中文題目：C 型肝炎病毒基因 1b 型感染患者接受長效干擾素/雷巴威林治療期間 PBMC 基因表達的動態研究

英文題目：Dynamics of PBMC gene expression during peginterferon/ribavirin combination therapy in hepatitis C virus genotype 1b-infected patients

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Background: Hepatitis C virus (HCV) can replicate in peripheral blood mononuclear cells (PBMCs). This study explored the dynamic gene expression profiles of PBMCs from chronic HCV-1 patients undergoing peginterferon/ribavirin (PR) therapy.

Methods: PBMCs were collected at baseline and on weeks 1 and 4 from 27 chronic HCV-1 patients treated with a 48-week PR regimen (screening dataset n=7; validation dataset n=20). A sustained virologic response (SVR) was defined as undetectable HCV RNA throughout the 24 weeks after the completion of therapy. An Affymetrix microarray was used to identify differentially expressed genes between SVR and non-SVR patients and was validated by quantitative PCR. **Results:** We found 13 genes at week 1 and 24 genes at week 4 were differentially expressed in the SVR group compared with the non-SVR group. Eight target genes (RSAD2, LOC26010, HERC5, HERC6, IFI44, SERPING1, IFITM3, and DDX60) were selected at week 1 as the major components of a scoring method to predict the treatment outcome for HCV-1 patients. This predictive model reliably stratified the responders and non-responders at week 1 [AUC=0.89, p=0.007 for SVR; AUC=0.95, p=0.003 for complete early virologic response (cEVR)), especially among patients carrying the favorable IL28B rs8099917 TT genotype (AUC=0.89, p=0.002 for SVR; AUC=1.0, p=0.008 for cEVR. The performance of this predictive model was superior to traditional predictors, including the rapid virologic response, viral load and IL28B genotype.

Conclusions: We established a cell sorting protocol to study the effects of viral loads in HCV-infected cell populations. The results demonstrated different capacities of damage-related gene expression. Our findings highlight the important role of viral load in the study of gene expression in viral infection-associated research.