Antimicrobials molecules from the Arctic: how about Giant Viruses?

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Throughout evolution, natural selection has favored the survival of organisms with the best strategies to overcome competition. One of these mechanisms is the production of antimicrobials molecules, which may have different modes of action and structures. Since about the 2000s, our research group, the Marine Bioprospecting group from the Arctic University of Norway, has explored the production of these molecules in more than 20 arctic marine organisms. The antibacterial activity of extracts from different samples of various species of fish, crab, shrimp, sea urchin, sponges, among others, have been tested against environmental and human pathogenic and non-pathogenic bacteria. For instance, many molecules were effective against *Escherichia coli, Pseudomonas aeruginosa, Cornyebacterium glutamicum* and *Staphylococcus aureus*. We can expect that even viruses may present antibacterial compounds in virus-host systems in which competition with bacteria takes place. In fact, the other way around has already been described, where free-living amoebas have a bacteria symbiont naturally present in their cytoplasm, abrogating the establishment of giant viruses' viral factory, thus impairing viral replication and allowing its host cell to survive. Considering that Giant Viruses have enormous genomes, with many genes that have unknown functions, there is a great potential for some of those genes to act against competition inside their host cells, such as by producing antimicrobials. Giant viruses' isolation attempts using more than 300 samples (various sources) from the arctic region in the north of Norway have been performed in the past 2 years. Until this moment, we successfully have acquired 6 giant virus positive samples, isolating Mimiviruses (identified as AP86, AC98 and AC87) and Marseilleviruses (AC41 and AC140) in *Acanthamoeba* spp. host cells. Amoeba cells infected by 2 of these Mimiviruses (AP86, AC98) and the other 2 Marseillevirus, separately, as well as the culture media that these amoebas were grown and infected into, have been processed through Liquid-liquid extraction, Solid-Phase extraction (80% acetonitrile only) and LC-MS/MS. A total of 142 compounds were identified from the washed cells sample of *A. castellanii* infected by the Mimivirus AC98, while the non-infected control had 147; and for the media of infected cells there was 228 compounds identified, and 254 for the control. Now considering the *A. castellanii* infected by the other 2 Marseillevirus, the number of compounds presented in the washed cells sample were 121 (AC41) and 145 (AC140). The control was the same as mentioned for the Mimivirus infection. As initial attempts, these final extracts containing all these compounds were tested against *P. aeruginosa, S. aureus, Bacillus subtilis, E. coli, C. glutamicum,* and until now, no antimicrobial activity has been detected. One of our next steps is to challenge the amoeba with these bacteria (and other environmental bacteria) while also being infected by the giant virus, to potentially stimulate the production of antimicrobial molecules. Furthermore, we plan to characterize these molecules presented in these extracts, as well as focus on the differences of these infections through global proteomics and metabolomics analysis. Overall, we hope that this project finds antimicrobials molecules that can be used for medical and environmental settings, and that our results bring deeper knowledge in the dynamics of host-virus interaction.

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