

UNTARGETED METABOLOMICS OF EARLY VASCULAR AGING IN HYPERTENSIVE PATIENTS



Renata Wawrzyniak ¹ Katarzyna Polonis ^{1, 2} Emilia Daghir-Wojtkowiak ¹ Anna Szyndler ¹ Marzena Chrostowska ¹ Olle Melander ³ Michał Hoffman ¹ Marta Kordalewska ¹ Joanna Raczak-Gutknecht ¹ Ewa Bartosińska ¹ Roman Kaliszan ¹ Krzysztof Narkiewicz ¹ Michał J. Markuszewski ¹ ¹ Medical University of Gdańsk; ² Mayo Clinic Rochester; ³ Lund University, Malmö

Introduction

Arterial stiffening is a hallmark of early vascular aging (EVA) syndrome and an independent predictor of cardiovascular morbidity and mortality. Early vascular ageing (EVA), reflected by increased pulse wave velocity, has been associated with premature CV diseases manifestation including coronary heart disease and stroke. Potential mechanisms underlying EVA process include arterial stiffening and impaired endothelial function. Small-molecule metabolites may reflect pathological state and serve as novel markers of EVA state.

Aim of the study

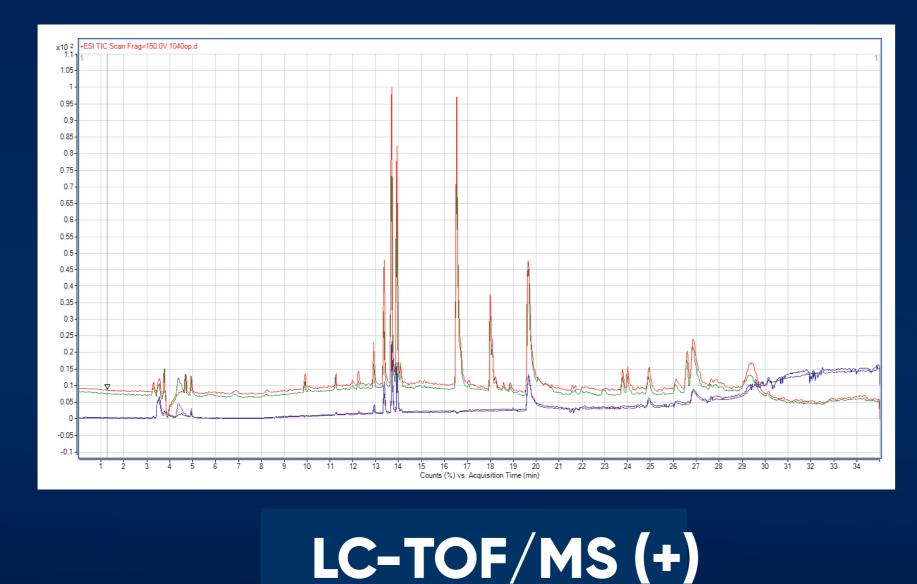
In this case-control study we sought to identify plasma metabolites associated with EVA syndrome in the setting of hypertension. An untargeted metabolomic approach was used to identify plasma metabolites in an age-, BMI-, and sex-matched groups of EVA (n = 79) and non-EVA (n = 73) individuals with hypertension. Principal component analysis (PCA) was used to evaluate quality of analyses and general trends in the data. Hotelling's T2 range was used to detect potential outliers. Least Absolute Shrinkage and Selection Operator (LASSO) were used to select metabolites which contribute the most to recognition between non-EVA and EVA group. A reproducibility of the results was assessed with a resampled-based bootstrap procedure.

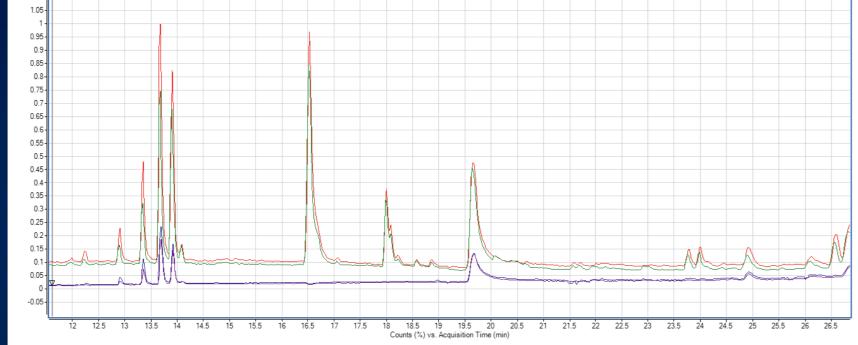
Plasma metabolic fingerprinting

LC-TOF/MS HPLC system (1200 series, Agilent) • RP column: (Discovery HS C18 Supelco, 2.1 x 150 mm, 3μm) • column temperature: 40°C flow rate 0.6 mL/min injection volume: 10 μl mobile phase: A1: H2O + 0.1% formic acid; B1: ACN + 0.1% formic acid gradient elution • time of analysis: 45 min TOF (Agilent 6240)

 polarity positive and negative • full scan from 50 to 1000 m/z capillary voltage - 3000 V(+) 4000V (-)

 scan rate of 1.0 scan per second • nebulizer gas flow rate - 10.5L/min • gas temperature 330°C • nebulizer pressure 52 psig

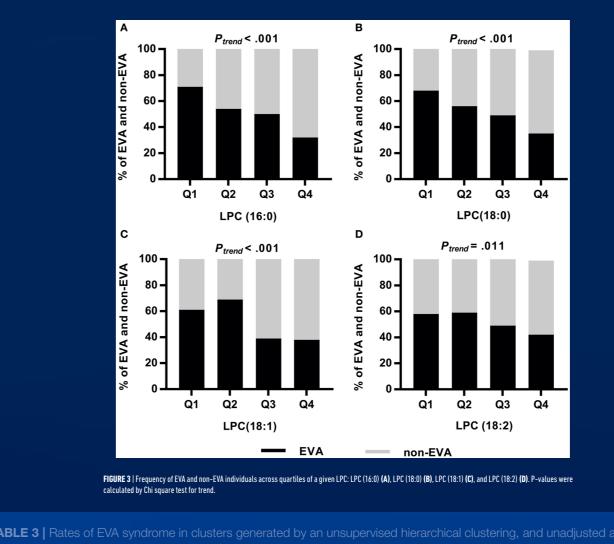




LC-TOF/MS (-)

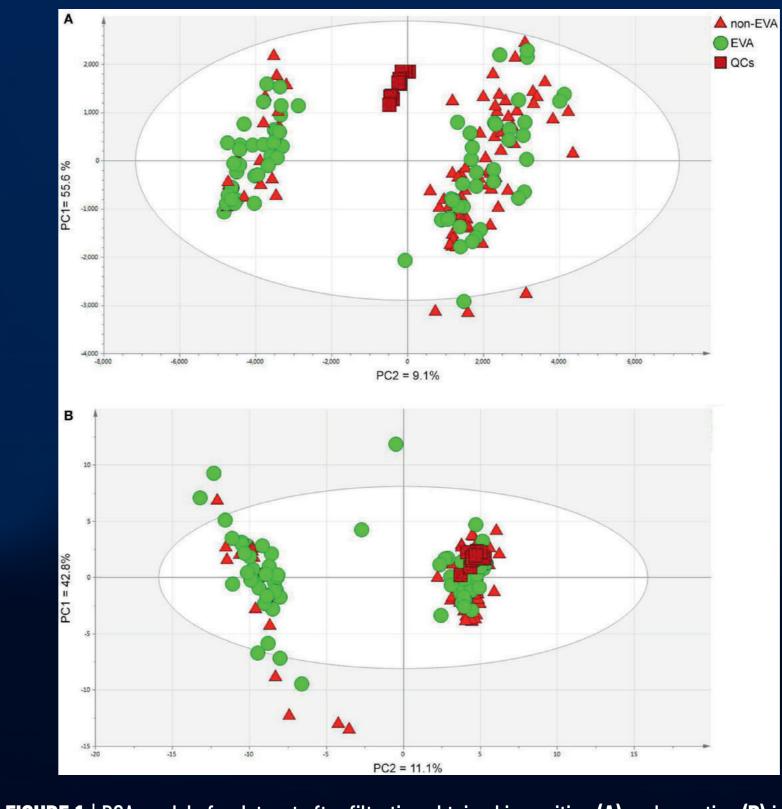
- ✓ The hypertensive individuals were characterized by 4 down-regulated LPCs had 3.8 times higher risk of EVA compared to those with higher LPC levels (OR = 3.8, 95% CI 1.7–8.5, P < 0.001).
- ✓ Our results provide new insights into a metabolomic phenotype of vascular aging and warrants further investigation of negative association of LPCs with EVA status.
- ✓ This study suggests that LPCs are potential candidates to be considered for further evaluation and validation as predictors of EVA in patients with hypertension.
- \checkmark The reproducibility of 4 selected metabolites was found to be within a relatively wide range (39–65%) which is likely a consequence of a relatively small sample size and variability present in the data.



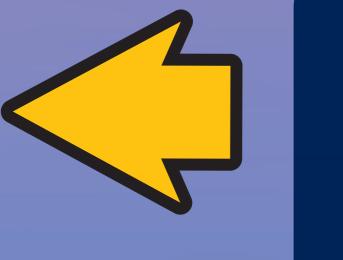


	Model 1 (4 clu	ısters)	Model 2 (3 clusters)			Model 3 (2 clusters)		
	n	% EVA		n	% EVA		n	% EVA
luster 1	107	61%	Cluster 1	107	61%	Cluster 1	107	61%
uster 2	38	29%	Cluster 2	43	33%	Cluster 2	45	31%
uster 3	5	60%	Cluster 3		0%			
luster 4		0%						
dd ratios (ORs): cluster 1	vs. cluster 2						
OR _{unadj} 3.8 (1.7–8.5), P = 0.001			OR _{unadj} 3.2 (1.5–6.7), P = 0.002			OR _{unadj} 3.4 (1.6–7.2), P = 0.001		
OR _{adj1} 5.5 (2.1–14.4), P < 0.001			OR _{adj1} 4.4 (1.8–10.9), P = 0.001			OR _{adj1} 4.8 (1.9–11.7), P < 0.001		
OR_{adi2} 4.9 (1.7–13.8), $P = 0.003$			OR_{adi2} 3.9 (1.5–10.6), $P = 0.007$			OR_{adi2} 4.2 (1.6–11.4), $P = 0.004$		

Checking of quality of analysis

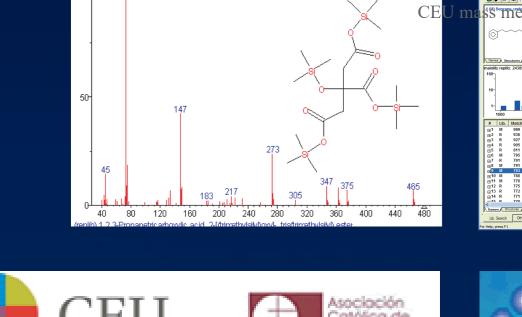


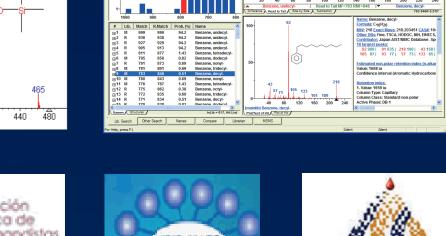
modes. PC1/2—principal component 1/2. Data were log transformed and Pareto or UV scaled in the case of positive and negative ionization modes, respectively. (A) PCs contribution (PC1 = 55.6%and PC2 = 9.1%), **(B)** PCs contribution (PC1 = 42.8%, PC2 = 11.1%).



Metabolite identification

- Accurate masses of features which represented statistically significant differences were searched for structure against the METLIN, KEGG, LIPIDMAPS, HMDB databases and CEU MASS mediator database
- Comparison of the structure of the proposed compound with the spectra obtained by LC-QTOF/MS fragmentation analyses confirms the identity of











Statistical analysis

• All analyses were performed with "penalized" and "rcorr" package in R Core Team (2014) to fit the LASSO model and perform the correlation analysis, respectively. PCAmodeling and plotting were performed with the use of SIMCA software (version P13, Umetrics, Umeå, Sweden).

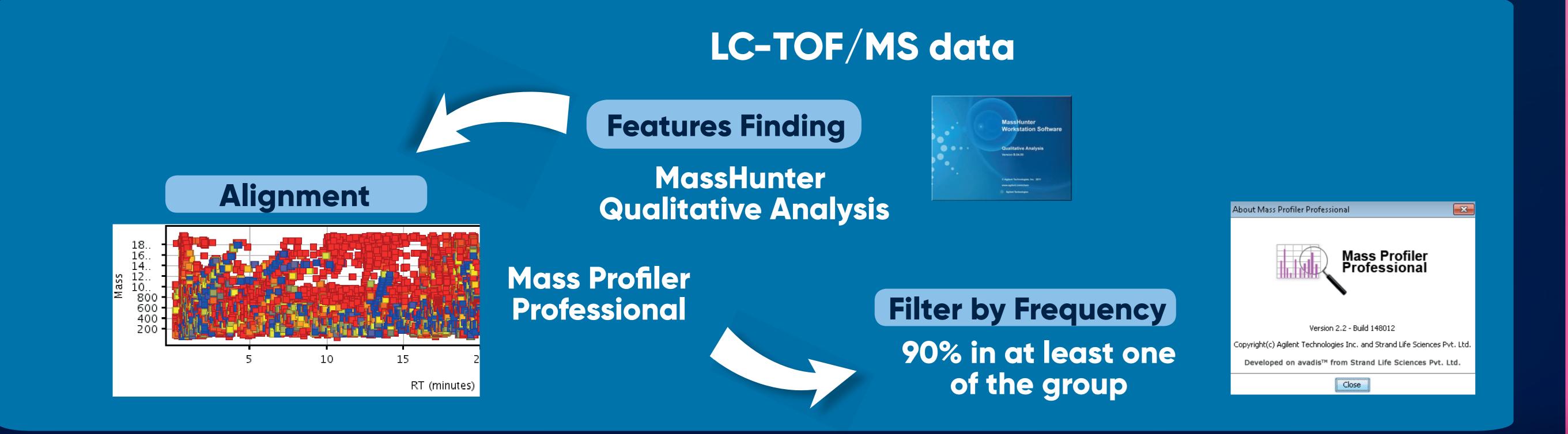
 An unsupervised hierarchical cluster analysis with Ward's method for defining distances between clusters was used to determine a metabolomic signature of EVA. Binary logistic regression was applied to calculate unadjusted and adjusted odds ratios (ORs), to assess the association between given clusters (profiles) and a risk of EVA.







fragmentor 175V



Acknowledgements

blood pressure (SBP) (**B**) and office diastolic blood pressure (**C**) in the entire study population.

• This project was supported by Polish-Norwegian Research Fund (EOG/2007/019), National Science Centre (DEC-2012/07/E/NZ7/04411), Ministry of Science and Higher Education in Poland (0042/IP1/2016/74, 01-0222/08/529), and by the in the field of MS/MS analyses with the use of LC-QTOF/MS (model 6546, Agilent European Union through the European Social Fund under the Operational Programme Knowledge Education Development Technologies, Waldbronn, Germany). 2014-2020 (project POWR.03.02.00-00-1026/17-00)

Authors would also like to thank Łukasz Nowicki from Perlan Technologies for support