

# Can natural preservatives serve as a new line of protective technology against bacterial pathogens in meat and meat products?

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Data from governmental agencies have indicated that the major foodborne pathogens implicated in foodborne illness may vary among different continents (top five in descending order of numbers of cases/infections): *Campylobacter*, *Salmonella*, *Yersinia*, Shiga toxin-producing *Escherichia coli* and *Listeria monocytogenes* in the European Union in 2021 (European Food Safety *et al.*, 2022); *Campylobacter*, *Salmonella*, Shiga toxin-producing *E. coli*, *Shigella* and *Yersinia* in the US in 2022 (Delahoy *et al.*, 2023); and *Salmonella*, *Vibrio parahaemolyticus*, pathogenic *E. coli*, *Staphylococcus aureus* and *Bacillus cereus* in China in 2020 (Li *et al.*, 2021). Presence of *L. monocytogenes*, particularly the ST87 strains in ready-to-eat foods, is also a risk factor in Chinese food system (Cheng *et al.*, 2022).

In addition to data on the main pathogens involved or confirmed in general foodborne outbreaks from individual years, two recent review articles reported on bacterial foodborne outbreaks specifically related to red meat and meat products (Omer *et al.*, 2018; Warmate and Onarinde, 2023). In one of the papers based on peer-reviewed journal articles in the period 1980–2015, the authors reported that most of the outbreaks were attributed to verotoxigenic *E. coli* and *Salmonella*, causing 33 and 21 outbreaks, respectively, mostly in Europe and the United States, and that the implicated food items included beef, lamb, pork, and meat products (Omer *et al.*, 2018). The other review reported their findings of major foodborne outbreaks linked to red meat and its products based on 1729 reports, 101 from peer-reviewed journals and 1628 from two official websites - the US Centers for Disease Control and Prevention and the European Centers for Disease Control and Prevention (Warmate and Onarinde, 2023). They found that most of the outbreaks were caused by *Salmonella* (469 or 27.1%), followed by *E. coli* (414 or 23.9%), and then *Clostridium* (294 or 17%). *S. aureus* and *L. monocytogenes* accounted for 134 (7.8%) and 120 (6.9%) of the outbreaks, respectively. Absence of *Campylobacter* in these lists is apparently due to exclusion from their analyses of the white meat (poultry meat) which is considered as a major contributor to human campylobacteriosis (Hermans *et al.*, 2012; Chlebicz and Slizewska, 2018; European Food Safety *et al.*, 2022). In some African countries, the major pathogens in the food systems included pathogenic *E. coli*, *S. aureus*, *Salmonella*, *Bacillus* and *L. monocytogenes* according to the meta-analytical data of publications from 2000 to 2015 (Paudyal *et al.*, 2017). It is obvious that *Campylobacter* was not targeted in the surveyed African studies.

By putting both the red and white meats together, the major bacterial pathogens in meats and meat products could be typified as *Salmonella*, *Campylobacter*, pathogenic *E. coli*, *L. monocytogenes* and *Clostridium*. This is quite similar to a review published a decade ago titled as “Food-borne diseases — The challenges of 20































reported RiLPs include goadvionins (Kozakai *et al.*, 2020), albopeptins (Oikawa *et al.*, 2022), selidamides (Hubrich *et al.*, 2022), and others (Pilz *et al.*, 2023).

Plant AMPs act as the first line of defense against phytopathogens, widespread in the plant kingdom and can be found in all plant organs (Lima *et al.*, 2022; Sharma *et al.*, 2022). Plant AMPs are ribosomally derived and share several common characteristics with those from microbes, insects and animals, such as their molecular forms, positive charge and amphipathic nature (Tam *et al.*, 2015). They are structurally diverse and can be divided into families based on their sequence similarity, cysteine (Cys) motifs, and distinctive disulfide bond patterns (i.e., characteristic Cys pattern with a defined number of non-Cys residues between the two neighboring Cys) which, in turn, determine their tertiary structure (Tam *et al.*, 2015). Plant AMP families include thionins, defensins, hevein-like peptides, knottins, stable-like peptides, lipid transfer proteins, snakins and cyclotides (Lima *et al.*, 2022).

Insect AMPs play an important role in the humoral immune system. In holometabolous species AMPs are biosynthesized mainly in the fat body and transferred into the hemolymph, while in heterometabolous species they are produced by hemocytes and secreted into the hemolymph following infection (Bulet and Stöcklin, 2005; Marmaras *et al.*, 2009). More than 200 AMPs have been identified from insects to date (Erdem Büyükkiraz and Kesmen, 2022). Insect AMPs are divided into three groups based on their amino acid sequence and structures: (1) cecropins, the linear peptides with  $\alpha$ -helix but lack Cys residues; (2) defensins with 6-8 conserved Cys residues and a stabilizing array of 3 or 4 disulfide bridges as well as 3 domains consisting in a flexible amino-terminal loop; and (3) proline and/or glycine-rich peptides (Wu *et al.*, 2018). The most explored insect AMPs are cecropins, drosocin, attacins, dipterocins, defensins, ponerocins, drosomycin and metchnikowin (Mylonakis *et al.*, 2016; Wu *et al.*, 2018). More new peptides can still be discovered by combined use of mass spectrometric techniques, antimicrobial assays and RNA-seq (Lin *et al.*, 2022; Scieuzo *et al.*, 2023).

LPs and AMPs from plants and insects possess antibacterial properties against fungal and bacterial pathogens, including those foodborne (Wu *et al.*, 2018; Kourmentza *et al.*, 2020; Lin *et al.*, 2022; Sharma *et al.*, 2022; Pilze *et al.*, 2023; Wang *et al.*, 2023). Mechanistically, the negatively charged bacterial cell membrane is the primary target for electrostatic interaction with the positively charged antimicrobial peptide residues, and the hydrophobic property, e.g., of tryptophan, leucine, etc., aids in insertion of LPs into the lipid bilayer, leading to depolarization of bacterial cell membrane and eventual bacterial lysis (Mylonakis *et al.*, 2016; Lima *et al.*, 2022; Pilz *et al.*, 2023). Some AMPs function via non-membrane target (i.e.,























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## **Author contributions**

CC and LJ contributed two parts each, XL and HS participated in the organization of sections and discussion; and WF involved in conceptualization and finalization of the manuscript.

## **Conflict of interest**

There is no conflict of interest.

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**Figure**

**Figure 1. Discovery of novel antimicrobial peptides via rational design**

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