# Forward Vaccinology: CTL Targeting Based upon Physical Detection of HLA-Bound Peptides

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VACCINES AND INFECTIOUS CHALLENGES

On a global scale, vaccines have had the greatest impact on human morbidity and mortality from infectious diseases relative to other medical interventions (1). Current FDA-approved vaccines are primarily, if not exclusively, antibody-based in their action, eliciting effective neutralizing antibody responses in pathogen-naïve individuals. Alum-based vaccines are of major clinical utility in facilitating this humoral response. However, these licensed vaccines are protective against pathogens with low antigenic variability. Thus, little to no antigen variation is detected in diphtheria, tetanus, H. influenzae B, polio virus, hepatitis A virus, hepatitis B virus, measles, mumps, or rubella viruses. Influenza A virus sequence variability, in contrast, being annual in timescale, requires educated guessing as to appropriate subtype for vaccine formulation to prophylax against future outbreaks. This forecasting approach is only partially successful.

Conventional vaccines against viruses with high mutational rates like hepatitis C virus (HCV) and human immunodeficiency virus-1 (HIV-1), which evolve changes daily under immune selection pressure, or even influenza viruses, which evolve mutations more slowly, will fall short due to intrinsic antibody-avoiding mechanisms (2). These viruses can avoid attack by immune memory cells through mutation, leaving “yesterday’s” adaptive immune system unable to cope with evolving changes in the viral proteins. Immune escape follows. While it has long been recognized that conserved segments of viral pathogens that cannot mutate due to detrimental effects on viral fitness would be ideal targets against which to engender cross-protective immunity via T cells, the way to implement such an approach has been unclear.

Abbreviations: CTL, cytotoxic T lymphocytes; LN, lymph node; MS, mass spectrometry; pMHC, peptide bound to major histocompatibility complex class I molecule; TCR, T cell receptor.

Forward vaccinology: CTL targeting based upon physical detection of HLA-bound peptides

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loading levels are defined only by the solution concentration of the peptide with neither the pMHCI density on the loaded APC or on the infected/transformed cell being known, the disparity in T cell avidity between recognizing loaded APCs and recognizing infected cells remains unknown. Beyond technical issues is a fundamental problem: in principle, reverse immunology identifies only antigenic peptides and not those non-antigenic foreign peptides that are displayed as surface pMHCI (vide infra).

As MS is the premiere analytical method for the sensitive identification of peptides in complex mixtures, the very limited literature reports of identifying pathogen-derived MHCI/peptide by MS proteomics is notable, but not surprising. The analytical challenge for MS is twofold. First, MHCI peptides are derivatives of total protein metabolism and this complex set is bound to a small set of different MHC proteins on the cell surface. T cells can recognize a few specific pMHCI copies per cell among 100,000 irrelevant other peptides on the same cell (11). Fundamental and practical constraints limit the number of infected or excised cells available for analysis, requiring both high dynamic range and high absolute sensitivity for immunologically useful MS analysis. Second, MHCI peptides are similar in amino acid residue number and hydrophobicity due to MHC-binding requirements resulting in crowding along both the \( m/z \) (mass/charge) axis and the chromatographic elution time axis that characterize peptides and their fragments. For samples like this, standard proteomics can identify thousands of the major components without identifying the immunologically important but quantitatively minor peptides within the pool.

Our laboratory has applied the theory of probabilistic measures for stochastic processes to recognize an ion’s fragmentation pattern when it is set among a complex set of other ion fragments. In general, ion arrival rates in different \( m/z \) channels of the mass spectrometer is a Poisson process and a Poisson measure is used to assign a magnitude of a target molecule’s fragmentation spectrum when it is buried among ion fragments from unrelated molecules. In one format, denoted MS\(^3\) Poisson detection, the measure has been applied to detecting MHCI peptides without LC separations. Using static nanospray, MS\(^3\) spectra are generated directly from the complex mixture by first isolating and fragmenting a precursor \( m/z \) and then isolating and fragmenting a selected fragment of the precursor. The MS\(^3\) spectrum is the mass spectrum of the fragment of a fragment of a molecular ion. Prior to analyzing the mixture, the pure molecule (e.g., synthetic peptide) will have been studied to determine the optimal MS\(^3\) spectra for detection and these spectra acquired for later use. MS\(^3\) spectra of the mixture are then acquired with the same \( m/z \) selection steps and the probabilistic measure determines if the target molecule’s MS\(^3\) spectra are present against the background of other molecules that had the same molecular \( m/z \) and generated the same fragment \( m/z \).

The two \( m/z \) selection steps act somewhat like chromatography in that they simplify the overall ion population while increasing the probability of detecting the ions that are derived from the target molecule. Two important features have been shown. First, the dynamic range of detection, defined as the target’s fraction of the total ion flux, can be directly estimated and is on the order of 10\(^5\). Second, the sensitivity of MS\(^3\) Poisson detection compares well with the most sensitive T cell clone that we have generated. The theory of the method and its use in identifying HPV antigens has been published (12–14).
In a second format, the Poisson measure is used to recognize a target ion’s MS² fragment spectrum against a complex background of other ion fragments in a data-independent acquisition (DIA) format. Here different mz ranges of precursor ions are selected and dissociated with the set of mz ranges selected covering all precursor ions of interest. When selecting an mz interval for fragmentation, ions outside the interval are lost. Better sensitivity is associated with selecting fewer, and therefore, wider, mz intervals. However, wider mz intervals increase the fragment background relative to the target’s fragments and here the Poisson measure is applied. The Poisson measure of any target is then calculated for each scan and plotted as a chromatogram. In a DIA format, prior knowledge of the target’s MS² spectrum is not required for data acquisition outside of the target ion’s mz being contained in at least one of the selected mz intervals. Knowledge of the MS² spectrum is required only later when the amassed data are being mined for a specific molecular ion. Using organic monolithic columns with flow rates of 10 nL/min and collecting a series of overlapped mz intervals, highly sensitive Poisson detection chromatograms for targets defined post-acquisition can be generated (Poisson segmented LC-MS²). Rapid electronic data capture, high resolution mass spectrometers and information-rich precursor, and ion fragment beams allow deep targeted interrogation and re-interrogation of precious samples after the sample is acquired and data archived. Poisson MS³ and segmented LC-MS³ have very different strengths and are highly orthogonal in the features that they employ for detection. Their combination we have found is considered to be most effective.

**DIRECT PRESENTATION VERSUS CROSS-PRESENTATION**

CD8 TCM and TEM are thought to circulate through blood, inter-converting while passing through lymphoid and non-lymphoid tissues (15, 16). Emerging evidence indicates that TRM reside long-term in the brain and mucosal tissues (such as the lungs, gut, and skin) and show only limited levels of egress and recirculation (17). These cells have a characteristic CD103⁺CD69hiCD27low phenotype and may express high levels of granzyme B. The signaling pathways and transcriptome components regulating formation of these heterogeneous populations are coming to light (18). TRM populations have been identified as embedded within barrier epithelial surfaces both in humans and rodents. CD8 TRM cells rapidly acquire cytotoxic function after encountering pMHC. For viral infection, the outcome at barrier surfaces is a competition between the production of new viral particles by infected host cells vs. immune protection afforded by CTL recognition and destruction of infected or transformed cells. The finite number of TRM cells at mucosal surfaces with limited scanning mobility places a great premium on matching TRM specificities to MHC class I presentation on infected cells. TRM cells link antigen specificity with tissue localization, in part through expressing integrins imprinted by draining lymph nodes (LN). Enriching the TRM population specific for pathogens that are likely to be encountered at a given site based on previous encounters makes immunological sense. However, T cell homing only connects the antigen display of professional APCs in draining LN with the antigen source in the periphery; it does not identify or instruct which pMHC should be recognized. The display of pathogen determinants in LN is dependent on antigen trafficking and cross-presentation, while the display at barrier surfaces reflects the direct presentation of infection. It is not sufficient that some of the determinants on professional APCs are displayed in common with infected tissue parenchyma. Stimulation of CTL by APC display that is functionally irrelevant for destruction of infected epithelium may even yield positive functional readouts in ELSpot or other assays, but this response is no biomarker of protection.

The objective for CTL vaccination is to establish an optimal, functionally avid TRM population focusing on the MHCI presentation of pathogen determinants displayed at the epithelial barrier of an infected organ. Cytotoxic response should target determinants that are displayed by infected host cells at early time points in order to eliminate these cells prior to significant viral replication. The cellular scale and sensitivity of the aforementioned MS Poisson detection methods permit such identification.

Of note, in cases where HPV-16 infection has induced epithelial transformation and cervical cancer in HLA-A*0201 hosts, only a single epitope from the E7 oncogene product, E7_{11-19}, is naturally processed and presented by this allele on those tumor cells. Pointedly, although E7_{11-20} is capable of binding equivalently to this same HLA allele, the 10-mer peptide, unlike the 9-mer, is not displayed on the primary epithelial cells. In contrast, when a large fragment of E7 as a synthetic peptide is exogenously added to HLA-A*0201 professional APCs, the E7_{11-20} is displayed to a very large extent (14). Since T cells are not strongly crossreactive and are particularly specified to a single peptide length (19, 20), this discordance misguides the immune response. It also explains, in significant part, why the 10-mer vaccine was without clinical effect in a therapeutic HPV-16 cancer trial (21).

**CD8 T CELLS: FUNCTIONAL AVIETY, ELICITATION, AND DEPLOYMENT**

Functional avidity refers to the sensitivity of a particular T cell to be triggered by pMHC on an APC. High-avidity T cells are capable of recognizing a very small number of pMHC/target cell (i.e., single digit), whereas low-avidity T cells may require hundreds (22–24). Avidity is dependent on the TCR–pMHC interaction, CD8 co-receptor expression, intracellular signaling molecules, and other factors (25). With respect to the TCR, the Vβ and Vα gene repertoire and the nature of the antigen itself both contribute. Unfeatured pMHC surfaces, like influenza A M158-66 bound to HLA-A*0201, strongly elicit T cells which, although plentiful, comprise a low-avidity immunodominant response (26, 27). As such, display requirements on infected epithelium for activation of those CTL may be at too high a copy number to be achieved during natural infection. Consequently, this CTL response would be non-protective. By using next generation sequencing technologies to identify T cell antigen-specific repertoires and rapid 8β TCR cloning and expression systems (28), their functional TCR-pMHC binding characteristics can be cataloged. In conjunction with quantitation of a given viral pMHC copy number on epithelium or other cells during early infection, the best epitopes can be selected for CTL elicitation through vaccination. In turn, slow release of these epitopes from nanovaccines or other biomaterials formulation (8) in conjunction with routes of administration and
chemokines to foster dissemination in relevant tissues (29) can afford optimal protection.

Imagine a time in which CTL-eliciting vaccines are predicated on knowledge of the actual HLA-linked viral peptide with epitope formulations reflecting peptides conserved in sequence among viral strains and displayed at the earliest time points of infection in numbers sufficient to elicit responding TCRs from the human repertoire. If this could be applied to influenza A, for example, a single vaccine incorporating a few such epitopes would be sufficient, in principle, to afford protection against both seasonal and pandemic variants and bird or swine flu (6). Assuming that we can amalgamate advances in ion physics, structural biology, immunology, computer science, and virology, there is no reason to expect such advances not to be achievable.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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