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Prediction of immunological T-cell epitopes of hepatitis C virus genotype 5a

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Background: Hepatitis C virus (HCV) is a public health problem with almost 170 million people estimated to be infected worldwide and is one of the leading cause hepatocellular carcinoma. Currently, there is no vaccine for HCV infection and the current treatment does not clear the infection in all patients. Because of HCV high diversity, protective vaccines will have to overcome significant viral antigenic diversity. The objective of this study was to predict conserved T-cell epitopes of HCV genotype 5a.

Methods & Materials: HCV near full-length sequences proteins were analyzed to predict T-cell epitopes that recognize both major histocompatibility complexes (MHC) I and II in HCV genotype 5a using Propred I and Propred, respectively. The Antigenecity of all the predicted epitopes were analysed using VaxiJen v2.0. All antigenic predicted epitopes were analysed for conservation using the IEDB database in comparison with 10 randomly selected sequences from each of the HCV genotypes 1, 2, 3, 4 and 6.

Results: A total of 33 and 51 antigenic epitopes that recognize MHC I and MHC II respectively were predicted. The highest number of MHC I binding epitopes were predicted within the NS3 protein (27.2%), followed by E2 (15.2%), and the least binding protein was the NS5A which was not predicted for any antigenic epitopes. The highest numbers of MHC II binding epitopes were predicted within the NS3 protein with 19.6% followed by NS4B (17.6%) and the E2 was the least binder with 1.9%. More than 80% of the predicted epitopes were conserved in genotype 5a sequences. However, in contrast to genotype 5a more than 45% of the predicted epitopes were conserved in other genotypes. The most conserved epitopes in all genotypes were predicted within the NS3 protein while the least conserved epitopes were predicted in the P7 protein.

Conclusion: The predicted conserved epitopes analysed in this study will contribute towards the future design of HCV vaccine candidate to avoid variation in genotypes and as such it will be able to induce broad HCV specific immune responses.

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Whole genome analyses of 21 human rotavirus strains in Africa

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Background: Rotaviruses remain a leading cause of viral mortality in children below the age of five years even after the introduction of rotavirus vaccines in several African countries. Data on whole genome of rotaviruses from Africa is very scarce. We carried out a study to evaluate the whole genome range of rotaviruses in Africa with the aim of determining the novel involvement of strains from the continent that make them unique from those collected in other parts of the world.

Methods & Materials: Selected strains included 11 G1P[8] (South Africa), 3 G8P[4] (Zimbabwe and Kenya), 2 G9P[8] (Cameroon and Zimbabwe), 2 G6P[6] (Guinea Bissau), 1 G2P[4] (South Africa), 1 G12P[6] (Zimbabwe) and 1 mixed G8,9P[4] (Swaziland). The dsRNA was extracted using Trizol and enriched using Lithium Chloride. Purified dsRNA was used to synthesize cDNA for sequencing. Sequences were generated using overlapping PCR amplicons spanning the genome. The amplicons were pooled by sample and then barcoded and sequenced using Illumina and Ion torrent Next Generation Sequencing platforms. The consensus sequences of the internal PCR primer hybridization sites were manually verified using reads from amplicons that spanned across the sites.

Results: The strains under binary classification G1P[8], G9P[8] and G12P[6] revealed a complete Wa-like genotype constellation of I1-R1-C1-M1-A1-N1-T1-E1-H1. Those under G2P[4], G8P[4], G6P[6] and G12P[6] exhibited DS-1-like I2-R2-C2-M2-A2-N2-T2-E2-H2. Strain G8,9P[4] presented multiple mixed infections in more than one genome segment under a DS-1-like genetic backbone as I2-R2-C2-M2-A2-N1/2-T2-E2-H2. Phylogenetic analysis of nucleotide sequences revealed that the genome segments grouped in small separate sub-clusters within their specific genotypes together with other global strains. Most clades were formed by strains from the same geographical location rather than their specific genotype for those that belonged in the same genogroup.

Conclusion: This study demonstrates that large-scale deep sequencing is crucial in providing genetic diversity at segment level and more precise evolutionally mechanisms of rotavirus strains. The study recommends the need to carry out more whole genome analyses of different rotavirus genome constellations to improve diagnostics and next generation vaccine candidates.

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