IR Biotyper®

Ready-to-use *Salmonella* Classifiers

Distinguishing *Salmonella enterica* serogroups and Typhi from Non-Typhi by AI-based classification

Salmonella species are a leading cause of foodborne infections worldwide. While non-typhoidal *Salmonella* typically results in self-limiting diarrhea, *Salmonella* Typhi causes typhoidal fever - a severe, potentially life-threatening disease requiring prompt antibiotic treatment. Rapid and reliable differentiation between Typhi and non-Typhi strains is therefore of high relevance. Traditional serotyping by agglutination is labor-intensive and relies on specialized antisera and expert handling. Fourier-transform infrared (FTIR) spectroscopy, combined with a new AI-based *Salmonella* classifier for the IR Biotyper, provides a practical alternative. The classifier enables an efficient differentiation of *Salmonella* Typhi from non-Typhi strains and is well suited for routine laboratory workflows - helping reduce hands-on time and operational costs.

Benefits of using Classifiers:

- Ready-to-use
- Immediate and clear result display by color coding and score values
- Easy and fast workflow improving lab efficiency
- Transparent, objective and standardized serotyping results
- Safe (no open slides) and animal friendly workflow (no rabbit antibodies)

What's a Classifier?

An FTIR classifier is a software tool that learns from infrared spectra of known training classes and uses AI-based algorithms to confidently classify new, unknown spectra (Fig.1).

How was the *Salmonella* Classifier developed?

The serotyping approach begins with a serogroup classifier that differentiates 36 *Salmonella* enterica serogroups. When serogroup O:9 is detected, a second classifier is automatically activated to distinguish *Salmonella* Typhi from non-Typhi isolates within this group.

To develop the *Salmonella* Typhi Classifier, *Salmonella* isolates of serogroup O:9 were used as the training set. This set contained a mix of Typhi and non-Typhi isolates with Enteritidis being the most common. In total, 1,000 spectra were used to train a support vector machine (SVM) algorithmn within the IR Biotyper software.

After training, the classifier was evaluated using a set of additional spectra from 643 isolates of serogroup O:9 that were not included in the previous training dataset. The test set comprised 69 Typhi isolates and 574 non-Typhi isolates. The accuracy of the unknown classification (Table 1) shows an accuracy of > 99 % with one isolate out of the 643 being misclassified.

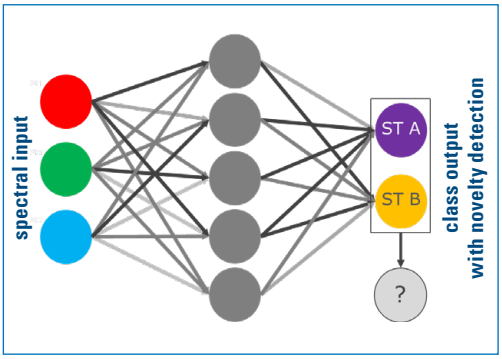

Fig. 1 Schematic depiction of Classifier that can be applied to unknown samples for their classification (right side). Classifier creation involves a training set of isolates (left side) to establish a recognition network (middle).

		Prediction				
		Typhi	non-Typhi	uncertain	∑ Actual	class recall
Actual	Typhi	69	0	0	69	100%
	non-Typhi	1	573	0	574	100%
	∑ Prediction	70	573	0	643	
	class precision	99%	100%	0%		

Table 1. Confusion matrix of the test results.

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Not for use in clinical diagnostic procedures.
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