Methodology for vaccine development against *Meningococcus B* using Revere Vaccinology

- Whole Genome Sequence of *Neisseria meningitidis* serogroup B (MenB) was analyzed to identify proteins that are to be secreted or exported to the outer membrane.
- Hundreds of genes were identified, these genes coded for potential surface-exposed antigens, these genes were then amplified, cloned in expression vectors and used to immunize mice.
- Out of 350 recombinant antigens, 28 were select as potentially protective, based on "antibody dependent, complement mediated, serum bactericidal activity assay".
- These antigens were then tested against a large strain collection that represented global cases of disease and carriage, which revealed that no single component would be sufficient for a universal vaccine and multiple antigens need to be used.
- Final antigens reflected the following features:
    - Cross-protective ability.
    - Maximum coverage of antigenic variability of MenB.
- Resulting vaccine consisted of 3 recombinant antigens:
    - Neisserial Heparin Binding Antigen (NHBA)
    - Factor H binding protein (fHbp)
    - Neisseria Adhesin A (NadA)
- Outer membrane vesicle component was obtained from epidemic New Zealand strain (OMVNz) and added to the formulation to improve immunogenicity and potential strain coverage.
- The resultant 4 component vaccine was named 4CMenB.
- Series of phase 2 and 3 clinical trials were conducted to evaluate safety and tolerability, in humans of different ages.
- 4CMenB was approved in Europe in 2013.

References:

- Masignani V, Pizza M, Moxon ER. The Development of a Vaccine Against Meningococcus B Using Reverse Vaccinology. Frontiers in Immunology 2019;10. https://doi.org/10.3389/fimmu.2019.00751.