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Background and Aims: Among the HDL atheroprotective function, the most known is the ability of promoting cholesterol efflux from macrophages, termed cholesterol efflux capacity (CEC) and considered a better predictor of cardiovascular disease (CVD) than HDL levels. Moreover, the capacity of serum to load macrophages with cholesterol (cholesterol loading capacity, CLC) represents an index of serum pro-atherogenic potential. As transgender individuals are exposed to lifelong exogenous hormone therapy, we investigated whether HDL-CEC, HDL subclasses and serum CLC are affected by hormone treatment.

Methods: HDL-CEC and serum CLC were evaluated in a cohort of 15 trans men and 15 trans women at baseline and after 12 months of hormone therapies. Total HDL-CEC and its main contributors ABCA1 and ABCG1 HDL-CEC and HDL-CEC by aqueous diffusion were determined by a cell radioisotopic technique, serum CLC by a fluorimetric assay, HDL subclass distribution by 2D electrophoresis.
Results: In trans women, total HDL-CEC decreased by 10.8% and ABCA1 HDL-CEC by 23.8%, independently of HDL-C changes; aqueous diffusion HDL-CEC decreased by 4.8%. In trans men, only aqueous diffusion HDL-CEC decreased significantly (-9.8%). HDL subclasses distribution (e.g. pre-beta HDL) were not modified by hormone therapy in both groups. Serum CLC was not affected by hormonal treatment.
Conclusions: In trans women total HDL-CEC decreased after hormone therapy, mainly due to a reduction in ABCA1 HDL-CEC however no changes in HDL levels and subclass distribution occurred. Serum CLC did not change after hormone therapy. These findings might contribute to a higher CVD risk in trans women during feminizing hormone therapy.

P225 / #1169, E-POSTERS TOPIC: *2. LIPIDS AND LIPOPROTEINS / 2.06 CHOLESTEROL EFFLUX AND REVERSE CHOLESTEROL TRANSPORT.* CHOLESTEROL EFFLUX CAPACITY IS ASSOCIATED WITH INFLAMMATION LEVEL AND MONOCYTE-PLATELET AGGREGATES IN HEALTHY MEN.

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Background and Aims: It is well established that HDL particles have antiatherogenic properties. However, there are conflicting evidence in regards to HDL particle function and its association with various CVD risk factors. The aim of our study was to analyze associations between the marker of HDL function - cholesterol efflux capacity (CEC) and traditional (age, serum lipids, CRP) and emerging (monocyte-platelet aggregates (MPAs)) CVD risk markers.

Methods: CEC of 62 apparently healthy men (aged 25-55 years) was measured using J774a.1 murine macrophage cell line and fluorescent NBD-cholesterol. ApoB-containing lipoproteins were removed from blood serum by PEG precipitation and the removal was evaluated by lipoprotein gel electrophoresis. Monocyte-platelet (MO/CD42a) and platelet-classical monocyte ($CD14^{++}/CD16^{-}$) aggregates were evaluated by flow-cytometry.
Results: CEC median of healthy men was 31.85 %. CEC in middle-aged (> 40 y.) men was significantly higher than in young men (34.88 % *vs.* 31.18 %, U = 245, p = 0.019). CEC was not associated with serum lipid markers. However, CEC differed significantly depending on serum CRP levels ($\chi^2(2) = 6.185$, p = 0.045, ≤ 1 mg/L *vs.* 1-3 mg/L *vs.* > 3 mg/L). Furthermore, we discovered statistically significant, but weak negative associations between cholesterol efflux capacity and platelet-monocyte (MO/CD42a) (r(62)= -0.251, p = 0.049) and platelet-classical monocyte ($CD14^{++}/CD16^{-}$) aggregates (MO1/CD42a) (r(62)= -0.293, p = 0.021).
Conclusions: Our findings suggest that CEC is associated with inflammation level and platelet monocyte-aggregates. However, CEC was not associated with serum lipid markers, such as total cholesterol, LDL-C, HDL-C and triacylglycerols.

P226 / #241, E-POSTERS TOPIC: *2. LIPIDS AND LIPOPROTEINS / 2.07LIPIDS BEYOND CHOLESTEROL AND TRIGLYCERIDES (LIPIDOMICS).* EFFORTLESS EXTRACTION OF INDIVIDUAL LIPID MOIETIES FROM LIPIDOMICS DATASETS: LIPUTILS, A PYTHON MODULE

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Background and Aims: Lipidomic analyses tackle the problem of characterizing the lipid components of given cells, tissues and organisms by means of chromatographic separations coupled to high-resolution, tandem mass spectrometry analyses. Like other -omic techniques, lipidomic analyses have rapidly transitioned from a niche commodity to a widespread tool. A number of software tools have been developed to help in the daunting task of mass spectrometry signal processing and cleaning, peak analysis and compound identification, and a typical finished lipidomic dataset contains hundreds to thousands of individual molecular lipid species. To provide all researchers - including those without specific technical expertise in mass spectrometry and bioinformatics skills - the possibility of broadening the exploration of their lipidomic datasets, squeezing out additional information that would otherwise be discarded, we have developed liputils.

Methods: It's a Python module that specializes in the extraction of fatty acid moieties from all individual molecular lipids of a lipidomic dataset.
Results: There is no prerequisite data format, as liputils extracts lipid residues from RefMet-compliant textual identifiers, as well as from annotations of other commercially available services. Plus, with its new graphical user interface (GUI), the processing of even the most complex datasets is performed with a couple of clicks.
Conclusions: We herein provide hands-on examples of real-world data processing with liputils.

P227 / #272, E-POSTERS TOPIC: *2. LIPIDS AND LIPOPROTEINS / 2.07LIPIDS BEYOND CHOLESTEROL AND TRIGLYCERIDES (LIPIDOMICS).* THE FEATURES OF SPHINGOLIPIDS' PROFILE IN YOUNG PATIENTS WITH ATHEROTHROMBOTIC STROKE

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Background and Aims: Sphingolipids may contribute to the development of early atherosclerosis. The aim of the study is to determine the features of sphingolipids profile in young patients with stroke.

Methods: The study included 47 lipid-lowering drug-naive patients (9 (19.1%) with early (at the age of under 55 for men and 60 for women) stroke, 38 (80.9%) has the stable manifestation of atherosclerosis or early dyslipidemia). A study of fasting blood lipids and sphingolipids parameters was performed on the first day from the stroke's onset. Sphingolipids were detected by chromatography-mass spectrometry method.
Results: In group of patients with stroke the level of sphingomyelins SM 18-0 (5152 vs 2888, p=0,017), SM 20-0 (38085 vs 19504, p<0,001), SM22-0 (10970 vs 7535, p=0,016), ceramides C22-1 (189,2 vs 42,5, p=0,019),