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CrossTope: How this database can impact new vaccine strategies development

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One of the greatest challenges in immunology is the discovery of appropriate targets for vaccine development. The choice relies on the identification of elements responsible for the stimulation of immune responses, such as the analysis of peptide loaded MHC-I molecules (pMHC). These features could define the physicochemical and structural fingerprints shared by pathogens. Focusing on this idea, our group developed the CrossTope Data Bank, a curated repository of 3D structures of pMHC-I complexes. The structures hosted by the CrossTope were obtained from either (i) modeling of MHC-I containing immunogenic epitopes through Docktope (tool developed by our group, hosted in CrossTope) or (ii) retrieving pMHC-I crystals from Protein Data Bank. At this moment, CrossTope contains nearly 460 non-redundant pMHC-I complexes. In the database query, the user can download either the structures or the topographical/charges images of the pMHC-I surface. These files can be used to cluster similar complexes, which could be applied to develop wide spectrum vaccines, or to identify viral and tumor mutations that can impact in the T cell structural recognition. The rational involves the analysis of electrostatic potential and accessible surface area from the TCR-interacting surface of these pMHC complexes, performing a Hierarchical Cluster Analysis (HCA). We were able to reproduce cross-reactivity networks, previously described *in vitro*, among different viral targets like HCV, PV, VV, IV, HIV, etc. Our ultimate goal is to provide a platform that allows scientists from all over the world to perform the prospection of new immunogenic targets, envisaging a new generation of vaccines and immunotherapies.

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Bluetongue virus in Morocco from 2004-2012

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Bluetongue (BT) is an infectious, non-contagious disease of domestic and wild ruminants caused by Bluetongue Virus (BTV). The disease is quite prevalent in Morocco where serotypes BTV-1 and BTV-4 were found circulating since 2006. Despite use of attenuated bivalent vaccine, outbreaks are not uncommon each year along with lack of knowledge in geographical evolution of each serotype. Here, in this retrospective study from 2004-2012, we have determined current status of BTV prevalence and its serotypes together with techniques used for virus isolation, its antigen and antibody detection. Overall the prevalence of BTV was found to be 77.61% (728/938) and 76.94% (307/339), respectively. Although, we noticed some variation in year-wise distribution of each serotype particularly BTV-1 where BTV-4 was more prevalent than BTV-1 (45.77% vs. 40.59%). The study provides a baseline data upon circulating serotypes of BTV in Morocco over the years that will certainly help devising its control strategies in future.

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