SUPPLEMENTARY MATERIALS

METHODS

Sample Collection, Isolation and Identification

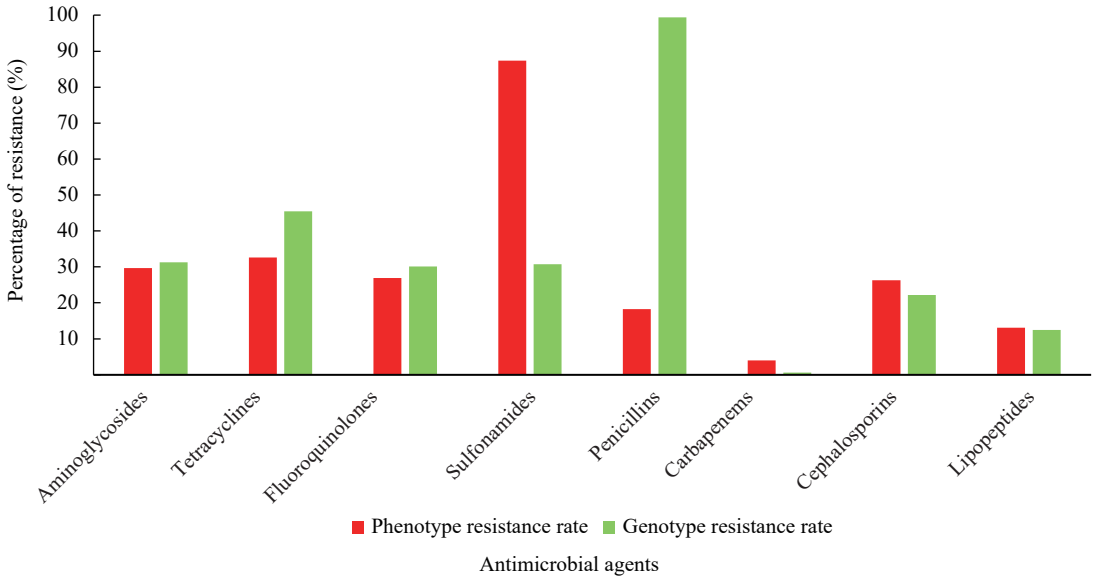
From July to October 2020, a total of 290 animal-derived food samples (91 pork and 199 chicken samples) were collected from 16 large supermarket chains and farmers' markets in 6 districts of Beijing Municipality. The specific collected samples commercially available cuts of pork meat and commercially available chicken cuts. All samples were placed in Labplas TWIRL'EM sterile homogeneous bags (Labplas, Canada) after being collected and brought to the laboratory for testing. A single sample was placed in a sterile sampling bag to prevent cross-contamination during sample collection. The target strains were isolated as previously described (*1*), and the brief description was shown as following: 10 mL brain heart infusion (BHI) broth (Land Bridge, Beijing, China) was used to wash the sample surface, transfer to a 10 mL EP tube, and incubation at 37 °C for 24 h. 0.5–1 mL of the enrichment culture obtained was cultured on CHROMagar^{TM} ECC medium (CHROMagar, France) and inoculated at 37 °C for 24 h. The blue colonies on the plate were further purified using Luria agar (LA) and identified by matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry analysis.

Antimicrobial Susceptibility Testing

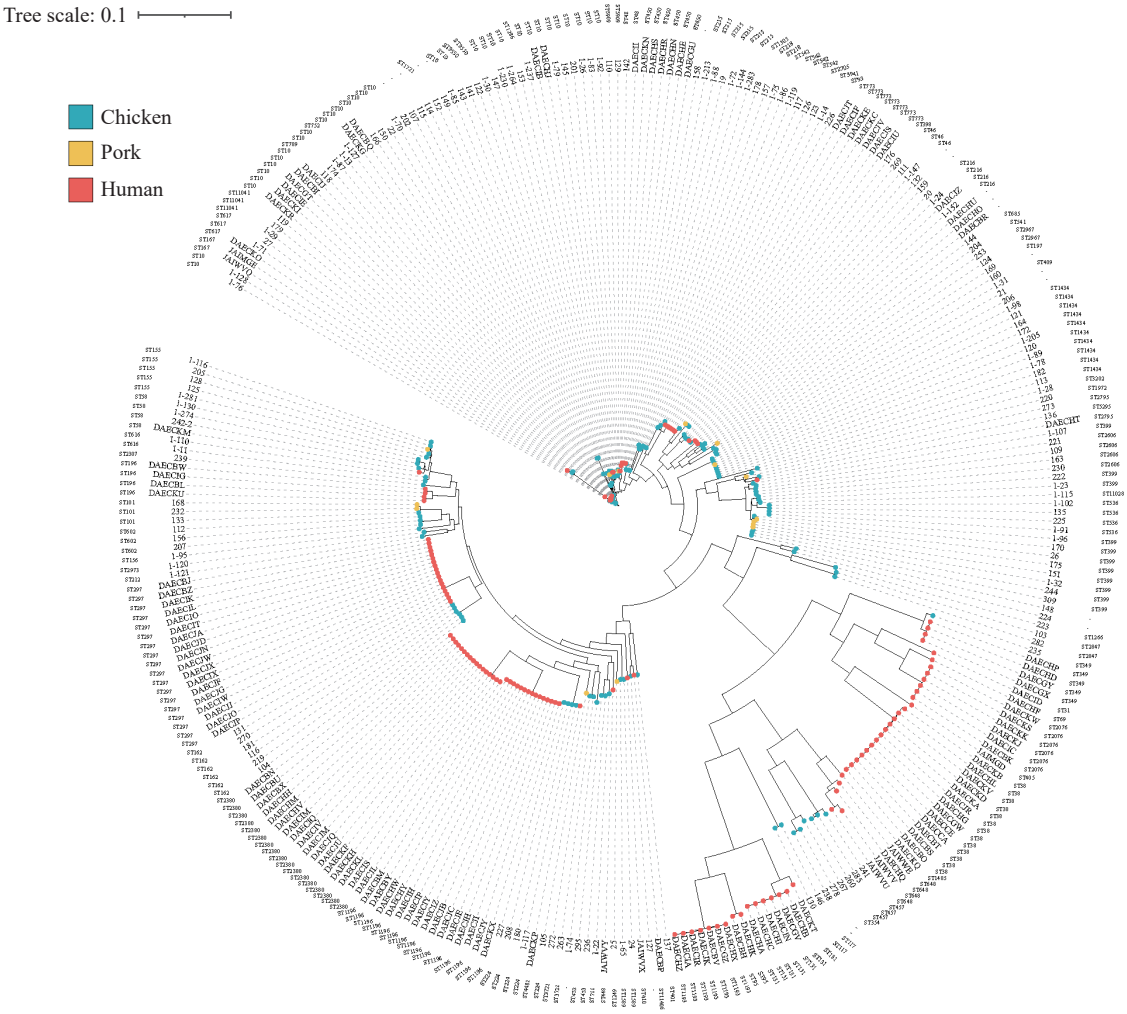
The gram-negative bacteria drug sensitivity plates Sensititre GNX3F were used for the antibiotic susceptibility test of the isolated strains according to the recommendations of the Clinical and Laboratory Standards Institute guidelines (CLSI, M100-S30) (*2*) and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) standard v10.0 (*3*). *E. coli* ATCC25922 was used as the quality control strain.

Whole Genome Sequencing

Genomic DNA from *E. coli* isolates was extracted for whole genome sequencing using the Wizard Genomic DNA Purification Kit (Promega, Madison, WI, US) following the manufacturer's instructions. The DNA libraries were constructed using a KAPA Hyper Prep Kit (Roche, Basel, Switzerland). Sequencing was carried out with Illumina Novaseq 6000 platform (Illumina, San Diego, CA), which generated 150-bp paired-end reads from a library with an average insert size of 350 bp. Raw sequence data of *E. coli* isolates were assembled using SPAdes v3.13.1 (*4*) via the



SUPPLEMENTARY FIGURE S1. Correlation analysis of antimicrobial resistance genotype and phenotype of *Escherichia coli* isolates.



SUPPLEMENTARY FIGURE S2. Phylogenetic analysis of *Escherichia coli* isolates of animal-derived foods (n=166) and human clinic (n=146).
Note: A midpoint-rooted maximum-likelihood phylogenetic tree was constructed using core-genome single-nucleotide polymorphisms (SNPs).

Unicycler v0.4.7 (*5*) assembly pipeline. Additional genomes were downloaded from the National Center for Biotechnology Information (NCBI) Pathogen detection database (https://www.ncbi.nlm.nih.gov/pathogens/isolates#/search/). There were n=806 isolates retrieved with the search criteria"species_taxid:562" and "geo_loc_name: Beijing*" (*E. coli* from Beijing) on November 12th 2021. Among which, 422 clinical isolates collected from *Homo sapiens* were selected. Furthermore, 146 *E. coli* genomes collected between 2018–2021 were downloaded using collection time and WGS accession as filter criteria.

Phylogenetic Analysis

The full set of 312 genomes were used to generate a core-genome SNP alignment and construct a phylogenetic tree, using Parsnp v1.1.2 in the Harvest package (*6*). The mid-point rooted phylogenetic tree was annotated in ITOL (https://itol.embl.de/). To estimate the *E. coli* population structure, we used hierBAPS v6.0 software (*7*) to identified the Bayesian model-based population structures. BAPS groups were assigned based on single-nucleotide polymorphisms (SNPs) were identified with SAMtools v1.3.1 (*8*) using RedDog v1bata.11 (https://github.com/katholt/RedDog) pipeline in the core genome of the *E. coli* strains.

SUPPLEMENTARY TABLE S1. Characteristic and prevalence of *Escherichia coli* isolates from the 6 districts, Beijing, China, 2020.

Region	Chicken		Pork		Total isolating rate (%)
	No. of isolates	Isolating rate (%)	No. of isolates	Isolating rate (%)	
Dongcheng	18	85.7	5	41.7	63.7
Xicheng	14	73.7	8	66.7	70.2
Haidian	32	94.7	5	33.3	60.6
Fengtai	24	50.0	10	45.5	47.7
Chaoyang	43	95.6	6	33.3	65.2
Changping	16	80.0	5	41.7	67.0
Total	147	73.9	39	42.9	64.1

Note: The six districts of Beijing includes Dongcheng, Xicheng, Haidian, Fengtai, Chaoyang, and Changping. The primary objective of the present study was to investigate the isolating rate and prevalence of *E. coli* isolates in Chicken and Pork from the six districts, Beijing, China, in 2020.

REFERENCES

1. Wang Y, Zhang R, Li J, Wu Z, Yin W, Schwarz S, et al. Comprehensive resistome analysis reveals the prevalence of NDM and MCR-1 in Chinese poultry production. Nat Microbiol 2017;2:16260. http://dx.doi.org/10.1038/nmicrobiol.2016.260.
2. CLSI. Performance Standards for Antimicrobial Susceptibility Testing (30th ed.), CLSI, Wayne, PA (2020) CLSI supplement M100. 2020.
3. European Committee on Antimicrobial Susceptibility Testing. EUCAST guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance, version 2.0. Accessed. 2017.
4. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 2012;19:455 – 77. http://dx.doi.org/10.1089/cmb.2012.0021.
5. Wick RR, Judd LM, Gorrie CL, Holt KE. Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol 2017;13:e1005595. http://dx.doi.org/10.1371/journal.pcbi.1005595.
6. Treangen TJ, Ondov BD, Koren S, Phillippy AM. The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. Genome Biol 2014;15:524. http://dx.doi.org/10.1186/s13059-014-0524-x.
7. Cheng L, Connor TR, Siren J, Aanensen DM, Corander J. Hierarchical and spatially explicit clustering of DNA sequences with BAPS software. Mol Biol Evol 2013;30:1224 – 8. http://dx.doi.org/10.1093/molbev/mst028.
8. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, et al. The Sequence Alignment/Map format and SAMtools. Bioinformatics 2009;25:2078 – 9. http://dx.doi.org/10.1093/bioinformatics/btp352.