Anthropogenic and environmental factors associated with high prevalence of *mcr-1* carriage in humans across China

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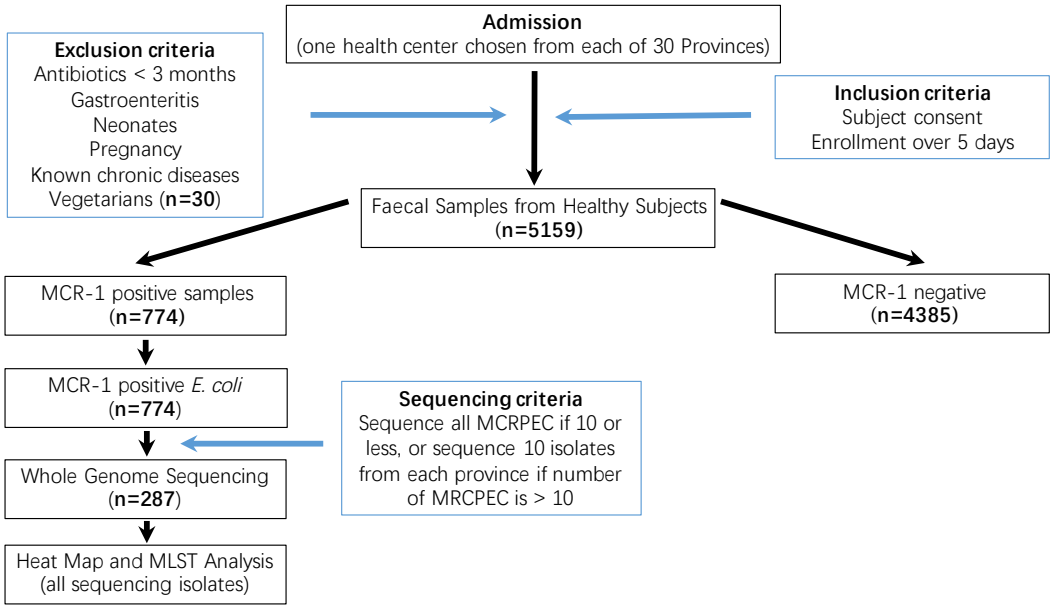
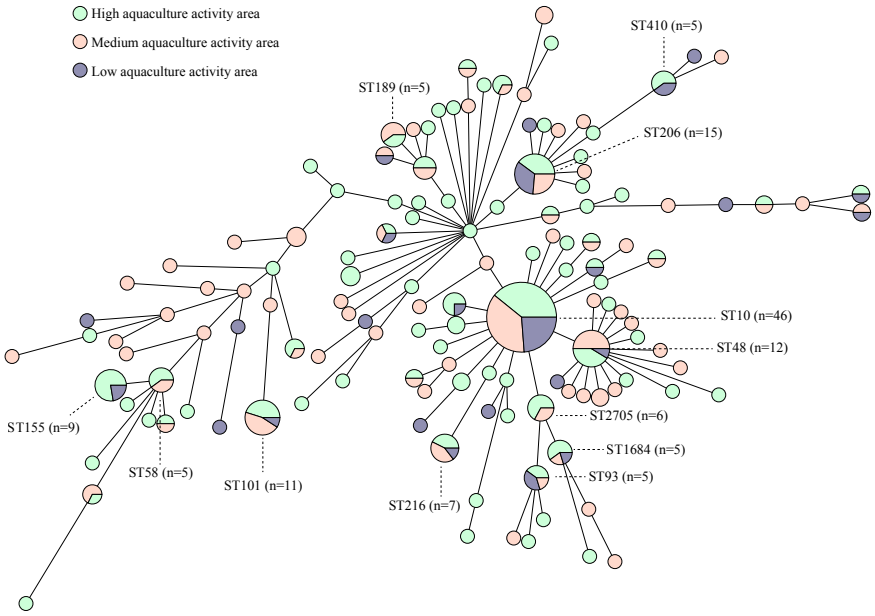
Supplementary Figure 1



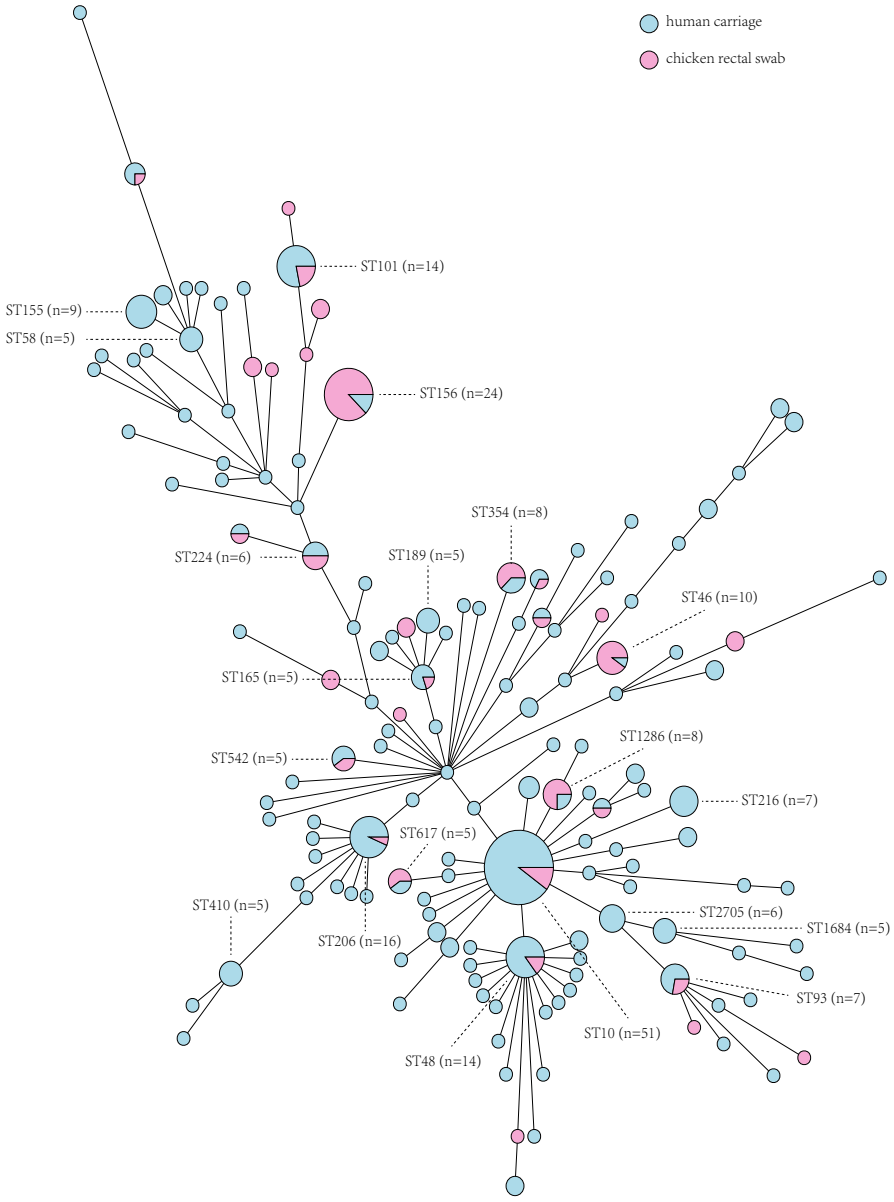
Supplementary Figure 1. Diagram of study design.

Supplementary Figure 2



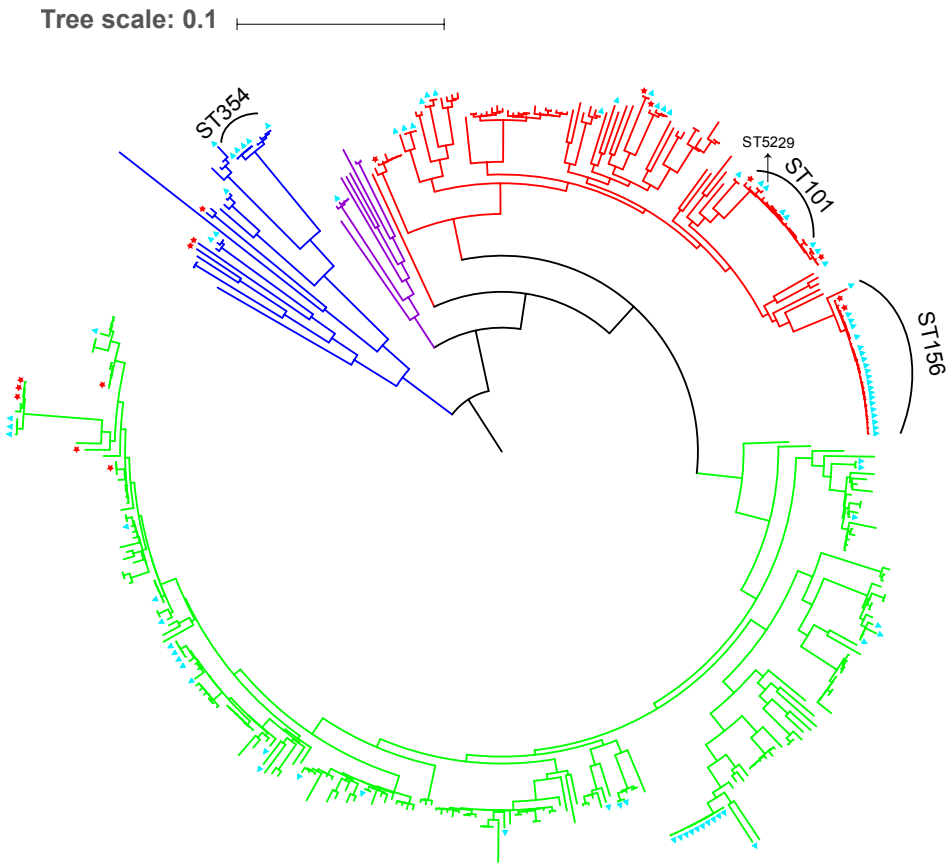
Supplementary Figure 2. Minimum spanning trees of all sequenced MCRPEC by MLST type and gene allele profile. Each node within the tree represents a single ST. The size of the nodes is proportional to the number of isolates represented by said node. Selected nodes are labelled with corresponding ST and number of isolates (at least five).

Supplementary Figure 3



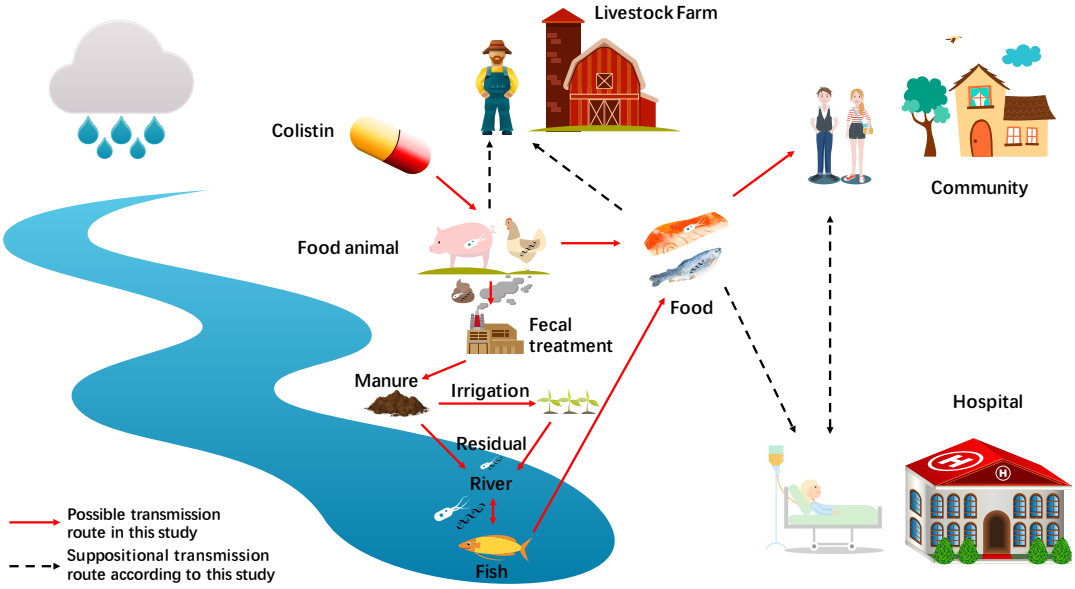
Supplementary Figure 3. Minimum spanning trees of MCRPEC by MLST type and gene allele profile for the human isolates of this study and chicken isolates from China of other studies. Each node within the tree represents a single ST. The size of the nodes is proportional to the number of isolates represented by said node. Selected nodes are labelled with corresponding ST and number of isolates (at least five).

Supplementary Figure 4



Supplementary Figure 4. Phylogenic tree of all *mcr-1*-carring *E. coli* from humans in this study and chicken MCRPEC from other studies. Each branch of isolates are denoted by four colours corresponding to four lineages. Red star and blue triangle represent the sixteen and eighty-eight isolates from other countries and chicken origin from China, respectively.

Supplementary Figure 5



Supplementary Figure 5. Diagram showing the possible transmission route of *mcr-1*/*mcr-1*-carrying isolates among animal, environment and humans.

Supplementary Table 4. Comparison of the MIC profiles of nine tested antimicrobials among the MCRPEC isolates of the different aquaculture conditional areas.

Antimicrobials	Number of Resistance (resistance rate %) in different aquaculture conditions area			*P* value (χ^2)
	Low activity (n=71)	Medium activity (n=236)	High activity (n=467)	
Cefepime	14 (19·72%)	58 (24.58%)	68 (14.29%)	**0.002****
Amikacin	0 (0%)	4 (1.69%)	5 (1.07%)	-
Piperacillin/Tazobactam	6 (8.45%)	9 (3.81%)	23 (4.93%)	0.309
Ceftazidime	12 (16.90%)	44 (18.64%)	51 (10.92%)	**0.018***
Ticarcillin/Clavulanic acid	39 (54.93%)	147 (62.29%)	262 (56.10%)	0.705
Ciprofloxacin	33 (46.48%)	106 (44.92%)	162 (34.69%)	**0.011***
Imipenem	1 (1.41%)	3 (1.27%)	6 (1.28%)	0.995
Colistin	43 (60.56%)	174 (73.73%)	333 (71.31%)	0.099
Cefoperazone/Sulbactam	4 (5.63%)	6 (2.54%)	8 (1.71%)	0.112

*P<0·05, **P<0·01

Supplementary Table 5. Information of worldwide mcr-1-positive E. coli isolates of human origin downloaded from NCBI.

isolate	Accession	species	collected time	country	source	ST
WI2	SAMEA19195918	*E.coli*	2016	France	clinical	1288
MDR_56	SAMN06344815	*E.coli*	2015.5	USA	clinical	117
3431F	SAMN06233851	*E.coli*	2014	Brazil	rectal swab	744
2016C-3936C1	SAMN061595501	*E.coli*	–	USA	clinical	2734
C153	SAMN06051286	*E.coli*	2016	Brazil	blood	410
O177:H21	SAMN05407982	*E.coli*	2015.4	Netherlands	faeces	359
204965	SAMN06163642	*E.coli*	2016.6.20	Austria	stool clinical	10
BJ10	SAMN04884976	*E.coli*	2015.2.21	China	clinical liver ascites	156
HC891	SAMN06043562	*E.coli*	2016.4.11	Brazil	blood	156
MRSN346355	MRSN346355	*E.coli*	2016.7	USA	clinical	617
MCR1_NJ	SAMN05294116	*E.coli*	2014.8	USA	clinical	405
MRSN346595	MRSN346595	*E.coli*	2016.7	USA	clinical	617
MRSN346638	MRSN346638	*E.coli*	2016.7	USA	clinical	617
MRSN388634	MRSN388634	*E.coli*	2016.7	USA	clinical	101
STEC_575	SAMN04002628	*E.coli*	2013.9	Netherlands	stool clinical	21
TN1	SAMN04423147	*E.coli*	2013.11	Vietnam	feces clinical	1589