



Project Number & Title: Pork CRC Project 2C-126
Utilization of next generation sequencing for identifying *Streptococcus suis* clones responsible for recurrent outbreaks and identifying effective *S. suis* autogenous vaccine candidates

Project Leader: Dr Sam Abraham

Project Participants:

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Aims and Objectives:

1. To identify the dominant clones of *S. suis* that colonise healthy pigs and cause clinical disease
2. To determine whether tonsillar sampling of live pigs is a feasible diagnostic method for rapid identification of circulating *S. suis* clones

Key Findings

- Tonsil swabs did not yield any isolates with genomic signatures indicative of pathogenic *S. suis* circulating in Australia, however a large number of *S. suis*-like organisms were isolated.
- Genomic comparison indicated that *S. suis* isolated from tonsils were genetically distinct from pathogenic *S. suis* causing invasive clinical infections in Australian pigs, and likely to be a separate subspecies.
- Whole genome sequencing of 148 clinical isolates from diseased pigs demonstrated serotypes 2, 3 and 1/2 are the predominant serotypes in Australia
- Phylogenetic analysis found ST1, ST25 and ST27 to be the main MLSTs identified in pathogenic clones
- Australian isolates belonging to ST1 (serotypes 1/2, 2 and 14) had a significantly higher number of potential virulence genes than other pathogenic clones.
- It is recommended that a trivalent, autogenous vaccine targeting the above serotypes and MLSTs be developed to control highly pathogenic *S. suis* infections

Application to Industry

This study has highlighted the major pathogenic *S. suis* strains found in Australian pigs, providing knowledge that will be fundamental to development of vaccines to combat disease. This study has demonstrated the advantage in the use of robotics methods over conventional methods for *S. suis* recovery; and that isolation of *S. suis* from tonsils of pigs is ineffective for isolating pathogenic strains.

Additionally, this study has refined and streamlined methods for processing and analysing *S. suis* with a whole genome sequencing pipeline developed in association with other studies, that will be highly useful for future genomic studies on Australian *S. suis* as well as for rapid typing in outbreaks;