

Molecular risk assessment of *Campylobacter jejuni* recovered from human and broiler carcasses

Mohamed Elhadidy, Alexandra Duarte, Katelijne Dierick, Nadine Botteldoorn

Campylobacter Jejuni.. Background

- One of the leading causes of gastrointestinal illness in humans in recent years
- Poultry is considered to be the main reservoir for infection in humans
- Most cases are sporadic and self-limiting



Study objectives



- 1-Evaluate a combination of molecular typing methods in the characterization of *C. jejuni* isolated from clinical samples and chicken meat
- 2-Investigate the dynamic of antibiotic resistance and to investigate the clonal structure and genetic determinants of resistance

Experimental approach



- A total of 415 *Campylobacter Jejuni* strains from 2006-2015:
 - Broiler carcasses (215 strains)
 - Human strains (200 strains)
- Reported symptoms (diarrhea, bloody diarrhea, hospitalization, fever)
- MIC antibiotic sensitivity profiles for 5 antibiotics

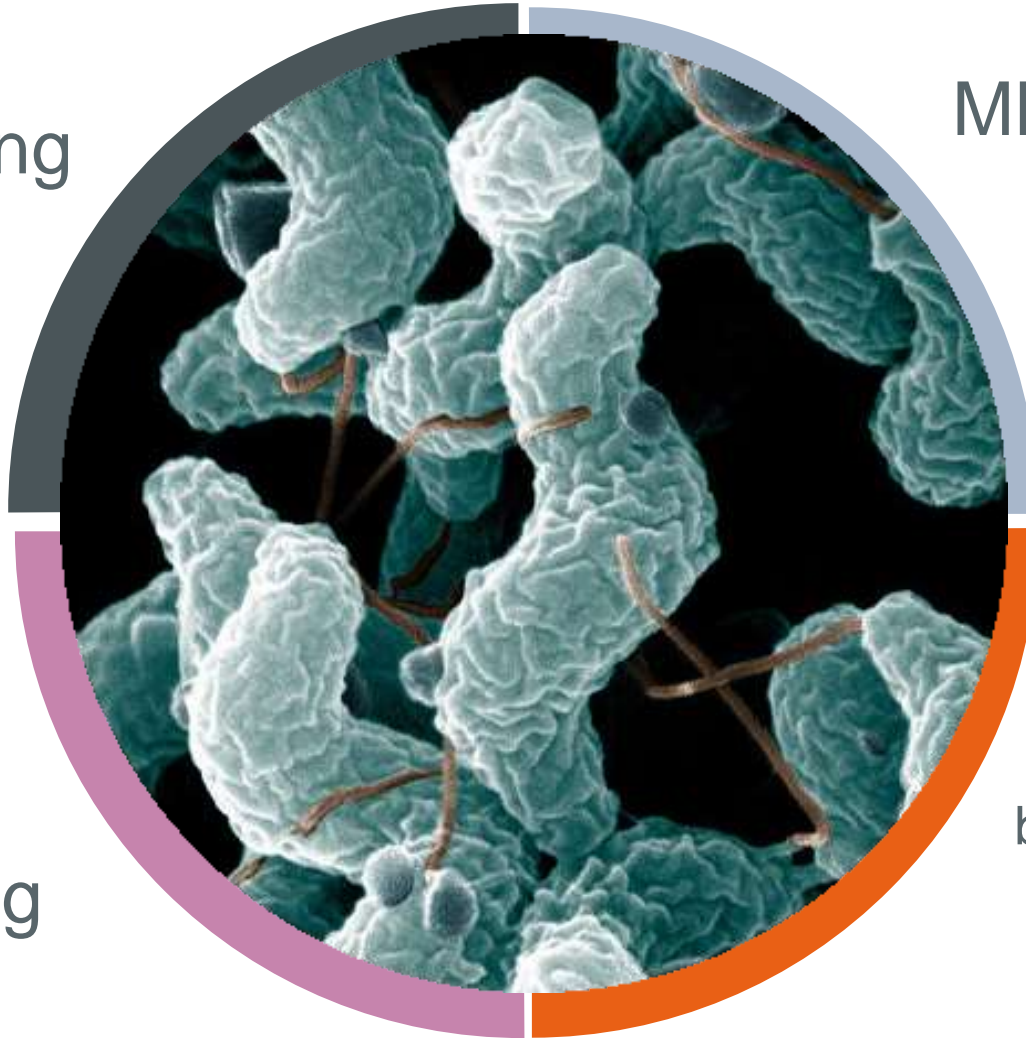
Typing methods

Binary typing

MLST

LOS typing

The molecular
basis of antibiotic
resistance



Population diversity of *C. jejuni*

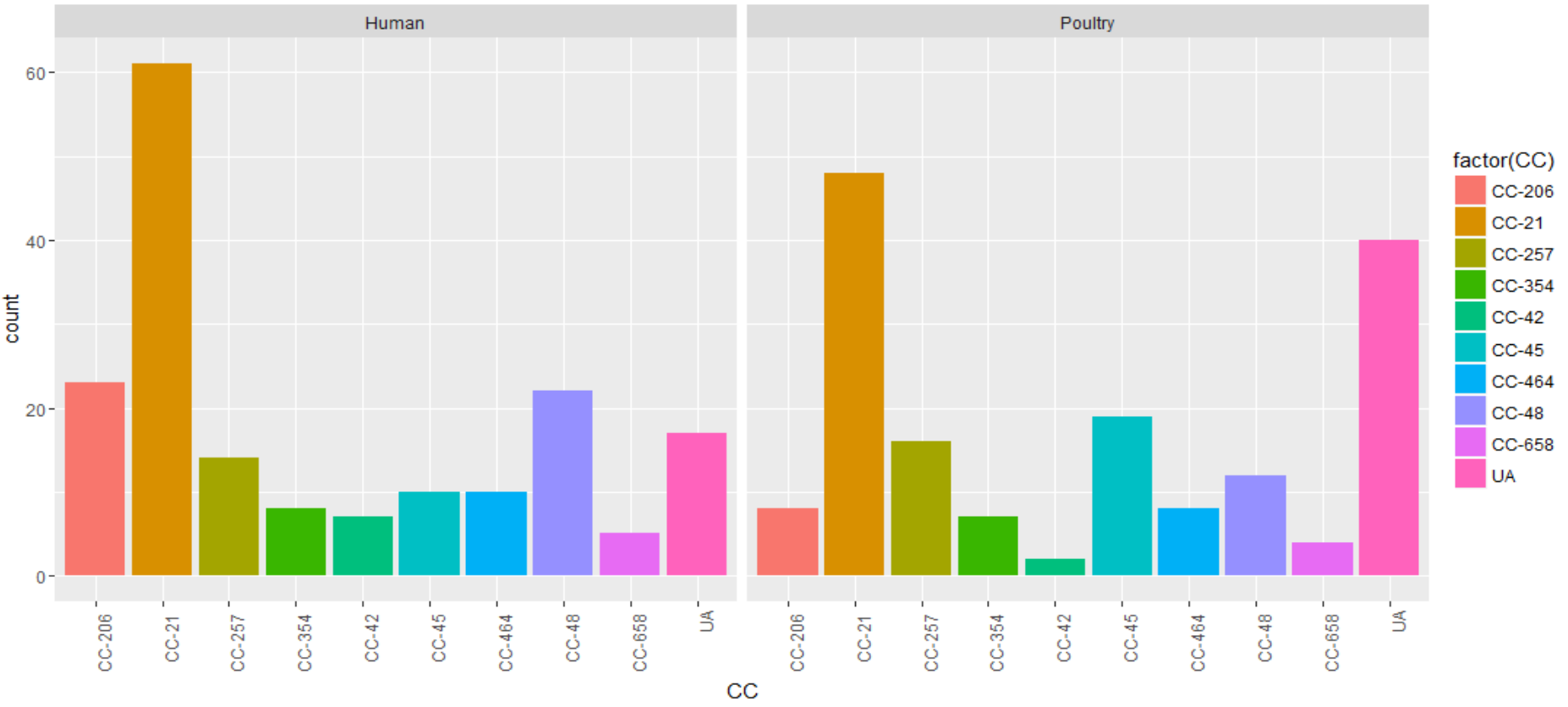
	Total	Human	Poultry
LOS	0,795	0,770	0,813
MLST	0,976	0,964	0,984
BIT	0,979	0,958	0,998

Binary coding

Isolate ID	cje629	Value	Cj0008	Value	gmhA2	Value	cgtA	Value	cje1733	Value	tetO	Value	cje1500	Value	cj0299	Value	pseE	Value	Cj0265	Value	Total binary score
144	1	512	1	256	1	128	0	0	1	32	1	16	1	8	0	0	1	2	0	0	954
806	1	512	0	0	0	0	0	0	1	32	1	16	1	8	0	0	1	2	0	0	570
1072	0	0	1	256	0	0	0	0	0	0	0	0	1	8	1	4	1	2	0	0	270
1270	0	0	1	256	1	128	0	0	0	0	1	16	1	8	0	0	1	2	0	0	410
1954	0	0	1	256	1	128	0	0	0	0	0	0	1	8	1	4	1	2	0	0	398
1955	1	512	1	256	1	128	0	0	1	32	1	16	1	8	0	0	1	2	0	0	954
2087	1	512	0	0	1	128	0	0	1	32	0	0	1	8	0	0	1	2	0	0	682
2088	0	0	1	256	0	0	0	0	0	0	0	0	0	0	1	4	1	2	0	0	262
2157	0	0	1	256	1	128	0	0	0	0	1	16	1	8	0	0	0	0	0	0	408
2158	0	0	1	256	1	128	0	0	0	0	0	0	1	8	1	4	1	2	0	0	398
2159	0	0	1	256	1	128	0	0	0	0	0	0	1	8	1	4	1	2	0	0	398
2285	1	512	1	256	0	0	0	0	1	32	1	16	1	8	0	0	1	2	0	0	826
2372	0	0	1	256	0	0	0	0	0	0	1	16	1	8	0	0	1	2	0	0	282
2402	0	0	0	256	1	128	0	0	0	0	0	0	0	0	1	4	0	0	0	0	388
2404	0	0	1	256	1	128	0	0	0	0	0	0	1	8	1	4	1	2	0	0	398
2481	0	0	1	256	1	128	0	0	0	0	0	0	0	0	1	4	0	0	0	0	388
2538	1	512	0	0	1	128	0	0	0	0	1	16	0	0	0	0	0	0	1	1	657



Clonal complexes (CCs)



Phylogenetic analysis by Maximum Likelihood method

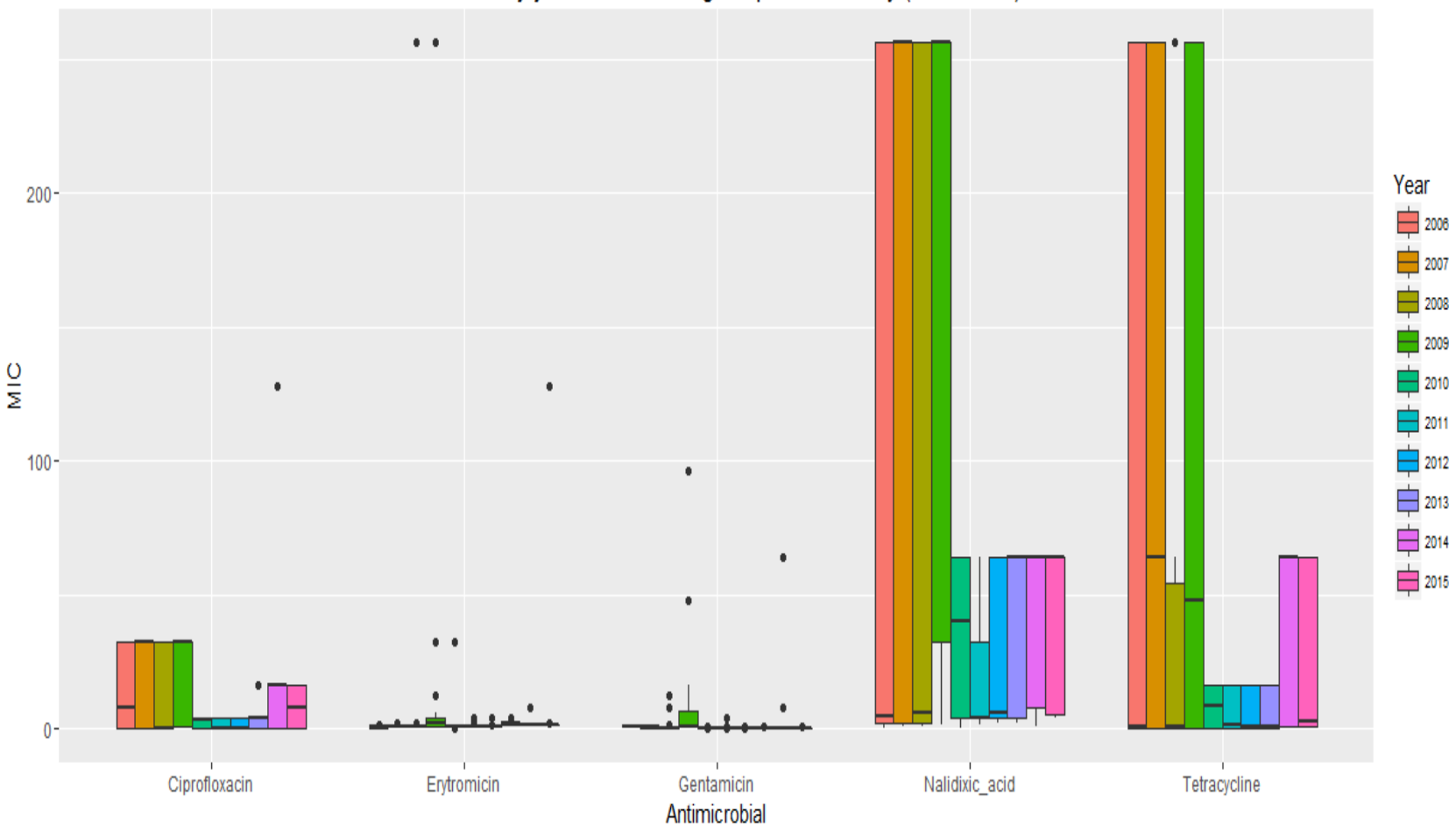
Only poultry isolates



Evolution of AMR during the period of study



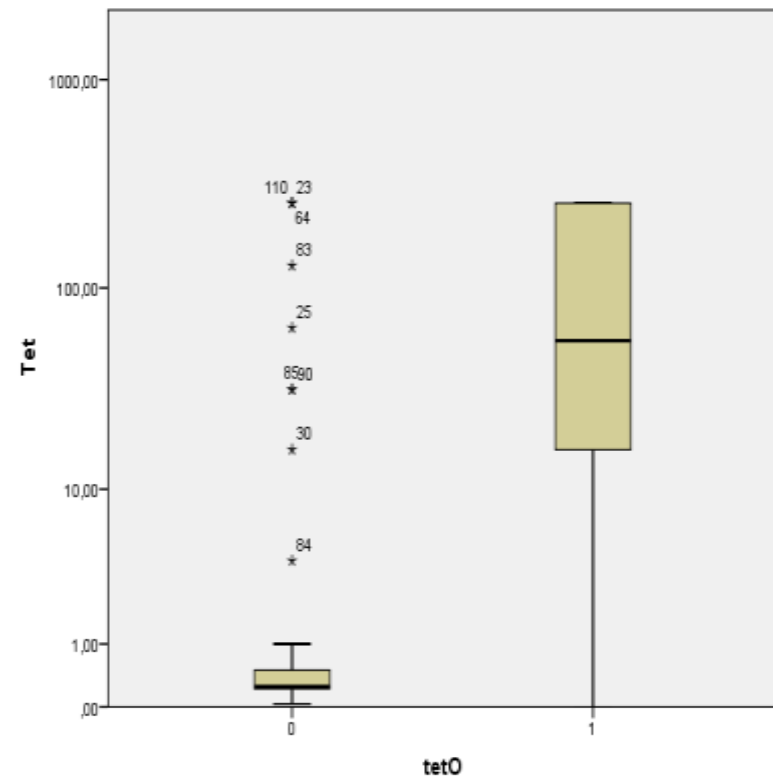
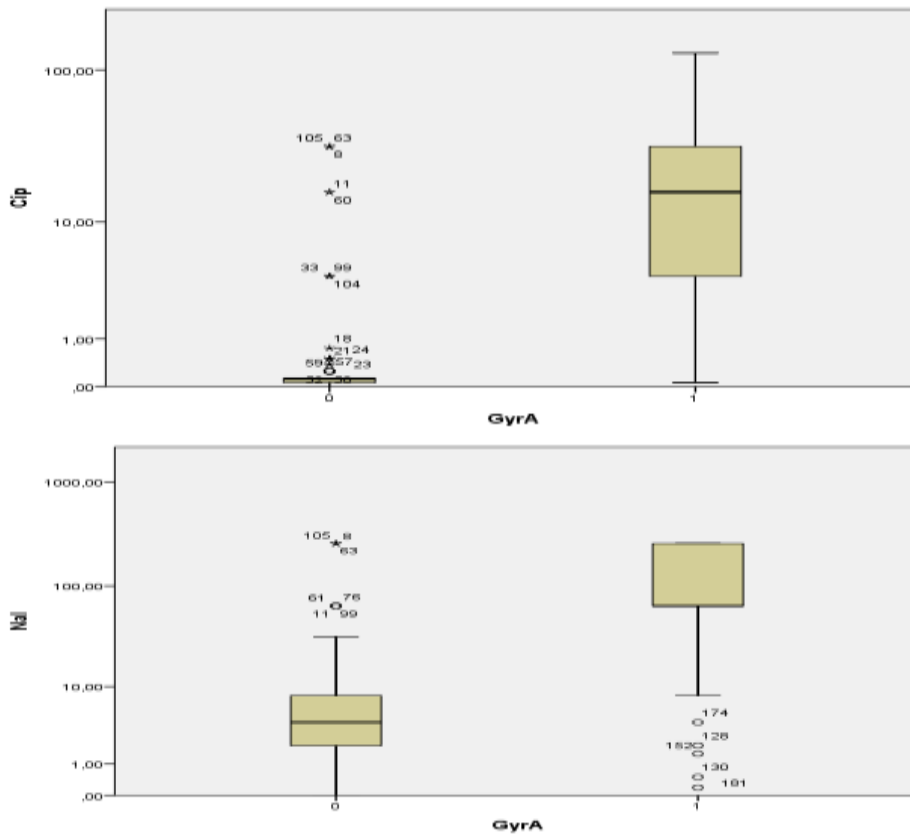
MICs of *C. jejuni* isolates during the period of study (2006-2015)



Molecular mechanisms of antibiotic resistance

Quinolones: Thr-86-Ile in the QRDR

Tetracycline: *tetO*

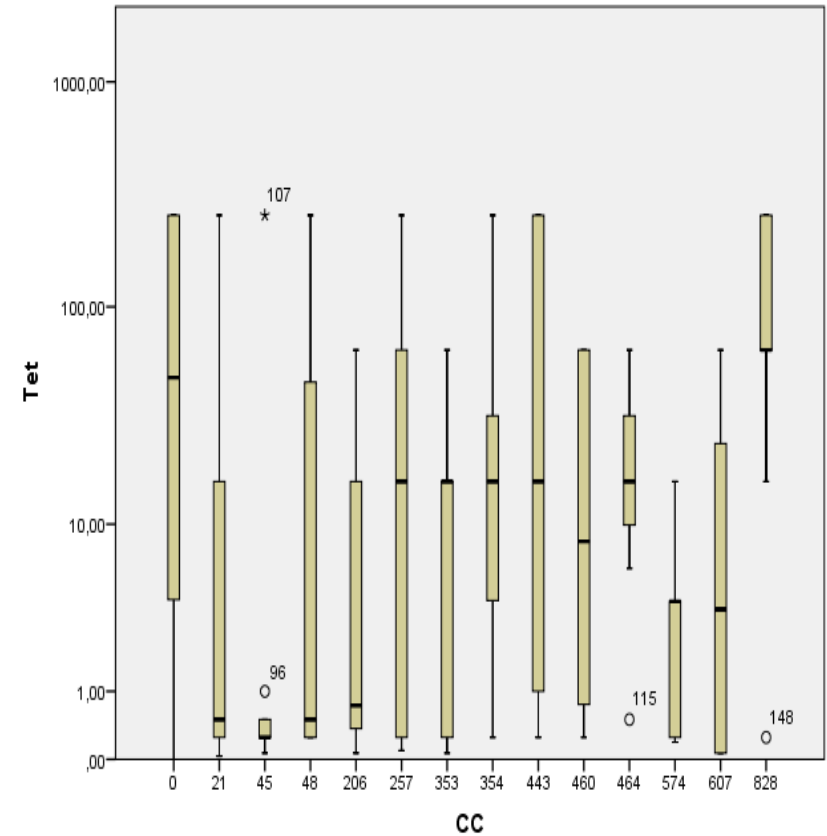
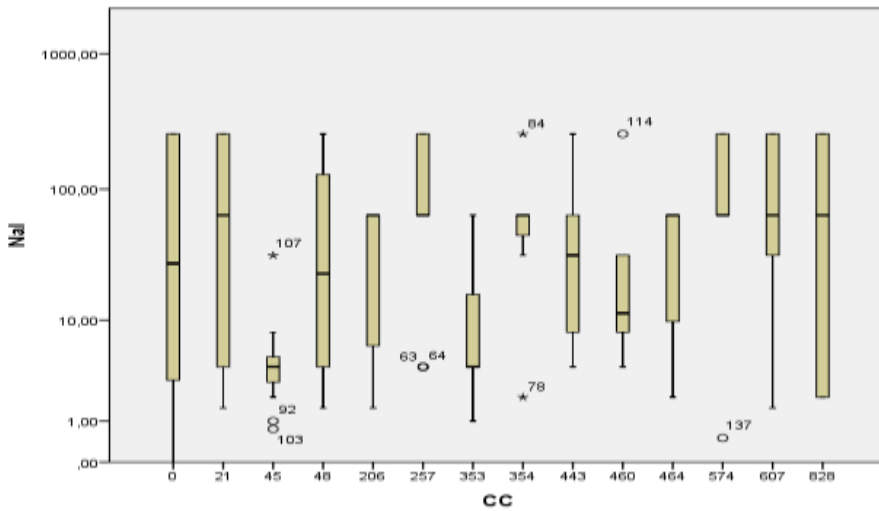
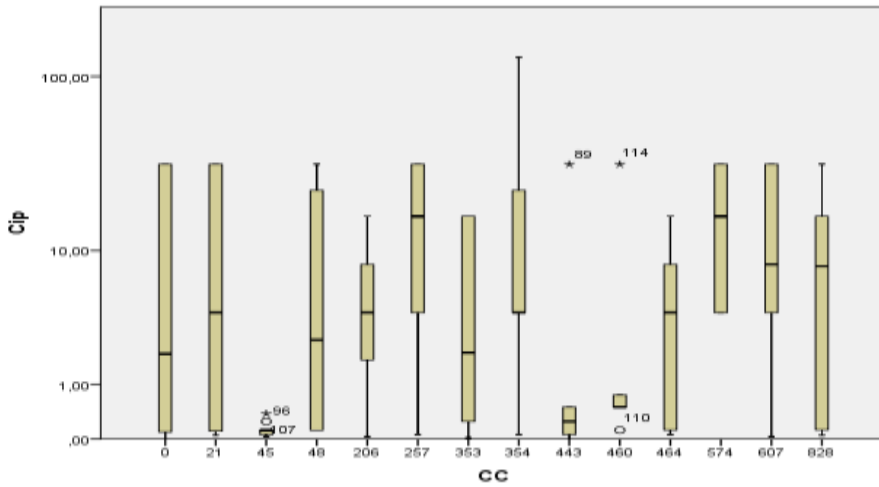


Strain	ERY MIC (µg/ml)	Mutation in 23S rRNA	Ribosomal gene Polymorphism		CME polymorphism	
			L4	L8	CmeR	Cme IR region
H15	128	A2075G	M192I	A103V, T109A, A111E, A114T	WT	WT
H127	128	A2075G	V121A, T177S	G74A, A105M, T109A	7	2
B810	256	A2075G	A196V	V65I, G74A, T109S, A111E, A114T	6	3
B1062	256	WT	A196V	V65I, G74A, T109S, A111E, A114T	5	WT
B1396	256	WT	WT	G74A, A103V, T109A, A111E, A114T	9	4
B2885	32	A2075G	WT	WT	1	1
B656	8	WT	WT	Q24R, V65I, G74A, T109A, A111E, A114T	4	2
B713	128	WT	A196V	V65I, G74A, T109S, A111E, A114T	WT	WT
B783	32	WT	A196V	V65I, G74A, T109S, A111E, A114T	6	3
B856	6	WT	M192I, V121A	G74A, T109A, A111E, A114T	4	2
B872	256	WT	WT	V65I, G74A, T109S, A111E, A114T	5	WT
B1680	256	WT	M192I, V121A, T177S	V65I, G74A, T109A A111E, A114	4	2
B2136	12	WT	A196V	V65I, G74A, T109S, A111E, A114T	10	4



**Erythromycin
resistance
mechanisms**

Heterogeneity in AMR by CC



Conclusion

- P-BIT is a useful approach for subtyping offering both high discriminatory power and potential for strain risk assessment in human
- Chromosomal target mutations and active efflux contribute to antimicrobial resistance

Acknowledgements



Scientific Institute of Public Health

(WIV-ISP)

Dr. Sarah Denayer
Dr. Bavo Verhaegen
Elke Wattijn



Belgian Science Policy Office

University of leon

Dr. Avelino Álvarez-Ordóñez
Dr. Hector Argüello



universidad
de león

USDA-ARS

Dr. William Miller
Emma Yee



Saint Pierre University Hospital

Dr. Olivier Vandenberg
Dr. Delphine Martiny



CHU St-Pierre | UMC St-Pieter



Public Health Microbiology,

Australia

Dr. Bixing Huang

Thanks for your attention!

Questions?