Bovine major histocompatibility complex (MHC) class I molecules and analysis of their peptide-binding specificities

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Major histocompatibility complex (MHC) class I molecules present endogenously derived peptides to circulating cytotoxic T-lymphocytes (CTLs). Individuals within a species express a diverse set of MHC molecules, which implies an individual specific T-cell response towards peptides. Characterization of the peptide binding specificity of bovine leukocyte antigen (BoLA; cattle MHC) is important in understanding the adaptive immune response towards intracellular pathogens, such as Foot and Mouth disease virus (FMDV). We describe the peptide-binding motif of four BoLA molecules using a positional scanning combinatorial peptide library approach (PSCPL), in combination with a computer algorithm, *NetMHCpan 2.9* to select peptides that are most likely to be CTL epitopes of FMDV. Peptide binding affinity was determined using a Luminescent Oxygen Channeling Immunoassay (LOCI). Eleven out of thirteen predicted FMDV peptides bound to BoLA 2*00801. Three out of nine predicted FMDV peptides bound to BoLA 2*01201. None of the predicted FMDV peptides were found to be strong binders to BoLA 1*01901 or 4*02401. In addition the functional diversity of known BoLA alleles was predicted using the *MHCcluster* tool. Results of these analyses showed that BoLA alleles can cluster into three distinct groups, with the potential to define BoLA supertypes. The data generated from this study will facilitate identification of MHC class I restricted T-cell epitopes within FMDV. Ultimately, providing insight into T-cell immunity following infection or vaccination.