**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>.