**OBJECTIVE:** Agricultural antimicrobial use may lead to the emergence of multidrug resistant microbes in food animal populations and at subsequent levels of the food chain. Multidrug resistance (MDR) poses a unique threat by limiting or eliminating treatment options for animal and human illness. Moreover, analyzing MDR poses challenges to researchers due to the complexity of the large number of possible MDR patterns that could be present across a given population. The objective of this study was to apply association rule mining to the analysis of MDR patterns present in cattle associated *Escherichia coli*, incorporating both phenotypic and genotypic indicators of resistance. Associations among MDR patterns were compared across years, resistance indicators, and sources (retail meats or slaughterhouse samples).

**METHODS:** Data were retrieved from the National Antimicrobial Resistance Monitoring System (NARMS) to include 12,932 isolates tested against 12 to 14 antimicrobials, spanning 19 years from 2002 to 2021. Data were divided into separate datasets based on year and source. Reported minimum inhibitory concentrations were used to determine each isolate’s phenotypic resistance profile based on NARMS interpretive criteria. Associations among these resistance profiles were mined using the machine learning method, association rule mining. Associations based on the presence of resistance genes were also mined for years where the genotypic data was available. A set of data driven approaches were employed to select the hyperparameters involved in rule assessment and pruning. The MDR patterns were also tabulated to compare a more traditional method to the association rule mining method.

**RESULTS:** Association rule mining was able to capture the MDR profile information yielded by the tabulation as well as the complex associations among these profiles. Association rules were analyzed with both graphical and numerical methods. Network graphs were constructed for each year/source dataset for both genotypic and phenotypic association rules. The networks graphs efficiently reflect both the prevalence and complexity of the associations among MDR patterns in the data, as well as indicate important differences among these associations across datasets. To compare associations across datasets, the percentage of associations from one dataset that were captured in another dataset were calculated. Phenotypic and genotypic association rules were compared by aggregating resistances and genes to the class level. An exceedingly high percentage (~98%) of phenotypic associations were captured by the genotypic associations; however, a much lower percentage of the genotypic associations were captured by the phenotypic associations.

**CONCLUSIONS:** Association rule mining was able to effectively provide insights into complex associations among MDR patterns present in cattle associated *Escherichia coli*. The high percentage of phenotypic associations represented in the genotypic associations suggests that genotype is a good predictor of phenotypic resistance; while the comparatively lower percentage of genotype associations represented within the phenotype associations is largely driven by drug-specific resistance genes. This discrepancy may suggest that more drugs need to be tested to have a fuller understanding of the variation in MDR patterns. It also may be important to consider how MDR status differentially relates to phenotypic and genotypic characterizations to promote consistency in MDR categorization.