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Increased expression of key SARS-CoV-2 entry points in multiple tissues in individuals with NAFLD

To the Editor:

Recently, Fondevila and colleagues¹ reported that individuals with non-alcoholic steatohepatitis (NASH), one of the more severe manifestations of non-alcoholic fatty liver disease (NAFLD), have increased hepatic expression of key entry points of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

Increased hepatic expression of the SARS-CoV-2 entry points angiotensin converting enzyme 2 (ACE2) and transmembrane protease serine 2 (TMPRSS2) in individuals with NAFLD possibly provides a mechanistic explanation for their increased susceptibility to hepatic complications. These findings are of relevance during the ongoing coronavirus disease 2019 (COVID-19) global health crisis, which has particularly affected those with underlying health conditions including NAFLD.²⁻⁴ Given the multifactorial and multi-organ nature of NAFLD, herein, we assess the multi-organ expression of SARS-CoV-2 entry points in tightly matched obese individuals with and without NAFLD.

To assess multi-organ expression of SARS-CoV-2-entry points in NAFLD, we included 56 women from our bariatric surgery cohort⁵ of whom RNA transcriptomic data was available from the liver, jejunum, visceral adipose tissue (VAT) and subcutaneous adipose tissue (SAT). Prior to surgery, every individual underwent a complete metabolic work-up (Table S1) including a 2-hour mixed meal tolerance test (MMT) to assess insulin resistance. In total, 23 individuals fulfilled the criteria for NAFLD (biopsy-proven) whereas 33 individuals did not. NAFLD ranged from grade 1 to grade 2 steatosis. Of note, none of the included individuals had hepatocyte ballooning, a prerequisite for NASH diagnosis according to the Steatosis Activity and Fibrosis (SAF) criteria. From the extensive list of baseline characteristics, only alanine aminotransferase was significantly higher in individuals with NAFLD. Moreover, insulin and glucose excursions during the MMT did not differ between groups (Fig. 1A and 1B). We hence have a very homogenous study population that differ only in presence or absence of NAFLD. ACE2 expression was significantly higher in the SAT, VAT and liver of individuals with NAFLD (Fig. 1C-E) but did not reach significance in jejunal tissue (Fig. 1F). Next, we addressed expression of the proteases, TMPRSS2, TMPRSS4 and Furin that assist ACE2-dependent cell entry of Sars-CoV-2. Although TMPRSS2 appeared higher in the VAT and liver of individuals with NAFLD, expression levels did not reach significance (Fig. 1H and 1I). In all tissues, TMPRSS2 and ACE2 correlated strong with each other. TMPRSS4 and Furin did not differ in the tissues analyzed (data not shown).

Since metabolic dysregulation has been shown to be an independent predictor of death and morbidity in previous infectious epidemics,⁶ we investigated the correlation between SARS-CoV-2-entry points and components of insulin resistance. Interestingly, liver ACE2 expression significantly correlated with insulin area

under the curve (AUC) but not with glucose AUC determined during the MMT.

In conclusion, we report that ACE2 is upregulated in the SAT, VAT and liver tissue of individuals with NAFLD. A presumably greater availability of ACE2 and the strong correlation with TMPRSS2 in these organs likely fosters viral penetration into cells. These results strengthen the obesity-independent link between NAFLD and severe COVID-19. Moreover, the strong correlation between insulin AUC and ACE2 in the liver might explain adverse clinical outcomes and laboratory results in SARS-CoV-2-infected individuals with T2D on insulin compared to those on other glucose-lowering agents.^{7,8} We thus presumably identified an additional mechanism that contributes to increased susceptibility to severe COVID-19 in individuals with NAFLD and individuals with insulin resistance or T2D. Last but not least, we underscore once more that "simple steatosis" is not as benign as sometimes assumed. Our results highlight the need to develop accurate, non-invasive diagnostic methods for the early detection of NAFLD and for subsequent COVID-19 risk stratification.

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Conflict of interest

The authors declare no conflict of interest.

Please refer to the accompanying ICMJE disclosure forms for further details.

Authors' contributions

A.K.G, M.N and H.H. supervised this work, - A.S.M & H.H. conducted conceptual design, data curation, data analysis, visualization and main manuscript preparation. S.B & A.S.M collected medical data and biopsies.

Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jhep.2020.12.007>.

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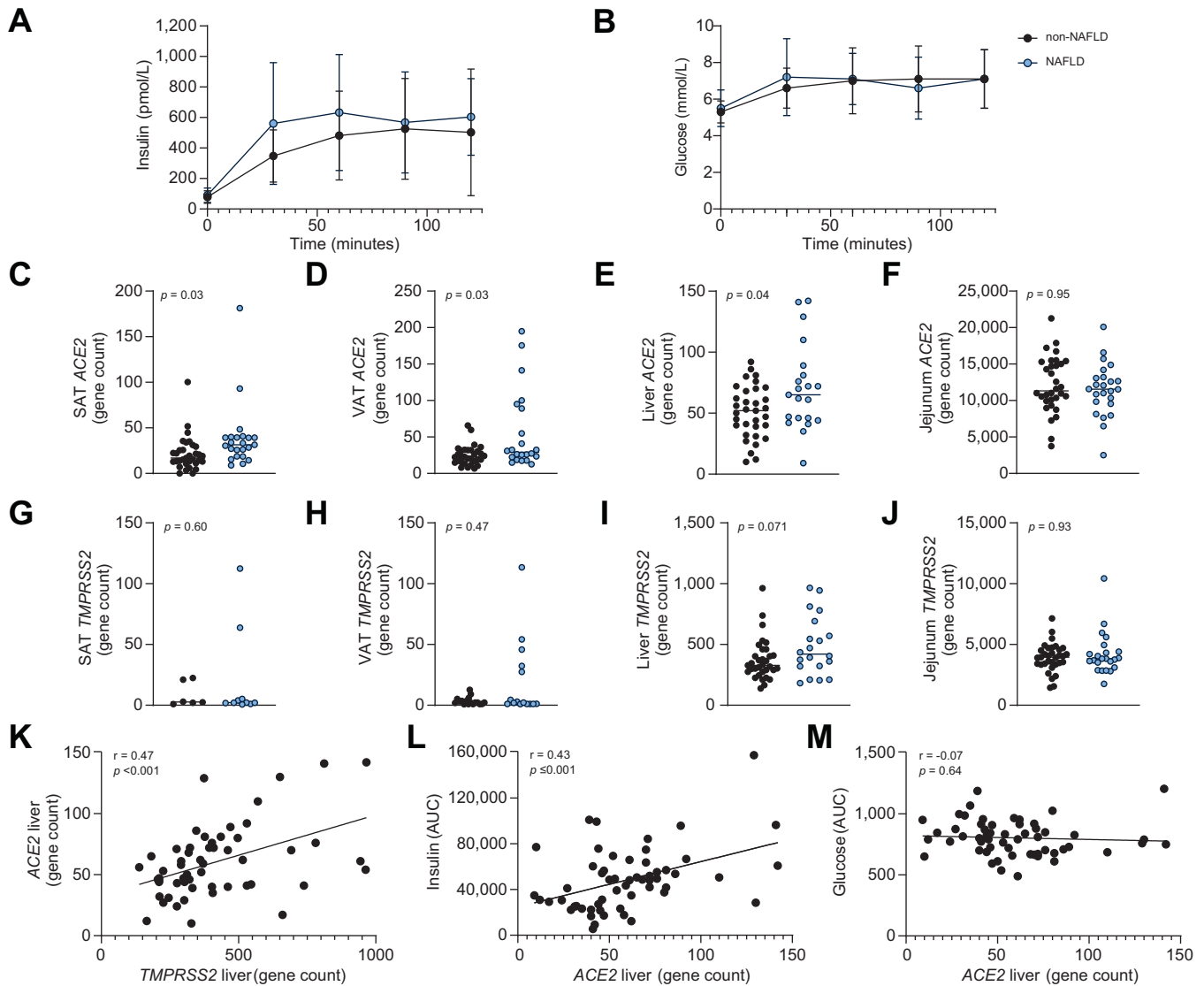


Fig. 1. SARS-CoV-2 entry point expression in patients with and without NAFLD. (A) Insulin and (B) glucose excursions during the MMT. (C–F) *ACE2* expression in individuals with and without NAFLD in different tissues. (G–J) *TMPRSS2* expression in individuals with and without NAFLD in different tissues. (K) Pearson correlation between hepatic *ACE2* and *TMPRSS2* expression. (L) Pearson correlation between hepatic *ACE2* expression and insulin AUC determined during the MMT. Pearson correlation between hepatic *ACE2* expression and glucose AUC determined during the MMT. For comparison between gene expression levels Mann-Whitney *U* test was used. *ACE2*, angiotensin converting enzyme 2; AUC, area under the curve; MMT, mixed meal tolerance test; NAFLD, non-alcoholic fatty liver disease; SAT, subcutaneous adipose tissue; *TMPRSS2*, transmembrane protease serine 2; VAT, visceral adipose tissue.

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