increase in hepatic steatosis in marmosets as observed in humans. Lipidomic studies were also performed using blood samples from male and female marmosets to investigate age-associated changes in specific lipid species, which are characteristic of aberrant lipid metabolism. Analysis of the results revealed significant decreases in several phosphatidylethanolamine, phosphatidylcholine, and sphingomyelin species in the plasma of old marmosets compared to young marmosets. We are now performing studies to determine whether the observed changes in different lipid species could influence the development of cardiovascular disease and provide new insights underlying the mechanisms of NAFLD development with aging.

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Generation of Affinity Purified Antibody Reagents for Specific Determination of Efruxifermin in Biological Matrices

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Efruxifermin (EFX) is a novel Fc-fusion analog of human fibroblast growth factor 21 (FGF21), currently in clinical development as a potential treatment for non-alcoholic steatohepatitis (NASH). Each molecule of EFX consists of two modified FGF21 molecules, each attached at their N-termini to a human IgG1 Fc domain by a short polyglycine-serine linker. The FGF21 moiety of EFX incorporates three amino acid substitutions (L98R, P171G, and A180E relative to native FGF21). Two of these are proximal to the C-terminus (P171G and A180E), and reduce cleavage and inactivation by an endogenous protease, fibroblast activation protein (FAP), thereby prolonging its half-life. Fusion to human IgG1 Fc domain further extends circulating half-life, enabling once-weekly subcutaneous dosing. Accordingly, to support on-going clinical development of EFX, a specific assay is needed to distinguish intact EFX from both endogenous FGF21 and any *in vivo* biotransformation products of EFX that display reduced pharmacology. To maximize the antigenicity of EFX, FGF21 amino acid sequences were compared across species. Based on this, an antibody generation campaign was initiated in both rabbits and chickens. Comparison of titer responses against EFX and human FGF21 suggested that antisera from chickens was superior to rabbit antisera. Following a scaled-up, 12-week antibody campaign, antisera were purified by a combination of batch and column chromatographic procedures. By exploiting differences in structure and amino acid sequence of EFX relative to human FGF21, a purification strategy was designed to isolate chicken antibodies with increased specificity for EFX unique sequences. This reagent is being used as a capture antibody in the development of a non-competitive ECLIA employing chemiluminescence detection. Presently, a number of different antibodies are being evaluated for potential pairing with the specific capture. We conclude that application of affinity purified chicken anti-EFX IgY will enable sensitive and specific determination of EFX in biological matrices with decreased cross-reactivity from endogenous hFGF21 and EFX metabolites.

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Identification of Diagnostic Plasma Biomarkers of Coronary Microvascular Disease in Postmenopausal Women Using Machine Learning Methods

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Introduction: Coronary microvascular disease (CMD) affects small arteries that feed the heart and is more prevalent in postmenopausal women. Since CMD and Coronary artery disease (CAD) have distinct pathologies, but are treated the same way, the majority of the patients with CMD do not receive a proper diagnosis and treatment, which in turn results in higher rates of adverse future events such as heart failure, sudden cardiac death, and acute coronary syndrome (ACS). Previously, we performed full metabolite profiling of plasma samples using GC-MS analysis and tested their classification performance using machine learning approaches. This initial proof-of-concept study showed that plasma metabolite profiles can be used to develop diagnostic signatures for CMD. In the current study, we hypothesize that plasma metabolite and protein composition is different for postmenopausal women with no heart disease, with CAD, or with CMD. **Methods:** We obtained plasma samples from 70 postmenopausal women who are healthy, women who have CMD, and women who have CAD at the time of blood collection. In addition to GC-MS metabolite profiles, we performed LC-MS metabolomic profiling, and proteomic profiling of a panel of 92 proteins that were implicated in cardiometabolic disease. We identified a combination of metabolites and proteins, and further tested their classification performance using machine learning approaches to identify potential circulating biomarkers for CMD. **Results:** We identified a comprehensive list of metabolites and proteins that were involved in endothelial cell function, nitric oxide metabolism and inflammation, which significantly different in plasma from women with CMD. We further validated difference in the level of several protein biomarkers, such as RAGE, PTX3, AGRP, CNTN1, and MMP-3, which are statistically significantly higher in postmenopausal women with CMD when compared with healthy women or women with CAD. **Conclusion:** Our research identified a group of potential molecules that can be used in the design of easy and low-cost blood biomarkers for the clinical diagnosis of CMD.

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Impact of Hypertriglyceridemia on Outcome of Adult Patient Admitted With Hyperthyroidism: Analysis of the National Inpatient Sample 2016–2017