

Press release – 16 February 2023

Poultry farming: better understanding and treating an emerging infectious bacterium

Around the world, poultry face a multitude of pathogens. Of particular concern is *Enterococcus cecorum*, a pathogenic bacterium that is increasingly behind severe disease and mortality on farms. Recently, researchers at INRAE and ANSES explored the biology of this species with a view to better protecting farm animals. The findings were published on February 16 in *mSphere* and *Journal of Clinical Microbiology*.

Enterococcus cecorum causes locomotor dysfunction and blood poisoning (i.e., septicæmia) in poultry, especially in fast-growing broilers. This pathogen has become progressively more problematic, as its incidence has risen 100-fold in 15 years.

Naturally present in the digestive tract of chickens, *E. cecorum* largely remains a biological black box for scientists, although certain strains seem to have greater pathogenic potential. Consequently, researchers at INRAE and ANSES have joined forces to find out more about this bacterium.

Deciphering DNA differences

First, the scientists characterised the genetic diversity found in *E. cecorum* strains circulating on French farms. To this end, they studied 100 strains isolated from sick animals. Strains of disease-causing bacteria are known as clinical variants; strains that do not cause disease are called non-clinical variants. Next, the variants' genomes were compared to create a comprehensive list of the bacterium's genes and identify those shared by all strains.

The results clearly revealed that clinical and non-clinical variants have followed distinct evolutionary trajectories. Among the clinical variants are most of the bacteria responsible for infections not just in France, but also in other European countries as well as in the US.

The scientists then identified six genes that could determine a variant's evolutionary origin 94% of the time, information that will facilitate farm monitoring efforts. They also described antibiotic resistance genes, data that can guide the development of targeted treatments.

Assessing antibiotic resistance

The researchers had gained knowledge about resistance-conferring genes in the clinical variants, but the state of affairs in non-clinical variants remained unknown.

Thus, in a second study, they tested the effects of antimicrobial compounds on over 200 variants. The goal was to develop better methods for identifying antibiotic-resistant variants. To this end, minimum inhibitory concentrations, inhibition zone diameters and epidemiological cut-offs were established.

These thresholds were determined for 29 antimicrobial compounds. This work underscored that many variants display resistance to the antibiotics used on livestock farms. That said, this resistance is not directed against the antibiotics used to treat humans.

Taken together, these two complementary studies illustrate the evolutionary dynamics of this bacterium, whose populations now harbour infectious variants. Their findings have shed light on genetic diversity and antibiotic resistance in *E. cecorum* and will help prevent and control severe infections.

References

Laurentie J, Mourand G, Gripon P, Furlan S, Chauvin C, Jouy E, Serror P, Kempf I. 16 February 2023. Determination of epidemiological cutoff values for antimicrobial resistance of *Enterococcus cecorum*. J Clin Microbiol <https://doi.org/10.1128/jcm.01445-22>.

Laurentie J, Loux V, Hennequet-Antier C, Chambellon E, Deschamps J, Trotereau A, Furlan S, Darrigo C, Kempf F, Lao J, Milhes M, Roques C, Quinquis B, Vandecasteele C, Boyer R, Bouchez O, Repoila F, Le Guennec J, Chiapello H, Briandet R, Helloin E, Schouler C, Kempf I, Serror P. 16 February 2023. Comparative genome analysis of *Enterococcus cecorum* reveals intercontinental spread of a lineage of clinical poultry isolates. mSphere <https://doi.org/10.1128/msphere.00495-22>.

Scientific Contacts:

Pascale Serror pascale.serror@inrae.fr

Joint Research Unit for Food Microbiology for Health (MICALIS)

Isabelle Kempf

Research Unit for Mycoplasma, Bacteriology, and Antimicrobial Resistance

Press contacts:

INRAE: 01 42 75 91 86 – presse@inrae.fr

Anses: 01 49 77 13 77 / 28 20 – presse@anes.fr