



Immunogenic epitopes prediction of SP15 protein of *Phlebotomus papatasi* salivary gland by bioimmunoinformatic

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Abstract: SP15 is one of the most immunogenic proteins of *Phlebotomus papatasi* saliva, the vector of *Leishmania major* that drives Th1 response in cutaneous leishmaniasis infection. Here, we tried to predict the immunogenic T-cell epitopes of SP15 using computational prediction for epitope-based vaccine design in future [1]. Online software including SYFPEITHI, RANKPED, NETMHC, and IEDB were used for both HLA class I (HLA-A*0201) and HLA class II (HLA-DRB*10101) prediction. EpiJen and NETCTL were also used for HLA class I prediction. IC50 below 500 for Machine Learning Methods and a score over 20 for SYFPEITHI was used as threshold of prediction [2,3]. Peptides were selected if predicted by at least 3 different algorithms. By evaluating the results, we observed that the epitope KADIRKIMEHCAKKVKKQA (amino acids 61-79) was made up of high scored T-helper epitopes (KADIRKIMEHCAKKV, DIRKIMEHCAKKVKK, IRKIMEHCAKKVKKQ, RKIMEHCAKKVKKQA). The hallmark of this peptide region is a 9-mer core sequence (IMEHCAKKV) that is a strong HLA-A*0201 binder potentially cleaved by proteasome. Two other peptides AIQEYDKTI and YQYYGFVAM were also predicted to be good binders to HLA-A*0201 predicted by at least 3 different software. Here we advantaged the potential of computational tools to predict T cell epitopes of SP15. SP15 is a potential vaccine candidate and here we demonstrated that this protein contains peptide regions that can strongly stimulate T cell responses (both CD4 and CD8). It is noteworthy to further evaluate the *in vitro* and *in vivo* immunogenicity of this epitope for further peptide vaccine design.

Keywords: *Phlebotomus papatasi*; SP15 epitope, HLA I/II.

References

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