

# Is possible to detect nonalcoholic fatty liver disease by a new index including single nucleotide polymorphisms (SNPs)?

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In the last decades, nonalcoholic fatty liver disease (NAFLD) has become an emerging health problem worldwide, and affects currently from 15% to 40% of the general population (1). The mechanisms involved in the pathogenesis and progression of NAFLD are probably due to a metabolic profile expressed within the context of a genetic predisposition and associated with a higher energy intake (2). Considering the epidemic border of NAFLD and the increased associated healthcare costs, better understanding of the diagnostic aspects related to NAFLD, is of great interest not only for the researchers and physicians, but also to improve the public health policy (3). Literature had shown that >20% of patients with NAFLD, may develop cirrhosis during their lifetime (4). In addition, strong evidence suggests that the prevalence of NAFLD has paralleled with obesity, diabetes, metabolic syndrome, and the development and progression of cardiovascular disease (5). Relevant genetic factors are usually copy number variants or single nucleotide polymorphisms (SNPs), that affect the function of one or more genes in a way that affects the probability of a subject to develop a certain trait, either increasing or decreasing it. It has been proven how epigenetic factors, can also affect the expression and function of several genes, including several ones involved in the occurrence and development of NAFLD, especially SNPs for those genes involved in lipid handling, insulin signaling, and oxidative stress (6,7). The identification of genetic and epigenetic factors can be important not only for the screening of individuals at risk, but also for the study of the pathogenic mechanisms underlying NAFLD. Recently,

a cross-sectional community-based study, conducted by Yang *et al.* in the Xiang Cheng District, Suzhou, China, investigated the feasibility of a new comprehensive index (CI) for the earlier detection of NAFLD in elder people (8). The CI consisting of six serum biomarkers in association with anthropometric parameters through multivariate logistic regression analysis. This research study group also analyzed the diagnostic value for NAFLD of five different SNPs: S1, rs2854116 of apolipoprotein C3 (*APOC3*); S2, rs4149267 of ATP-binding cassette transporter (*ABCA1*); S3, rs13702 of lipoprotein lipase (*LPL*), S4: rs738409 of patatin-like phospholipase domain containing protein 3 (*PNPLA3*); S5, rs780094 of glucokinase regulatory protein gene (*GCKR*) (8). The authors found that the diagnostic value for NAFLD of the CI combined with *APOC3* SNP rs2854116 resulted better than the one of CI alone. Therefore, the combined value of CI and *APOC3* rs2854116 can provide a better non-invasive method for the diagnosis of NAFLD in the near future. However, to confirm these results is necessary to replicate the analysis in a larger population study and different ethnic groups, not only with the “gold standard” represented by liver biopsy and other non-invasive methods, such as transient elastography and ultrasound. Finally, in a near future genetic variants may be expected to influence efficacy of potential treatment and allow for greater personalization of therapy in NAFLD patients.

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## Footnote

*Conflicts of Interest:* The authors have no conflicts of interest to declare.

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