Genomic characterization of fecal Escherichia coli isolates with reduced susceptibility to beta-lactam antimicrobials from wild hogs and Coyotes

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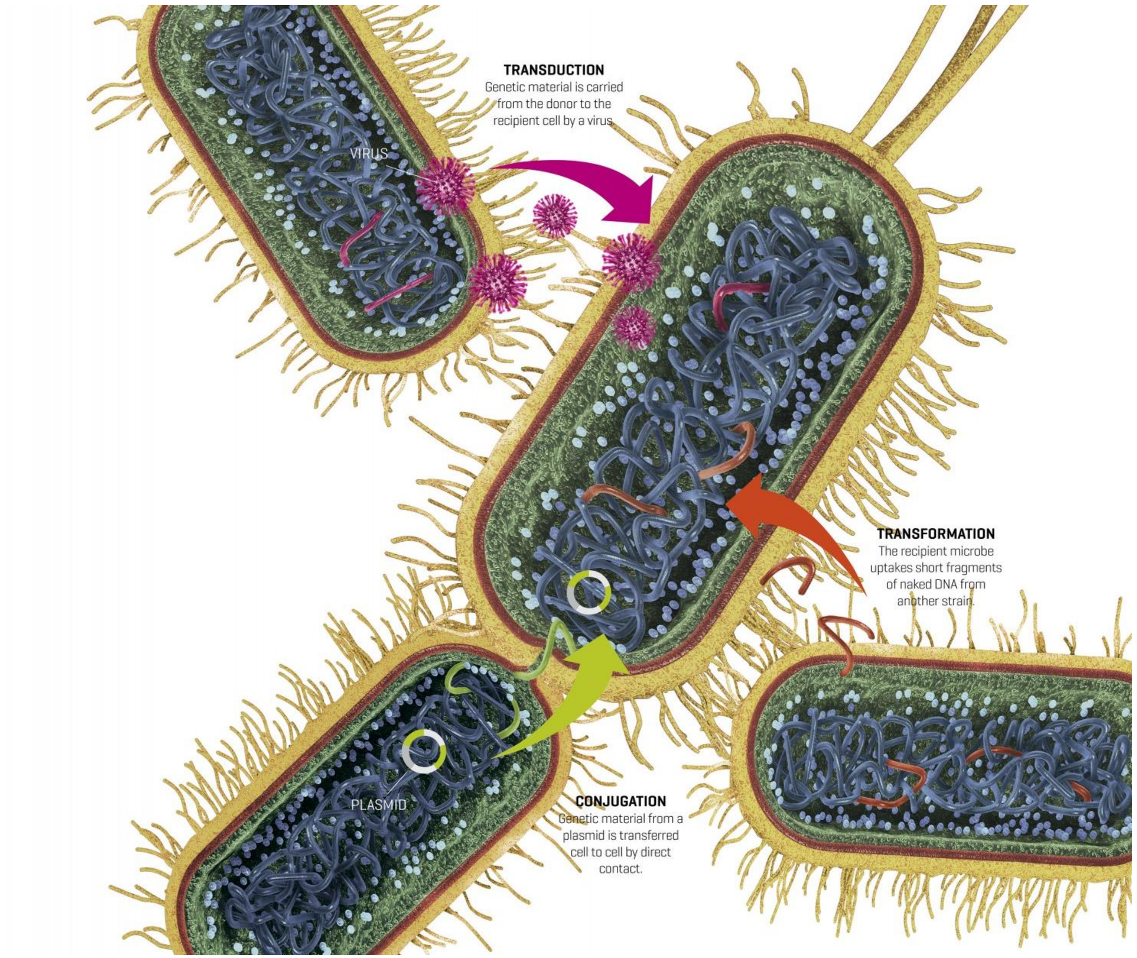
Background

- Antimicrobial resistant (AMR) genes is the most significant global health threats
- It could be threat in one health interface- Human, animal, industry and environment
- *E. coli* is a commensal, colonizes the gastrointestinal tract of mammalian and avian hosts
- *E. coli* is also a highly ubiquitous environmental microbe

- *E. coli*'s genome adapts and thrives through mobile genetic elements like plasmids and transposons
- Enhancing adaptability and survival in various hosts and environments, including horizontal gene transfer



- Wildlife encountering clinically employed antimicrobial treatments is an uncommon event

- However, wild animals can acquire resistant bacteria by encountering humans, domesticated animals, and the environment

- Coyotes and feral hogs influence AMR resistance dynamics at the wildlife-livestock interface

Objectives

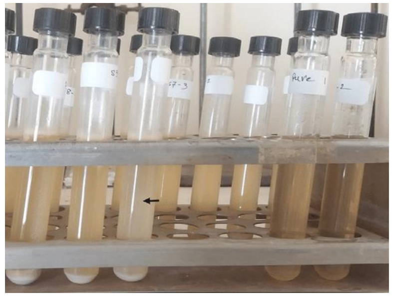
- To characterize AMR genes and Mobile genetic elements of *E. coli* isolates that were recovered from the fecal samples of coyotes and wild hogs from West Texas.

Methods

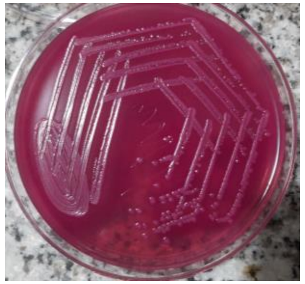
n= 9

n= 7

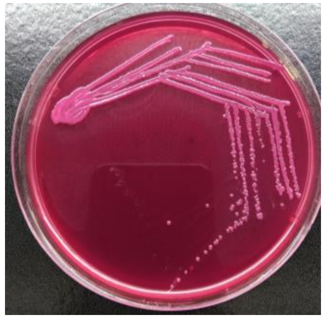
Feces



Pre-enrichment in buffered peptone water

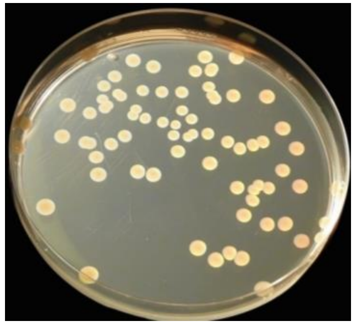


MacConkey agar with 1 ug/mL of ceftazidime



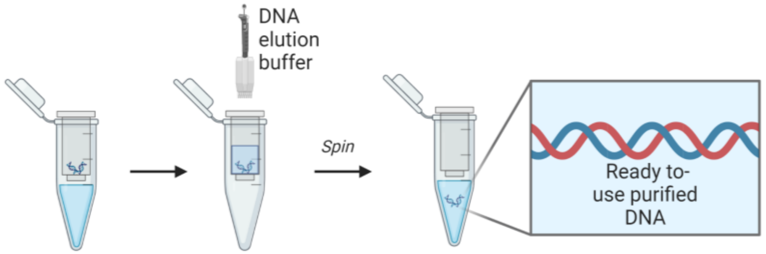
Presumptive ESBL-*E. coli*

sub-cultured on fresh MacConkey agar without ceftazidime



Further purified on Tryptic soy agar

E. coli isolates were further confirmed using MALDI-TOF



Genomic DNA of *E. coli* extracted using the InstaGene™ Matrix

DNA quantified

WGS on the Illumina MiSeq platform

Finally, bioinformatics analyses was done

Results

- All the 16 *E. coli* isolates were carriers of the *mdf(A)* resistance gene

- 5 isolates harbored at least 1 beta-lactamase gene
    - $bla_{\text{CMY-2}}$ – 1 coyote and 1 wild hog
    - $bla_{\text{CTX-M-55}}$ – 2 coyotes
    - $bla_{\text{CTX-M-27}}$ – 1 coyote

- several isolates were carried tetracycline resistant genes
    - *tet(A)* –2 coyotes
    - *tet(B)* –1 coyotes
    - *tet(C)* –1 wild hog

- 11 isolates were positive for aminoglycoside resistance genes
    - *aac(3)-IId* (2/16)
    - aadA5(2/16)
    - *ant(3")-Ia* (2/16)
    - *aph(3')-Ia* (1/16)
    - *aph(3")-Ib* (2/16)
    - *aph(6)-Id* (2/16)

- Some other resistance genes were identified
    - Sulfonamide resistance- *sul1, sul2, and sul3*
    - Amphenicol resistance- *flo*R
    - Trimethoprim resistance- dfrA1 and dfrA17
    - macrolide, lincosamide, streptogramin B resistance- lnu(F), *erm*(B), and *mph*(A)

- 10 isolates showed chromosomal mutations in the promoter region G of ampC beta-lactamase, with mutation in the amino acid G > A

- Additional chromosomal mutations observed in ampC beta-lactamase include promoter region P with change in amino acid C > T (7/16) and R25H cgc > cac (1/16)

- Three isolates showed chromosomal mutations in gyrA (3/16), parC (2/16), and parE (1/16) quinolone resistance-determining regions

- IncF (13/16) was the most common plasmid groups among the isolates

- Various virulence genes were detected: fimH, yehA, yehB, yehC, yehD, and fdec

- One $\mathit{bla}_{\text{CMY-2}}$ positive E. coli isolated from a wild hog was Shiga toxin-producing stx2A virulence toxin subtype

- Few isolates identified enterotoxin producing genes (*ast*A, *eltIIAB*-c3, and *cdt*-IIB)

Conclusions

- Coyotes and wild hogs in the Texas panhandle region harbor *E. coli* strains with virulence factors, antimicrobial resistance genes, and mobile genetic elements
- Wildlife's role in disseminating multidrug-resistant bacteria can carry important consequences for human and animal well-being, as well as environmental health.
- Environmental contamination with bodily secretions can taint water, soil, and vegetation, potentially driving the proliferation of multidrug-resistant bacteria in wildlife or vice versa.

Thank you!