Innovative HIV-1-specific CD8+ T-cell epitopes revealed in human recipients of conserved-proteome T-cell vaccine

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Background: Optimum characterization of targeted CD8+ T-cell epitopes and their human leucocyte antigen (HLA) class I restriction enlightens iterative improvements of HIV-1 T-cell vaccine designs and may predict early vaccine success or failure. In our study, lymphocytes from volunteers, who had received candidate HIVconsv DNA vectoredvaccines expressing sub-protein conserved regions of HIV-1, were used to define the optimum-length target epitopes and their HLA restriction. In HIV-1-positive patients, CD8+ T-cell responses predominantly recognize immunodominant, but hypervariable and therefore less protective epitopes. The less variable, more protective epitopes in conserved regions are typically subdominant. Therefore, induction of strong responses to conserved regions by vaccination provides an opportunity to discover novel protective epitopes.

Methods: Cryopreserved lymphocytes from vaccine recipients were expanded by stimulation with 15-mer responder peptides for 10 days to establish short term-cell-line STCL) effector cells. These were subjected to intracellular cytokine staining using serially truncated peptides and peptide-pulsed K562 cells, engineered to express individual.

HLA class I alleles, to define minimal epitope sequence and HLA restriction by stimulation of IFN-γ production.

Results: Using lymphocyte samples of 20 vaccine recipients, we defined 8 previously unreported optimal CD8+ T-cell HIV-1 epitopes and their four-digit HLA allele restriction tentatively. Further 13 predicted, but un-reported epitopes with incomplete information were revealed.

Conclusions: The high rate of discovery of novel CD8+ T-cell effector epitopes warrants further epitope mapping in recipients of the conserved-region vaccines in other populations and informs development of HIV-1/AIDS vaccines.

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Eosinophilic gastroenteritis: An atypical cause for chronic diarrhea in human immunodeficiency virus-associated immunosuppression

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Eosinophilic gastroenteritis is an uncommon disease in both immunocompetent and immunocompromised patients.

We describe a 57-year-old male with human immunodeficiency virus (HIV) who presented with chronic diarrhea. He had no history of allergies, had significant weight loss, normal systemic examination and a complete blood count showing no eosinophilia. On further evaluation, the diagnosis of eosinophilic gastroenteritis was made by histopathological findings.

Primary Eosinophilic Gastroenteritis has not been reported before in HIV associated immunosuppression and should be kept as a differential diagnosis in HIV patients with chronic diarrhea.

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Detection of Metallo β- Lactamase producing Pseudomonas aeruginosa isolated from patients in Saudi Arabia

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Background: Pseudomonas aeruginosa is the most common opportunistic pathogen associated with community and hospital-acquired infections worldwide. Treatment of P.aeruginosa infections is becoming more challenging over years due to its ability to rapidly develop resistance against multiple classes of antibiotics including carbapenems. Carbapenems are considered one of the last resort choice of treatment for severe infections caused by P. aeruginosa. The main resistance mechanism is the production of Metallo β-Lactamase (MBLs), through the acquisition of resistance genes encoding carbapenem-hydrolyzing enzymes related to class B β-Lactamase such as IMP, VIM and NDM. These enzymes are encoded by genes located within mobile genetic elements that facilitate their speared among strains and across species. Therefore, detection of MBL is crucial for the optimal treatment and control of drug resistance among patients.

Objective: To detect the presence of MBLs in P.aeruginosa using genotypic method and to assess the efficiency of phenotypic assays for MBL detection.

Materials and Methods: A total of 184 P.aeruginosa isolates were collected from five different hospitals in Saudi Arabia throughout National Guard Health Affairs AMR surveillance program. Susceptibility testing was performed using the Vitek II system with AST-N292 card, Modified Hodge Test (MHT) and manual MICs. Selected isolates were screened using PCR for the presence of MBLs (IMP, VIM and NDM) encoding genes.

Results and Discussion: The results of Vitek II system indicate that 39 isolates were resistant to meropenem and imipenem. PCR analysis showed that 7 out of 39 carry bla VIM resistant gene and none of the isolates found to carry either bla IMP or bla NDM-1