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Alteration of plasma acylcarnitines and glycerophospholipids between metabolically healthy and unhealthy overweight subjects

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The objective of this study is to check metabolic profiles of metabolically healthy and unhealthy overweight individuals in order to verify metabolic biomarkers or pathways regulating the different metabolic characteristics of overweight. Metabolic characteristics were obtained from 109 overweight (25kg/m2 ≤ BMI < 30kg/m2) subjects aged 30-65 year. Among them, 34 individuals, whose veceral fat adiposity at L4 is over 100 cm2, were included as metabolically unhealthy overweight group. Metabolically healthy overweight group (n=34), matched for age, gender, and BMI, set as a control group. Despite similar body fat % and total fat mass, measured by using DEXA, metabolically unhealthy overweight group showed higher visceral fat area at L1 and L4 than metabolically healthy overweight group. Metabolically unhealthy overweight subjects had higher blood pressure, lipid profiles, hs-CRP, malondialdehyde, and oxidized LDL, HOMI-IR, and had lower HDL-cholesterol and adiponectin. In metabolic profile analysis, methoxybenzepropanoic acid, α-linolenic acid, docosahexaenoic acid, dodecenoylcarnintine (C12:1), dodecanoylcarnintine (C12), tetradecenoylcarnitine (C14:1), hexadecenoylcarnitine (C16:1), palmitoylcarnitine (C16) and urobillinogen were higher in metabolically unhealthy overweight group than those of metabolically healthy overweight group. In addition, the two groups were distinguished by glycerophospholipid pathway, which showed higher levels of lysophosphatidylethanolamine (lysoPE) (22:6), lysophosphatidylcholine (lysoPC) (22:6) and lysoPC (22:5) in metabolically unhealthy overweight group. In conclusion, inidviduals who have same age, gender, BMI, body fat %, and total fat mass are able to be classified according to metabolic status including long-chain fatty acids, medium chain (C12:1, C12) acylcarnitine (AC), and long chain (C14;1, C16:1, C16) AC levels and glycerophospholipid pathway.

Biography

Seung Han Baek has completed his PhD in 2014 at Cancer Biology Lab, Dept. of Biology, College of Life Science and Biotechnology, Yonsei University which is in connection with Yonsei University Research Institute of Science for Aging. At present he is pursuing his Postdoctoral research at Dr. Min Songs lab Department of Library & Information Science, Yonsei University and is working on bio-text and bio-medical text mining.

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