



Using genomic sequences to develop new diagnostic methods for Glässer's disease

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INTRODUCTION

Glässer's Disease and *Haemophilus parasuis* (HPS)

Symptoms:

- Fibrinous polyserositis - Meningitis, Arthritis, Pericarditis, Septicaemia
- Also able to cause pneumonia

Occurrence:

- Used to be a sporadic disease in recently weaned pigs.
- Current production practices (multi-site, high health) have coincided with more frequent larger outbreaks, affecting various ages with increased mortality and morbidity
- Multisourcing of weaners has been a major driver to increased disease prevalence

Diagnostics:

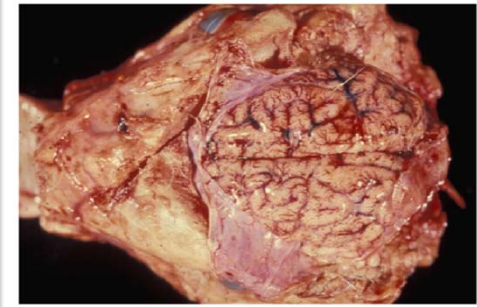
- Most commonly used technique is serotyping, but no labs in the UK perform this test.

Treatment & Disease Control

- Antibiotics (penicillin based)
- Prophylactic antibiotic treatment in feed is common
- Several vaccines are available but they are serotype specific.

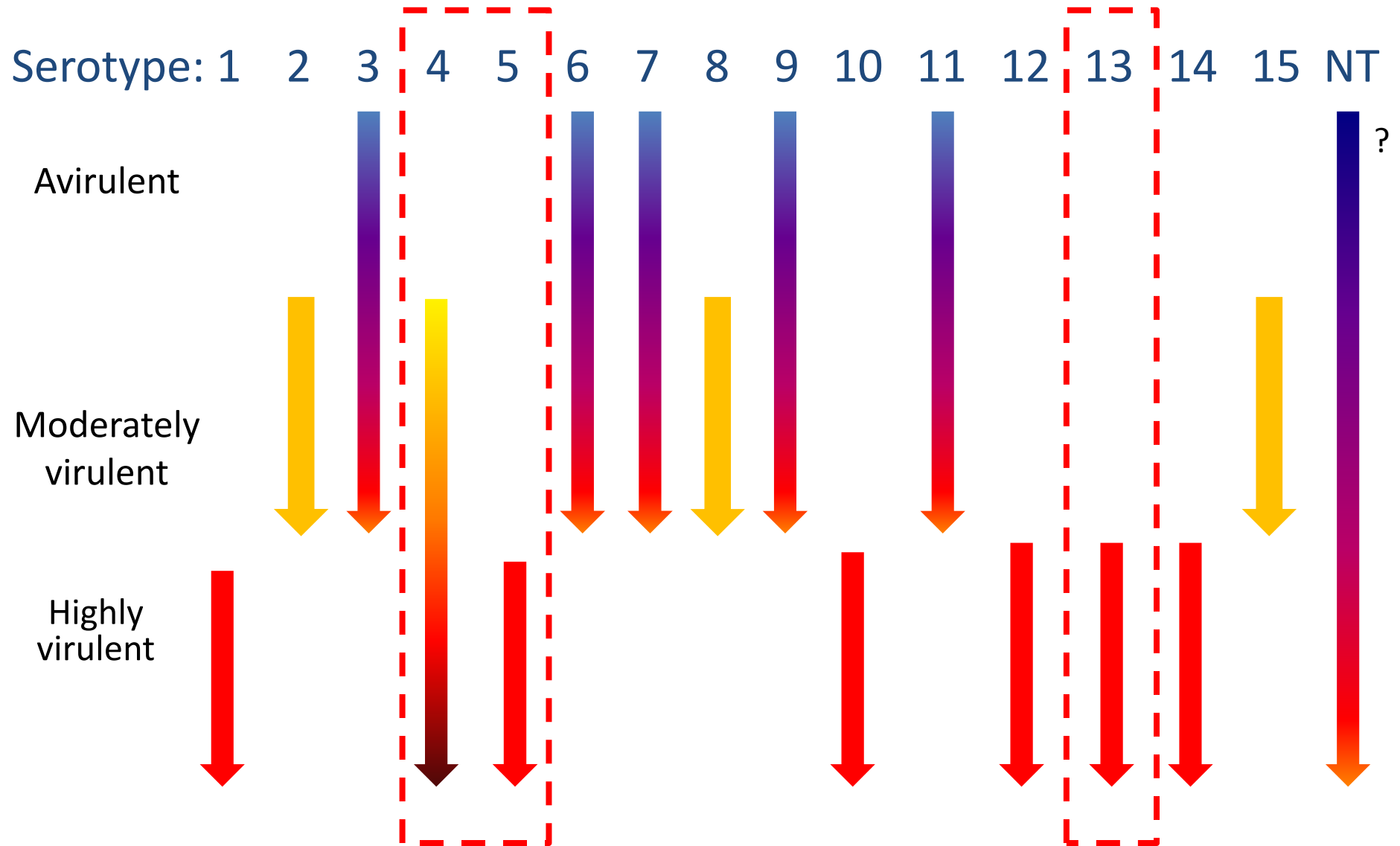
Management of disease

- Optimise maternal antibody delivery
- Optimise acquired immunity
- Minimise introduction of new strains of HPS



INTRODUCTION

Scale of Virulence by Serotype



OBJECTIVES

Aims to fill technology gaps in respiratory disease control by designing efficient diagnostics

Identify molecular markers from variation in the genetic sequences of *H. parasuis*

Two main strategies:

1. Molecular serotyping

- Identify genes or markers characteristic of serotypes
- Would indicate usefulness of vaccination & useful for stock mixing

2. Virulence Associated Gene Identification

- Compare clinical and non-clinical strains of *H. parasuis*

GENOME SEQUENCES + CLINICAL DATA + SEROTYPING DATA

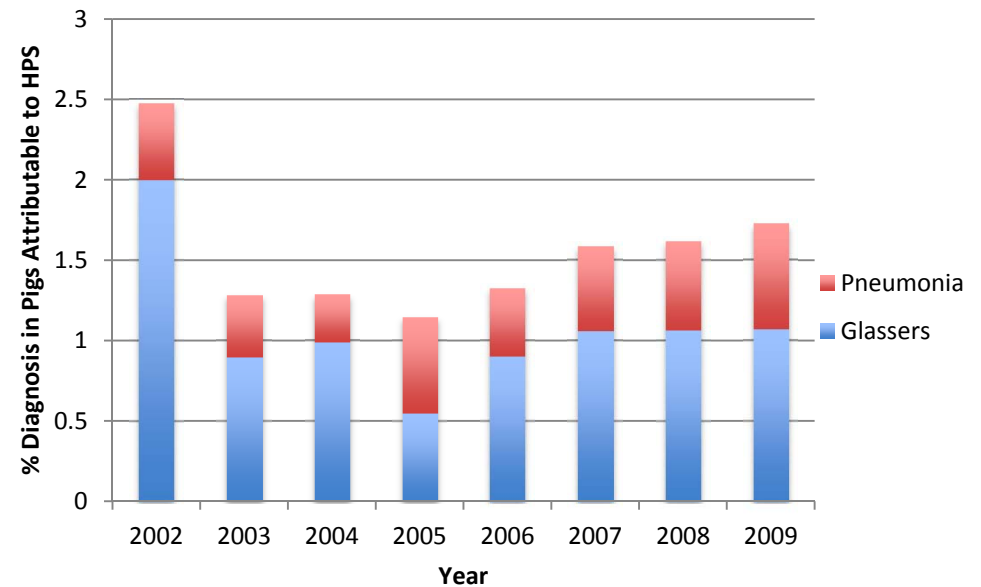
INDUSTRY FOCUS

1. For diagnosis of HPS disease
2. For management of disease
3. For surveillance and herd monitoring prior to trade



Economic Impact on the UK Industry is ~ £27/pig for an outbreak and £20/pig/year for vaccination (White 2010).

UK Statistics: 5% of systemic swine disease and 5% respiratory disease attributable to HPS in 2010 AHVLA surveillance report

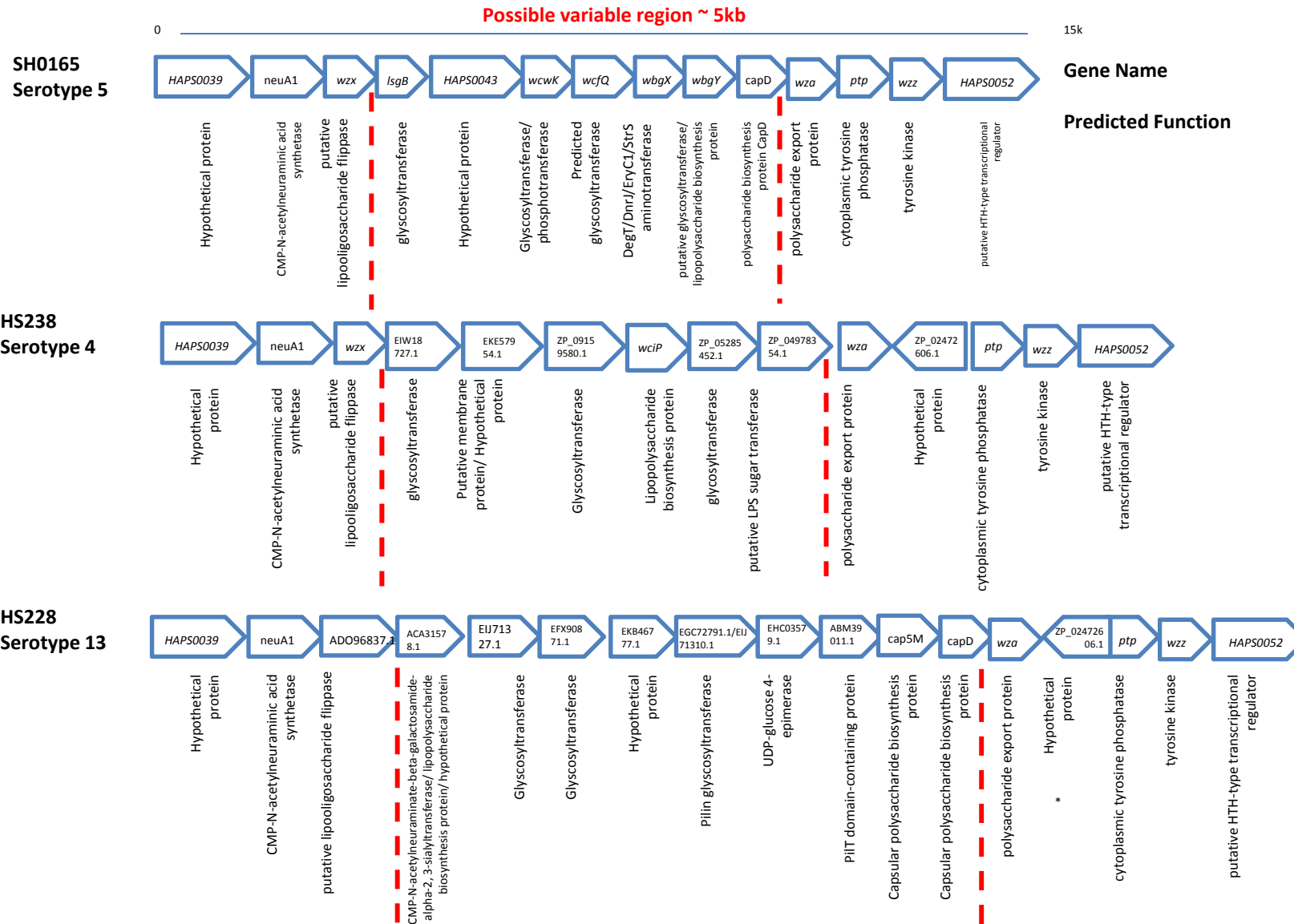


MATERIALS & METHODS

1. Strains were collected by the AHVLA which were both **disease-associated** and **non-disease associated** (carrier strains), with clinical data.
2. Strains were also supplied by collaborators in Denmark & Spain including reference strains used in the current serotyping assays
3. All of these strains were sent for whole genome sequencing
4. Subset of strains sent for serotyping
5. Bioinformatics analysis
 - Assembly of sequencing data into draft sequences
 - Core genome built
 - Capsule loci identified & compared
 - Phylogenetic trees built for genes of interest
 - Pangenomes built – core & accessory genes identified – analysis continuing.

RESULTS

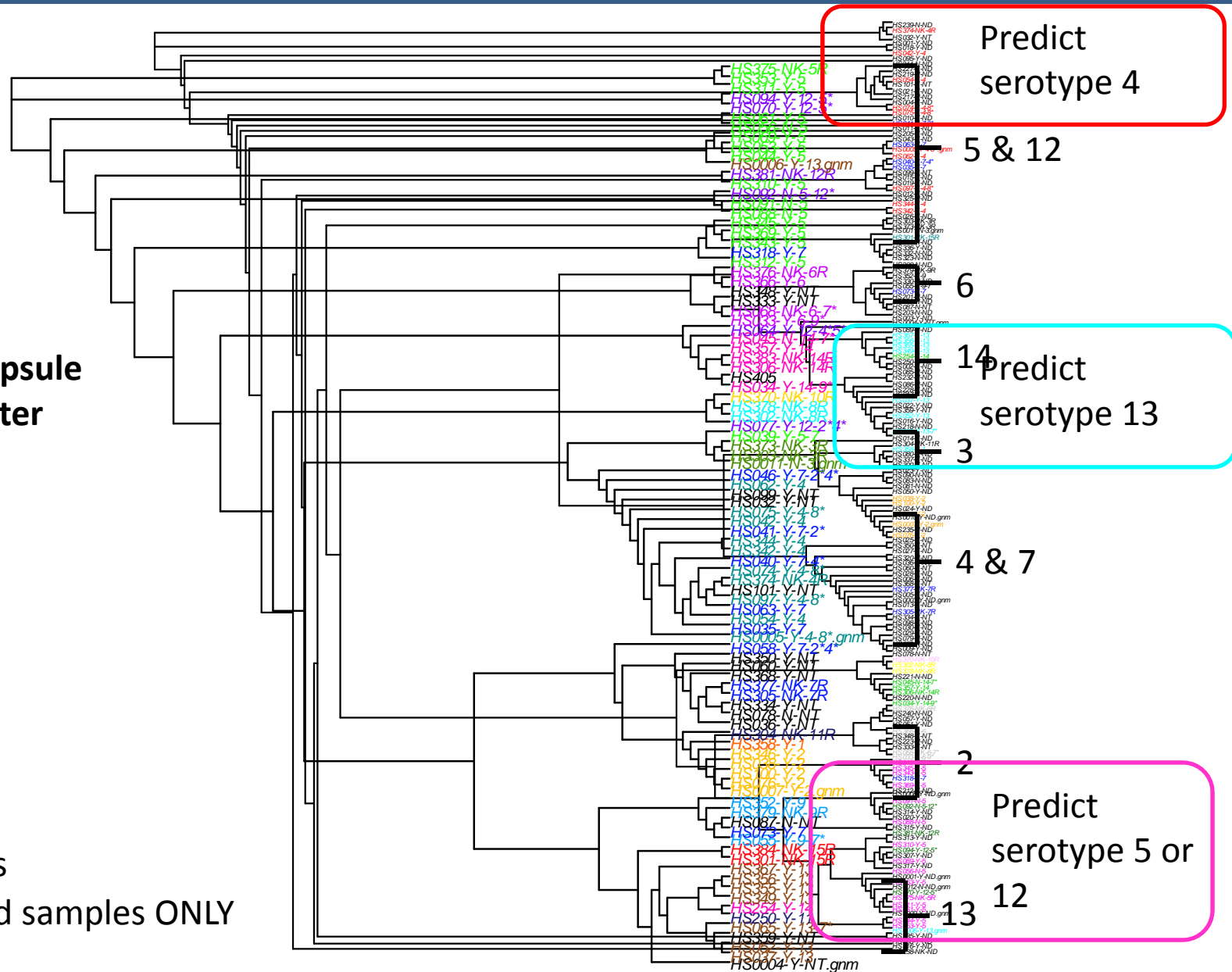
Predicted Gene Functions between dominant serotypes



CONCLUSIONS

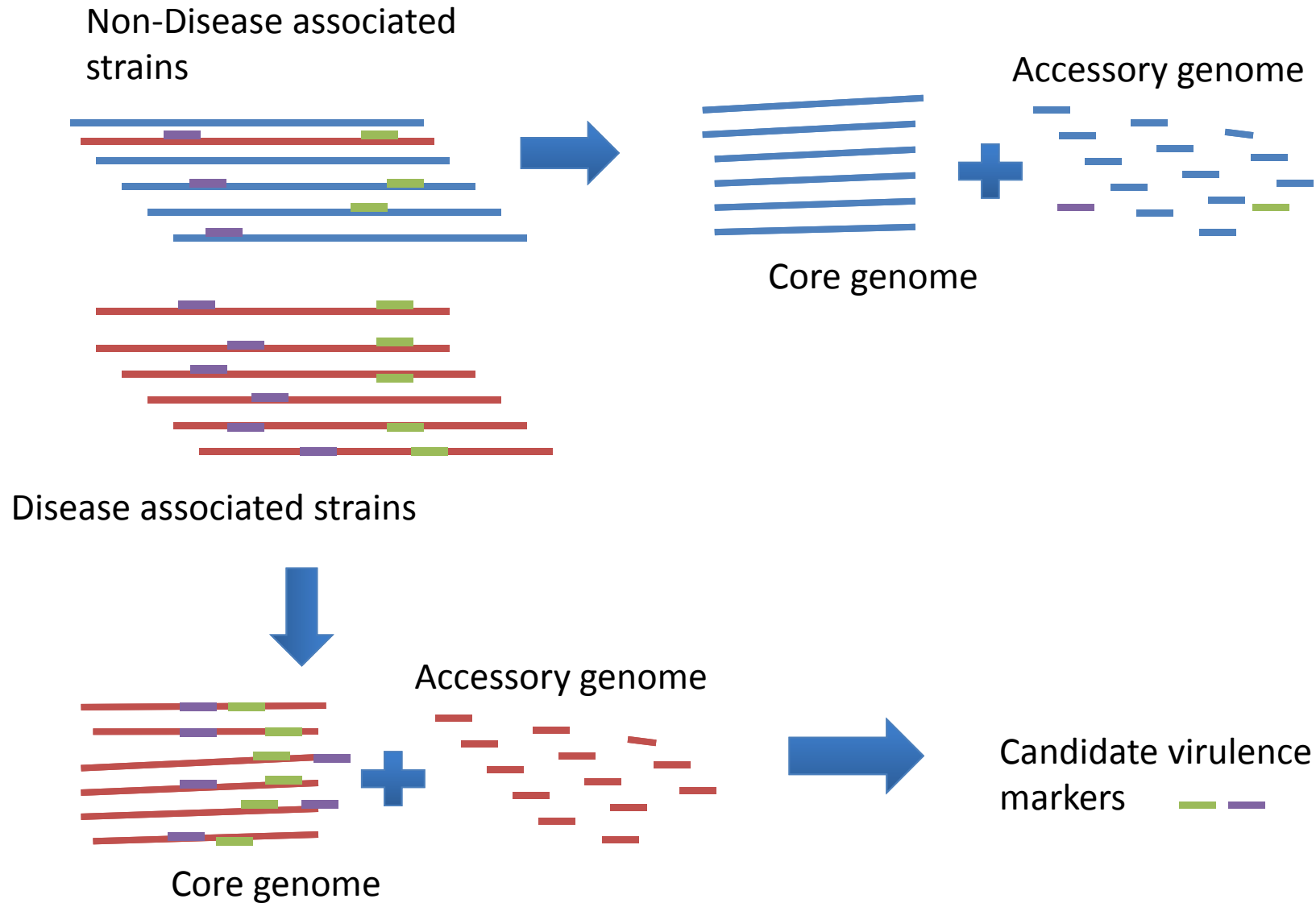
Tree of Capsule Gene Cluster

All Strains
Serotyped samples ONLY



NEXT STEPS

Virulence Gene Identification - Strategy



Acknowledgements & References

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