Development of Veterinary Vaccines

Protecting livestock against infectious diseases

Wageningen Bioveterinary Research

Safeguarding human and animal health through veterinary and biomedical research

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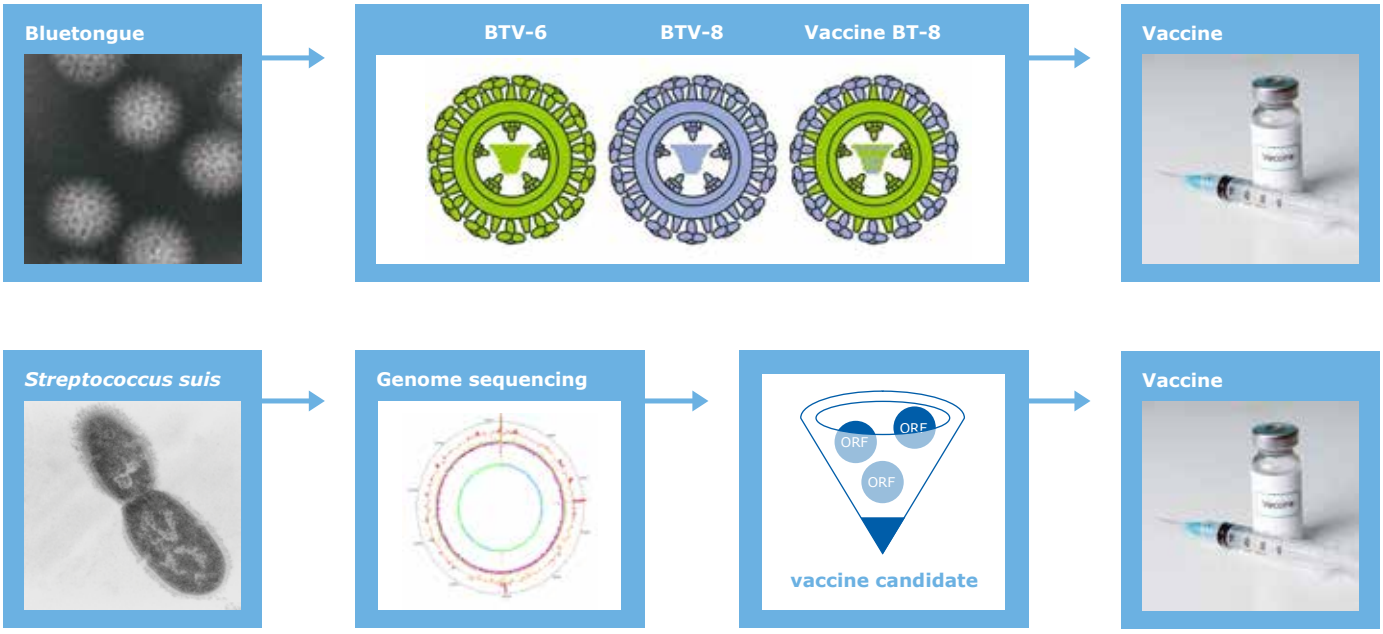

Vaccine development for viral and bacterial pathogens

Wageningen Bioveterinary Research is a contract research organisation with excellent facilities for developing vaccines to safeguard against and support the control of animal and zoonotic diseases. We have facilities for research on pathogens up to biosafety level 3. State-of-the-art whole genome-based technologies (like reverse vaccinology) are used to identify bacterial vaccine candidates, for example from *Streptococcus uberis* and *Coxiella burnetii* (Q fever).
Reverse genetics techniques are used to develop vaccines for a wide range of viral diseases like Influenza and Bluetongue. We develop vaccines and the associated diagnostic assays that differentiate infected from vaccinated animals (DIVA principle). Vaccination-challenge experiments in natural hosts are used to evaluate the protective efficacy of vaccines, and to study immune responses in detail using transcriptome analyses.

Examples from our current vaccine development

Vaccine development based on whole genome bacterial sequences

Reverse vaccinology is used to predict novel vaccine candidates *in silico* using bacterial genome sequences. At Wageningen Bioveterinary Research genomes of *Coxiella burnetii* as well as several streptococcal species were sequenced and analysed to identify vaccine candidates using in-house bioinformatics pipelines.

Extensive strain collections as well as convalescent and field sera were used to validate the *in silico* results. Another method to select vaccine candidates uses genome-wide transposon libraries to select genes that are essential for *Streptococcus suis* infection in piglets. Essential genes were identified by profiling the relative abundance of each gene using transposon insertion site sequencing. To confirm the results, directed mutants were generated by allelic exchange and tested for virulence in an experimental infection in piglets.

Vaccine development for Bluetongue

Bluetongue virus (BTV) includes 26 serotypes and is endemic in large parts of the world, e.g. the Americas, Australia, Africa and Asia. In 2006, a huge BT outbreak caused by serotype 8 started in Northwest Europe.
The possible emergence/re-emergence of BTV serotypes in countries requires the rapid supply of vaccines of the circulating serotype. Reverse genetics for BT vaccine virus were developed, which allowed the exchange of serotype specific proteins. This created so-called 'serotyped' vaccine viruses. These vaccines are completely protective. Reverse genetics is also used to incorporate more advantageous properties into vaccines, such as improved safety and the DIVA principle. This ongoing research is supporting new strategies for vaccine development against related viruses such as African horse sickness virus.

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