FISHGUARD: a fast, cost-effective, user-friendly and in-field screening test

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CONTEXT

FISH FARMS IN EUROPE, NORTH AMERICA, JAPAN

DEADLY VIRUSES with up to 95% mortality

Viral hemorrhagic septicemia virus (VHSV) & Infectious hematopoietic necrosis virus (IHNV)

Highly contagious viruses: **NEED FOR RAPID TESTS**

BUT: current methods are expensive and long (2-3 weeks).

GOAL

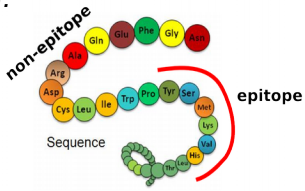
Developing a **fast and cost-effective immuno-assay** to detect the virus in-field

requires...

Building an **antibody** against each virus

which requires...

Predicting **epitopes** *in silico* (machine learning).



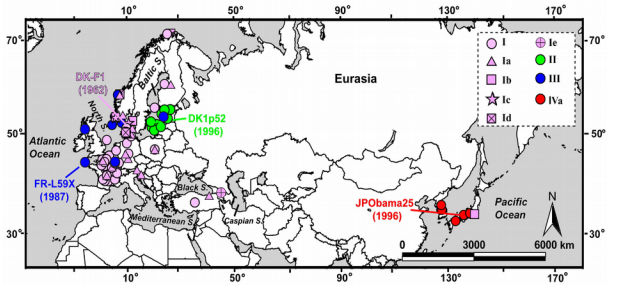
METHODS

1. Protein characterization

Identify abundant proteins, trans-membrane domains, post-translation modifications.

2. Conserved sequences

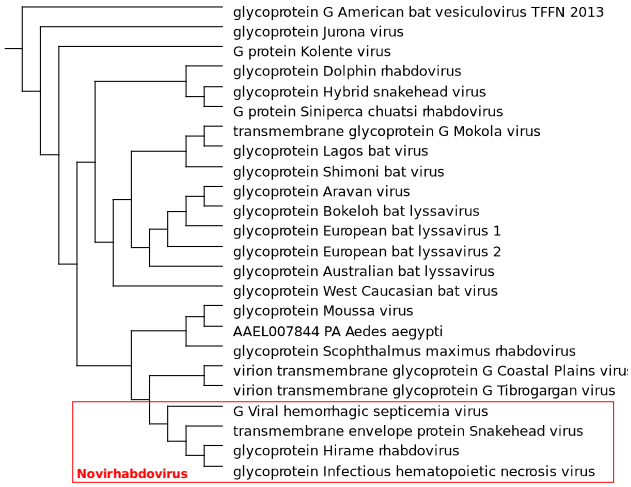
Identify sequences conserved among virus isolates.



Pierce & Stepien 2012

3. Low homology

Identify sequences with low identity in other species.



4. Position-specific evolutionary rates

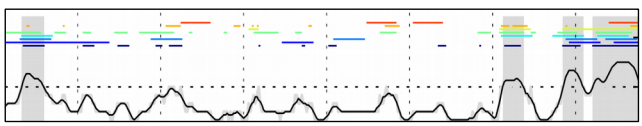
Predict slowly evolving residues [1].

5. In silico mapping of epitopes

- **BepiPred** [2], **CBTope** [3], **AAP** [4], **BCPred** [5], **SVMTriP** [6]: list of antigenic residues.
- **ABCPred** [7]: list of overlapping epitopes. The top 20% scoring epitopes are used to calculate a residue-based score. Only residues with a positive score are kept.
- **COBEPro** [8]: list of most-likely and least-likely epitopes of different sizes, used to calculate a residue-based score. Residues with a positive score are kept.
- **TEPRF** [9]: All the possible sliding windows of some fixed length are scored as epitope/non-epitope. Keeping the top 20% scoring epitopes and non-epitopes, a residue-based score is calculated. Residues with positive score are kept.

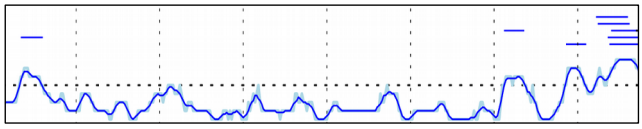
6. Consensus epitopes

Find antigenic residues with >50% consensus (gray).



7. Best epitopes of length 11-20aa

Identify peak scores and extend epitopes from there.



References – [1] PMID: 15201400 [2] PMID: 16635264 [3] PMID: 20961417 [4] PMID:17252308 [5] PMID: 18496882 [6] PMID: 22984622 [7] PMID: 16894596 [8] PMID: 19074155 [9] PMID: 24721579

NEXT

- Use predicted tertiary structures to map epitopes.
- Automate the implemented "jury vote" pipeline and use benchmark datasets to test its performance. Add new features (e.g. Bayesian estimation of evolutionary rates) to improve its performance.