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CTL epitopes of FMDV determined by the NetMHCpan-driven predictions of SLA/peptide binding, confirmed by tetramer complex formation and staining

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Abstract

In this study, we have measured peptide-protein binding interactions using the recently developed Tetramer technology. Tetramer binding is the dominant determinant for the function of the immune system and is the major determinant for the function of the immune system. To measure peptide-protein binding interactions, we used Tetramer technology and the recently developed Tetramer technology. The tetramers showed that we have identified a porcine FMDV-specific T cell epitope.

Introduction

Major Histocompatibility Complex class I (MHC-I) molecules are highly polymorphic peptides that are expressed across the entire population in a species or in a single individual. They are encoded in all species and are involved in antigen presentation, which is the fundamental step in the immune response. Peptide-MHC-I binding is the dominant determinant for CTL function.

approach

1. Select peptide specimens using the FMDV viral sequence
2. Predict the FMDV sequences that bind to MHC-I molecules
3. Measure peptide-MHC-I binding interactions using Tetramer technology

Conclusions

Tetramer-based predictions of FMDV-specific CTL epitopes have shown potential for the identification of T cell epitopes. The tetramers showed that we have identified a porcine FMDV-specific T cell epitope.

Selected peptides were tested and their Kβ binding was measured using anti-MHC-II antibodies and the recently developed Tetramer technology. The tetramers showed that we have identified a porcine FMDV-specific T cell epitope.