Identification of peptides from foot-and-mouth disease virus structural proteins bound by class I swine leukocyte antigen (SLA) alleles, SLA-1*0401 and SLA-2*0401

Characterization of the peptide-binding specificity of swine leukocyte antigen (SLA) class I and II molecules is critical to the understanding of adaptive immune responses of swine toward infectious pathogens. Here, we describe the complete binding motif of the SLA-2*0401 molecule based on a positional scanning combinatorial peptide library approach. By combining this binding motif with data achieved by applying the NetMHCpan peptide prediction algorithm to both SLA-1*0401 and SLA-2*0401, we identified high-affinity binding peptides. A total of 727 different 9mer and 726 different 10mer peptides within the structural proteins of foot-and-mouth disease virus (FMDV), strain A24 were analyzed as candidate T-cell epitopes. Peptides predicted by the NetMHCpan were tested in ELISA for binding to the SLA-1*0401 and SLA-2*0401 major histocompatibility complex class I proteins. Four of the 10 predicted FMDV peptides bound to SLA-2*0401, whereas five of the nine predicted FMDV peptides bound to SLA-1*0401. These methods provide the characterization of T-cell epitopes in response to pathogens in more detail. The development of such approaches to analyze vaccine performance will contribute to a more accelerated improvement of livestock vaccines by virtue of identifying and focusing analysis on bona fide T-cell epitopes.

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