

JEMRA Report 2018

Shiga toxin-producing Escherichia coli (STEC) and food: attribution, characterization, and monitoring

- The STEC serotype is not a reliable predictor of the potential of the STEC strain to cause severe diseases.
- Risk of D, BD or HUS for STEC infections is best predicted using STEC virulence factors (encoded by genes).
- Based on existing scientific knowledge, STEC strains belonging to the Stx2a subtype and with adherence genes eae or aggR are considered to pose the highest risk of illness and have the strongest potential to cause HUS.
- All STEC, regardless of the Stx subtype they produce, should be considered as potentially diarrhoeagenic, especially in susceptible individuals.



JEMRA Report 2019

Attributing illness caused by STEC to specific foods

«Here, beef, produce (fruits and vegetables), dairy products, other unspecified types of meat, and chicken all emerged as significant sources of STEC, depending on geographic region (AMR, EUR and WPR) and whether the illnesses being considered were from outbreaks or were sporadic cases. Care must be taken in extrapolating data from these regions to other regions for which there are no data. Similarly, absence of data for food categories, and absence of food items from any of the studies, does not necessarily mean that said food items are safe».

Journal of Food Protection, Vol. 82, No. 5, 2019, Pages 724–767 https://doi.org/10.4315/0362-028X.JFP-18-479
Published 2019 by the International Association for Food Protection
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General Interest

Response to Questions Posed by the Food and Drug Administration Regarding Virulence Factors and Attributes that Define Foodborne Shiga Toxin-Producing *Escherichia coli* (STEC) as Severe Human Pathogens[†]

ADOPTED 7 AUGUST 2018, WASHINGTON, D.C.
NATIONAL ADVISORY COMMITTEE ON MICROBIOLOGICAL CRITERIA FOR FOODS

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MS 18-479: Received 2 October 2018/Accepted 14 December 2018/Published Online 10 April 2019

Key words: Escherichia coli; Shiga toxin; virulence factor

NACMCF Report

STEC disease prevention has been and will continue to be driven by **improvement in outbreak detection**, **investigation**, **and food industry practices**. Highlights of Committee recommendations include the following:

- Develop a new universal enrichment culture medium that can be broadly used for all STEC in any food.
- Explore high-throughput methods that can detect STEC virulence factor genes directly from enrichment medium
- Expand systematic sampling of food, animals, and water for STEC
- Explore ways for industry to share test data anonymously.
- Link standardized epidemiological, clinical, and STEC WGS data to monitor trends in recognized and emerging
- virulence attributes
- Fund academic research

EFSA Opinion 2019

Pathogenicity assessment of STEC and analysis of outbreak data for the source attrubution

Expected to be published soon