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Designing Short Peptides as Viral Vaccines

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Abstract

The genetic diversity across global population (Black, Caucasoid, oriental, Hispanic, mixed race, Pacific Islander, American Indian and Australian aboriginal) are other vital issues in personalized/population based medicine. The human leukocyte antigen (HLA) genes in human chromosome 6 are extensively studied across global population using genetic data and about a 2000 HLA alleles have been named so far at IMGT/HLA database. Extensive HLA polymorphism and peptide diversity are critical issues in HLA-peptide binding estimation for T-cell mediated immune response. The precise evaluation of HLA peptide binding finds application in epitope design for the development of vaccines and diagnostics of diseases associated with CD4+ (example, type 1 diabetes, malaria) and CD8+ (example, several viral infections) T-cellular immunity. HLA class II binding peptides have an extended conformation at the binding groove unlike class I. This increases peptide binding combinations of varying length at the groove having eventual effect in the host immune response to infectious agents. Discussion on the significance of prediction models to large HLA allele coverage representing sampled global population towards the development of diagnostics and vaccines will be presented.

Biography

Dr. P. Kanguane received his B. Tech in Industrial Biotechnology from Anna University, Chennai, India (1997) and PhD in Bioinformatics from National University of Singapore (2000). He served as Scientist Bioinformatics, S* BIO, Singapore - Technology Transfer Bioinformatics Scientist, Chrion Corporation, USA (2001). He then served as an Assistant Professor of Bioinformatics at Nanyang Technological University, Singapore (2002-2006). He is an author of about 45 journal articles, 22 book chapters, 1 book, 1 book editor, and 40 proceeding articles. He had advised PhD students in several aspects of Bioinformatics. He founded BIOINFORMATION, an online open access journal and an executive founding member of Holo-genomics society, USA. He is Professor, AIMST University, Malaysia, Board of Directors, Biomedical Informatics, India, Visiting Professor, VITU, Associate Editor, BMC Bioinformatics, and Managing Editor, Frontiers in Bioscience, Executive Editor, Journal of Bioinformatics and Systems Biology. He is an Ambassador for Peace, Universal Peace Federation for Contribution in Science and Technology and a recipient of Merit award in Science, State Government of Pondicherry. His research interest is in Bioinformation discovery, Peptide vaccine design, Protein subunits interaction and Genome design.

Speaker Info

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