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Approximately 85% of HCV patients do not eliminate the virus, leading to a chronic infection with various complications such as the development of hepatocellular carcinoma. The mechanisms involved in the persistence of HCV are not yet fully understood. Therefore, to better understand the relations between the virus, host, and mechanisms of cure, we employed a shotgun proteomic approach to assess plasma samples collected from three HCV infected patients at the beginning of the infection (PSCT0) and after six months (PSCT1). A total of 15 samples were analyzed including nine from healthy donors. Identification of plasma samples are challenging as abundant proteins shadow the detection of the least abundant ones, thus we depleted the six most abundant plasma proteins. The samples were then digested and analyzed by reverse phase chromatography online with tandem mass spectrometry using an Orbitrap Velos mass spectrometer. Protein identification was performed using the ProLuCID search engine and then filtered to meet a 1% FDR using the Search Engine Processor (SEPro). Differentially expressed proteins were pinpointed using the PatternLab for proteomics suit. A total of 667 proteins were identified, 29 were exclusive from PSCT0, three from PCST1 and 117 from healthy donors. Thirty two proteins were differentially expressed between PSCT0 and healthy donors, 18 between PSCT1 and healthy donors and two between PSCT0 and PSCT1 samples. The identified proteins play a role in liver function, inflammatory, and immune responses. Taken together, the protein panel described in this work can lead to a better understanding of this disease at the molecular level.

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