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Differential regulation of cytotoxicity pathway discriminating between HIV, HCV mono and co-infection identified by transcriptome profiling of PBMCs

There has not been a study focusing on the global dysregulations of biological pathways in PBMCs from HIV, HCV mono- and co-infected individuals. This study aimed at identifying the transcriptome distinctions of PBMCs between these patient groups. Genome-wide transcriptomes of PBMCs from 10 HIV/HCV co-infected patients, 7 HIV+ patients, 5 HCV+ patients, and 5 HIV/HCV sero-negative healthy controls were analyzed using Illumina microarray. Pairwise comparisons were performed to identify differentially expressed genes (DEGs), followed by gene set enrichment analysis (GSEA) to detect the dysregulated biological pathways between HIV, HCV mono- and co-infection. 41, 262, and 44 DEGs with fold change >1.5 and FDR (false discovery rate) <0.05 for the comparisons of HCV versus co-infection, HIV versus co-infection and HIV versus HCV were identified, respectively. Significantly altered pathways (FDR<0.05), featured by those involved in immune system, signaling transduction, and cell cycle, were detected. The differential regulation of cytotoxicity pathway discriminated between HIV, HCV mono- and co-infection (up-regulated in the former versus the latter group: Co-infection versus HIV or HCV, HIV versus HCV; FDR <0.001~0.019). The cytokine-cytokine receptor interaction pathway was down-regulated in co-infection versus either HCV (FDR=0.003) or HIV (FDR=0.028). For the comparison of HIV versus HCV, the cell cycle (FDR=0.016) and WNT signaling (FDR=0.006) pathways were up- and down-regulated, respectively. The differential regulation of cytotoxicity pathway may reflect the distinct patterns of virus-host cell interactions. Between HIV and HCV, the altered cell cycle and WNT signaling pathways may suggest the different impact of HIV and HCV on cell proliferation and differentiation.

Biography

Jingqin Wu has completed her PhD in 2009 from the University of Sydney and is a Research Fellow at the Universtiy of Newcastle, Australia. She specializes in genome-wide association and transcriptome analyses of schizophrenia and infectious dieseases (HIV and HCV). She is a NHMRC early career fellow and has published more than 35 papers in reputed journals and has been serving as an Editorial Board Member of Austin Virology and Retro Virology.

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