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Significance of the beef, pork and poultry sectors in the occurrence of *Clostridium perfringens* food poisoning outbreaks in France

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► To cite this version:

Christina Tran, Typhaine Poezevara, Véronique Maladen, Laurent Guillier, Narjes Mtimet, et al.. Significance of the beef, pork and poultry sectors in the occurrence of *Clostridium perfringens* food poisoning outbreaks in France. 14th International Conference on the Molecular Biology and Pathogenesis of Clostridia (ClostPath 2025), Sep 2025, PARIS, France. 133, 2026, <10.1016/j.fm.2025.104898>. <anses-05601454>

HAL Id: anses-05601454

<https://anses.hal.science/anses-05601454v1>

Submitted on 24 Apr 2026

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INTRODUCTION

Clostridium perfringens is a spore-forming anaerobic bacterium that is both widespread in the environment and recognized as a foodborne pathogen. In France, 39% of foodborne outbreaks caused by *C. perfringens* are associated with the use of contaminated raw materials in the preparation of meat-based ready meals^[1]. Contamination in the food chain is suspected to occur during the evisceration step in slaughterhouses. However, the origins of *C. perfringens* contamination remain poorly studied.

As part of the **ANR ClostAbat project**, a previous investigation^[2] confirmed the presence of *C. perfringens* in French slaughterhouses in the cattle, pig or poultry sectors. The aim of this study is to characterize the dissemination and persistence potential of 286 *C. perfringens* isolates collected from slaughterhouses, as well as to assess their virulence and antimicrobial resistance profiles.

RESULTS

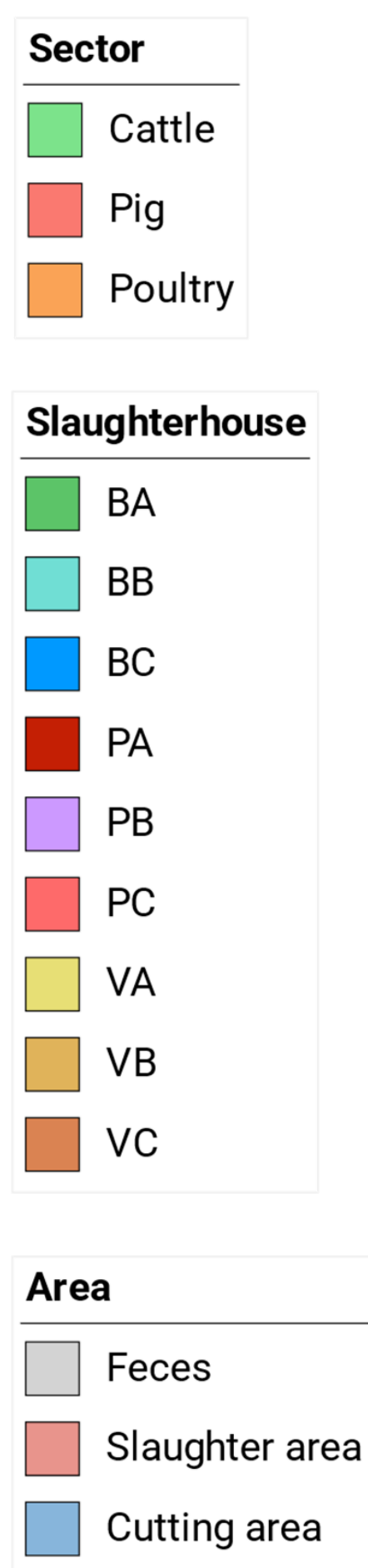
Phylogenetic analysis

- Isolates are not grouped by their sector origin, apart from one branch only containing **pig** isolates
- Dissemination** of *C. perfringens* along the slaughter process (detection in **meat, air** and **surface** samples) and across all sectors
- Detection in the **air** of slaughterhouse, suggesting that **airborne transmission** may be a potential route of dissemination
- Potential **persistence** was observed in the **pig** and **poultry** sectors: genetically closely related isolates were recovered during at least two distinct sampling campaigns

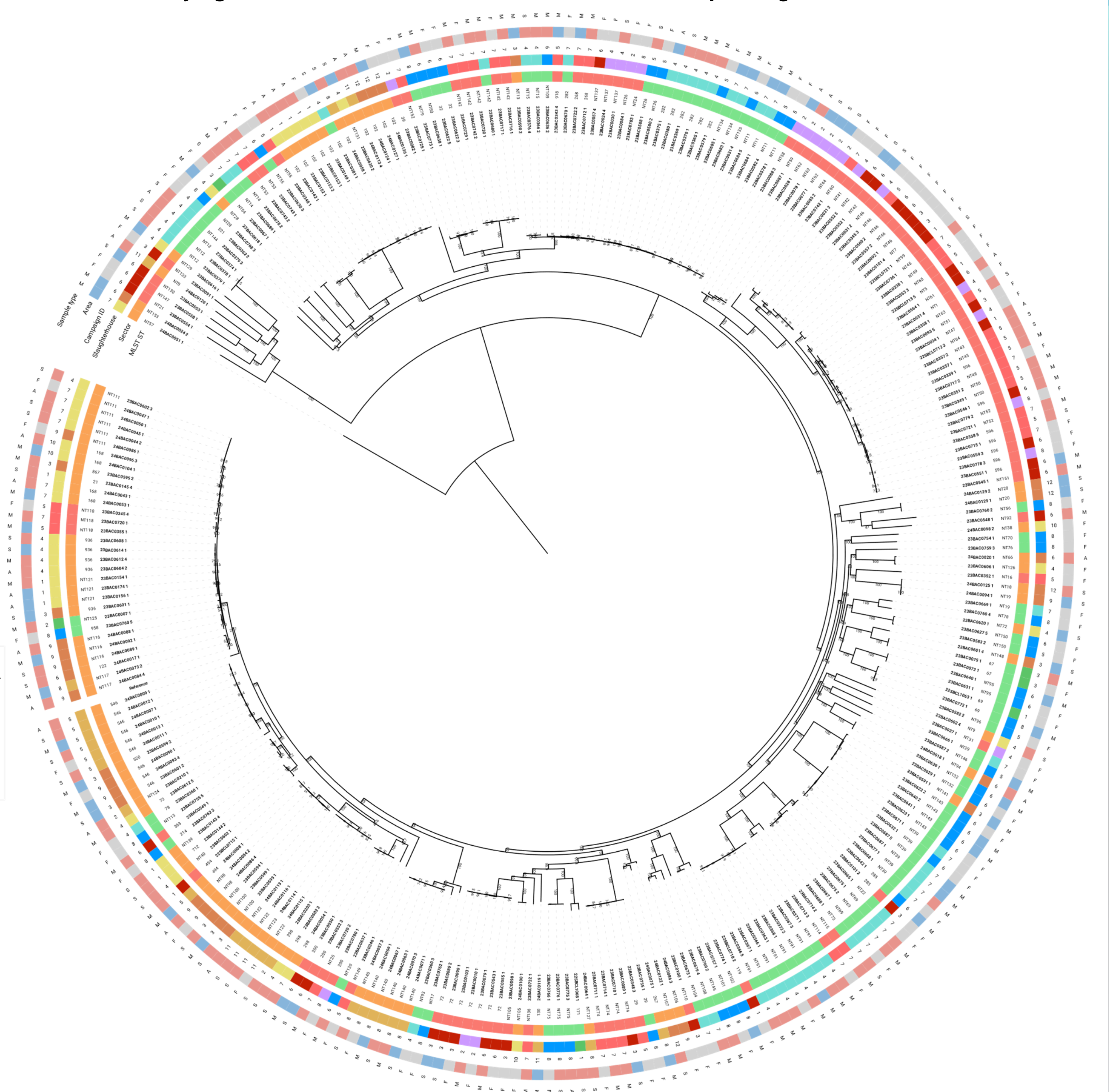
Antimicrobial resistance genes (ABRicate, CARD database)

- 67% isolates carried at least one more resistance gene alongside *mprF*
- Common AMR gene carriage (*tetA(P)*, *tetB(P)*, *ErmQ*, *LnuP*) is similar to existing literature
- 2% are **multidrug resistant (MDR)** isolates
- tetA(P)* and *tetB(P)* are significantly more frequently detected in the pig and poultry sectors than the cattle sector

Tree scale: 0.1



Phylogenetic tree based on the core SNP of the 286 *C. perfringens* isolates



Virulence related genes (ABRicate, custom database of 60 genes)

- 98% (280/286) of isolates were **type A**
- Type D** was detected in **pig** and **cattle** sector
- Type G** was only isolated from the **poultry** sector
- Average virulence related gene carriage was 28 ± 2 genes
- 19 genes including toxin genes (*cpa*, *colA*, *ccp*, and sialidases) were carried by all isolates
- 14 toxin genes were carried by none of the isolates
- Sector specific virulence genes: *ureABC* (**cattle** sector); *dlpA*, *ldpB*, *ldpC* (**poultry** sector)

Gene	Cattle		Pig		Poultry		Total	
	n	(%)	n	(%)	n	(%)	n	(%)
<i>mprF</i>	96	100	95	100	95	100	286	100
<i>ANT(6)-Ib</i>	0	0	7	7	0	0	7	2.4
<i>APH(3'')-Ib</i>	1	1	0	0	0	0	1	0.3
<i>APH(3')-IIIa</i>	1	1	0	0	0	0	1	0.3
<i>APH(3')-Ia</i>	1	1	0	0	0	0	1	0.3
<i>APH(6)-Id</i>	1	1	0	0	0	0	1	0.3
<i>ErmQ</i>	1	1	11	12	3	3	15	5.2
<i>LnuP</i>	0	0	10	11	23	24	33	11.5
<i>SAT-4</i>	1	1	0	0	0	0	1	0.3
<i>TEM-104</i>	1	1	0	0	0	0	1	0.3
<i>aad(6)</i>	1	1	0	0	0	0	1	0.3
<i>lnuC</i>	0	0	0	0	2	2	2	0.7
<i>sul2</i>	1	1	0	0	0	0	1	0.3
<i>tet44</i>	0	0	7	7	0	0	7	2.4
<i>tetA(P)</i>	31	32	83	87	75	79	189	66.1
<i>tetB(P)</i>	16	17	63	66	60	63	139	48.6
Total isolates	96		95		95		286	

Frequency of antibiotic resistance genes detected in *C. perfringens* isolates by sector

DISCUSSION & CONCLUSION

This study highlighted the dissemination of *C. perfringens* strains through cross-contamination between feces, meat, and the environment of slaughterhouses, with airborne transmission being a possible route. Additionally, characterization of isolated strains revealed various virulence potential and AMR gene carriage, with some genes possibly related to specific sectors. Overall, multiple AMR gene carriage was not frequent and intrinsic resistance was rare, which is similar to other studies conducted in the world. Nevertheless, the widespread presence of *C. perfringens* throughout the slaughter process should be considered a potential risk and, therefore, closely monitored. These data provide a basis for source attribution analyses to better characterize public health risks associated with foodborne outbreaks caused by *C. perfringens*.

[1] Santé publique France (SPF). Surveillance des toxi-infections alimentaires collectives (TIAC). Données de la déclaration obligatoire, 2022. 2024

[2] Tran, C., et al. 2026. Isolation rate, genetic diversity, and toxinotyping of *Clostridium perfringens* isolated from French cattle, pig or poultry slaughterhouses. Food Microbiology 133, 104898. <https://doi.org/10.1016/j.fm.2025.104898>