Background. ‘One Health’ recognizes the interconnectivity 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=3398; see Figure captions) were collected from humans, canines, bovines from the Midwest USA. We identified beta-lactamase gene targets for third-generation cepheid 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. UMAP is a dimensionality reduction technique similar to principal component analysis (PCA), except that it uses a non-linear combination of the underlying dimensions, which highlights the local structure and grouping of the cases. For more details see: Diaz-Papkovich, A., Anderson-Trocmé, L., & Gravel, S. (2021). A review of UMAP in population genetics. Journal of Human Genetics, 66(1), 85–91. Infection isolates: bovine n=190, human n=115. Surveillance isolates: bovine n=175, canine n=747, human n=2171.

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 animals and humans, and resistant isolates in animals and humans in the study region (see Figure captions).

Methods.

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 animals and humans, and resistant isolates in animals and humans in the study region (see Figure captions). The dark bars show the proportion of cases falling into each cluster for each county. The light bars provide a reference point for interpreting the dark bars by showing the proportion of cases falling into each cluster across all four counties. When the dark bars exceed the light bars it indicates that the proportion of cases in that cluster exceeds that of the neighboring counties, such as Cluster 2 for Taylor county and Cluster 3 for Marathon county. All counties shown include a population of at least 20,000. These stipulations are in compliance with federal (HIPAA) guidelines.

Conclusion. 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.

Disclosures. All Authors: No reported disclosures