

Diversity of Pathogenic Bacteria in Commercially Available Mango Fruits in Western Province, Sri Lanka

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Foodborne illnesses are reported every year throughout the world due to contaminations with pathogenic microorganisms such as *Escherichia coli* and *Salmonella*. Preventing contaminations during any stages of a post or pre-harvesting, transportation, and storage conditions is important in reducing the risk of foodborne illnesses. The present study was aimed to determine the pathogenic bacterial diversity and abundance in the fresh mango samples from Moratuwa, Pettah and Wellawatte areas in Western Province, Sri Lanka. Four varieties of purchased mango (n=200) from every 50 samples from commercial markets were used for analysis. Isolated microorganisms were then identified by conventional standard methods using Biochemical keys. Biochemical tests included Indole, Citrate, MRVP, Triple sugar iron agar, Motility test and microbiological culture methods such as MacConkey, Chromogenic culture and Gram staining. Along with the bacterial characteristics of lactose fermentation and non-lactose fermentation, bacterial chemical reaction to each biochemical test and overall colony characteristics on Chromogenic culture media were used for identifying each pathogenic bacterium in mango samples. Distance-Based Redundancy Analysis (dbRDA) was used to identify the distribution pattern of bacterial isolates from different mango collection sites. Seven pathogenic bacterial species namely; *Escherichia coli* (25%), *Shigella sonnei* (25%), *Klebsiella pneumonia* (30%), *Enterobacter intermedius* (15%), *Proteus vulgaris* (5%) and *Salmonella enterica* (30%) were identified from mangoes. As indicated by Distance-Based Redundancy Analysis (dbRDA) on Bray- Curtis Similarity, the bacteria in mango varieties of study regions were significantly different from each other ($\chi^2=556.167$; $P < 0.001$). As indicated by the loadings of the dbRDA axes, the bacterial diversity in mangoes from Moratuwa and Pettah indicated similarity of 72.46%. The dbRDA 1 axis was significantly influenced by the abundance of *E. coli* and dbRDA 2 axis was significantly subjective with the abundance of *Klebsiella oxytoca*, and *Proteus vulgaris*. Poor hygiene and handling practices of the vendors, storage in unsafe containers and in high-temperature for long periods, and unsafe marketing environments were identified as key facts contributing to the pathogenic contamination of mangoes.

Keywords: contamination, culture, isolate, mango, microbiological