

Reverse Vaccinology

MIC 3004. Cellular and Molecular Immunology

MSc Microbiology

Dr Shilpa Deshpande Kaistha

Department of Biosciences & Biotechnology

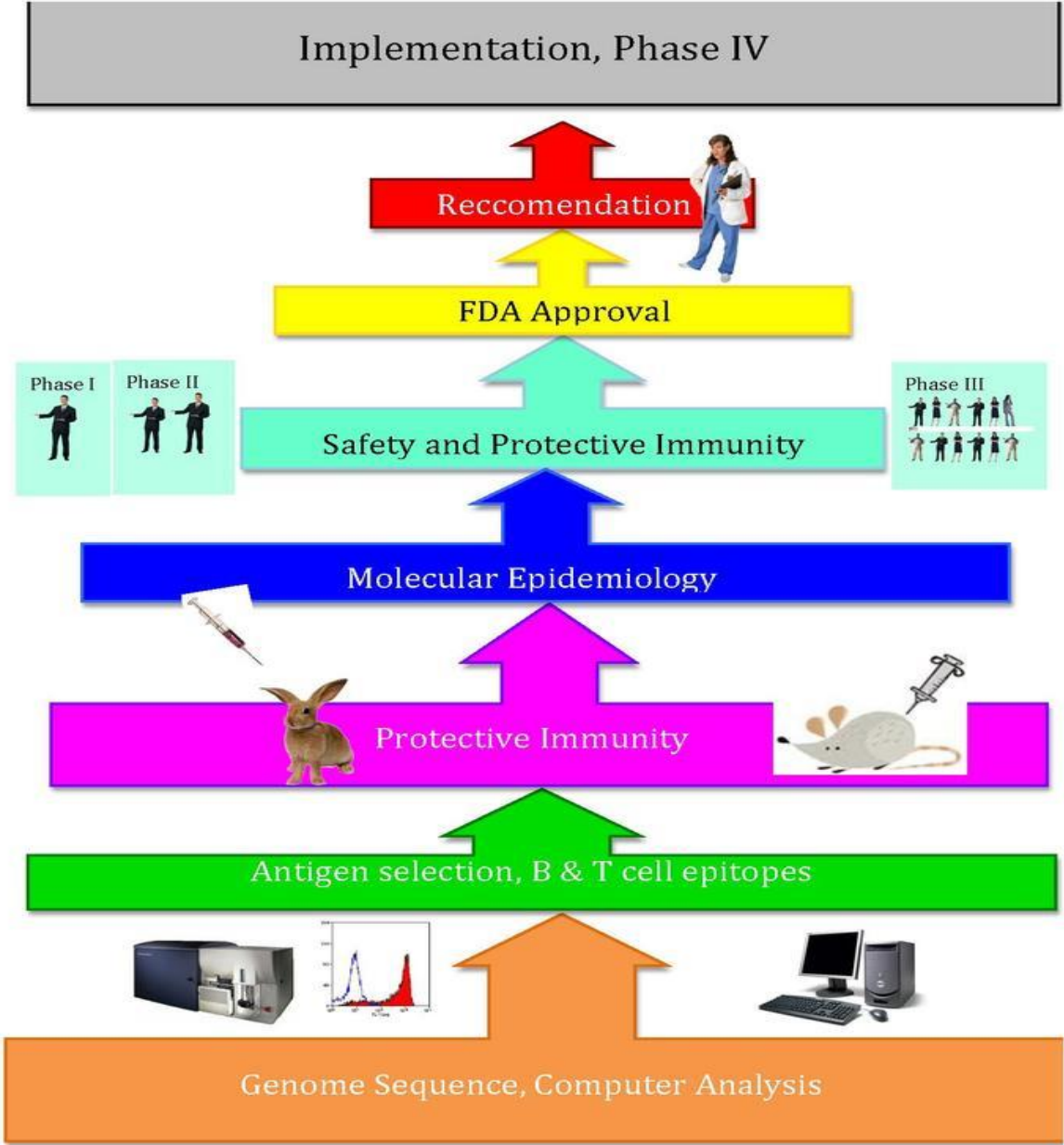
CSJM University Kanpur

Introduction

- Reverse vaccinology refers to the discovery of potential vaccine candidates (PVCs) prior to experimental validation
- 1995-2001. Human Genome Project
- Rappuoli, Rino. Reverse Vaccinology Current Opinion in Microbiology 2000, 3:445–450.
- Serogroup B Meningococcal vaccine candidate- Rappuoli and Craig Venter Institute develop first reverse vaccine
- Extended to *Streptococcus A*, *Streptococcus B*, *Staphylococcus aureus*, and *Streptococcus pneumoniae*
- Genome sequence of organism is screened for potential vaccine candidate genes- bioinformatics and computational biology approach to search for vaccine epitopes without traditional wet lab experiments

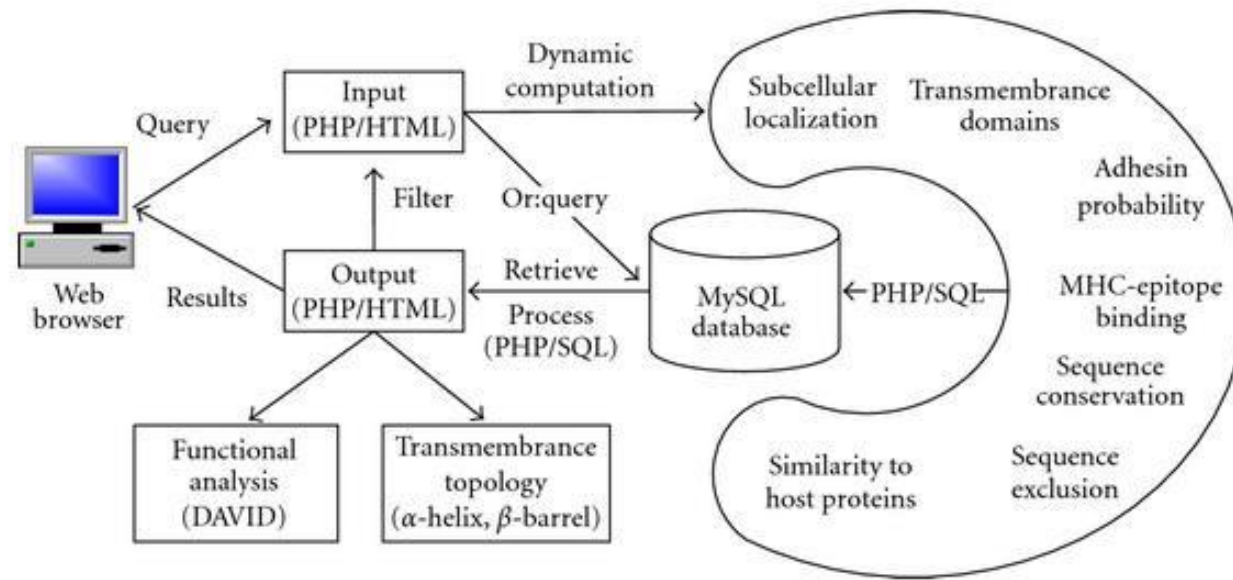
Reverse Vaccinology pipeline

- Select candidate genes and protein based on software prediction tools in immunoinformatics, immunoproteomics and reverse pharmacology
- Clone select genes in E. coli to create vaccine gene library
- Purify proteins
- Add adjuvants to enhance immunogenicity
- Experimental animal trials conducted



Softwares used to screen pathogenic genes

- Vaxign is the first web-based vaccine design system that predicts vaccine targets based on genome sequences using the strategy of reverse vaccinology





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Welcome to Vaxign: Vaccine Design!

Vaxign2 is now available! [Click here to try it out.](#)

Vaxign (Vaccine Design) is a vaccine target prediction and analysis system based on the principle of reverse vaccinology. Two programs exist in Vaxign: (1) Vaxign Query: provide precomputed Vaxign results for users to explore, and (2) Dynamic Vaxign Analysis: allow sequence input and dynamic Vaxign execution and result visualization.

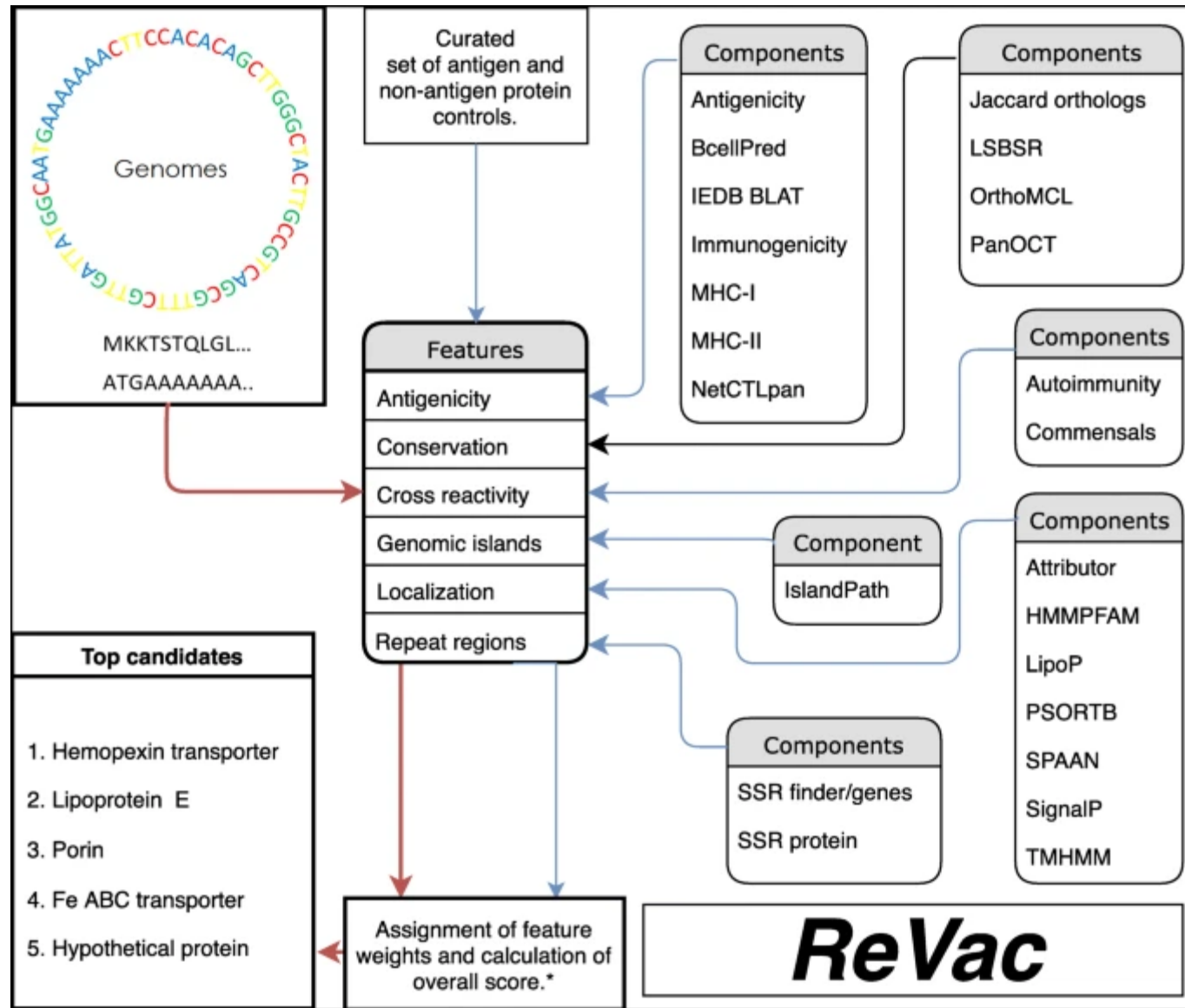
NOTE: Vaxign is freely available for academic uses. The Vaxign vaccine design pipeline runs some [open-access third-party software programs/algorithms](#) in the background. For commercial users, you may want to check all licenses for these [third-party programs](#) used in Vaxign.

1. Vaxign Query:

This program allows users to search precomputed Vaxign results for [> 350 genomes](#). A user can either select a genome(s) for all possible vaccine targets based on desired parameters, or query a protein sequence(s) from a genome to find possible vaccine target(s):

Select a Genome(s), Query a Protein (Optional), and Set up Parameters (Optional)	
Select a Genome Group (Required)	Please select a genome group <input type="text"/>
Select a Genome (Required)	Please select a genome <input type="text"/>
Sequence ID(s)	NCBI Protein Accession <input type="text"/> (One ID per line, or use comma, tab-delimited format)
	Or load IDs from file <input type="button" value="Choose File"/> No file chosen
Keywords	Gene Symbol <input type="text"/>
Sort by	NCBI Protein RefSeq <input type="text"/> Ascending <input type="text"/>
Filter Options:	





Advantages

- Finding vaccine targets quickly and efficiently
- Does not require extensive wet lab experiments to screen several candidates. Can focus on validation of select suitable screened candidates
- Increased research focus for pathogenomics and pathoproteomics
- Led to Discovery of new genes example : pili in Gram positive cocci, complement binding proteins in *Streptococci*
- Web based software allow extensive research without need of experimental set up
- Reverse Pharmacology can be used to study vaccine dynamics upon delivery prior to clinical trails

Disadvantage

- Requires extensive genome sequencing and proteomics pipeline
- Requires computational tools and bioinformatics analysis pipeline development
- Currently targets protein targets. Polysaccharide antigens still used by traditional vaccinology