New Tool for Bacteriological Analysis of Milk

An accurate, fast, and cost-effective tool to improve udder health

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Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF) is a new tool used in many veterinary and milk quality laboratories to identify microorganisms present in milk.

Observation of clinical symptoms and measurement of somatic cell count are important methods of detecting mastitis; however, they cannot identify specific mastitis-causing pathogens.

MALDI-TOF provides a clearer picture of the microorganisms that may be contributing to mastitis, including bacteria, fungi, and algae.

How does MALDI-TOF work?

MALDI-TOF creates a unique protein spectrum pattern of an unknown microorganism - like a unique fingerprint for each microorganism.

This result is then compared with patterns in a reference database of thousands of known microorganisms, allowing the genus- or species-level identification of a microorganism.

This process of creating a fingerprint for each microorganism strain and comparing it to other strains is like the DNA tests crime laboratories use to identify suspects.

Similar to each person having unique DNA, microorganisms have unique markers that allow them to be identified through MALDI-TOF analysis.

Key Points

There are many species now identified in milk, and for many of them the relevance to udder health is unknown.

The MALDI-TOF databases used to identify microorganisms are expanding. This may lead to valuable information on new mastitis prevention and control strategies.

You may receive a milk bacteriology result reporting an uncommon bacterial species - these microorganisms are not new, it is just that we can now identify them.

If you see unfamiliar microorganism names on your mastitis reports, ask your veterinarian or the diagnostic laboratory to provide further information on these species.

MALDI-TOF equipment for analyzing milk samples.

What does this mean for mastitis-causing pathogens?

Researchers from the University of Montreal have used MALDI-TOF to determine the diversity and proportion of different microorganisms isolated from milk. The microorganisms present in 94,353 milk samples collected in Canada, the US, and Brazil were identified. The milk samples came from both apparently healthy cows and cows with clinical mastitis. The results showed a great diversity of microorganisms in both types of samples, with 294 species present.

The microorganisms were mapped based on what is known and unknown about their relevance to udder health. For most of the microorganism species identified (206), little is known about their relevance to udder health.

> **For instance, microorganisms can be commensal microorganisms, meaning they are present in milk but not harmful to the cow.**

Some identified microorganisms may be part of a healthy skin or teat canal microbiome, while others may be pathogenic and cause subclinical and clinical mastitis.

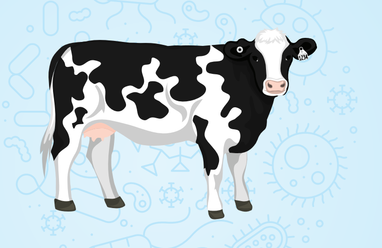
The microorganisms present in 94,353 milk samples collected in Canada, the US, and Brazil were identified

The results show that at least 85 different microorganisms can cause an elevation of SCC and/or clinical mastitis in dairy cattle. **You can find the complete list of the 294 microorganisms by scanning the QR code:**

A difference was found in the microorganism species' identified from apparently healthy cows compared to cows with clinical mastitis.

APPARENTLY HEALTHY COWS

When looking at the most frequently identified microorganisms from the milk of apparently healthy cows, **the following 5 microorganisms were most prevalent:**



- *Staphylococcus chromogenes* | **6.7%**
- *Aerococcus viridans* | **1.6%**
- *Staphylococcus aureus* | **1.5%**
- *Staphylococcus haemolyticus* | **0.9%**
- *Staphylococcus epidermidis* | **0.7%**

COWS WITH CLINICAL MASTITIS

When looking at the most frequently identified microorganisms from the milk of cows with clinical mastitis, **the following 5 microorganisms were most prevalent:**

- *Escherichia coli* | **11.0%**
- *Streptococcus uberis* | **8.5%**
- *Streptococcus dysgalactiae* | **7.8%**
- *Staphylococcus aureus* | **7.8%**
- *Klebsiella pneumoniae* | **5.6%**

Funding Partners

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