The cattle slurry virome and the potential spread of antibiotic resistance

Ryan Cook
Steven Hooton
Urmi Trivedi
Liz King
Christine Dodd
Jon Hobman
Dov Stekel
Michael Jones
Andrew Millard

Video Byte

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Abstract

Livestock waste is a common fertilizer for crop fields. Many farms remove the solids from manure and store only the remaining liquid, called slurry, for later use, but little is known about the microbial contents of slurries, especially the viruses. To close this gap, researchers sequenced the slurry virome of a cattle farm over a 5-month period. They used a hybrid approach, combining short and long sequencing reads, which provided more comprehensive results than using only one method. The farm's virome was dominated by lytic bacteriophages and 98% were from novel genera. The overall diversity and composition was stable over time. In fact, over half of the operational taxonomic units were detected in all the samples. Functional analysis found a range of metabolic genes, diversity-generating retroelements, putative antibiotic resistance genes, and virulence factors. These results mean that spreading slurry may allow phages to spread those virulence and antibiotic resistance genes to bacterial pathogens. Some of these specific virulence factors, such as *vapE*, are found in agricultural pathogens like *Streptococcus* spp., which causes mastitis in cows. The prevalence of virulence factors in this system warrant further investigation to determine if they are being spread to pathogens in fields.