

Lipid profile of epicardial adipose tissue in obese individuals – preliminary data

Bijelić N¹, Zjalić M², Rođak E¹, Vučić D³, Debeljak Ž^{4,5}, Dumenčić B^{6,7}, Rajc J⁶, Belovari T¹, Selthofer-Relatić K.^{8,9}

¹Department of Histology and Embryology, Faculty of Medicine, J. Huttlera 4, 31000 Osijek, Croatia; ²Laboratory of Neurobiology, Department of Medical Biology and Genetics, Faculty of Medicine Osijek, Josip Juraj Strossmayer University of Osijek, J. Huttlera 4, HR-31000 Osijek, Croatia.; ³Department for Internal Medicine, Division of Cardiology, General Hospital Doctor Josip Benčević, Ul. Andrije Štampara, HR-35000, Slavonski Brod, Croatia; ⁴Clinical Institute of Laboratory Diagnostics, University Hospital Osijek, J. Huttlera 4, HR-31000 Osijek, Croatia; ⁵Department of Pharmacology, Faculty of Medicine Osijek, Josip Juraj Strossmayer University of Osijek, J. Huttlera 4, HR-31000 Osijek, Croatia; ⁶Department of Pathology and Forensic Medicine, University Hospital Center Osijek, Huttlera 4, HR-31000 Osijek, Croatia; ⁷Department of Pathology and Forensic Medicine, Faculty of Medicine, J. Huttlera 4, 31000 Osijek, Croatia; ⁸Department of Internal Medicine, Faculty of Medicine, University Josip Juraj Strossmayer in Osijek, Huttlera 4, HR-31000 Osijek, Croatia; ⁹Department of Heart and Vascular Diseases, University Center Hospital Osijek, Huttlera 4, HR-31000 Osijek, Croatia

Introduction

With its endocrine and metabolic activity, visceral adipose tissue (VAT) is more than a storage organ. Research shows that VAT has a role in the development of cardiovascular disorders. The influence of epicardial adipose tissue (EAT, a subset of VAT) morphology on cardiovascular function and health is still limited (1). Furthermore, the data on the content of lipids and their metabolites in the EAT depending on the amount of VAT are scarce or non-existent. The aim of this pilot study was to characterize lipids and their metabolites in EAT in relation to visceral obesity.

Materials & methods

EAT from 6 obese and 6 non-obese subjects (based on waist circumference) was collected post-mortem and homogenized in 20mM ammonium acetate buffer using Dounce homogenizer. Lipid extraction from the homogenate was performed with Bligh and Dyer's two-phase method (2). Both polar and nonpolar phases were imaged in positive and negative imaging mode on Bruker UltrafleXtreme MALDI-TOF device in the 200-1500 m/z range. The matrices used were dihydrobenzoic acid and 9-aminoacridine, respectively. Collected data were analyzed using R statistical software with FELLA and KEGGEST packages.

Results

Out of 106 determined putative metabolites, C08320 – Lignoceric acid was 2.37 times more abundant in the obese group ($p=0.0396$). Out of the 106 molecules, 13.5% were upregulated, 11.9% were downregulated in the obese group and the rest were unchanged compared to the non-obese group. FELLA enrichment revealed alteration in fatty acid biosynthesis and degradation accompanied with upregulation in glycosphingolipid biosynthesis.

Conclusion

Preliminary data indicate a metabolic difference in EAT of obese patients. None of the subjects suffered from Gaucher's disease, so it may be assumed that lignoceric acid is exogenous in nature (from food). This also explains upregulation in glycosphingolipid biosynthesis, lignoceric acid being one of its precursors. The preliminary data showed some changes in EAT of obese patients which are potentially food-related. Larger groups are necessary to draw more definite conclusions.

References

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Table 1. Altered human metabolic pathways in the obese group compared to the control (normal weight) group. p values represent the statistical possibility that a pathway is altered in the obese group.

KEGG ID	Type	Name	p value
hsa01040	pathway	Biosynthesis of unsaturated fatty acids	0.002766
hsa01212	pathway	Fatty acid metabolism	0.007535
hsa00534	pathway	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	0.017895
hsa00532	pathway	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	0.018234
hsa04672	pathway	Intestinal immune network for IgA production	0.018344
hsa00515	Pathway	Mannose type O-glycan biosynthesis	0.020204
hsa00514	Pathway	Other types of O-glycan biosynthesis	0.024774
hsa00140	Pathway	Steroid hormone biosynthesis	0.026294
hsa00062	Pathway	Fatty acid elongation	0.026634
hsa00601	pathway	Glycosphingolipid biosynthesis - lacto and neolacto series	0.030063
hsa00512	pathway	Mucin type O-glycan biosynthesis	0.032563
hsa00533	pathway	Glycosaminoglycan biosynthesis - keratan sulfate	0.034133
hsa00513	pathway	Various types of N-glycan biosynthesis	0.042402
hsa00830	pathway	Retinol metabolism	0.046212
hsa00603	pathway	Glycosphingolipid biosynthesis - globo and isoglobo series	0.046232
hsa05207	pathway	Chemical carcinogenesis - receptor activation	0.049112
hsa04976	pathway	Bile secretion	0.049552

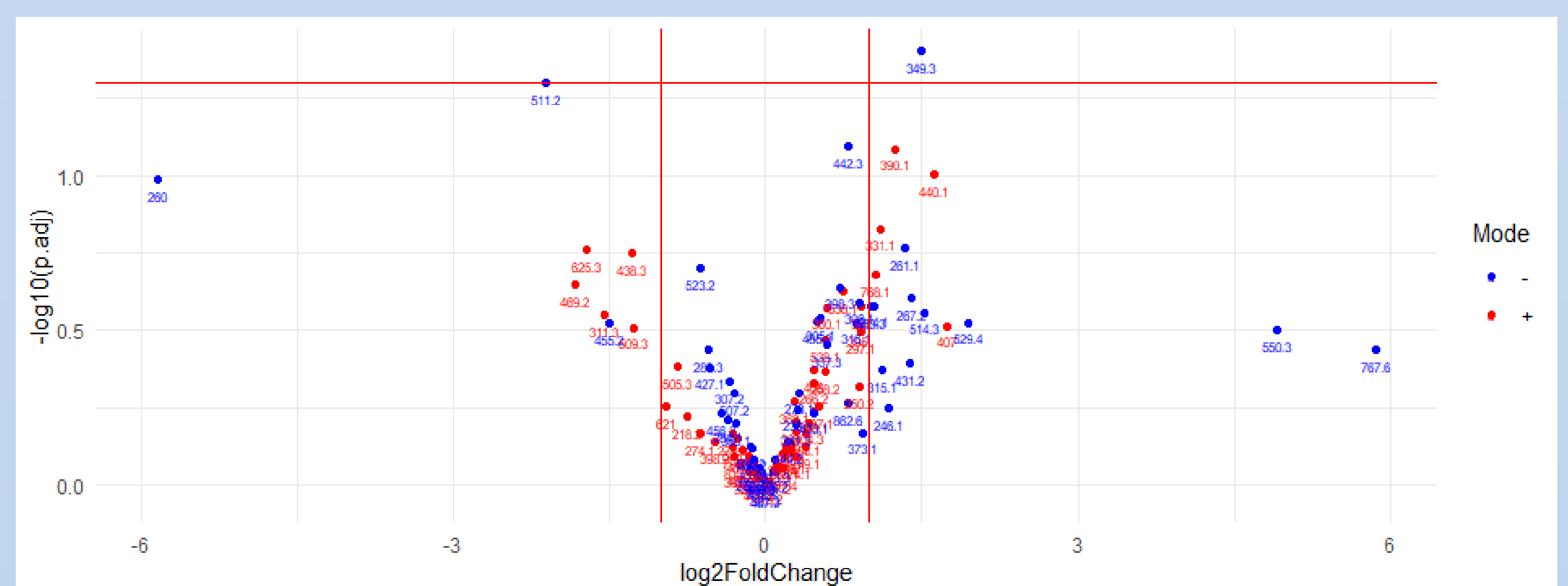


Figure 1. Volcano plot representing data distribution based on two parameters. First parameter is the fold-change of signal intensity compared to the control group (denoted by vertical red lines), and second is statistical significance after false discovery rate correction of p values (denoted by horizontal red line). Analysis was performed in R statistical software.

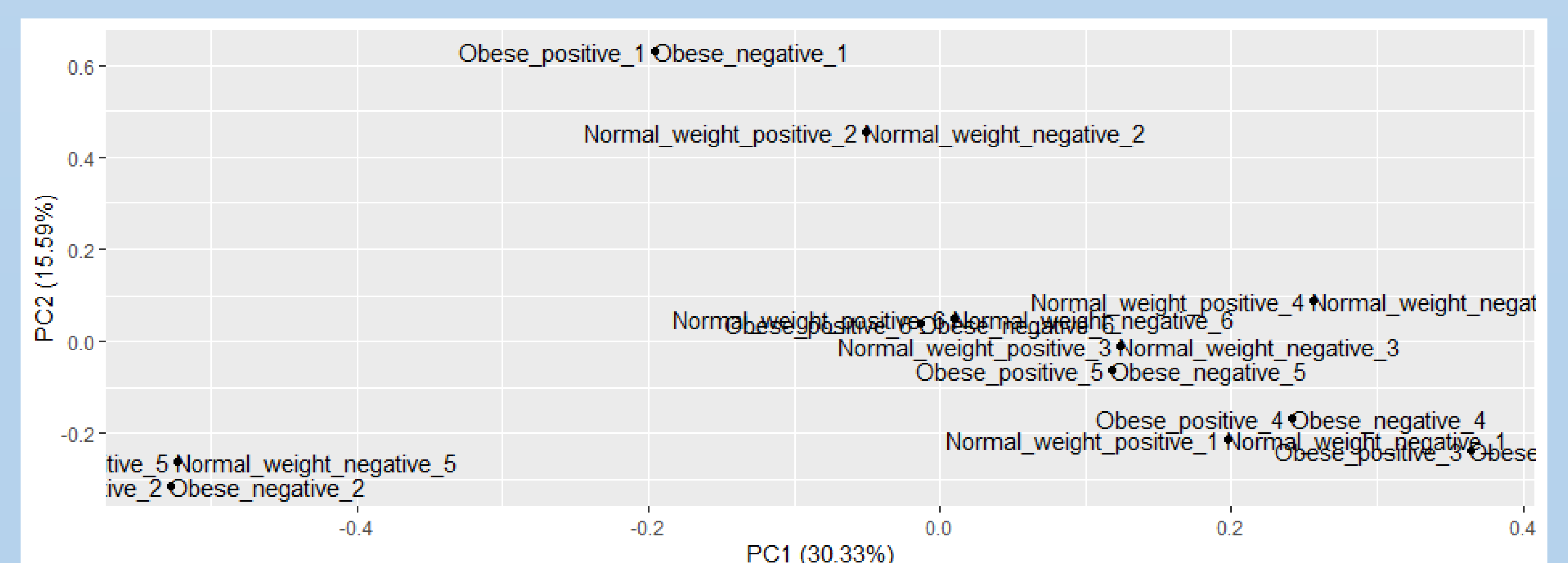


Figure 2. Principal component analysis (PCA) of m/z values from control (normal weight) and obese groups. Data from both positive and negative imaging modes were used in analysis and graph plotting. Analysis was performed in R statistical software.

