EVALUATING CORRELATIONS IN SALMONELLA SEROTYPES IN SWINE IN FOUR LONGITUDINAL DATASET

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S. enterica serovars surveillance program have been established for many years in the United State of America (USA). Data from long running surveillance programs provides the opportunity to compare prevalence of serotypes within and across surveillance programs, observed patterns and generate hypothesis. To this end, the aim of this project was to estimate the correlation between changes in the yearly changes in serotypes proportions in concurrent years and lagged years from swine, beef and avian longitudinal datasets: (The Iowa State University Veterinary Diagnostic Laboratory (VDL), The National Antimicrobial Resistance Monitoring System (NARMS animal-based isolates only), compared to data from The Centers for Disease Control (CDC) Laboratory-based Enteric Disease Surveillance (LEDS) Program. The lagged correlations were as follows: a) 1-year lag with the animal data preceding the human data and b) The correlation across a 2-year lag with the human data preceding the animal data. We calculated correlations and corresponding intervals for the following comparisons

- CDC-LEDS correlation with ISU VDL swine, avian and bovine data-sets.
- CDC-LEDS correlation with NARMS-USDA swine, avian and bovine data-sets.
- CDC-LEDS correlation with NARMS-FDA retail pork, poultry and beef data-sets.

Using the 10 most common serotypes found in swine based on the ISU database, some of the correlations observed included: 1) positive correlations between concurrent yearly proportional in changes in S. enterica 4,[5],12:i:- in swine VDL submissions, bovine VDL submissions, NARMS bovine submissions with the LEDS yearly proportional changes and 2) positive correlations for concurrent yearly proportions changes S. Anatum between LEDS and the NARMS swine dataset. No correlations where found for the lagged correlations.