English abstract

Heart failure (HF) is characterized by a complex clinical syndrome with a multifactorial etiology and elevated rates of morbidity and mortality. High-throughput metabolomics, the comprehensive analysis of metabolites produced by cellular processes, holds potential for elucidating the underlying mechanisms of HF. Despite the growing popularity of this technique, its application to HF has been limited. In this study, identification of a metabolomic signature linked to the development and progression of HF was pursued, utilizing data from a prospective observational cohort in the UK Biobank. Utilizing Nightingale Health's nuclear magnetic resonance platform, 249 metabolite measures were quantified. Emphasis was placed on examining the prospective associations between these metabolite measures and incident HF during the follow-up period. Relationships between metabolite levels and left ventricular function, as determined through magnetic resonance imaging, were also scrutinized, as were survival outcomes in participants with prevalent HF. An inverse association with HF risk was observed in elevated levels of certain metabolite measures, such as omega-3 fatty acids, small HDL particles, albumin, and specific amino acids like alanine and histidine. On the other hand, metabolite measures such as ketone bodies, very large HDL particles, and glycoprotein acetyls were found to have a positive association with HF risk. This study offers observational evidence that may support identification of new metabolic biomarkers in HF.