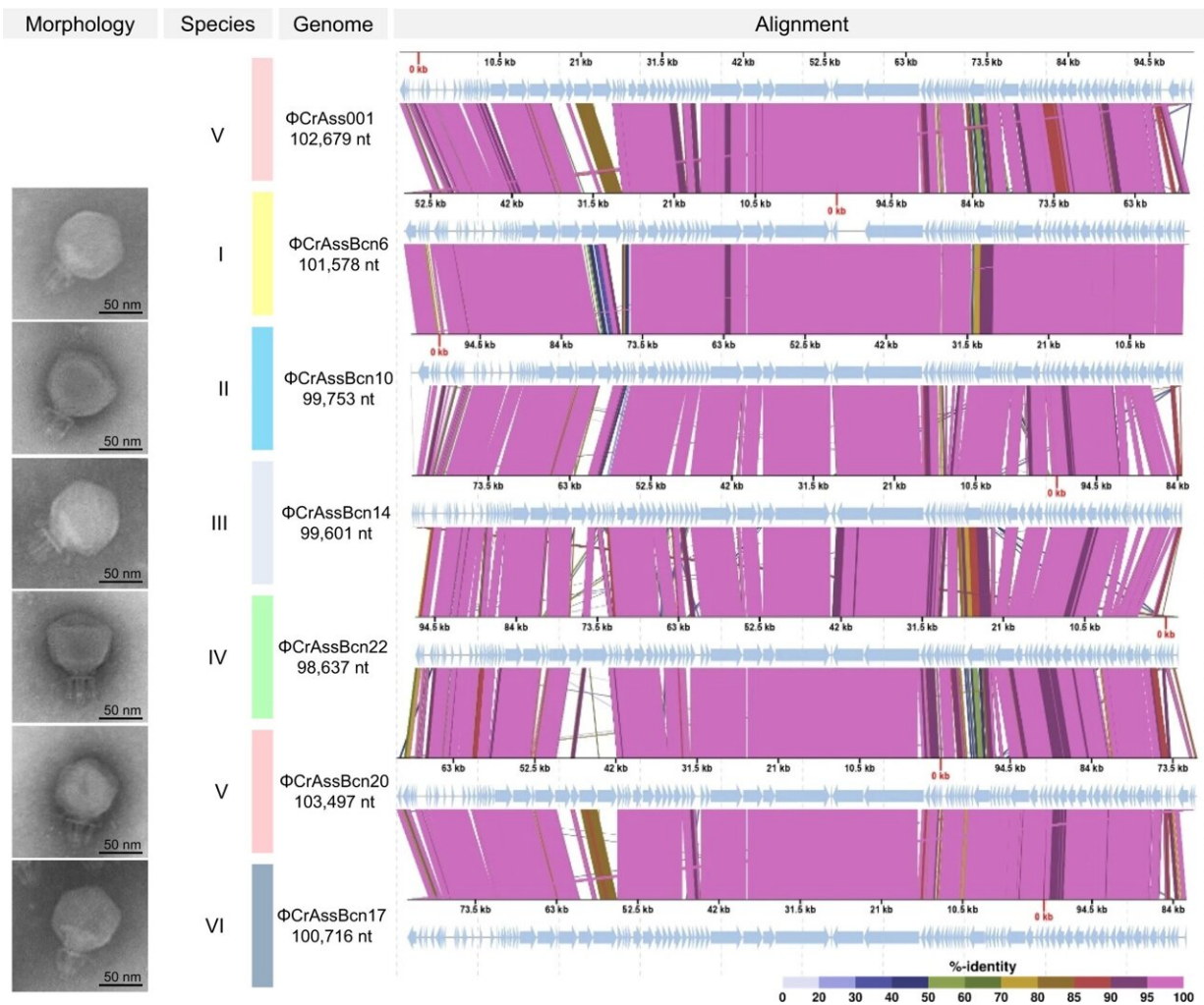


# Research team identifies 25 new viruses in Barcelona's wastewaters

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Comparison of the six representative crAssBcn phages of each species and ΦCrAss001. Electron micrographs and CDS alignment of the genomes of six crAssBcn phages representative of the six species (groups I-VI). Light blue arrows indicate the ORFs. The color of the bands between the seven genetic

maps shows the percentage of identity between each sequence as indicated in the legend at the bottom of the figure. Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-40098-z

A team from the University of Barcelona has identified 25 new viruses that infect bacteria in the human intestinal tract in wastewaters around the city's metropolitan area and in some towns nearby.

These viruses, of the Crassvirales order, infect some species of the *Bacteroides* genus, which are very abundant in the intestinal microbiota of humans. The viruses now isolated have a completely different genome to any other crAss [virus](#) described to date in the scientific literature and have been named crAssBcn phages.

The findings, published in [Nature Communications](#), were carried out by a team led by Professor Maite Muniesa, from the Research Group on Microbiology of Waters related to the Health (MARS) of the UB's Faculty of Biology.

Due to their characteristics, the new viruses are seen as potential indicators of fecal contamination in humans. In addition, the group wants to focus on studying whether the presence and the abundance of crAss phages—specifically crAssBcn phages—is different between healthy individuals and people affected by certain diseases (intestinal, metabolic or even nervous system).

"As far as we know, crAssBcn phages are very specific to the human microbiota and so far, we have not found them in the microbiota of other animals," notes Maite Muniesa, lecturer at the Microbiology section of the UB's Department of Genetics, Microbiology and Statistics.

"Their biological role is still unknown, but being such abundant phages that infect a bacterial genus (*Bacteroides*) also abundant in the human intestine, it is suspected that they may have a regulatory role in bacterial populations and some influence on the human intestinal [microbiota](#)."

Since 2014, only four groups had been able to isolate a total of seven crAssphage-like viruses. Now, the UB team has identified 25 new phages at once, significantly expanding the global map of this group of [viruses](#) that are highly prevalent in the world population. Moreover, crAssBcn, despite being native to the Barcelona area, are widely distributed and have been detected in 51% of intestinal metagenomes worldwide.

**More information:** María Dolores Ramos-Barbero et al, Characterization of crAss-like phage isolates highlights Crassvirales genetic heterogeneity and worldwide distribution, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-40098-z](https://doi.org/10.1038/s41467-023-40098-z)

Provided by University of Barcelona

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