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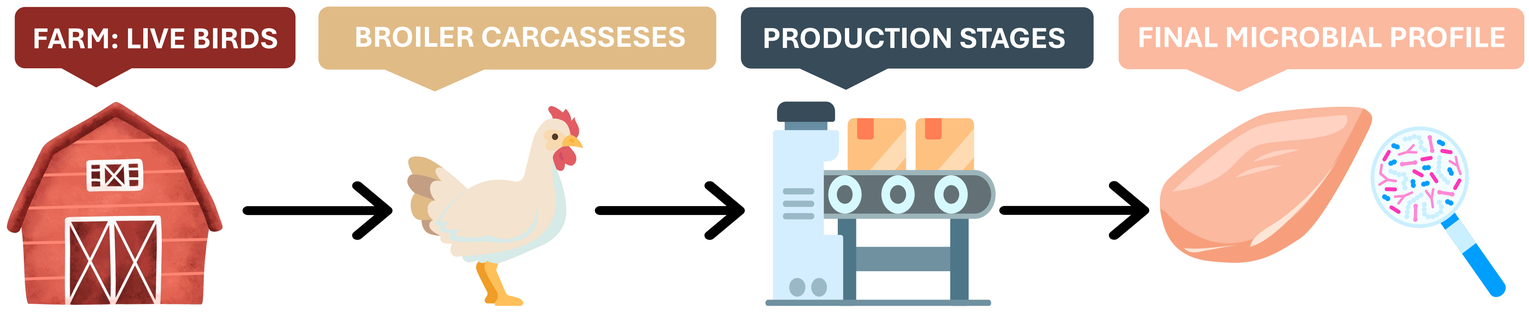
Meta-Taxonomic Analysis of Poultry and Slaughterhouse Microbiota: A Comprehensive Examination of Resident Microbial Communities

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INTRODUCTION & AIMS

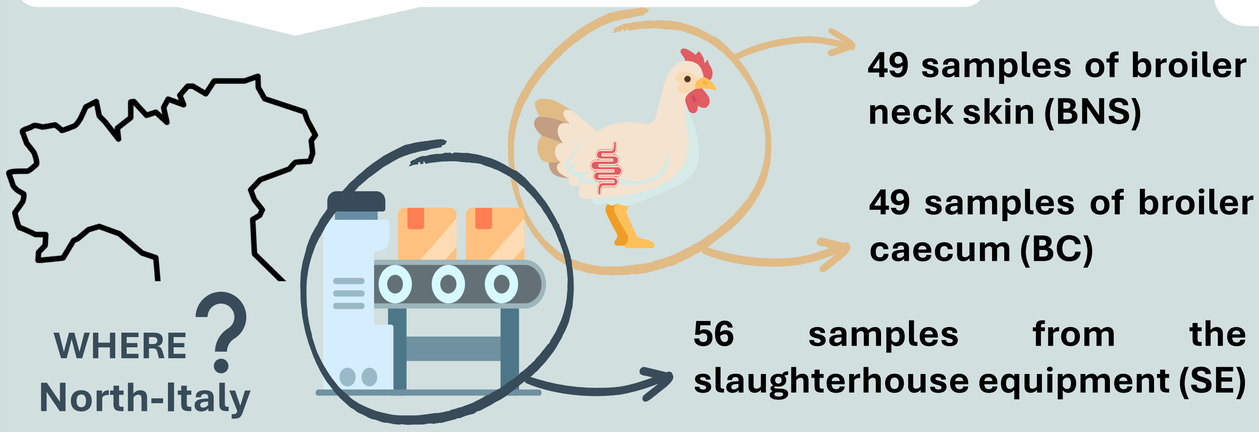
Poultry contaminations occur during the processing chain and are found from farm to table.
The final microbial profile of poultry meat is influenced by each step of the process.
The consumption of contaminated poultry poses a significant threat to public health. It is associated to infections caused by pathogens such as: *Campylobacter*, *Salmonella*, *Listeria monocytogenes* and *Arcobacter*.



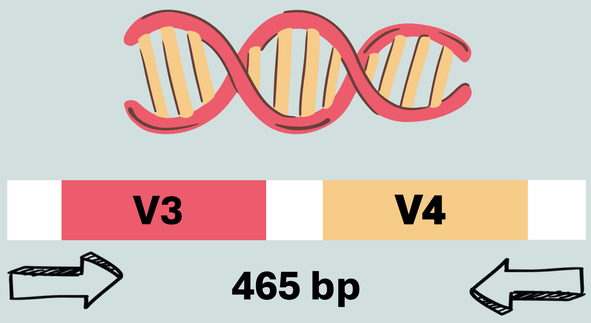
The **objective** is to assess the contribution of broiler skin and gut to the indigenous slaughterhouse microbiota. In addition, the study aims to clarify how the **persistence** and **environmental distribution of *Arcobacter* spp.** are influenced by the **cross-contamination** patterns associated with these specific sources.

MATERIALS & METHODS

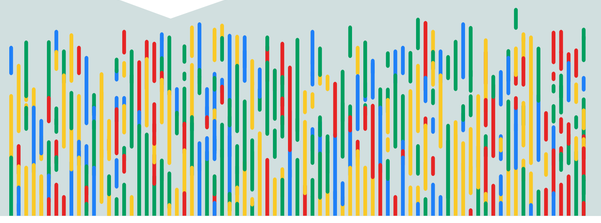
1. BROILERS AND ENVIRONMENTAL SAMPLING
154 samples were collected from a local poultry abattoir



2. DNA extraction
3. V3-V4 region library constructed from the 16S rRNA gene region



4. BIOINFORMATIC ANALYSIS: taxonomy was assigned with a 99% of sequence similarity by matching ASVs to the Silva prokaryotic reference database



RESULTS & DISCUSSIONS

The BC microbial community is significantly distinct from the BNS and SE community (Fig. 1, 2).

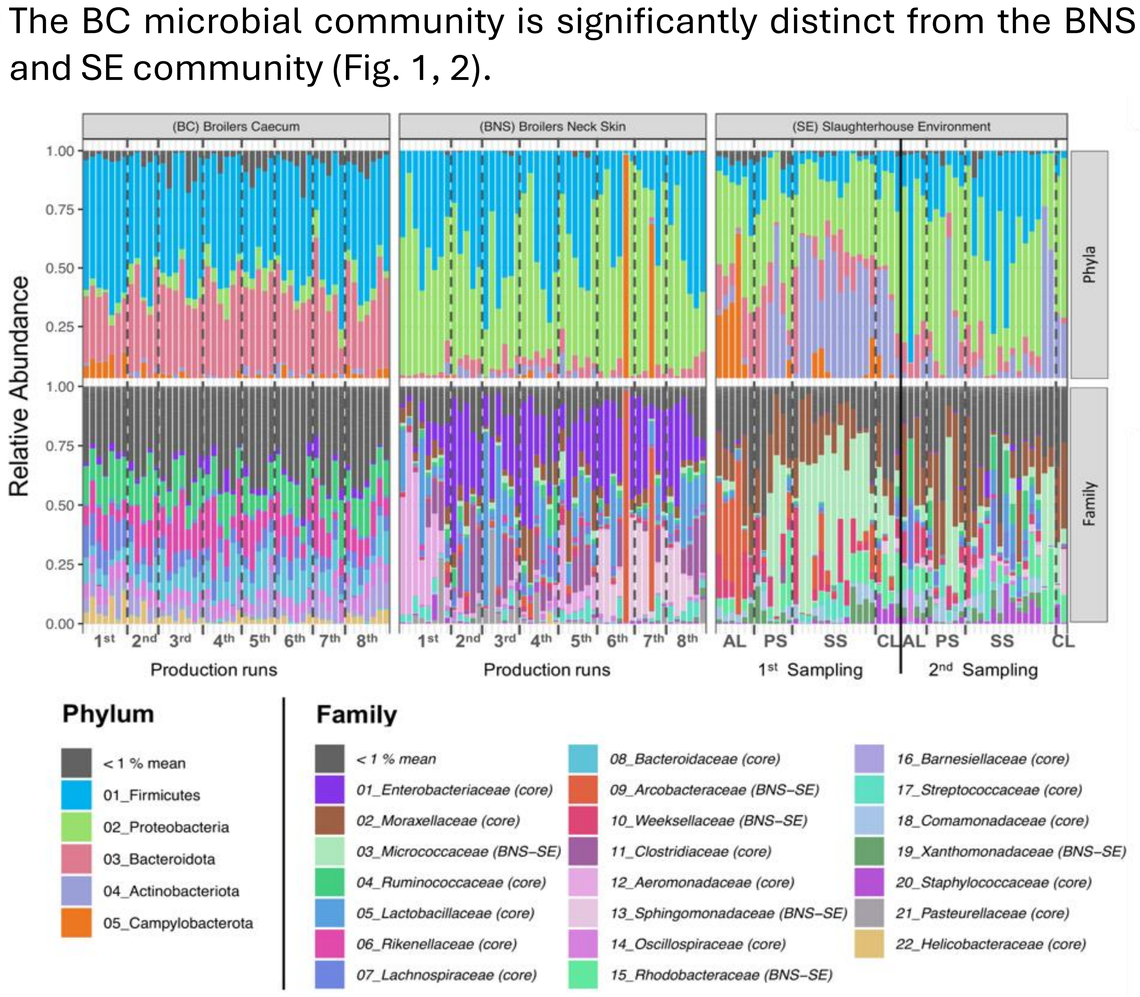


Figure 2. Microbiota composition and distribution in phylum and family taxa. The samples are grouped according to the temporal order of the sampling and according to the order of the slaughter of the flock and the processing stage, BC-BNS and SE. Slaughterhouse sectors and transport lines are indicated: FL = first row; PS = plucking sector; SS = slaughter sector; SL = second row. Taxa are ordered in the legend from most to least abundant (mean >1%).

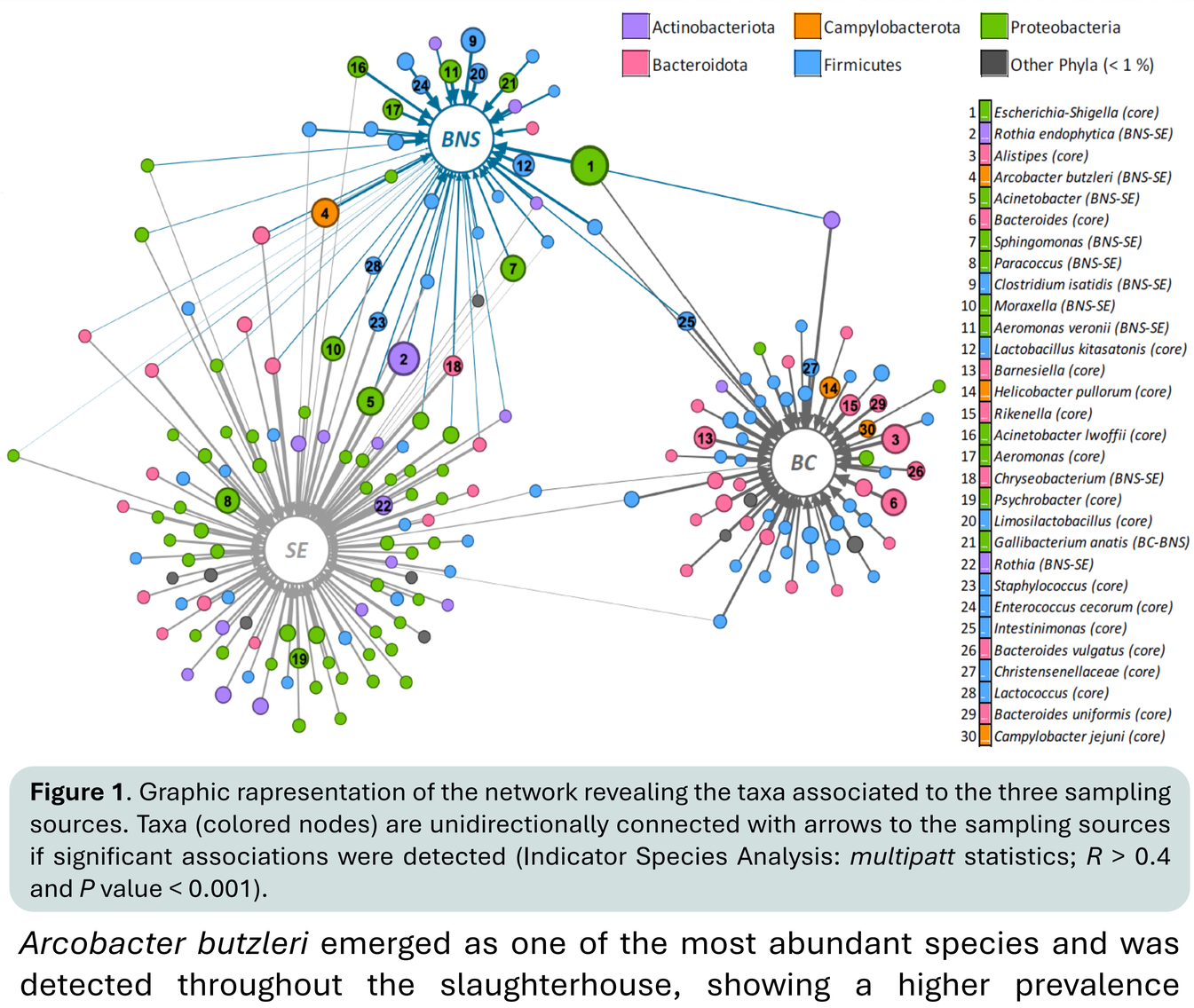


Figure 1. Graphic rapresentation of the network revealing the taxa associated to the three sampling sources. Taxa (colored nodes) are unidirectionally connected with arrows to the sampling sources if significant associations were detected (Indicator Species Analysis: *multipatt* statistics; $R > 0.4$ and P value < 0.001).

Arcobacter butzleri emerged as one of the most abundant species and was detected throughout the slaughterhouse, showing a higher prevalence compared to other Campylobacterota (Fig. 1, 2). It was uniquely and significantly associated with BNS and SE, while *Helicobacter pullorum* and *Campylobacter jejuni* were indicators of BC (Fig. 1). *A. butzleri* was constantly present on BNS along production runs, but significantly more abundant the first sampling day in SE (Fig.2).

CONCLUSIONS & IMPORTANCE

Our findings have emphasised the **persistence of *A. butzleri*** in a modern poultry abattoir and its establishment as part of the **resident microbiota** in specific environmental niches. The analysis conducted underlines the significance of early monitoring of food pathogens in the production chain, supported by meta-taxonomic analysis. Using these detection approaches, the presence of these pathogens could soon be considered an indicator of food safety and quality in slaughtered poultry.

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Applied and Environmental Microbiology
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Microbial contamination pathways in a poultry abattoir provided clues on the distribution and persistence of *Arcobacter* spp.
Cristian Botta,[1] Davide Buzzanca,[1] Elisabetta Chiarini,[1] Francesco Chiesa,[2] Selene Rubiola,[2] Ilario Ferrocino,[1] Edoardo Fontanella,[3] Kalliopi Rantsiou,[1] Kurt Houf,[4] Valentina Alessandria[1]

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Buzzanca D, Kerkhof P-J, Alessandria V, Rantsiou K, Houf K. 2023. *Arcobacteraceae* comparative genome analysis demonstrates genome heterogeneity and reduction in species isolated from animals and associated with human illness. Heliyon 9:e17652.
Ramees TP, Dhama K, Karthik K, Rathore RS, Kumar A, Saminathan M, Tiwari R, Malik YS, Singh RK. 2017. *Arcobacter*: an emerging food-borne zoonotic pathogen, its public health concerns and advances in diagnosis and control – a comprehensive review. Vet Q 37:136–161.

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