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Studying and enlightening food microbial ecosystem and microbiome

03.10

Exploring associations between metataxonomic profiles and pathogen presence along infant food production chain

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Food industries have not yet ceased the challenge conducted by pathogens that tend to persist after diverse stages of the process line. This critical issue is fundamental for infant food industries since their end users belong to a group of the population that has not yet thoroughly developed its immune system. Therefore, the presence of foodborne pathogens can cause severe illness and death on infants.

This study aimed to investigate presumable correlations among metataxonomic analysis and pathogens prevalence, through enrichment, isolation and molecular approaches.

Hundreds of samples were collected during various stages in the production of infant food in a commercial facility. Samples included environmental swabs, raw material, intermediate and final products. On every sample, 16S rRNA amplicon - based sequencing has been performed and Amplicon Sequence Variants (ASVs) distribution was examined thoroughly. Furthermore, the presence of *Listeria monocytogenes*, *Bacillus cereus*, *Salmonella* spp. *Staphylococcus aureus* and *Clostridium perfringens* was inspected prior and subsequent to twenty - four hours of enrichment, whereupon pathogens isolation, species specific PCR and Real - Time PCR were performed.

Heterogeneous bacterial communities were observed between food samples in relation to their composition, while in the case of the environmental samples a clear segregation was not easily discerned. Metataxonomic analysis seems not sufficient to directly detect low abundant microbial taxa, like the cases of pathogens. Nevertheless, identification of pathogens could feasibly be reached in cases of samples with high biodiversity, carrying narrow bacterial concentration. The presence of low abundance microorganisms should not be underestimated; because within them could be found new emerging microorganisms with potentiality in pathogenesis. This does not exclude the possibility to correlate specific metataxonomic profiles with potential pathogen's presence.

Our outcomes suggest that metataxonomic and other multi - omics approaches could be contributing elements in understanding and possibly predicting the distribution of pathogens (in time and space) during food processing.



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