

The Virtual Laboratory

Partnership EU-China

The UCD-Centre for Food Safety (UCD-CFS) is recognised for its long track record describing the application of molecular-based methods for risk assessment. Use of these approaches historically supported the more traditional culture-based methods when assessing the human health impact posed by a bacterial pathogen of interest. With technical advancements in DNA sequencing technologies, UCD-CFS has been able to extend these molecular-based methods to now implement superior precision food safety assessment of risk, based on a high resolution analysis of bacterial genome sequences.

The China National Centre for Food Safety Risk Assessment (CFSA) has been a long-standing collaborator of UCD-CFS. CFSA's technological evolution has followed a similar pathway to that of UCDs, but with a much-enhanced scale. Both of these laboratories have now joined in a collaboration, along with the Polytechnical University of Hong Kong (PUHK) to develop standard operating procedures (SOP) to roll out whole genome sequencing (WGS) of selected zoonotic bacterial pathogens of importance to food safety, thereby enabling a more refined definition of risk to human health.

Definition of the problem

Conventional food safety risk assessment of biological hazards, such as bacteria has been applied based on the use of bacteriological culture-based methods. This approach not only supports the isolation in pure culture of a bacterium of interest, but also provides additional information describing its serotype; antimicrobial resistance susceptibilities; and its phylogeny, based on pulsed-field gel electrophoresis (PFGE).

Technological advances in DNA sequencing, through massively parallel analysis of multiple target bacteria, along with a high resolution computational based analysis of its genomic content, has resulted in a paradigm shift, in how modern risk assessment can be delivered.

This problem to be addressed in this component part of the EU-China Safe project was formulated to provide the means to implement WGS-based analysis of bacterial hazards in both jurisdictions.

Pathway to solution

To create the solution and enable the development of a sustainable SOP that could be applied in both locations, UCD-CFS selected a small collection of food-borne bacterial pathogens, of known provenance, (including *Cronobacter* species [of importance to powder infant formula production]; *Salmonella* species [important for the poultry and pig industries] and *Listeria monocytogenes* [relevant to seafood and dairy foods]) to test the sequencing capabilities of all partners. Initial WGS protocols were shared, and sequencing commenced, using a dedicated Illumina MiSeq platform. Raw read sequences were then shared with UCD and analysed jointly, to ascertain the detailed features mentioned above. This approach facilitated the direct comparison of outputs from all three laboratories.

Finally, the approach resulted in the creation of a standardised SOP for WGS and bioinformatic analysis of bacteria that can be applied in both jurisdictions. In this way computational data can be exchanged and analysed in a unified manner such that the interpretation will be the same, independent of which laboratory provides these data.

This creates a truly harmonised approach to WGS analysis and high-resolution risk assessment.

Long-term impact

The collaborations and partnerships developed and strengthened through the EU-China Safe project will continue to work together, over the longer term. New biological hazards can be added to the portfolio. To this end protocols useful for whole virus genome sequencing (WvGS) particularly in the case of SARS-CoV-2 have been developed and implemented. In the future, where funding opportunities allow, joint projects will be designed and submitted, thereby securing the long-term future and impact of the original programme.