

Sequencing finds antibiotic resistance in bacteria moving from livestock to humans

The following is an editorial summary.

While it has long been suspected that using “judicious” use antibiotics in livestock could cause the development of antibiotic resistance in bacteria that would then find its way into human infections, efforts to demonstrate the connection between the development or resistance in livestock and the emergence of resistant infections from the same bacteria have been largely unsatisfactory. As the author puts it:

The policy difficulty regarding this long-recognized problem has never been the emergence of resistant bacteria on farms; no one seriously disputes that resistance emerges whenever antibiotics exert selective pressure on bacteria, killing the vulnerable and opening an ecological niche into which the surviving not-vulnerable can expand. The sticking point has been the difficulty of *proving* that those resistant bacteria depart from farms, cross to humans, and cause resistant illness in them.

A new Dutch study, using extremely precise sequencing techniques, may finally be the “smoking gun” needed to implicate livestock. Using modern genetics, the researchers were able to demonstrate that the similarity of the infections and infer their passage from livestock to human by taking whole genome sequences of the bacteria in drug-resistant staph infections that arose on farms.

View the original article here: [Gene Sequencing Pinpoints Antibiotic Resistance Moving From Livestock to Humans](#)