RES-339

Genomic Characterization and Transferability of *bla*$_{\text{CTX-M-55}}$-Carrying Plasmids in *Escherichia coli* from Malawian Broiler Chickens

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Introduction

- The global spread of extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* poses a growing public health concern.
- While poultry is recognized as a major reservoir of ESBLs, data on the mobility and genetic context of ESBL genes in African settings remain limited.
- This study investigated the genomic characteristics and transferability of *E. coli* isolates carrying *bla*$_{\text{CTX-M-55}}$, a commonly detected ESBL genes globally, from Malawian broilers and compared their plasmids with those from other sectors.

Methodology

- Whole-genome sequencing of 21 *bla*$_{\text{CTX-M-55}}$ -positive *E. coli* isolates in Malawi was performed using short-read sequencing and nine isolates underwent long-read sequencing to resolve complete genome structures, including plasmids.
- Bacterial conjugation assays were performed to evaluate plasmid transferability using an *E. coli* recipient.
- Comparative genomic analyses were performed between plasmids in this study and reference plasmids from humans, animals, and environmental sources.

Results

Characteristics of *E. coli* plasmids carrying *bla*$_{\text{CTX-M-55}}$ gene

Fifteen isolates were conjugative, including seven harbouring *bla*$_{\text{CTX-M-55}}$ on diverse plasmid types: IncFIB (n=1), IncFII (n=1), IncFII::IncN (n=2), IncHI2 (n=3) (Table 1). Several antimicrobial resistance genes (e.g., *sul2*, *tetA*, and *floR)* were frequently identified.

Table 1: Genomic characteristics of *E. coli* plasmids carrying *bla*$_{\text{CTX-M-55}}$

Plasmid	pMLST	Host range	Replicon	AMR	Size (bp)
BT08F36	ST2	IV	IncHI2;IncHI2A	*aac(3)-IId, aph(3')-Ia, aph(6)-Id, ARR-2, bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{LAP-2}}$*, bla*$_{\text{TEM-1B}}$*, dfrA14, floR, mph(A), qnrS1, sul3, tet(A)*	331,316
DW03F4	ST2	IV	IncHI2;IncHI2A	*aac(3)-IId, aadA22, aph(3')-Ia, aph(6)-Id, ARR-2, bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{LAP-2}}$*, bla*$_{\text{TEM-1B}}$*, dfrA14, floR, lnu(F), mph(A), qnrS1, sul3, tet(A)*	291,889
LL01C3	F33:A-:B-::repN	-	IncFII(pHN7A8); IncN	*aph(3'')-Ib, aph(6)-Id, bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{TEM-214}}$*, fosA3, sul2, tet(A)*	93,869
DZ08F97	ST2	IV	IncHI2;IncHI2A	*aac(3)-IId, aadA22, aph(3')-Ia, aph(6)-Id, ARR-2, bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{LAP-2}}$*, bla*$_{\text{TEM-1B}}$*, dfrA14, floR, lnu(F), mph(A), qnrS1, sul3, tet(A)*	295,410
LL12F51	X1	-	IncX1	*aac(3)-IId, aadA2, aph(3'')-Ib, aph(3')-IIa, aph(6)-Id, bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{TEM-1B}}$*, bla*$_{\text{TEM-216}}$*, dfrA12, floR, rmtB, sul1, sul2, tet(A)*	46,794
MZ16F86	F24:A-:B1::repN	III	IncFIB(AP001918);IncFII	*aac(3)-IId, aadA2, aph(3'')-Ib, aph(3')-Ia, aph(6)-Id, bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{TEM-1B}}$*, bla*$_{\text{TEM-214}}$*, dfrA12, floR, fosA3, mph(A), sul2, tet(A), tet(A)*	170,682
MZ16F87	F33:A-:B-	III	IncFII(pHN7A8)	*bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{TEM-57}}$*, fosA3*	82,812
MZ16F88	F33:A-:B-	-	IncFII(pHN7A8); IncN	*bla*$_{\text{CTX-M-55}}$*, bla*$_{\text{TEM-214}}$*, fosA3*	93,587

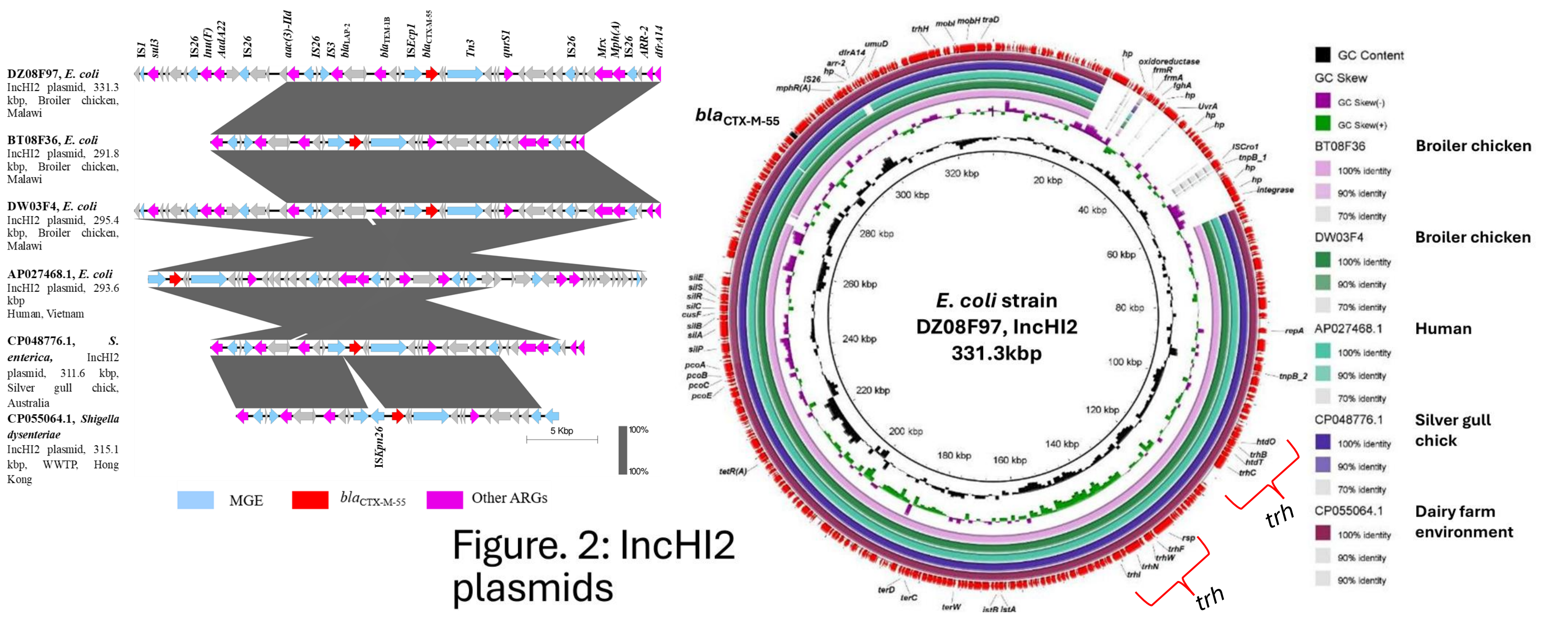

Figure. 2: IncHI2 plasmids

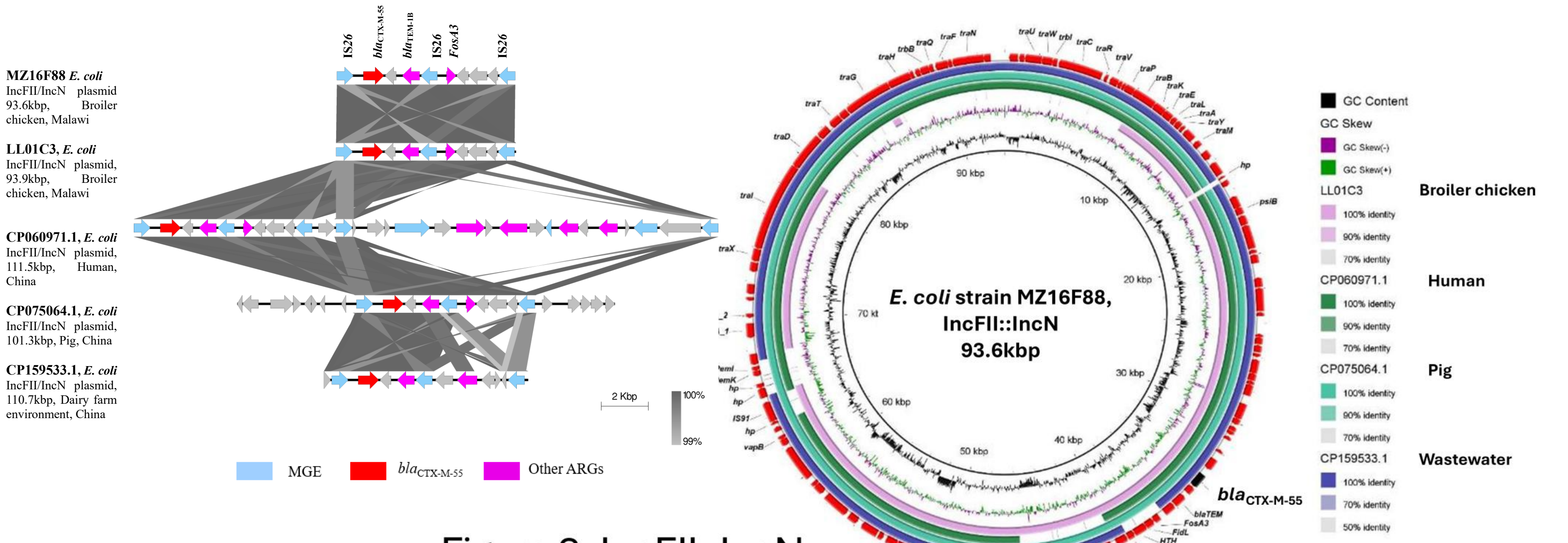

Figure 3: IncFII::IncN plasmids

Plasmid structures and the genetic context of *bla*$_{\text{CTX-M-55}}$ gene

Conserved genetic structures flanking *bla*$_{\text{CTX-M-55}}$ were observed across diverse plasmid types and sources (Figures 1 – 5). The aligned regions also included conjugation machinery genes like *tra*, *trh* involved in plasmid mobilization through horizontal gene transfer. Virulence genes (*iro* and *sit*) were detected only in IncFIB plasmid (Figure 5).

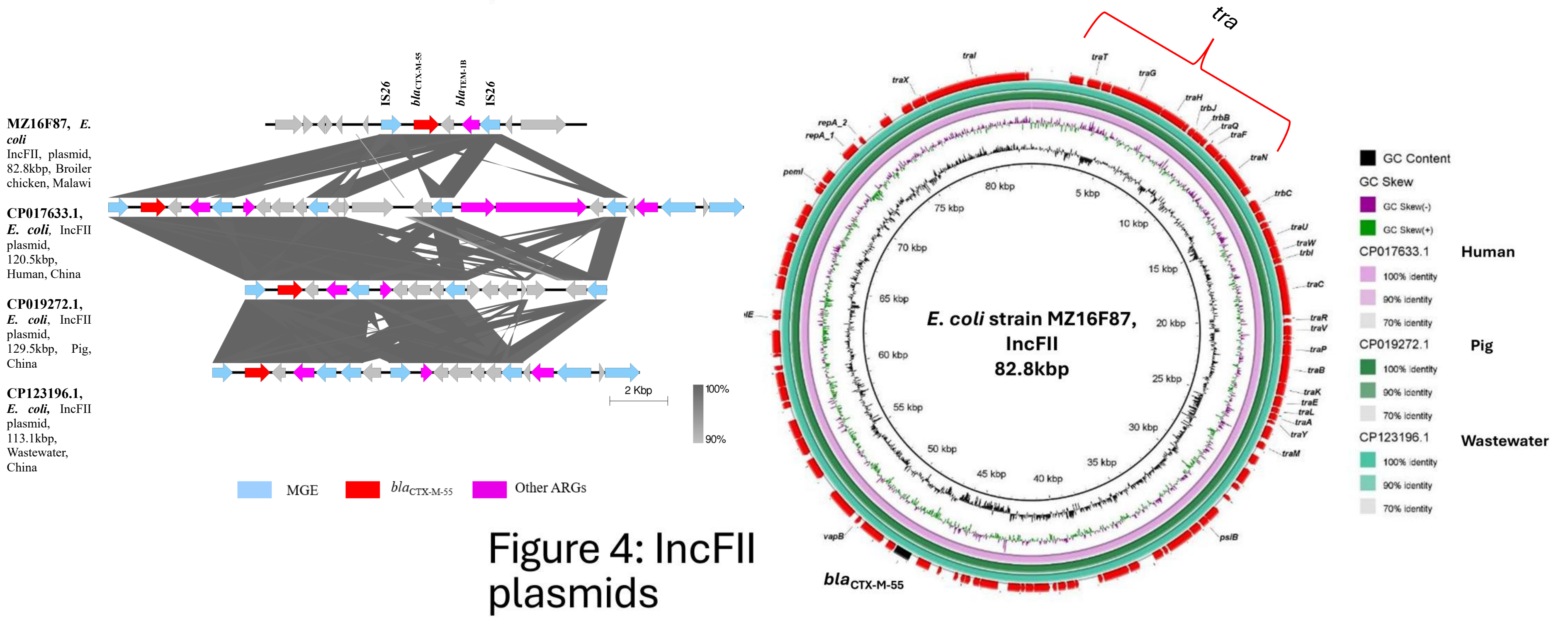

Figure 4: IncFII plasmids

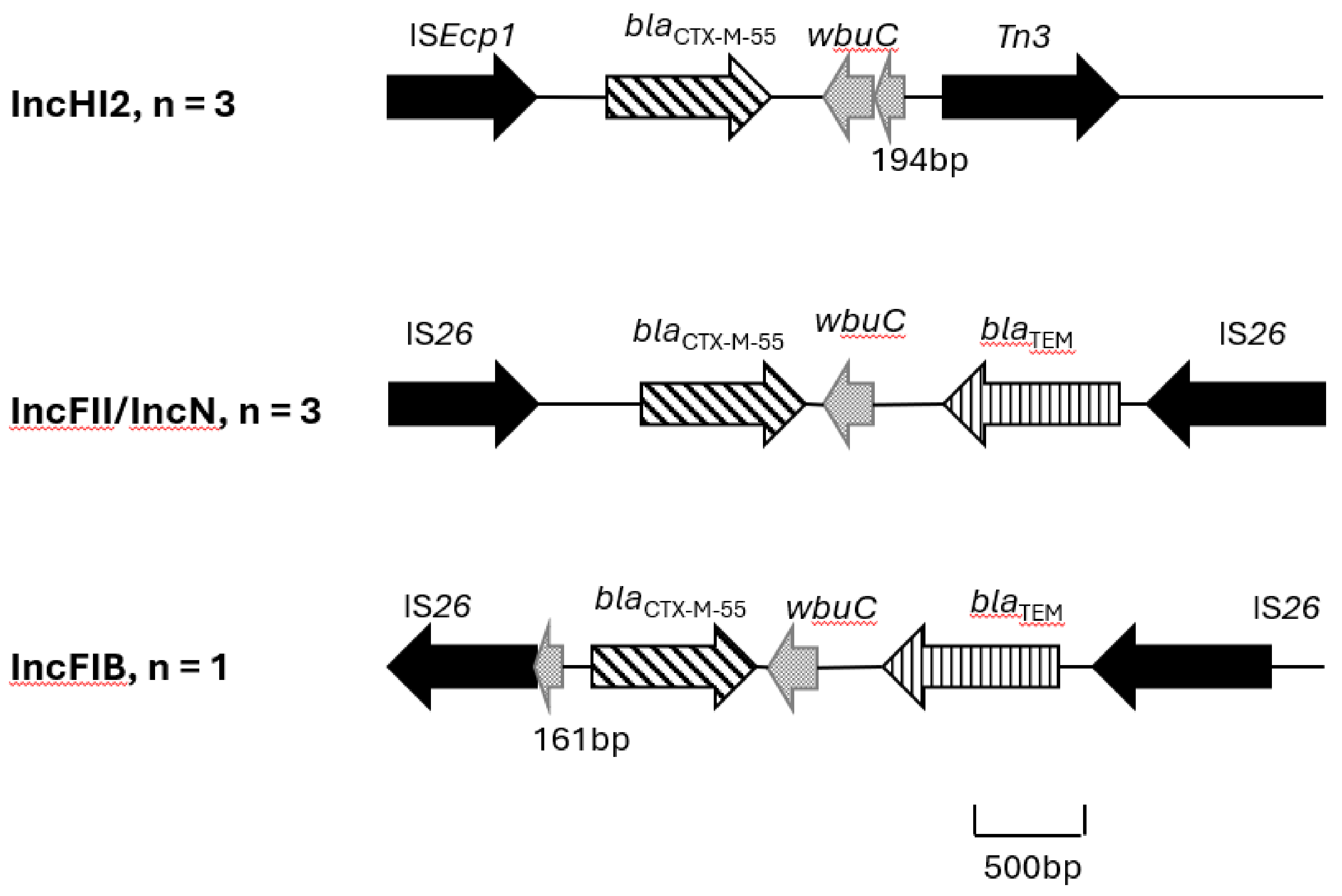

Figure 1: Genetic regions surrounding *bla*$_{\text{CTX-M-55}}$

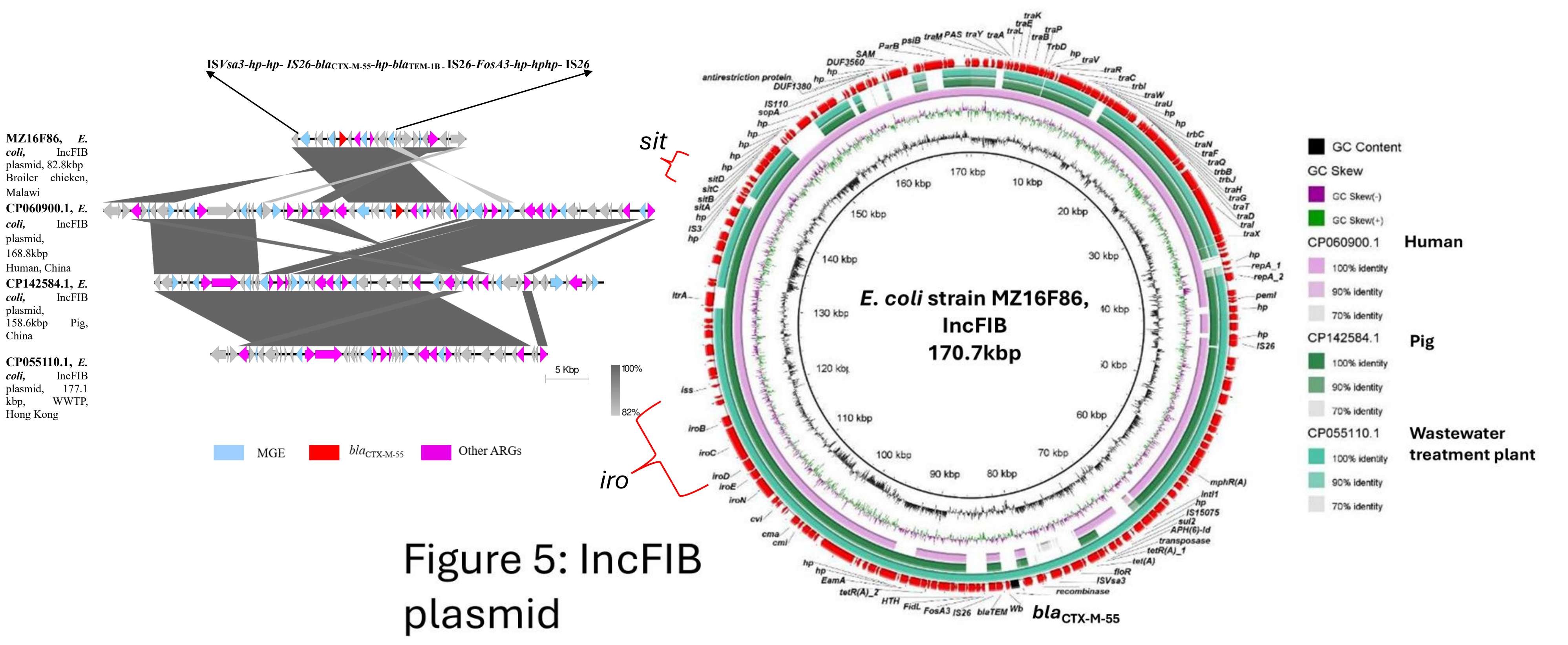

Figure 5: IncFIB plasmid

Conclusion

- The presence of multiple incompatibility groups carrying *bla*$_{\text{CTX-M-55}}$ gene shows that it can be hosted by diverse plasmid backbones which increases its dissemination potential.
- The observed similarities and transferability of poultry-derived plasmids indicate the potential for cross-sectoral transmission of *bla*$_{\text{CTX-M-55}}$ -carrying plasmids through horizontal gene transfer worldwide mediated by mobile genetic elements. These findings support the importance of the One Health approach in antimicrobial resistance surveillance.

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