E. coli isolates were common among \( \beta \)-lactam resistant \( E. coli \) from US hospitals. These isolates were significantly more resistant than their counterparts, despite the elevated resistance rates of the overall WGS collection. ST131 and ST131-O25b isolates had the potential to present a challenge for antimicrobial treatment. Specific therapies that are effective against these isolates should be investigated.

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229. A Novel ‘One Health’ Approach to Understanding the Relationship of Antimicrobial Resistance Characteristics Among Humans, Bovines, and Canines

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Background. ‘One Health’ recognizes the interconnectedness of humans with their production and companion animals, and the environment. Emergence and transmission of antimicrobial resistance (AMR) within and between these compartments is a recognized global threat that requires further understanding to design interventions protecting both human and animal health. In this study we identified resistance gene targets and clonotypes of Escherichia coli recovered from human, canine and bovine hosts and applied non-linear dimensionality reduction and visualization techniques to identify genetic relationships that may otherwise be unobservable within the data.

Methods. Non-duplicative E. coli isolates (N=3,398; see Figure captions) were collected from humans, canines, bovines from the Midwest USA. We identified beta-lactamase gene targets for third-generation cephem multidrug resistant isolates and performed clonotype analysis on each. Uniform Manifold Approximation (UMAP) was used to create a two-dimensional "map" of the high dimensional space of the genetic results to identify genetic relationships that may otherwise be unobservable within the data.

Results. The resulting "map" highlights similarities in: 1) genetic patterns of AMR among animals and humans, and 2) links between isolates that are infecting and colonizing isolates, and between susceptible and resistant isolates in humans and animals in the study region (see Figure captions).

Conclusions. The results support that UMAP is a valuable tool for visualizing genetic AMR links across species. Human-animal transmission is likely for disparate and common clonotypes.

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Figure 2. Distribution of resistant and susceptible isolates shows the resistant cases are distributed in small clusters surrounding a large cluster of predominantly susceptible cases.

Figure 3. The proportion of cases from each cluster in four adjoining counties varies considerably.