Foods 2024 Conference
The 5th International Electronic Conference on Foods
28–30 October 2024 | Online
MDPI

# Comparison between two different mass spectrometry platforms (MALDI-TOF MS) for rapid Shiga toxin-producing *Escherichia coli* O157:H7 detection in food.

Manfredi E, Rocca F, Gentiluomo J, Miliwebsky E

*INEI-ANLIS "Dr. Carlos G. Malbrán"- Buenos Aires Argentina*

## INTRODUCTION & AIM

*Escherichia coli* O157:H7 is the most frequent Shiga toxin-producing (STEC) serotype associated with severe humans diseases related to foodborne illnesses. Different STEC contaminated foods, such as undercooked ground beef, hamburgers, fermented sausages, lettuce, among others, have been identified as source of contamination in sporadic cases or outbreaks associated with STEC infection.

**Mass spectrometry (MALDI-TOF MS)** is a simple and rapid technique that can be applied for STEC O157:H7 strains detection from the presumptive colony on a culture plate. The technology is based on the analysis of protein spectra resulting from the impact of a laser on a sample crystallized with an organic matrix. The presence of some of the 9 biomarker peaks (BP) and the absence of 9060m/z would allow the detection of STEC O157:H7 according to previous work carried out on Microflex LT (Bruker Daltonics). A comparative analysis with **Vitek MS Prime (VMSP,** *bioMeriéux)* was necessary to investigated the presence of the same typical BP.

## METHOD

**Samples analyzed**
**178 isolations**

**163- *E. coli***

- **86 STEC O157:H7**
- **77 Others *E. coli***

| pathotypes (Others *E. coli*) | STEC (no O157) | EPEC | ETEC | EIEC | EAEC | O157 NT |
|---|---|---|---|---|---|---|
| | 26 | 13 | 10 | 6 | 13 | 9 |

| Serogroups (STEC no O157) | 145 | 121 | 26 | 103 | 123 | 111 | 59 | 112 |
|---|---|---|---|---|---|---|---|---|
| | 14 | 6 | 1 | 1 | 1 | 1 | 1 | 1 |

**15- *Shigella spp***

| flexneri 1 | flexneri 2 | flexneri 6 | dysenteriae 1 | Dysenteriae 2 | boydii | sonneii |
|---|---|---|---|---|---|---|
| 3 | 4 | 2 | 1 | 2 | 1 | 2 |

### PROCEDURE

Food freezing samples

-Isolation in Mueller Hinton and *E. coli* strain on blood agar (calibration)


-Direct sowing on plate (in duplicate)

-Added MATRIX (produced by the manufacturer) → Crystallization (By evaporation)


Machine

→ Reading

The IVD library was used to corroborate the identification and the RUO database to search for BP.

## RESULTS & DISCUSSION

Due to the characteristics of the VMSP equipment and the peaks analysis software, differences were found between the BP detected. The presence of low intensity peaks (<2000000) in other *E. coli* did not allow the same algorithm to be applied. In parallel, for the detection of STEC O157:H7 with VMSP, BPs between 10163-10168 m/z and 5234-5238 m/z were found, in addition to the presence of three or more BPs previously defined. The rest of *E. coli*/*Shigella* presented BPs between 10137-10142 m/z and 5229-5232 m/z, in addition to 9060 m/z peak; and generally less than two of the other BPs obtained by Bruker.

*Escherichia coli*

81% (the 2 markers)

| m/z | 9060 | 3017 | 3083 | 3595 | 3770 | 4012 | 4939 | 5234-5238 | 5229-5232 | 6037 | 6169 | 10163-10168 | 10137-10142 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| STEC O157 | 3% | 74% | 76% | 67% | 51% | 94% | 65% | 96.5% | 0% | 86% | 50% | 84% | 0% |
| Otras *E.coli* | 97,4% | 9% | 5% | 8% | 14% | 45% | 0 | 2,50% | 91% | 10% | 0 | 0% | 92% |

85% (the 2 markers)

| c/0 | c/1 | c/2 | c/3 | c/4 | c/5 | c/6 | c/7 | c/8 |
|---|---|---|---|---|---|---|---|---|
| 0 | 6 | 8 | 6 | 6 | 4 | 13 | 21 | 21 |
| 28 | 31 | 17 | 1 | 0 | 0 | | | |

→ c/+3 peaks 82,5%

→ c/up to 2 peaks 99%

Table 1: Bruker BP percentages using the VMSP platform in *E. coli* samples (STEC O157:H7 yellow and other *E.coli* green)

*Shigella spp*

| m/z | 9060 | 3017 | 3083 | 3595 | 3770 | 4012 | 4939 | 5234-5238 | 5229-5232 | 6037 | 6169 | 10163-10168 | 10137-10142 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 9 | 1 | 3 | 2 | 6 | 6 | 0 | 1 | 11 | 0 | 0 | 0 | 15 |
| | 60% | 6% | 20% | 13% | 40% | 40% | 0% | 6% | 73% | 0% | 0% | 0% | 100% |

*S.flexneri* c/5236 low intensity + 10137

| c/0 | c/1 | c/2 | c/3 | c/4 | c/5 |
|---|---|---|---|---|---|
| 7 | 2 | 4 | 1 | 0 | 1 |

87%

Table 2: Bruker BP percentages using the VMSP platform in *Shigella* samples

As by Bruker, *Shigella* showed great similarity with the other *E. coli.*
In STEC O157:H7 strains, the presence of the 2 peaks found at the same time, represented 81% and in the other *E. coli*/*Shigella*, the 3 peaks represented 83%

Presence of Biomarkers (Biomerieux)

**STEC O157**

| 10163-10168 | 5234-5238 | 9060-9065 | |
|---|---|---|---|
| + | + | - | **81%** |
| + | - | - | 6.5% |
| - | + | - | 8% |
| - | - | - | REPEAT |

***Others E.coli /Shigella***

| 10137-10142 | 5229-5232 | 9060-9065 | Presence |
|---|---|---|---|
| + | + | + | 83% |
| + | + | - | 1.3% |
| + | - | + | 6.5% |
| - | + | + | 6.5% |
| + | - | - | 0% |
| - | + | - | 0% |
| - | - | + | 0% |

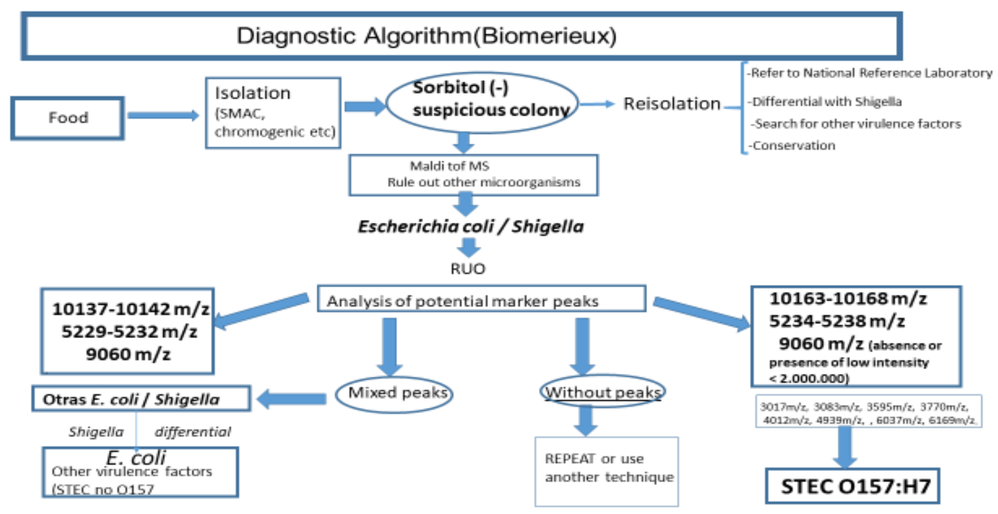
**Mixed peaks**

- c/characteristic peaks of STECO157 with **9060** (low intensity) → STEC O157
- *c/ peaks of others E.coli/Shigella* with **5234-5238** → *E. coli/Shigella*

A small percentage presents mixed peaks, but they are easily identifiable by the BP described.

## CONCLUSION

Applying the algorithm designed for VMSP equipment, it was possible to identify STEC O157:H7 in 99% of the isolates. This screening method to detect the suspicious colony from a primary culture, is highly recommended as it is quick, easy and economical to implement in those food analysis laboratories that can count on this technology.




## FUTURE WORK / REFERENCES

**"Rapid and accurate detection of Shiga toxin-producing *Escherichia coli* (STEC) serotype O157:H7 by mass spectrometry directly from the isolate, using 10 potential biomarkers peaks and machine learning predictive models."**
**Manfredi Eduardo**, Rocca María Florencia, Zintgraff Jonathan, Irazu Lucía, Miliwebsky Elizabeth, Carbonari Carolina, Deza Natalia, Prieto Mónica , Chinen Isabel. **Journal of Medical Microbiology 2023;72:001675**