Predicted B-cell epitopes on 18 kDa antigen of *Haemophilus ducreyi*

Sir,

Chancroid is an important sexually transmitted infection. This infection is caused by *Haemophilus ducreyi*.[1] This fastidious, gram-negative coccobacilli dies rapidly outside the human host, making diagnostic testing using culture methods difficult.[1] *Haemophilus ducreyi* infection is predominantly seen in tropical resource-poor regions of the world, where it is frequently the most common etiological cause of genital ulceration.[2] One major goal of current chancroid research is to identify antigens which are immunogenic and could form the basis of a vaccine against *Haemophilus ducreyi* infection.[2] Based on the advance in bioinformatics, the immunomics becomes a new alternative in vaccine development.[3-4]

Advanced technologies for vaccine development, such as genome sequence analysis, microarrays, proteomics approach and high-throughput cloning, bioinformatics database tools and computational vaccinology, can be applied for vaccine development for several diseases, including emerging diseases. Faced with the expanding volume of information now available from genome databases, vaccinologists are turning to epitope mapping tools to screen vaccine candidates.[3-4] New databases have been launched in order to facilitate epitope prediction.[3-4]

Immunity to *Haemophilus ducreyi* involves B lymphocytes that provide *Haemophilus ducreyi*–specific antibodies. Spinola *et al.* found that *Haemophilus ducreyi* expressed an 18,000–molecular weight outer membrane protein (18 kDa) that contained a conserved surface–exposed epitope recognized by monoclonal antibody 3B9, and monoclonal antibody 3B9 cross-reacted with proteins of similar molecular weight found in many *Haemophilus* sp. strains, including P6, a candidate vaccine for *Haemophilus influenzae*.[5-6] Finding specific epitope from this region can be expected. The main aim of this study is to find potential B-cell–specific epitopes of *Haemophilus ducreyi*. Here, the author reports the data from the computational analysis of *Haemophilus ducreyi* to find potential B-cell epitopes using a new immunomics technology.

The author performed computation analysis of available *Haemophilus ducreyi* 18 kDa sequence to find potential B-cell

epitopes using a bioinformatics tool, namely BCEPred.[7] This online tool is a B-cell epitope prediction using physicochemical properties (BCEPred.) This tool allows users to predict B-cell epitopes using any of the physicochemical properties (hydrophilicity, flexibility/mobility, accessibility, polarity, exposed surface, and turns) or combination of properties.[7] The algorithm used for the search are Parker method for hydrophilicity, Karplus method for flexibility/mobility, Emini method for accessibility, Ponnuswamy method for polarity, Janin method for exposed surface, and Pellequer method for turns.[7] Available *Haemophilus ducreyi* 18 kDa sequence (AAC44382) is used for further epitope finding. According to the analysis, the B-cell epitope peptides are presented in Table 1. The peptides 16VLTACSSSSGKT27 and 78AAYLTSSNSK88 are the areas with the highest epitope property [Table 1].

Haemophilus ducreyi 18 kDa, the major capsid antigen, is presently the target for vaccine development.[5-6] *Haemophilus ducreyi* 18 kDa is a highly immunogenic major membrane protein that may be useful as a subunit vaccine. Identification of epitopes capable of binding multiple HLA types will significantly rationalize the development of epitope-based vaccines. In this work, the author used a new bioinformatic tool to predict potential B-cell epitopes of *Haemophilus ducreyi* 18 kDa. The determined peptides are useful for further vaccine development, because the bioinformatics tool can reduce the time and minimize the total number of required tests to find the possible proper epitopes, the target for vaccine development. The design of multi-epitope vaccines can also be based on these identified epitopes.

However, some limitations of this study should be mentioned. The results from this study are only predicted results from advanced immunomics technique. Apart from antigenicity, several other factors are important in vaccine development, like possible collateral effects due to cross reactions. Linear epitopes are more likely to be relevant for molecular assays like Western blot or ELISA. To conclude, the author used a computational analysis to determine the potential B-cell epitopes of *Haemophilus ducreyi* 18 kDa. According to this work, 16VLTACSSSSGKT27 is the peptide with the best epitope property. Further confirmation is required. Further *in vitro* synthesis of the determined peptide and *in vivo* experimental study to test the efficacy are the future steps for vaccine development.

Table 1: Showing the epitope with high antigenic property (>2+) activity of Haemophilus ducreyi 18 kDa

Antigenic property	Epitopes
> 3 +	16VLTACSSSSGKT27, 78AAYLTSSNSK88
2 + to 3 +	1MKKIA5, 20SSSSGKTDAN30, 50LQTRYNT57

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