Strategy based on data mining and MALDI-mass spectrometry for control disease of SRS in salmo salar

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Piscirickettsia salmonis is a highly transmissible pathogens that cause high mortality in farmed salmonids. In this way, new techniques based on mass spectrometry (MS) and machine learning were applied and combined in an automatized platform in order to classify and predict this pathogen, in a faster and effective way. MALDI-MS was used to analyze serum samples from salmonid fishes (healthy and diseased) coupled to machine learning analysis in order to obtain a specific and sensitive pattern (m/z) for every pathogen with high reproducibility. The results probed that combining these two techniques are a powerful tool in the correct detection of this pathogen, in an early state of the infection process. Accuracy was >80%, which affords the good performance of our platform as a potential tool for the early disease control in the salmon farming industry. © 2018 IEEE.

Data mining

Databases

Disease control

Fingerprint recognition

Machine learning

Automation

Database systems

Disease control

Industry 4.0

Learning systems

Machine learning

Mass spectrometry

Pathogens

Pattern recognition

Process control

Fingerprint Recognition

High reproducibility

Infection process

MALDI-mass spectrometry

Potential tool

Salmon farming industry

Salmonid fish

Serum samples

Data mining