for 6 months did not significantly influence middle aged women's physical health. Although young aged women benefited physically, according to SF-12 results, compared baseline to 6 months after intervention.

Yoga practice for 6 months did influence young aged women's mental wellbeing and did not have significant effects to middle aged women.

According to SF-12 questionnaire, yoga practice for 6 months is more beneficial to young aged women.

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Assessment of Reliability and Validity of the Lithuanian Version of the P-QOL Questionnaire

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Introduction

Pelvic organ prolapse (POP) is defined as the downward displacement of one or more pelvic structures, including the anterior or posterior vaginal wall, the vaginal apex, or the uterus [1]. POP is a prevalent condition affecting approximately 40% of women across all age groups [2].

Over recent decades, the assessment of quality of life in women with POP using self-administered questionnaires has gained increasing importance, as symptom relief and improvement of quality of life have become the primary goals of treatment [3]. The Prolapse Quality-of-Life (P-QOL) questionnaire was developed by Digesu et al. in 2005 [4]. It has been recognized as a simple, valid instrument for assessing the severity of POP symptoms and their effect on quality of life. In addition, it facilitates the identification of women requiring treatment and enables evaluation of treatment outcomes.

Aim

The aim of this study was to translate and validate the Lithuanian version of the P-QOL questionnaire for use in Lithuanian women with urogenital prolapse.

Methods

The study was carried out between January and December 2020 at the outpatient Obstetrics and Gynaecology Clinic of the Lithuanian University of Health Sciences, a tertiary referral

centre. The original English version of the questionnaire was independently translated by two English-Lithuanian translators. Women older than 18 years of age whose native language was Lithuanian were eligible for inclusion. Exclusion criteria included pregnancy, ongoing treatment for oncological disease and neurological or psychiatric conditions that could interfere with the completion of the questionnaire.

The form contained 20 questions representing nine quality-of-life domains. Scores for each domain ranged from 0 to 100, with higher scores indicating greater impairment in quality of life, whereas lower scores reflected better quality of life. In addition, the questionnaire included 18 items assessing urinary, bowel, and vaginal symptoms. These items were not incorporated into the overall scoring system.

Based on symptom presence, participants were classified into two groups: symptomatic women (reporting a vaginal bulge or a sensation of something protruding from the vagina) and asymptomatic women (without symptoms of POP, who attended the clinic for unrelated gynaecological complaints). Questionnaire validity was evaluated by assessing the proportion of missing data and by comparing symptom scores between symptomatic and asymptomatic women using the Mann-Whitney U test. Reliability was assessed by calculating Cronbach's alpha coefficients. A Cronbach's alpha coefficient >0.70 was considered indicative of acceptable internal consistency. To evaluate test-retest reliability, a subgroup of 22 symptomatic women completed the questionnaire for a second time after an interval of two to three weeks. Test-retest reliability was assessed using Spearman's correlation coefficient (SCC). A p-value <0.05 was regarded as statistically significant.

Results

A total of 274 women (98.2%) correctly completed the questionnaire. The study population consisted of 137 symptomatic and 137 asymptomatic women. Significant differences in quality-of-life domain scores were observed between the two groups ($p < 0.001$). Furthermore, P-QOL scores demonstrated significant correlations with the stage of prolapse across most domains, suggesting that more advanced prolapse stages were associated with a greater negative impact on quality of life. Exceptions were noted in the "social limitations" and "personal relationships" domains, where no significant association was observed. Internal consistency was high across all questionnaire domains, with Cronbach's alpha coefficients ranging from 0.775 to 0.958. However, the "social limitations" domain demonstrated acceptable internal consistency with a Cronbach's alpha value of 0.647. Test-retest analysis revealed a highly significant correlation between repeated questionnaire scores across all common domains.

Conclusions

The Lithuanian version of the P-QOL questionnaire was shown to be a valid, reliable and easily understandable instrument for evaluating symptom severity and the impact of

urogenital prolapse on the quality of life of Lithuanian women.

Effects of visual stimulus intensity on dynamic subjective visual vertical performance in multiple sclerosis

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Introduction

Dynamic subjective visual vertical (SVV) testing evaluates visual - vestibular interaction and visual dependence by measuring perceived verticality during moving visual stimulation [1,2]. In multiple sclerosis (MS), impaired central vestibular processing may increase susceptibility to visually induced verticality errors [3]. However, there is no consensus regarding the optimal visual stimulus velocity for dynamic SVV testing.

Aim

To evaluate how different visual stimulus rotation velocities affect dynamic SVV performance and diagnostic accuracy in patients with MS.

Methods

A cross-sectional observational study included 31 patients with relapsing-remitting MS and dizziness, and 32 age- and sex-matched healthy controls. Static and dynamic SVV were assessed using a virtual reality system [4]. Dynamic stimuli consisted of rotating spheres presented at velocities of 10°/s, 30°/s, and 60°/s. Median SVV deviations, visual dependence (VD), and visually induced dizziness were compared between groups. Receiver operating characteristic (ROC) analysis was used to evaluate discriminatory performance.

Results

MS patients demonstrated significantly greater SVV deviations than controls during static and all dynamic conditions. Median dynamic SVV deviations in the MS group were 4.3° at 10°/s, 6.2° at 30°/s, and 5.6° at 60°/s, compared to 2.1°, 3.7°, and 3.8° in controls, respectively ($p < 0.05$). The 10°/s stimulus yielded the highest diagnostic accuracy for differentiating MS patients from controls (AUC = 0.897; $p < 0.001$). VD discriminatory performance was also greatest at 10°/s (AUC = 0.828; $p < 0.001$). Higher stimulus velocities induced significantly greater dizziness in both groups. Differences in SVV deviations between 30°/s and 60°/s were not significant in the MS group.

Conclusions

Lower visual stimulus rotation velocity during dynamic SVV testing demonstrated superior discriminatory performance and reduced test - induced dizziness compared with stronger stimuli. A velocity of 10°/s may represent the most clinically applicable parameter for assessing altered verticality perception and visual dependence in MS.

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Poster session

Unresolved infertility cases and reproductive outcomes: towards genome-wide diagnostics

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Introduction

Infertility affects a substantial proportion of couples, yet many cases remain genetically unexplained despite routine diagnostic testing. Conventional approaches, including karyotyping and targeted assays, have limited diagnostic yield, particularly in unexplained infertility and recurrent pregnancy loss.

Aim

To evaluate the diagnostic yield of routine genetic testing in infertility patients and assess reproductive outcomes, with additional follow-up and prospective whole genome sequencing in undiagnosed cases.

Methods

A retrospective study included 900 patients (473 males, 427 females) evaluated between 2020 and 2024. All underwent karyotyping, with targeted testing performed by indication. A subgroup of 566 patients with azoospermia, oligospermia, unexplained infertility, or recurrent pregnancy loss was analysed. Undiagnosed patients were recontacted and invited to participate in a prospective study involving whole genome sequencing. Reproductive outcomes were assessed through follow-up.

Results

Karyotype abnormalities were identified in 3.22% (29/900) of all patients and 5.12% (29/566) of the study subgroup. The highest diagnostic yield was observed in azoospermia (33.3%), followed by oligospermia (6.6%), recurrent pregnancy loss (5.3%), and unexplained infertility (3.1%). Follow-up data showed that in azoospermia/oligospermia, 50.4% did not achieve pregnancy, 17% conceived spontaneously, and 26.7% after assisted reproduction. In unexplained infertility, 46.5% did not achieve pregnancy, 9.7% conceived spontaneously, and 41% after assisted reproduction. In recurrent pregnancy loss, 44.2% did not achieve pregnancy, 47% conceived spontaneously, and 7.8% after assisted reproduction. Prospective whole genome sequencing data analysis is ongoing in previously undiagnosed cases.

Conclusions

Routine genetic testing provides clinically relevant diagnoses in a subset of infertility patients, with the highest yield in azoospermia. However, many cases remain unexplained. Follow-up data highlight differing reproductive outcomes across subgroups and the role of assisted reproduction. Ongoing whole genome sequencing may improve diagnostic resolution and support personalized reproductive care.

References

Performance comparison of supervised machine learning models for sensor-based classification of metabolic and udder health disorders in dairy cows

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Introduction

Early detection of metabolic and udder health disorders is essential for improving dairy cow welfare, productivity, and herd sustainability. Precision livestock technologies allow continuous monitoring of milk composition and behavioural parameters, creating new opportunities for earlier disease recognition through machine learning methods (1,2).

Aim

The aim of this study was to compare the predictive performance of supervised machine learning models for classifying dairy cows into health-related groups using sensor-derived data collected during early lactation.

Methods

A total of 206 Holstein cows from two commercial dairy farms in Lithuania were enrolled during the first 100 days in milk. Automated systems continuously recorded milk yield, fat, protein, lactose, fat-to-protein ratio, somatic cell count, rumination time, and milk temperature. According to these indicators, cows were classified as clinically healthy, subclinical ketosis risk, subclinical mastitis, or clinical mastitis. Five supervised machine

learning models were evaluated: Decision Tree, Logistic Regression, Multilayer Perceptron, Random Forest, and Gradient Boosting. Model performance was assessed using accuracy, precision, sensitivity, F1 score, and Matthews correlation coefficient.

Results

All models demonstrated satisfactory classification ability. Random Forest achieved the highest overall accuracy (85.7%), with precision of 1.000, sensitivity of 0.938, F1 score of 0.968, and MCC of 0.950. Logistic Regression and Gradient Boosting each reached an accuracy of 83.3%. Logistic Regression also showed excellent precision (1.000) and F1 score (0.968). Decision Tree and Multilayer Perceptron both achieved an accuracy of 81.0%.

Conclusions

Supervised machine learning models can successfully classify dairy cows according to metabolic and udder health status using automatically collected sensor data. Random Forest showed the strongest predictive performance, while Logistic Regression also provided accurate and interpretable results.

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Combined Cellular and Exosomal miRNA Profiling Reveals Potential Regulators of Colorectal Cancer Cell Line Aggressiveness

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Introduction

Colorectal cancer (CRC) progression is driven by molecular changes that distinguish malignant from normal epithelial cells and contribute to differences in tumor aggressiveness, including proliferative, invasive and metastatic potential [1]. Although many expression studies compare CRC tissue or cells with healthy controls [2,3], less is known about miRNA-related regulatory changes associated with increasing aggressiveness within CRC. MicroRNAs (miRNAs) are important post-transcriptional regulators that may affect cancer-related pathways both intracellularly and through exosome-mediated intercellular communication [4].

Aim

This study aimed to identify miRNAs associated with an aggressiveness-related expression gradient in CRC cell lines and to determine which of these candidates are shared between cellular and exosomal compartments.

Methods

Small RNA sequencing data from normal colonic epithelial cells (HCoEpic) and two CRC cell lines, HTB37 and HCT116, were analyzed. Tumor aggressiveness-associated cellular candidates were identified by selecting commonly deregulated miRNAs showing stronger changes in the more aggressive HCT116 cell line compared with HTB37 [5]. Further prioritization was performed using quartile-based delta log₂FC filtering. Candidate cellular miRNAs were then integrated with exosomal miRNA datasets. Shared candidates were retained only if they were detected in both exosomal datasets, showed concordant

deregulation direction with cellular data and met the significance threshold of $\text{padj} < 0.05$. KEGG pathway enrichment analysis was performed separately for predicted target genes of upregulated and downregulated shared cellular-exosomal miRNAs.

Results

Principal coordinate analysis of cellular miRNA expression profiles clearly separated non-malignant HCoEpic cells from CRC cell lines, while HTB37 and HCT116 also formed distinct groups, reflecting differences in tumor aggressiveness. The first two principal coordinates explained 45.3% and 30.8% of total variance, respectively. In total, 29 tumor aggressiveness-associated cellular miRNA candidates were identified. Among these, 7 miRNAs were shared between cellular and exosomal compartments: hsa-miR-1224-5p, hsa-miR-140-5p, hsa-miR-138-5p, hsa-miR-1271-5p, hsa-miR-30a-3p, hsa-miR-30a-5p and hsa-miR-30c-2-3p. The strongest expression changes were observed for hsa-miR-1224-5p (FC = 3.63), hsa-miR-30a-3p (FC = -4.68) and hsa-miR-30c-2-3p (FC = -6.18). Functional enrichment analysis of predicted target genes identified several cancer-related and regulatory pathways, including proteoglycans in cancer, endocytosis, cell cycle, cellular senescence, focal adhesion, adherens junction, MAPK signaling and Hippo signaling. Additional enriched pathways were related to autophagy, protein processing in the endoplasmic reticulum and ubiquitin-mediated proteolysis.

Conclusions

This study identified 7 shared cellular-exosomal miRNAs associated with increasing CRC aggressiveness across cell lines. These miRNAs may contribute to both intracellular regulatory changes and exosome-mediated communication during CRC progression. The findings suggest that shared cellular and exosomal miRNA profiles may help reveal molecular regulators of tumor aggressiveness and provide candidate targets for further functional investigation.

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Influence of Dietary Cholesterol on Microbial Metabolism and Lipid Imbalance in Ulcerative Colitis

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Introduction

The interplay between diet, gut microbiota, and host metabolism is central to inflammatory bowel disease (IBD). Cholesterol-derived bile acids may mediate these interactions via FXR and TGR5 signaling (1). High cholesterol intake may promote inflammation by altering microbial bile acid metabolism and is associated with systemic metabolic changes in IBD (1,2). However, the relevant microbial functional pathways and metabolites remain unclear.

Aim

To investigate the association between dietary cholesterol intake and microbial functional profiles, and to evaluate metabolomic changes in ulcerative colitis alongside the effects of 7-keto-lithocholic acid in organoids.

Methods

A pilot cohort (n=30) was analyzed using Food Frequency Questionnaires and shotgun metagenomic sequencing (Illumina NovaSeq X) to profile microbial metabolic pathways. Plasma metabolomics (GC-MS) was performed in patients with active ulcerative colitis (UC), UC in remission, and non-IBD controls (n=15 per group). Statistical analyses included Kruskal-Wallis and Dunn's tests with Benjamini-Hochberg correction (padj<0.05). UC and control-derived organoids were co-treated with inflammatory cytokines (TNF- α , IFN- γ) and 7-keto-LCA, followed by qRT-PCR analysis to evaluate inflammation, bile acid signaling and epithelial barrier integrity.

Results

Dietary cholesterol intake showed high variability. No global microbiome shifts were detected (PERMANOVA, p=0.184), but 19 microbial metabolic pathways were significantly associated with high cholesterol intake (>400 mg/day). This was linked to a shift from recycling-associated state, including reduced putrescine biosynthesis and purine degradation, toward increased de novo nucleotide and amino acid biosynthesis. Plasma metabolomics revealed lipid imbalance in active UC, including elevated saturated fatty acids (palmitic, myristic) and 2-hydroxybutyrate. In organoids, 7-keto-LCA did not reduce inflammatory markers but significantly increased *NR0B2* expression in non-IBD controls (p<0.05).

Conclusions

High dietary cholesterol is associated with a shift toward anabolic microbial metabolism, while UC is characterized by systemic lipid imbalance and oxidative stress markers. Modulation of *NR0B2* by 7-keto-LCA suggests a potential role for bile acid-mediated signaling in regulating epithelial metabolic responses.

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Semi-solid extrusion 3D printing enhances epidermal menthol accumulation from PVA-based transdermal films: ex vivo comparative study

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Introduction: Transdermal drug delivery avoids first-pass metabolism and improves patient compliance. PVA-based polymeric films are a promising platform; however, the effect of manufacturing method on epidermal drug accumulation remains poorly characterized.

Aim: To compare epidermal menthol accumulation from PVA-based films manufactured by semi-solid extrusion (SSE) 3D printing and solvent casting (SC).

Methods: Identical PVA-based films containing 5% menthol were manufactured by SSE 3D printing and SC. Ex vivo permeation studies were conducted using porcine ear skin in Franz diffusion cells (n=6). Epidermal menthol accumulation was quantified by GC/FID. Film microstructure was analyzed by scanning electron microscopy (SEM).

Results: SSE 3D-printed films demonstrated 4.4-fold higher epidermal menthol accumulation compared to SC films (p=0.0004, Cohen's d=1.79). SEM revealed interconnected porous microstructure in 3D-printed films facilitating enhanced drug-skin contact.

Conclusions: SSE 3D printing significantly enhances epidermal menthol accumulation from PVA-based films versus solvent casting. Interconnected porous microstructure of 3D-printed films is identified as a key mechanistic factor.

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Manufacturing quality assessment of PVA-based pharmaceutical films: microstructural analysis and USP compliance evaluation

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Introduction: Quality assessment of pharmaceutical films requires evaluation of both microstructural properties and content uniformity. Comparative analysis across different manufacturing methods is essential for regulatory compliance and process optimization.

Aim: To assess and compare manufacturing quality of PVA-based pharmaceutical films produced by semi-solid extrusion (SSE) 3D printing, solvent casting (SC), and electrospinning (ES).

Methods: Identical PVA-based films containing 5% menthol were manufactured by SSE 3D printing, SC, and ES using a DOBOT MG400 robotic arm-assisted system. Content uniformity was evaluated per USP <905>. Microstructural analysis was performed by scanning electron microscopy (SEM). Mechanical properties were assessed by texture analysis.

Results: All three manufacturing methods achieved USP <905> compliance for content uniformity. SEM revealed distinct microstructural differences: interconnected porous network in 3D-printed films, dense homogeneous structure in SC films, and fibrous morphology in ES films. Mechanical properties varied significantly between methods.

Conclusions: All three manufacturing methods produce USP <905>-compliant PVA-based pharmaceutical films with distinct microstructural characteristics. Manufacturing method selection should consider the intended drug delivery application.

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Association of serum IL-17A and IL-33 levels with relapsing-remitting multiple sclerosis

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Introduction

Multiple sclerosis (MS) is a chronic inflammatory disease of the central nervous system characterised by immune-mediated damage to myelin and subsequent neurodegeneration. The mechanism involves interactions between immune-derived signals and glial cells, particularly astrocytes and microglia. The most common clinical form, relapsing-remitting MS (RRMS), is characterised by periods of neurological worsening followed by partial or complete recovery, reflecting fluctuating inflammatory activity within the CNS (1).

IL-17A, produced by Th17 cells, contributes to the initiation and maintenance of neuroinflammation by activating astrocytes and promoting the release of inflammatory mediators, which sustain and amplify the local immune response (2). IL-33 is released from damaged CNS cells and acts as a danger signal, further enhancing glial activation (3). It promotes activation of both astrocytes and microglia, strengthening the inflammatory environment. As a result of this sustained inflammation, oligodendrocytes are damaged, leading to demyelination, followed by axonal injury and ultimately neurodegeneration, which is responsible for progressive neurological impairment in MS (4) (**Figure 1**).

Aim

To determine serum levels of IL-17A and IL-33 in patients with RRMS and healthy controls.

Methods

Peripheral blood samples were collected and processed to obtain serum. After incubation at room temperature, samples were centrifuged, and the serum was aliquoted and stored at -80°C until analysis. Serum levels of IL-17A and IL-33 in control and MS patient groups were measured using a standard sandwich ELISA according to the manufacturer's instructions. Optical density was read at 450 nm using a microplate reader, and concentrations were calculated from standard curves. Statistical comparisons between groups were performed using the Mann-Whitney U test.

Results

No statistically significant differences in IL-17A serum levels were observed between RRMS patients and healthy controls (median (IQR): 747.00 (3304.00) vs. 987.00 (5115.00),

p = 0.551) (Figure 2).

IL-33 serum levels were significantly lower in RRMS patients compared to healthy controls (median (IQR): 6.56 (4.29) vs. 7.89 (8.28), p = 0.034) (Figure 3).

Conclusions

No significant differences in IL-17A serum levels were observed between RRMS patients and controls. In contrast, IL-33 levels were significantly higher in the control group. These findings demonstrate differential patterns of cytokine expression in RRMS. The study is limited by a small sample size and the use of peripheral blood only.

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Proteomic Signatures of Systemic and Local Inflammation in Patients with Non-Obstructive Coronary Artery Disease

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Introduction

Atherosclerosis is a chronic inflammatory disease driven by interactions between immune responses and metabolic dysregulation [1]. While systemic inflammatory markers such as high-sensitivity C-reactive protein (hs-CRP) predict cardiovascular risk, local vascular inflammation also contributes to plaque development and instability [2,3]. Distinct systemic and local inflammatory pathways may differentially contribute to atherosclerosis and be reflected in circulating proteomic profiles.

Aim

To perform exploratory proteomic analysis in patients with non-obstructive coronary artery disease (CAD) and identify proteins associated with systemic and local vascular inflammation.

Methods

Eight patients with non-obstructive CAD confirmed by coronary computed tomography angiography were included. Blood samples were collected during the same visit. Perivascular adipose tissue (PVAT) fat attenuation index (FAI) was measured in the proximal 40 mm of the right coronary artery using Vitrea® software. Proteomic profiling covering approximately 11000 proteins was performed using the Illumina Somalogic platform. Protein expression differences were analyzed using DESeq2 in R. Correlations between FAI and protein levels were assessed with adjustment for CAD burden and risk factors.

Results

Patients with higher PVAT density showed reduced AHSG (fetuin-A) expression (fold change -1 ; $p < 0.05$) and increased PRR5L expression (fold change 1.94 ; $p < 0.05$). PVAT FAI negatively correlated with AHSG and positively with PRR5L. PRKRA expression was higher in patients with elevated hs-CRP but was not associated with PVAT FAI ($p < 0.05$).

Conclusions

Proteomic profiling identified proteins associated with PVAT-related inflammation in non-obstructive CAD. AHSG and PRR5L may reflect local coronary inflammation, while PRKRA may be linked to systemic inflammation. These findings support distinct roles of local and systemic inflammatory pathways in atherosclerosis. Larger studies are needed to confirm these results.

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Effects of fireweed (*Chamerion angustifolium* L.) leaf extract and its main component Oenothlein B on the viability and cell death of colon cancer (Caco-2) cells

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Introduction

Fireweed (*Chamerion angustifolium* L.) is a medicinal plant, widely used to treat gastrointestinal disorders, such as inflammation and irritation, acid reflux, mucous membrane lesions, wounds healing, swelling [1]. Fireweed is included in a European Medicines Agency (EMA) monograph stating that it can be used to relieve lower urinary tract symptoms associated with benign prostatic hyperplasia [2]. Extracts obtained from fireweed leaf are abundant in polyphenolic compounds (tannins, flavonoids, phenolic acids) and show a variety of pharmacological effects, such as anti-inflammatory, anti-oxidant, anti-proliferative, anti-cancer, anti-microbial, anti-bacterial properties [3]. The main compound which is detected in high concentrations in fireweed extract is Oenothlein B, a dimeric macrocyclic ellagitannin [1]. Due to the high incidence of colorectal cancer and the need for novel bioactive compounds targeting tumor cell survival, colon cancer is a relevant model to assess the therapeutic potential of fireweed leaf extract and Oenothlein B.

Aim

The aim of the study was to determine the effect of fireweed (*Chamerion angustifolium* L.) leaf extract and its main component Oenothlein B on colon cancer (Caco-2) cell death.

Methods

The fireweed leaves were collected in Jonava district, Šafarka village (55°00'22" N; 24°12'22" E) in 2023 July. The aqueous extracts from unfermented leaves were prepared from plants grown under natural conditions. Colon cancer cells (Caco-2) were treated with

different fireweed extract (0.5 mg/mL; 1 mg/mL; 1.5 mg/mL) and Oenothien B (0.05 mg/mL; 0.1 mg/mL; 0.15 mg/mL) concentrations for 48 hours. Control group were untreated colon cancer cells. The amount of viable, apoptotic and necrotic cells was evaluated by Hoechst 33342 (20 µg/mL) and propidium iodide (PI) (10 µg/mL) staining and analyzed with a EVOS M7000 Imaging System (Invitrogen, Thermo Fisher Scientific, Waltham, Massachusetts, U.S.) at 20x magnification.

Results

We found that the effect of fireweed extract and Oenothien B to colon cancer cell count and viability was dose dependent. An increase in fireweed leaf extract concentration from 0.5 to 1.5 mg/mL resulted in a significant reduction in colon cancer cells by 52-69% ($p < 0.05$). Similarly, increasing the concentration of Oenothien B from 0.05 mg/mL to 0.15 mg/mL, resulted in a significant reduction of cell number by 50-65% ($p < 0.05$). The cell viability decreased by 15-91% ($p < 0.05$) after treatment with fireweed extract (0.5-1.5 mg/mL) and by 11-88% ($p < 0.05$) after Oenothien B (0.05-0.15 mg/mL). Moreover, a concentration-dependent increase in necrotic cell death was observed following treatment with fireweed extract and Oenothien B. Treatment with fireweed extract (0.5-1.5 mg/mL) resulted in an 11-91% increase in necrotic cells, compared to an 8-88% increase observed in the oenothien B-treated group ($p < 0.05$). Additionally, there was an insignificant amount of apoptotic cell death, 4% in fireweed treated group (0.5 mg/mL) and 2% in Oenothien B treated group (0.05 mg/mL), which completely diminished with increasing concentrations of both the fireweed extract and Oenothien B.

Conclusions

The aqueous extract of fireweed (*Chamerion angustifolium* L.) leaves and its main component Oenothien B significantly suppresses the viability of colon cancer cells (Caco-2) in a dose-dependent manner. Notably, both the fireweed leaf extract and Oenothien B exhibited comparable cytotoxic effects, suggesting that Oenothien B may substantially contribute to the anti-cancer activity of the fireweed extract.

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miR-4492 expression in laryngeal squamous cell carcinoma

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Introduction

Approximately 30% to 40% of head and neck cancers are laryngeal (1). Laryngeal squamous cell carcinoma (LSCC) is the most prevalent kind of laryngeal cancer (2), and its location within the larynx affects its development, prognosis, and course of therapy. Due of its high recurrence rate and delayed detection, this illness has a dismal prognosis (3). MicroRNAs serve as key regulators of essential cellular processes, including proliferation, apoptosis, differentiation, and metastasis, and their dysregulation represents a hallmark of cancer development and progression (4). MiR-4492 plays a key role in several cancers such as, breast cancer, bladder cancer, osteosarcoma, glioblastoma multiforme, hepatocellular carcinoma, colorectal cancer, and ovarian cancer (5). Putting it all together, identifying the mechanisms of miR-4492 in the pathogenesis of cancer, could pave the way to find better diagnostic and therapeutic strategies for LSCC.

Aim

to investigate the association of miR-4492 expression with the occurrence and clinical characteristics of laryngeal squamous cell carcinoma.

Methods

RNA was isolated from tumor tissue, adjacent healthy tissue, and blood plasma, and miR-4492 expression was quantified using the QIAcuity One Digital PCR system, enabling absolute quantification without standard curves. Statistical analyses were conducted using IBM SPSS Statistics 31.0.0.0.

Results

MiR-4492 expression was significantly lower in healthy tissues compared with tumor tissues (median: 16.99 vs. 45.47 copies/ μ L; $p = 0.017$) and was significantly lower in blood plasma samples compared with tumor tissues (median: 3.88 vs. 45.47 copies/ μ L; $p < 0.001$). Spearman's correlation analysis revealed no significant associations between miR-4492 expression and clinicopathological parameters.

Conclusions

MiR-4492 expression was significantly upregulated in laryngeal squamous cell carcinoma tumor tissues compared with healthy tissues and plasma samples. However, miR-4492 expression was not significantly associated with clinicopathological parameters. These preliminary findings suggest that miR-4492 may be involved in LSCC tumor biology.

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Innovative sensor-based assessment of body-milk temperature difference for early detection of bacterial load in dairy cows

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Introduction

Subclinical mastitis remains a major challenge in dairy production due to the presence of bacterial pathogens in apparently healthy cows. Sensor-based monitoring systems may provide novel opportunities for early detection of changes associated with bacterial presence in milk.

Aim

To quantify the association between body-milk temperature difference and bacterial load in milk using sensor-derived data in dairy cows.

Methods

An observational study with repeated measurements was conducted using data from 24 dairy cows. Body temperature was continuously recorded every 10 minutes using an intraruminal bolus system (smaXtec, smaXtec animal care GmbH, Austria, 2023), while milk temperature was recorded twice daily during milking using an automated herd management system (HerdLine, Brolis Semiconductors UAB, Lithuania). Daily mean values were calculated over a 31-day period. Milk samples were microbiologically analysed and cows were classified into three groups: no bacterial growth (0), single pathogen (1), and ≥ 2 pathogens (2). The temperature difference (body-milk) was analysed using a linear mixed-effects model with cow as a random effect.

Results

Groups had a statistically significant effect on temperature difference. Compared to group 0 (mean 3.08°C), the difference was significantly lower in group 1 (−0.67°C, $p = 0.015$) and group 2 (−0.23°C, $p = 0.012$). A consistent reduction in temperature difference was observed with increasing bacterial load.

Conclusions

A smaller difference between body and milk temperature is associated with increased bacterial presence in milk. These findings suggest that body-milk temperature difference may have potential as an early indicator of bacterial load in dairy cows.

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Circulating protein signature for early detection of pancreatic ductal adenocarcinoma: a pilot study using Olink panels

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Introduction

Pancreatic ductal adenocarcinoma (PDAC) is often diagnosed at advanced stages and is associated with poor survival, highlighting the need for minimally invasive biomarkers for early detection. Circulating proteins may reflect tumor-associated systemic alterations and represent a promising source of diagnostic biomarkers.

Aim

To investigate serum protein profiles associated with early-stage PDAC using targeted Olink proteomic panels.

Methods

Serum samples from 22 stage I-II PDAC patients (11 M/11 F; 59.7 ± 7.7 y.) and 22 healthy controls (HC) (11 M/11 F; 62.4 ± 7.9 y.) were analyzed. Protein profiling was performed using Oncology II and Immuno-Oncology panels. Differential protein abundance analysis was conducted using the Limma statistical framework. Classification performance was preliminarily assessed using LOOCV and AUC analysis for proteins exhibiting the most pronounced differences.

Results

Onco II panel identified significant associations for PPY, RSPO3 and EGF (adj. p-values < 0.05). The Immuno-Onco panel revealed significant differences in multiple circulating proteins, incl. EGF, CSF-1, MCP-3, CAIX, TNFSF14, CCL20, MCP-1, MUC-16, CD40-L, IL-8 and ARG1 (all adj. p-values < 0.05). Preliminary classification analysis demonstrated moderate discriminatory performance (LOOCV AUC = 0.75, 95% CI: 0.62–0.88). All proteins identified in the Immuno-Onco panel were upregulated in PDAC compared to HC. They are involved in immune regulation, inflammatory signaling and tumor microenvironment interactions, supporting their relevance in early PDAC development.

Conclusions

This pilot study identified a circulating protein signature associated with early-stage PDAC, highlighting its potential as a minimally invasive biomarker. Upregulation of immune-related proteins suggests systemic immune alterations are present already in early PDAC. These findings will be validated in an ongoing study incl. 290 stage I-IV PDAC patients and 150 HC using the Immuno-Onco panel.

References

Please replace this text with your own content (list of literature resources which were used during your study - citations should be written in Vancouver Citation Style).

Relationship between musculoskeletal ultrasound changes and functional status in hand and foot osteoarthritis

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Introduction: Hand and foot osteoarthritis (OA) involves inflammatory and structural changes. Musculoskeletal ultrasound (MSUS) assesses synovial hypertrophy (SH), effusion (SE), and osteophytes (OPH), but the relationship of these findings to small-joint functional impairment remains unclear. Limited data exists on how US findings relate to combined hand and foot function in OA.

Aim: to evaluate the link between US inflammatory and structural changes and functional impairment of small hand and foot joints in OA patients.

Methods: 102 patients with hand and foot OA were included. Hand function was assessed using HAMIS, finger-to-palm distance, and the Modified Kapandji Index (MKI); lower-extremity function was evaluated using OARSI-recommended performance (30-second chair stand, 40-meter walk, heel-rise, single-leg stance, and 9-step stair-climb). Pain, stiffness, and tenderness were clinically assessed. MSUS was used to evaluate OPH, SH, and joint SE in the hand and foot in accordance with international guidelines. Patient-reported outcomes (FAOS, MOxFQ, pain, stiffness, FIHOA, MHQ) were recorded. Associations between US findings and functional outcomes were analysed using Spearman's rank correlation coefficient (ρ). This study represents a secondary analysis of a randomised controlled trial investigating rehabilitation outcomes in patients with OA. Participant recruitment began in August 2024.

Results: 102 patients with hand and foot OA were included. Mean BMI was 30.2 (SD 5.2) kg/m², and 89.9% were postmenopausal. Long symptom duration (≥ 5 years) was common in hand (51.0%) and foot OA (40.2%). Poorer finger flexion correlated with greater OPH burden and, to a lesser extent, inflammatory US findings in PIP and DIP joints ($\rho = -0.24$ to -0.44 , all $p < 0.05$). Higher HAMIS scores were associated with greater OPH burden in PIP and DIP joints ($\rho = 0.20$ to 0.33 , $p < 0.05$). Greater MCP OPH burden was associated with poorer hand dexterity (MKI), whereas symptoms and foot functional measures showed weak or no associations with MSUS findings.

Conclusion: US abnormalities, especially OPH, relate more to impaired hand function than inflammatory findings. Pain and stiffness weakly linked to US abnormalities, showing limited symptom-imaging correlation in small-joint OA. Age, but not BMI, correlates with higher OPH burden.

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Association of CXCL12 Gene Haplotypes with Pituitary Neuroendocrine Tumour Susceptibility: A Gender-Stratified Analysis

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Introduction

Pituitary neuroendocrine tumour (PitNET) is one of the most common intracranial tumours and is associated with molecular mechanisms involving cell proliferation, angiogenesis, and tumour microenvironment regulation (1). The CXCL12 signaling pathway plays an important role in tumour development and progression, while single-nucleotide variants (SNVs) within the *CXCL12* gene may influence susceptibility to PitNET (2,3).

Aim

To investigate the association of *CXCL12* haplotypes (rs1029153, rs1201157, and rs2297630) with PitNET susceptibility and to evaluate possible gender-specific genetic predispositions.

Methods

A case-control study was conducted involving 585 subjects, divided into two groups: the control group (n = 387) and the PitNET group (n = 198). DNA samples from peripheral blood leukocytes were purified using the DNA salting-out method. Single-nucleotide variants (rs1029153, rs1801157, rs2297630) were identified using real-time polymerase chain reaction (RT-PCR). The results were analyzed using the IBM SPSS Statistics 31 software.

Results

We found that the G-C-A haplotype was associated with a 1.6-fold increased odds of PitNET occurrence (OR = 1.60; CI: 1.16-2.21, p = 0.004), while the G-C-G haplotype also demonstrated a significant association with a 2.9-fold increased PitNET occurrence (OR = 2.91; CI: 1.16-7.28, p = 0.023). We found that in females, the G-C-A haplotype was associated with a 1.9-fold increased PitNET occurrence (OR = 1.86; CI: 1.19-2.89, p = 0.006), while the G-C-G haplotype showed an even stronger association with disease occurrence (OR = 4.23; CI: 1.36-13.17, p = 0.013). No statistically significant haplotype associations were identified in males.

Conclusions

CXCL12 haplotypes were significantly associated with PitNET susceptibility. The G-C-A and G-C-G haplotypes were associated with increased odds of PitNET occurrence, while gender-stratified analysis revealed significant associations only in females.

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Effectiveness of oxidative therapies in mature oral biofilms: a systematic review and meta-analysis

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Introduction

Mature oral biofilms (≥ 48 h) exhibit increased resistance to conventional antimicrobial therapies due to their complex structure and limited agent penetration. Oxidative therapies based on reactive oxygen species (ROS) have emerged as potential strategies for biofilm disruption.

Aim

To evaluate the effectiveness of oxidative therapies in disrupting and reducing mature oral biofilms and to compare their antimicrobial efficacy across different treatment modalities.

Methods

A systematic review and meta-analysis were conducted following PRISMA 2020 guidelines. A total of 23 studies (in vitro, in situ, ex vivo, and clinical) were included. Quantitative synthesis was performed using a random-effects model with restricted maximum likelihood estimation. Outcomes included percentage reduction in bacterial viability and $\log_{10}$ CFU reduction. Heterogeneity was assessed using I^2 and Cochran's Q test. Subgroup analyses were conducted based on therapy type, and publication bias was evaluated using funnel plots and Egger's test.

Results

Oxidative therapies significantly reduced bacterial viability compared with controls, with a pooled mean difference of 40.47% (95% CI: 29.80–51.15) and $-2.97 \log_{10}$ CFU (95% CI: -3.79 to -2.16) ($p < 0.0001$). Antimicrobial photodynamic therapy demonstrated the most consistent effects, while plasma and hydrogen peroxide-based therapies showed greater variability. High heterogeneity was observed ($I^2 > 97\%$), although all studies favored oxidative therapies. Structural disruption of the biofilm matrix was reported; however, complete eradication was rarely achieved.

Conclusions

Oxidative therapies demonstrate significant antimicrobial activity against mature oral biofilms, although their effectiveness depends on treatment parameters and biofilm characteristics.

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Mosaic Pathogenic STR Expansions: Insights into Diagnostic and Prognostic Challenges

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Introduction

Progressive ataxias are neurodegenerative disorders frequently caused by short tandem repeat (STR) expansions in specific genome loci. Detecting STR expansions is challenging, as short read sequencing can not detect longer STRs, underestimate repeat sizes or miss repeat interruptions, complicating diagnosis. Long read sequencing improves STR resolution, but is not yet standard practice. We present a case of progressive ataxia with onset in the third decade of life and dysarthria, assessed with short read genome and long read targeted sequencing.

Aim

To evaluate the utility of combined short read genome and long read targeted sequencing for characterizing STR expansions in ataxia, and their relevance to the clinical phenotype.

Methods

Whole genome sequencing (WGS) was performed on blood DNA with Illumina PCR-free library preparation kit and were sequenced on NovaSeqX Plus. Secondary analysis performed using Dragen and ExpansionHunter¹. Long read libraries (ONT ligation kit) were sequenced on PromethION. Secondary analysis done with Dorado basecalling using super-accurate model and STR analysis by Straglr².

Results

No pathogenic variants explaining the phenotype were found in standard WGS analysis. ExpansionHunter identified multiple false positive STR expansions, as well as a pathogenic CTG expansion in the *TCF4* gene (103 repeats). ONT sequencing confirmed a single phased *TCF4* allele with repeat sizes from 104 to 245, indicating marked mosaicism.

Conclusions

STR expansion in *TCF4* is associated with Fuchs endothelial corneal dystrophy type 3³,

typically manifesting later in life. In this case, short read sequencing detected the pathogenic expansion due to a simple CTG repeat motif, but failed to resolve mosaicism observed with long reads. This highlights the added value of long read sequencing for identifying and characterizing complex STR mosaics that may have clinical relevance, even when findings do not yet match the neurological presentation.

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Perioperative pain management in patients undergoing brain tumor resection.

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Introduction

Craniotomy for brain tumor resection is frequently associated with substantial acute and persistent postoperative pain, largely due to nociceptive stimulation of scalp, bone, and meningeal structures [1-4]. Multimodal perioperative analgesia, including regional techniques such as scalp nerve block (SNB) and incision-site infiltration, is now commonly included in enhanced recovery protocols, yet the optimal strategy and timing remain uncertain and no standardized protocol has been established for oncological craniotomy [5-12].

Aim

We aimed to compare the effect of preincision scalp nerve blockade versus wound infiltration (WI) on intraoperative opioid consumption, hemodynamic stability, and postoperative pain after supratentorial craniotomy for tumor resection.

Methods

A prospective, single-center, randomized, double-blind trial. 105 adults (ASA I-III) undergoing supratentorial craniotomy were randomized to bilateral SNB (Group B) or WI (Group I) after induction and before incision. Both received 0.25% bupivacaine + 1% lidocaine with epinephrine. Total intraoperative fentanyl consumption, intraoperative hemodynamics, time to first rescue analgesic, and total postoperative analgesic consumption over the first 48 hours were compared between groups. Postoperative pain intensity was assessed using visual analogue scale (VAS) at 1, 3, 24, and 48 hours postoperatively.

Results

Baseline characteristics and operative duration were similar. Total intraoperative fentanyl was lower in the SNB group compared to WI group (4.62 [3.89-5.36] vs 6.25 [5.1-6.94], $p < 0.001$). Median MAP after Mayfield head holder application was lower in group B compared with group I: 76.3 [67.7-81.3] vs 85.0 [78.0-92.0] mmHg. No difference in median VAS at 1 h and 3 h ($p = 0.829$, $p = 0.939$). Significantly lower VAS scores were observed in

SNB group at 24 h (median 8 [0-20] vs 20 [8-33], $p=0.014$) and 48 h (3 [0-12.5] vs 10 [0-20], $p=0.030$). Time to first rescue analgesic and total paracetamol consumption were comparable between groups (315 [132.5-360] vs 300 [133-375] minutes, $p=0.869$; 3000 [2000-3000] vs 3000 [2000-4000] mg, $p=0.88$). Ketorolac consumption was lower in SNB group (median 60 [60-90] mg vs 120 [60-150] mg, $p<0.001$).

Conclusions

Conclusions: Preincision scalp nerve blockade reduced intraoperative fentanyl requirement, lowered VAS scores at 24 and 48 hours, decreased ketorolac use compared with wound infiltration after supratentorial craniotomy. SNB may enhance pain control throughout the perioperative period.

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Left ventricular hemodynamic forces as novel biomarkers of reverse remodelling after transcatheter versus surgical aortic valve replacement: a CMR study

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Introduction

LV mass regression after aortic valve replacement (AVR) predicts improved survival, yet traditional metrics, including LVEF, fail to detect early functional recovery [1]. Hemodynamic forces (HDFs) – CMR-derived biomarkers quantifying intraventricular blood flow dynamics – predict cardiovascular events independently of LVEF in heart failure populations [2]. Whether HDF detects functional recovery during reverse remodelling after AVR and whether recovery patterns differ between transcatheter (TAVR) and surgical (SAVR) approaches remain unknown.

Aim

To characterize temporal changes in LV mass and HDF at 6 months following TAVR versus SAVR, and determine whether HDF parameters correlate with structural reverse remodelling.

Methods

This single-centre prospective CMR study enrolled 37 patients with severe symptomatic aortic stenosis (AS) with preserved LVEF $\geq 50\%$ and no significant concomitant valvular disease undergoing clinically indicated TAVR (n=19) or SAVR (n=18). CMR imaging was performed on a 3T MRI scanner at baseline and 6 months post-intervention. Quantitative analysis included LV volumes, LVEF, myocardial mass, and four HDF parameters: LV longitudinal force (LVLF), LV systolic longitudinal force (LVsysLF), LV impulse force, and LV suction force (Medis Suite: QMass 8.1, QStrain 4.4). Paired t-tests compared pre- and post-intervention parameters; Pearson correlation assessed relationships between HDF changes

and LV mass regression.

Results

Both groups demonstrated significant LV mass regression at 6 months: TAVR (LVM: 125.12 ± 29.69 g vs. 102.49 ± 18.22 g, $p=0.016$; LVMi: 69.09 ± 14.31 vs. 58.14 ± 10.82 g/m², $p<0.001$) and SAVR (LVM: 164.02 ± 54.19 g vs. 119.27 ± 32.68 g, $p<0.001$; LVMi: 80.04 ± 22.56 vs. 59.44 ± 14.55 g/m², $p<0.001$). LVEDV, LVESV, and LVEF remained unchanged in both groups.

HDF analysis revealed differential recovery patterns. TAVR patients demonstrated significant increases in LVLf (12.95 ± 3.75 % vs. 17.19 ± 6.93 %, $p=0.007$), LVsysLf (15.43 ± 4.33 % vs. 22.26 ± 8.4 %, $p<0.001$), and LV impulse force (15.43 ± 5.12 % vs. 24.26 ± 8.84 %, $p<0.001$). In contrast, SAVR patients - despite greater mass regression - showed significant improvement only in LV impulse force (17.64 ± 7.01 % vs. 21.38 ± 7.57 %, $p=0.039$).

In TAVR patients, LV mass demonstrated inverse correlations with all HDF parameters (LVLf: $r=-0.488$, $p=0.034$; LVsysLf: $r=-0.502$, $p=0.029$; LV impulse force: $r=-0.504$, $p=0.028$; LV suction force: $r=-0.554$, $p=0.014$), while LVEF positively correlated with LVsysLf ($r=0.544$, $p=0.016$) and LV impulse force ($r=0.602$, $p=0.006$). In SAVR patients, only LV suction force correlated with LV mass ($r=-0.474$, $p=0.047$).

Conclusions

CMR-derived HDFs detect functional recovery after AVR independently of LVEF. More comprehensive HDF improvement in TAVR despite less mass regression suggests distinct adaptation pathways between valve replacement strategies. Validation with clinical outcomes is warranted.

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Relationship between left ventricular strain and hemodynamic forces assessed by CMR in severe aortic stenosis patients undergoing transcatheter or surgical aortic valve replacement

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Introduction

Severe aortic stenosis (AS) results in chronic left ventricular (LV) pressure overload, leading to myocardial remodeling and progressive ventricular dysfunction. Cardiac magnetic resonance (CMR)-derived strain imaging enables sensitive detection of subclinical LV dysfunction and reverse remodeling after valve replacement, while assessment of LV hemodynamic forces (HDF) has emerged as a novel approach for evaluating intracavitary flow dynamics and ventricular performance [1,2]. However, the relationship between myocardial deformation and HDF following transcatheter (TAVR) versus surgical aortic valve replacement (SAVR) remains poorly understood.

Aim

To evaluate changes in LV global longitudinal strain (GLS), global circumferential strain (GCS), and LV hemodynamic forces following TAVR or SAVR, and to investigate their relationship during post-procedural ventricular remodeling.

Methods

This prospective single-center CMR study included 37 patients with symptomatic severe AS and preserved LV ejection fraction ($\geq 50\%$) undergoing TAVR ($n=19$) or SAVR ($n=18$). Patients underwent 3T CMR imaging before intervention and at 6-month follow-up. GLS, GCS, and four HDF parameters—LV longitudinal force (LVLF), LV systolic longitudinal force (LVsysLF), LV impulse force, and LV suction force—were quantified using Medis Suite (QMass 8.1). Pre- and post-procedural changes were assessed using paired t-tests, and correlations between strain and HDF parameters were evaluated using Pearson correlation

analysis.

Results

At 6 months, the SAVR group demonstrated a significant reduction in GLS ($-16.96 \pm 4.37\%$ vs. $-8.50 \pm 5.21\%$, $p=0.012$), whereas GLS remained stable following TAVR. GCS did not significantly change in either group.

Both treatment strategies were associated with increased LV hemodynamic forces during follow-up, although changes were more pronounced after TAVR. In the TAVR cohort, significant increases were observed in LVLF ($12.95 \pm 3.71\%$ vs. $17.19 \pm 6.93\%$, $p=0.007$), LVsysLF ($12.95 \pm 3.71\%$ vs. $22.26 \pm 8.40\%$, $p<0.001$), and LV impulse force ($16.73 \pm 5.11\%$ vs. $24.26 \pm 8.84\%$, $p<0.001$). In the SAVR group, only LV impulse force significantly increased following intervention ($17.64 \pm 7.01\%$ vs. $21.38 \pm 7.57\%$, $p=0.039$). In the TAVR group, GLS demonstrated significant inverse correlations with LVLF ($r=-0.556$, $p=0.013$), LVsysLF ($r=-0.605$, $p=0.006$), and particularly LV impulse force ($r=-0.765$, $p<0.001$). In contrast, the SAVR group showed inverse correlations between LV suction force and both GLS ($r=-0.626$, $p=0.005$) and GCS ($r=-0.653$, $p=0.003$).

Conclusions

TAVR and SAVR are associated with distinct patterns of LV functional adaptation and flow dynamic remodeling after valve replacement. TAVR demonstrated greater augmentation of longitudinal hemodynamic forces with preserved strain parameters, whereas SAVR was associated with reduced GLS and different HDF interaction patterns. These findings suggest that combined assessment of myocardial strain and LV hemodynamic forces may provide additional insight into ventricular recovery mechanisms following interventional and surgical treatment of severe aortic stenosis.

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Association of cranial base and upper cervical spine ossification changes with tooth agenesis and impaction: a systematic review

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Introduction

Sella turcica bridging (STB) and ponticulus posticus (PP) can be identified on lateral cephalometric radiographs (LCRs) [1]. The sella turcica, cervical vertebrae and dentition are related in embryological development through neural crest cells [1-5]. Therefore, cranial base and upper cervical spine anomalies may be associated with dental developmental anomalies [4].

Aim

To evaluate the associations of STB and PP with tooth impaction and tooth agenesis.

Methods

A systematic literature review was performed according to the PRISMA statement. The search was performed using PubMed, Web of Science, and Google Scholar databases. The inclusion criteria comprised English-language retrospective studies published between 2022 and 2026 that assessed STB and PP using LCRs. A total of 7 studies were included. The risk of bias was assessed using the Newcastle-Ottawa Scale.

Results

PP was significantly more prevalent in patients with maxillary impacted canines (MIC) ($p < 0.05$) but not in those with palatally impacted canines (PIC) alone [1, 3]. Moreover, no significant association was found between PP and overall tooth impaction [2, 4] or tooth agenesis [2-4]. Partial and complete STB were more common in patients with MIC ($p < 0.001$) [1], whereas only complete STB was more frequent in patients with PIC ($p < 0.05$) [6]. Three studies investigated the association of STB with overall tooth impaction and agenesis [2, 5, 7]. In two studies, STB was significantly more common in patients with tooth impaction ($p < 0.05$) [5, 7], whereas one study found no significant correlation ($p > 0.05$) [2]. Overall, only one study found a significant association between STB and tooth agenesis ($p < 0.05$) [5].

Conclusions

The present findings indicate that PP may be associated with maxillary canine impaction, whereas STB is linked to overall tooth impaction. However, the association with tooth agenesis is inconsistent across studies. Further research is needed to clarify these relationships.

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Molecular Allergy Profile Changes During One Year of House Dust Mite Allergen-Specific Immunotherapy: A Pilot Study

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Introduction

House dust mite allergy is a major cause of persistent allergic rhinitis. Compared with traditional extract-based allergy diagnostics, molecular allergy diagnostics allows more precise identification of sensitization to individual allergen components and may improve selection of allergen-specific immunotherapy. However, data on how allergen-specific immunotherapy can change molecular sensitization profiles remains limited. This pilot study aimed to evaluate changes in sensitization profiles to house dust mite allergen molecules during the first year of allergen-specific immunotherapy.

Aim

To evaluate changes in molecular sensitization profiles to house dust mite allergen components during the first year of allergen-specific immunotherapy.

Methods

Peripheral blood samples from five patients with allergic rhinitis were collected before initiation of house dust mite (HDM) allergen-specific immunotherapy and after 1 year of treatment. A molecular allergy diagnostic system was used to evaluate changes in sensitization profiles to HDM allergen components.

Results

Due to the very small sample size, no statistically significant changes in molecular sensitization profiles were observed after one year of allergen-specific immunotherapy. Evaluation of *Dermatophagoides pteronyssinus* allergen components showed a decrease in Der p 2 sIgE levels from 4.40 (2.28-9.26) at baseline to 3.41 (2.18-7.55) kUA/L at 12 months of treatment, and in Der p 21, sIgE levels decreased from 1.80 (1.46-5.09) to 1.20 (1.10-3.05) kUA/L. In contrast, Der p 23 sIgE levels increased in four patients, from 0.28 (0.15-0.60) to 0.73 (0.39-0.94) kUA/L, two patients developed new sensitization to Der p 23.

Evaluation of *Dermatophagoides farinae* allergen components revealed a consistent decrease in Der f 2 sIgE levels from 5.03 (1.63-8.29) kUA/L to 2.50 (1.60-6.14) kUA/L.

Conclusions

Molecular sensitization profiles may change during HDM allergen-specific immunotherapy. Decreasing sIgE levels were observed for Der p 2, Der p 21 and Der f 2, while increasing levels were observed for Der p 23. Given the small sample size, these findings should be confirmed in larger studies.

Integrating Endocrine Biomarker with Ultrasonography for Precision Reproductive Management in Warmblood Mares

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Introduction

Efficient reproductive management is essential in equine artificial insemination programs due to the high economic cost of stallion semen and pregnancy rates maximisation. [1,2]. Transrectal ultrasonography remains the gold standard for reproductive evaluation, structural findings do not always reflect functional reproductive competence [4]. Successful conception depends on multiple endocrine and inflammatory processes that cannot be fully assessed using ultrasonography alone [1,3]. Increasing attention is being given to biomarkers that may provide additional insight into mare reproductive potential and improve fertility prediction [4].

Aim

To evaluate if estradiol (E2) concentration at the time of insemination could provide additional information about reproductive competence and pregnancy outcome in Warmblood mares, beyond routine ultrasonographic assessment.

Methods

Thirty-one Warmblood mares aged 3–21 years were artificially inseminated at the Lithuanian University of Health Sciences Large Animal Clinic in 2025. Mares were monitored daily during estrus using transrectal ultrasonography to evaluate dominant follicle size and uterine edema. Ovulation was induced with hCG when a follicle ≥ 35 mm was detected, and artificial insemination with fresh cooled semen was performed within 24 h.

Blood samples were collected aseptically from jugular vein immediately prior to insemination, and serum E2 concentration were determined using ELISA assays. The analyses were performed in duplicate

Pregnancy diagnosis was performed 14 days after ovulation using transrectal ultrasonography.

The evaluated parameters included mare age, parity, follicle size, uterine edema score, serum E2 and pregnancy outcome. Statistical analysis was performed using IBM SPSS Statistics non-parametric tests, with significance set at $p < 0.05$.

Results

E2 concentration measured at the time of insemination was significantly higher in pregnant mares compared to non-pregnant mares ($p < 0.01$). Mares with estradiol concentrations ≤ 95 pg/mL had a markedly lower pregnancy rate (12.5%) compared to mares with concentrations of 96–382 pg/mL (73.3%) and >382 pg/mL (75.0%).

Conclusion



E2 concentration at the time of insemination was associated with pregnancy outcome, suggesting its potential as a biomarker of functional follicular competence in mares. Further studies are needed to validate its clinical applicability and establish reliable thresholds.

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Recovery dynamics of milk yield, feeding time and fat-to-protein ratio after herd-level stress in dairy cows

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Introduction

Stressors in dairy cattle can affect feeding-related behaviour, physiological adaptation responses, milk synthesis and metabolic processes (1). Management-related stress events, including collective handling and vaccination procedures, may influence feeding behaviour, milk production and milk composition in dairy herds. Evaluating short-term recovery after such events is important for understanding the magnitude and duration of their impact (1, 2).

Aim

To analyse the short-term dynamics of milk yield, feeding time and fat-to-protein ratio in dairy cows following a herd-level stress event.

Methods

In this longitudinal observational study, automatically recorded data from automated milking system were analysed in 50 dairy cows over a 13-day period surrounding a herd-level stress event associated with vaccination. Milk yield, feeding time and fat-to-protein ratio were evaluated. Cow-level pre- and post-event values were compared using paired-sample analysis, and changes were expressed as absolute and percentage differences from the pre-event baseline.

Results

Milk yield showed a transient decrease after the stress event, reaching its lowest value on day +1 (46.47 kg; -8.26% from baseline) and recovering to baseline by day +6 (50.88 kg). Overall post-event milk yield was significantly reduced compared with the pre-event period (-1.66 kg; -3.27%; $p = 0.0001$). Feeding time also decreased, with the greatest reduction on day +1 (-26.48 min; -14.12% from baseline) and a significant overall post-event decline (-10.82 min; -5.77%; $p = 0.0016$). Fat-to-protein ratio increased significantly after the event

(+0.047; +4.13%; $p < 0.0001$), with the most pronounced rise observed on day +2.

Conclusions

The herd-level stress event was associated with acute but reversible changes in productivity and feeding behaviour. Milk yield recovered to baseline by day +6, whereas the post-event increase in fat-to-protein ratio may reflect a transient alteration in energy balance. These findings highlight the value of automated monitoring for detecting short-term stress responses in dairy cows.

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UNUSUAL PROGRESSIVE TEAT LESIONS IN PRIMIPAROUS DAIRY COWS IN AN AUTOMATED MILKING HERD: A CASE SERIES

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Introduction

Teat lesions in dairy cows negatively affect udder health, milk production, and animal welfare (1). However, progressing teat lesions with rapid fibrosis in primiparous cows remain poorly described (2).

Aim

To describe an outbreak of progressive teat lesions in primiparous dairy cows and investigate potential contributing factors.

Methods

An observational case series investigation was conducted on a Lithuanian dairy farm with 1,500 lactating Holstein cows. Between January and May 2026, 35 primiparous cows with teat lesions were identified. Clinical examination, photographic documentation, herd management assessment, and epidemiological investigation were performed during two herd visits. Blood and milk samples were collected from affected cows for serum biochemistry, Infectious bovine rhinotracheitis (IBR) serology, bacteriological culture, and antimicrobial susceptibility testing. Additional cows with newly developed lesions were tested for blood β -hydroxybutyrate concentrations.

Results

Most affected cows originated from two groups composed exclusively of primiparous cows milked with automated milking systems. Abrasive teat lesions were first observed 2–3 weeks after calving, typically affecting a single teat on the medial surface. Lesions were frequently associated with fibrosis, teat induration, impaired milk flow, and loss of teat functionality.

Self-trauma and teat biting were observed in several cows, while mastitis occurred as a secondary complication. All tested cows were positive for IBR gB and gE antibodies. Milk cultures revealed no consistent pathogen. Biochemical analysis demonstrated decreased magnesium and increased GGT concentrations in all tested cows. No associations with genetics, introduction of new animals, or technical deficiencies were identified.

Conclusions

This case highlights the diagnostic challenges of atypical teat lesions in primiparous dairy cows and suggests possible multifactorial involvement of infectious, managemental, and immunological factors.

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