



## Insulin resistance, viral load and response to peginterferon and ribavirin in patients with chronic hepatitis C virus infection

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*Gut* 2010 59: 418

doi: 10.1136/gut.2009.199224

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**Competing interests** None.

**Provenance and peer review** Not commissioned; not externally peer reviewed.

*Gut* 2010;**59**:417–418. doi:10.1136/gut.2009.198382

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## Insulin resistance, viral load and response to peginterferon and ribavirin in patients with chronic hepatitis C virus infection

We read the article by Moucari *et al* in *Gut* recently<sup>1</sup> with great interest. The authors concluded that insulin resistance (IR) is correlated independently with serum hepatitis C virus (HCV)-RNA and frequently encountered in patients with HCV genotype 4 (HCV-4) infection. Also IR is a major predictor of response to peginterferon and ribavirin in 108 HCV-4 patients receiving a 48-week course of peginterferon plus ribavirin.

In our previous study we enrolled 330 Taiwanese patients with chronic hepatitis C (CHC) (150 HCV genotype 1 (HCV-1) and 180 genotype non 1 (HCV-non 1) to evaluate the association between homeostasis model assessment of IR (HOMA-IR) and response to therapy.<sup>2</sup> We checked the association between HOMA-IR and serum HCV-RNA level. The mean serum HCV RNA levels were similar between high HOMA-IR (>2.5) and low IR ( $\leq 2.5$ ) in all 330 patients ( $5.25 \pm 1.14$  vs  $5.19 \pm 1.00$  log IU/ml,  $p = 0.117$ ) and in 150 HCV-1 patients ( $5.56 \pm 0.94$  vs  $5.36 \pm 0.99$  log

IU/ml,  $p = 0.417$ ). The mean serum HCV RNA level was lower between high HOMA-IR (>2.5) and low IR ( $\leq 2.5$ ) in 180 HCV-non 1 patients with borderline statistical significance ( $4.97 \pm 1.23$  vs  $5.05 \pm 0.99$  log IU/ml,  $p = 0.056$ ). When using HOMA-IR 2 as a cut-off of high and low HOMA-IR as Moucari *et al*, we found the mean serum HCV RNA levels were similar between high HOMA-IR (>2) and low IR ( $\leq 2$ ) in all 330 patients ( $5.26 \pm 1.12$  vs  $5.18 \pm 1.00$  log IU/ml,  $p = 0.260$ ) and in 150 HCV-1 patients ( $5.54 \pm 0.94$  vs  $5.36 \pm 1.00$  log IU/ml,  $p = 0.464$ ). The mean serum HCV RNA level was lower between high HOMA-IR (>2) and low IR ( $\leq 2$ ) in 180 HCV-non 1 with borderline statistical significance ( $5.04 \pm 1.20$  vs  $5.02 \pm 0.98$  log IU/ml,  $p = 0.067$ ). Since Moucari *et al* elucidated that the IR was correlated independently with serum HCV-RNA in HCV-4 patients, whether there is association between HOMA-IR and different HCV genotypes needs further studies.

Moucari *et al* reported that IR is a major predictor of response to peginterferon and ribavirin in HCV-4 patients, which indeed meets with applause. We have found that HOMA-IR was associated with SVR to peginterferon plus ribavirin in HCV-1 patients, but not in HCV-non 1 patients. Romero-Gomez *et al*<sup>3</sup> and Conjeevaram *et al*<sup>4</sup> have also reported the high HOMA-IR impairs the response to combination therapy in HCV-1 patients in different countries and all the studies strengthen the important role of IR on the response to anti-HCV combination therapy in HCV-1 and -4 patients. By the way, the HCV viral load was an independent factor, in addition to HOMA-IR, associated with SVR in HCV-1<sup>2</sup>–4 patients. In HCV-4 patients Kamal *et al* reported that the viral load was highly correlated with and the best predictive marker for peginterferon plus ribavirin responsiveness.<sup>5</sup> It is noteworthy that Moucari *et al* reported the HOMA-IR rather than the HCV RNA level is a predictor of viral response in HCV-4 patients which minimised the role of pretreatment HCV RNA level on the viral response when taking the HOMA-IR into consideration in HCV-4 patients.<sup>1</sup> We just wonder whether the association between the HOMA-IR and HCV RNA level still exists in these 108 HCV-4 patients? On the other hand, the impact of HOMA-IR on SVR rate was especially discovered among patients with HCV-1 infection and high serum HCV RNA level (defined as 'difficult-to-treat' patients) in our previous study. It seems interesting that whether this finding can also be depicted among the HCV-4 patients in the study of Moucari *et al*.

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**Competing interests** None.

**Ethics approval** This study was conducted with the approval of the local institute.

**Provenance and peer review** Not commissioned; not externally peer reviewed.

*Gut* 2010;**59**:418. doi:10.1136/gut.2009.199224

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## Coeliac disease: emerging in China?

We read with interest the leading article by Hunt and van Heel on recent advances in coeliac disease (CD) genetics.<sup>1</sup> They suggested that further investigation of the coeliac-associated single nucleotide polymorphisms (SNPs) in other populations was needed. Our recent work may help to push this research work in the Chinese population. Here we report on a serological screening for CD in China. CD has been historically considered to be absent in the Far East (China, Japan, Korea, Malaysia, etc.).<sup>2</sup> However, since the major known risk factors for CD are common in China, we used serological tests for immunoglobulin G (IgG) anti-glutadin antibodies (AGAs) and IgA anti-tissue transglutaminase antibodies (tTGs) to screen for CD in high risk patients,<sup>3</sup> 4 comprising 73 cases of diarrhoea-predominant irritable bowel syndrome (IBS-D) and five cases of insulin-dependent diabetes mellitus (IDDM), 30 women and 48 men, mean age  $50 \pm 15$  years old. Patients with IBS fulfilled symptom-based diagnostic ROME II criteria and in addition had loose stools with undigested food, frequent stools after eating