



From Viral genome to specific peptide epitopes - Methods for identifying porcine T cell epitopes based on in silico predictions, in vitro identification and ex vivo verification

Pedersen, Lasse Eggers; Rasmussen, Michael ; Harndahl, Mikkel ; Nielsen, Morten; Buus, Søren; Jungersen, Gregers

Publication date:
2012

Document Version
Early version, also known as pre-print

[Link back to DTU Orbit](#)

Citation (APA):
Pedersen, L. E., Rasmussen, M., Harndahl, M., Nielsen, M., Buus, S., & Jungersen, G. (2012). From Viral genome to specific peptide epitopes - Methods for identifying porcine T cell epitopes based on in silico predictions, in vitro identification and ex vivo verification. Abstract from 4th European Veterinary Immunology Workshop (EVIW), Edinburgh, United Kingdom.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

(SLA-3 paper) Abstract Edinburg

Authors:

Lasse Eggers Pedersen¹, Michael Rasmussen², Mikkel Harndahl², Morten Nielsen³, Søren Buus², Gregers Jungersen^{1,4}

¹ National Veterinary Institute, Technical University of Denmark

² Laboratory of Experimental Immunology, Faculty of Health Sciences, University of Copenhagen

³ Center for Biological Sequence Analysis, Technical University of Denmark

⁴ Correspondence to professor Gregers Jungersen, National Veterinary Institute, Technical University of Denmark, Bülowsvej 27, 1790 Copenhagen V, Denmark, (grju@vet.dtu.dk).

Title (26 words):

From Viral genome to specific peptide epitopes - Methods for identifying porcine T cell epitopes based on *in silico* predictions, *in vitro* identification and *ex vivo* verification.

Abstract (250 words):

The affinity for and stability of peptides bound by major histocompatibility complex (MHC) class I molecules are instrumental factors in presentation of viral epitopes to cytotoxic T lymphocytes (CTLs). In swine, such peptide presentations by swine leukocyte antigens (SLA) are crucial for swine immunity during viral infections and disease. Here we combine the ability of complete nonamer peptide based binding matrices for three different SLA proteins to predict good candidates for peptide-SLA (pSLA) binding with that of an online available algorithm, NetMHCpan. Further we analyze the correlation between high affinity and high stability peptides bound by the highly expressed SLA molecules, SLA-1*0401, SLA-2*0401, and SLA-3*0401, using a luminescence oxygen channeling (LOCI) and a scintillation proximity assay, respectively. With this procedure, high affinity and highly stable SLA peptide epitopes can be identified within a given viral genome, along with the elimination of hundreds, or even thousands, of peptide sequences, which are not likely to be bound. Applying these methods can save enormous amounts of time and costs of epitope discovery studies and MHC binding analysis not only in swine but in almost any species of interest. Finally, peptide candidates of interest were verified as actual T cell epitopes using peptide-SLA complexes assembled into fluorescent tetramers to stain influenza-specific CTLs derived from vaccinated animals. From 20 such animals 16 had the correct SLA allele match and 7 of these qualified as potential candidates for tetramer staining. From the 7 animals 3 responded with a positive tetramer staining of 1% or higher.