

HAXHRAA



Next-Generation Bacterial mRNA Vaccines

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Rationale & Approach

Diversifying the tuberculosis vaccine development pipeline is recognized as an important strategy to find an effective vaccine and curb the tuberculosis crisis. The EU-funded project BAXERNA (www.baxerna.eu) aims to identify highly presented Mycobacterium tuberculosis (MTB) antigens, generate improved vaccine formulations, and bring a new tuberculosis vaccine to Phase I. BAXERNA's pipeline brings two key innovations: 1) a state-of-the-art immunopeptidomics workflow that allows highly sensitive, empirical discovery of the bacterial epitopes presented on infected cells, and 2) the Galsome platform, an mRNA vaccine formulation that incorportates the adjuvant alpha-galactosylceramide and elicits strong innate and adaptive immune responses.

Immunopeptidomics

Bacterial antigen identification using mass spectrometry





Adjuvanted mRNA Vaccine Platform







MTB Antigen Discovery Data

MHC Class I antigens identified in infected macrophage cell lines & primary macrophages

Proof of Concept

mRNA vaccine formulations against Listeria monocytogenes



A. MHC Class I immunopeptides were detected in *Listeria monocytogenes*-infected HeLa and HCT-116 cells using immunopeptidomics. Histogram showing the number of identified immunopeptides for all 42 detected Listeria antigens. B. C57BL/6 mice were IM vaccinated with a prime-boost regime with 2µg m1µ modified mRNA encoding a newly discovered *Listeria* protein antigen (Imon_0149) formulated in C12-200 LNPs alone or co-formulated with αGC adjuvant. Injection of PBS was included as a negative control, while 2x low-dose infections with *Listeria monocytogenes* EGD (5x10⁴ CFUs) were included as a positive control mimicking natural immune responses against infection. The animals were challenged by IV injection of a lethal dose of 7.5x10⁵ bacteria. After mice were euthanized, the bacterial load in spleen and liver was assessed by counting colony-forming units (CFU) via serial dilution and replating.

