

Abstract

American Society for Histocompatibility and Immunogenetics

TITLE: Next generation HLA peptide mapping using fluorescence polarization competition reveals expanded epitope landscape of influenza A hemagglutinin

CURRENT CATEGORY: Basic/Translational Research: Immunotherapy

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ABSTRACT BODY:

Aim: Identification of HLA-presented viral epitopes is often limited by incomplete peptide coverage, prediction bias, and inconsistent validation strategies. We applied a next-generation HLA peptide mapping platform using fluorescence polarization competition assays to systematically define the epitope landscape of influenza A hemagglutinin (HA) with improved resolution and coverage.

Methods: A fluorescence polarization–based competition assay was established using biotinylated soluble HLA complexes and a truncated overlap peptide library spanning the full influenza A HA protein sequence. Peptides were evaluated through competitive displacement to quantify relative HLA binding across overlapping sequence windows. This approach enabled systematic mapping of binding intensity, identification of region-specific enrichment, and refinement of epitope boundaries at high resolution.

Results: The expanded mapping approach revealed a broader and more structured epitope landscape of influenza A HA than previously characterized. Multiple distinct binding regions were identified across the antigen, with clear clustering of high-affinity peptide hotspots. Truncated overlap resolution enabled precise delineation of epitope boundaries and uncovered additional binding regions not resolved in prior limited datasets. The fluorescence polarization competition format provided robust ranking of peptide–HLA interactions and improved discrimination between closely related sequences within immunodominant regions.

Conclusion: Fluorescence polarization competition–based HLA peptide mapping enables high-resolution and systematic identification of influenza A hemagglutinin epitopes. Compared to prior limited analyses, this expanded dataset reveals a more comprehensive and structured epitope landscape. This platform improves confidence in viral epitope discovery and supports more accurate downstream immune monitoring and immunotherapy target selection.



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