NEWSLETTER Viraqua

Vol. 1, Issue 1, February 2017

The project so far...

By Professor Davey Jones, Bangor University

The NERC and FSA funded Viraqua project was established to protect human health from the threat of viral infection that exists in the environment. Its specific focus is on understanding the behavior, fate and risk posed by human pathogenic viruses such as norovirus and hepatitis A and E viruses within the land-to-sea continuum. Ultimately, the project aims to devise new management strategies to help reduce and manage the risk posed by these pathogens. The project is collaborative and combines expertise from both academic (Bangor, Liverpool and Cambridge University) and research institutions (The Centre for Ecology and Hydrology, CEH and The Centre for Environment, Fisheries and Aquaculture Science, CEFAS) with key stakeholders; the Food Standards Agency (FSA), Welsh Water, Public Health Wales and The Shellfish Association of Great Britain (SAGB). Led by the team at Bangor University much of the work to date, has focused on the development of novel techniques for viral detection and the surveillance of viruses in the environment as well as developing computer models to predict the flow of viruses through the river network and out into the coastal zone. 2017 will see us identify the full diversity of viruses in our target sampling areas (metaviromes) and develop new methods to quantify the infective status of viruses present in the environment.

Impact of the project

By Dr Kata Farkas, Bangor University

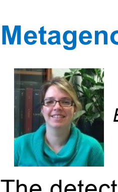
Increasing pressure on wastewater infrastructure, sewer misconnections and increasing incidence of sewer overflow discharge is impacting the waterborne disease burden in our rivers and coastal zone. The pathogens of interest are enteric viruses, such as norovirus (commonly known as winter vomiting bug) responsible for waterborne and shellfish-related outbreaks throughout the winter months. Resistant to wastewater treatment, they are often present in wastewater discharged into rivers which ends up in coastal waters and is then ingested by shellfish farmed for human consumption. The Viraqua project aims to develop, validate and standardize novel approaches for the detection and quantification of these viruses in surface water, aquatic sediment and shellfish which could then be made available to laboratories worldwide. Developing models to improve prediction of viral flow from diffuse and point sources (wastewater treatment plant discharges) through the catchment and out into 'high risk' coastal zones (bathing waters and shellfish harvesting areas). Our project involves extensive sampling in the Conwy river and estuary (North Wales). The samples are then used for method development and for monitoring virus numbers in the environment.

Modelling Virus Transport

By Dr Peter Robins, Bangor University and Dr David Cooper, CEH

By modelling virus dynamics across the catchment (river Conwy) and coastal zone (Conwy estuary), we improve our understanding of viruses in the environment and are better equipped to assess infection risk. The catchment model is composed of factors which influence the virus loads and concentrations entering the estuary. Field measurements, lab work and modelling provide estimates of: 1) source magnitudes and dilution 2) the rate of movement of viruses down the river and 3) estimated time series of virus concentrations entering the estuary. The catchment model is linked at the tidal limit to a model of virus flow within the Conwy estuary extending off shore to include the Menai Strait and the southwestern Liverpool Bay. The hydrodynamic model can simulate depth-averaged or 3D flows (tidally– and density-driven) that predict the transport of viruses down through the estuary and coastal system. Using this coupled model system we can predict the controls on viral transport: sensitivity to virus load, river flows, weather and tidal conditions. Future work will model the rate of loss of viability and the retention in the river bed. All the animations produced by the project showing simulations and predicted transit of viruses can be viewed on our YouTube channel.

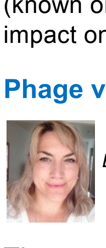
Metagenomics - A new approach in virus identification



By Dr Evelien Adriaenssens, University of Liverpool

The detection of pathogenic viruses in any environment, whether it be food, humans, or waterways, has traditionally been done with molecular methods which are targeted at a specific known gene or a short genomic segment of the target virus. These methods, while rapid and sensitive, are based on what is already known and cannot detect unknown targets. We are now using a novel approach, called metagenomics, used to recover all the genetic material from a sample without any prior knowledge of the target. Our research group at the University of Liverpool is implementing this state-of-the-art technology to recover and identify viral genomes (known or unknown) from the environment and assess their potential impact on human health.

Phage viability to validate inactivation treatments



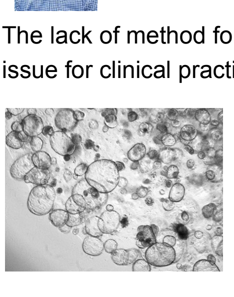
By Dr Lisa Cross, Cefas

The most widely used method to detect human enteric viruses usually involves the quantification of a short segment of the viral genome and unfortunately gives no information on the infectivity state of the viruses. There is therefore a dilemma in assessing the risk to human health from, for example, shellfish samples detected as positive for norovirus and given that enteric viruses cannot be easily cultured in the laboratory research is made more problematic. At CEFAS, we have been focusing on alternative approaches to overcome this problem. Through the use of bacteriophages (stable viruses associated with bacteria) which can be easily and rapidly cultured and are found in high numbers in wastewater and in areas contaminated by wastewater, we have been able to develop a method to assess norovirus infectivity. In addition we have been working on techniques using bacteriophage viability to assess the effectiveness of viral inactivation treatments (heat, UV) on environmental samples.

Replication of Norovirus

By Professor Ian Goodfellow, Cambridge University

The lack of method for the detection of infectious norovirus has been an issue for clinical practitioners as well as for environmental pollution investigators. If the infectious state of norovirus found in water samples remains unknown the risks associated with contaminated water cannot be determined. In 2016, Dr Ettayebi and his research team (Baylor Collage of Medicine, Texas) published a method using stem cells that allowed the laboratory propagation of human noroviruses (DOI:10.1126/science.aaf5211). Our research group has successfully adapted the method and now we are investigating the usefulness of the technique using different matrices.



2016 Publications

Last year saw the publication of key research by project members in the area of foodborne and waterborne enteric viruses :

Winterbourn, JB; Clements, K; Lowther, JA; Malham, SK; McDonald, JE; Jones, DL (2016) Use of *Mytilus edulis* biosentinels to investigate spatial patterns of norovirus and faecal indicator organism contamination around coastal sewage discharges. *Water Research* 105, 241-250.

Hassard, F., Gwyther, C. L., Farkas, K., Andrews, A., Jones, V., Cox, B., Brett, H., Jones, D., McDonald, J. E., and Malham, S. K. (2016) Abundance and Distribution of Enteric Bacteria and Viruses in Coastal and Estuarine Sediments—a Review. *Frontiers in Microbiology* 7: 1692. http://journal.frontiersin.org/article/10.3389/fmicb.2016.01692

Campos, C. J., Kershaw, S., Morgan, O.C. & Lees, D. N. (2017). Risk factors for norovirus contamination of shellfish water catchments in England and Wales. *International Journal of Food Microbiology* 241, 318 - 324. http://dx.doi.org/10.1016/j.ijfoodmicro.2016.10.028

Boxman, I. L., L. Verhoef, H. Vennema, S. Ngui, I. H. Friesema, C. Whiteside, D. Lees, and Koopmans, M. (2016). International linkage of two food-borne hepatitis A clusters through traceback of mussels, the Netherlands, 2012. *Eurosurveillance*, 21(3), 30113-30121.

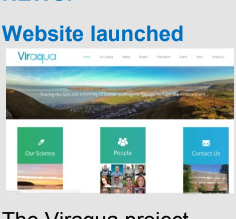
All references are available on the website (www.viraqua.uk). For full text PDFs please contact k.farkas@bangor.ac.uk

February 2017

The Viraqua Project Newsletter is a quarterly publication offering partners and stakeholders an insight into the impact of the project and findings to date.

NEWS:

Website launched

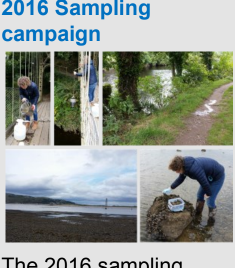


The Viraqua project launched its website in 2016. To learn more about the project and what we do visit us at: www.viraqua.uk

For more frequent updates, connect with us on social media:

follow us on twitter YouTube

2016 Sampling campaign

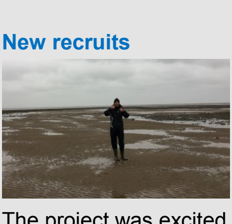


The 2016 sampling campaign was a great success. Water samples were taken upstream and downstream from a wastewater treatment plant along the river Conwy and water, sediment and mussel samples were taken near a combined sewage overflow in the estuary at Deganwy and Conwy. Samples were tested for the presence of enteric viruses.

PIG conference

December saw the inaugural meeting of the NERC Environmental Microbiology and Human Health (EMHH) programme integration group (PIG) at the Watershed in Bristol. The conference was well attended and was a good opportunity for the EMHH projects to share ideas.

New recruits



The project was excited to recruit two M degree students to the world of environmental microbiology. In November, Vanessa Kienmoser and John Maloney joined the team at Bangor and their research projects will focus on; enteric virus concentrations in wastewater shellfish and sediment samples.

First Project Paper

The new year kicked off with the first Viraqua project publication with Kata Farkas, Francis Hassard, James McDonald, Shelagh Malham and Davey Jones all co-authors on a paper in *Frontiers in Microbiology* evaluating molecular methods for the detection and quantification of pathogen-derived nucleic acids in sediment." Full references can be found on the publications page of the website: www.viraqua.uk

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NERC SCIENCE OF THE ENVIRONMENT EMHH

Food Standards Agency