

Occurrence of extended-spectrum beta-lactamase Gram-negative bacteria among various types of produce results in different level of ingestion risks

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-Background: Unsafe food can cause over 200 types of diseases and the risk of illness might increase due to ingestion of raw food. Previous studies from around the world have reported the presence of extended spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae* in retailed vegetables. In this study, we performed a comparative analysis on the produce-associated microbiota in three types of produces, namely lettuce, cucumbers and tomatoes that were collected over a period of 1.5 years. This study was also aiming to determine if different produce would result in differing risks upon ingestion.

-Material/Methods: Food sampling of raw vegetables were collected from Taif, Thuwal and Jeddah. Then through cultivation on selective media (MacConkey with 8 µg/mL meropenem or 8 µg/mL ceftazidime). The samples were also subjected to molecular-based approaches to determine species, sequence types and antibiotic resistance determinants. Two ESBL producing *Klebsiella pneumoniae* were selected for whole genome sequencing (Illumina MiSeq) to further describe their genomic makeup. Quantitative microbial risk assessment was used to estimate the risk arising from ingestion of these produces.

-Results: Microbiological investigations revealed sporadic presence of (ESBL) producing *K. pneumoniae* and multidrug resistant *A. baumannii* in lettuce and cucumbers but not tomatoes. Positive PCR amplification of the correct anticipated size were observed for *bla*_{CTX-M-15} gene among 13 out of the 21 *K. pneumoniae* isolates from lettuce. Two *A. baumannii* were isolated from cucumbers and were positive for *bla*_{OXA-51} gene. Further, whole genome sequencing data of the two of the *K. pneumoniae* isolates further suggested the presence of *bla*_{CTX-M-15} gene in conjugative plasmids, as well as other antibiotic resistance genes and virulence-associated traits in either conjugative plasmid or chromosomal genome. According to the quantitative microbial risk assessment in particular, the risks arising from ESBL-positive *K. pneumoniae* in the lettuce, but not in other types of vegetables, were higher than the acceptable annual risk of 10⁻⁴.

-Conclusion: Most of the current reports of ESBL-positive bacterial isolates were identified in nosocomial environment. However, the carriage of such drug-resistant bacteria in food that is consumed daily suggests a possible connection between daily diet and human health. This report suggests further research is needed to assist the risk of consuming the lettuce in community acquired carriage of multidrug resistant antigens. Also, further research should be conducted to assist the impact of water quality and farming practice on bacterial pathogens