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EU Virus-X Consortium Awarded $9M to Mine Viral Biological Diversity

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NEW YORK (GenomeWeb) – A consortium of private companies and public researchers recently snagged €8 million ($9 million) to explore viral genomic diversity, with the additional aims of crafting new sequencing approaches, bioinformatics tools, and targeted gene products.

The effort, called "Virus-X: Viral Metagenomics for Innovation Value," has been funded through Horizon 2020, the European Framework Programme for Research and Innovation. Virus-X is slated to run for the next four years and includes 15 participants from eight countries. Prokazyme, an Icelandic enzyme supplier, is coordinating the project.

Prokazyme CEO Arnthor Ævarsson told GenomeWeb that the main thrust of Virus-X is to exploit the genetic diversity of the virosphere and its potential for the development of unique products of industrial value.

"Looking at the viral proteins from only the well-known bacteriophages T4 and T7 of E. coli that have found use in molecular biology applications, it seems clear that the viral protein universe out there must have so much more to offer," Ævarsson said. "However, this requires extensive efforts for the discovery of new viral proteins, careful analysis of their structural and functional properties, and development of selected proteins as products for molecular applications."

To accomplish this, Ævarsson said that Virus-X will construct a "massive biodiscovery pipeline" that will extend from environmental sampling to metagenome sequencing, bioinformatics, annotation, selection of targets, cloning, expression, protein production, functional characterization, 3-dimensional structure determination, and eventually, target gene products.

Based in Reykjavik, Prokazyme has for the past decade worked to exploit the biodiversity of the volcanic island country's microbial ecosystems, especially the thermophilic bacteria and viruses found in its diverse geothermal areas. The company previously coordinated the European Commission-funded Exgenomes Project, which ran from 2011 to 2013 and led to the commercialization of six enzyme products by Prokazyme and Poland's A&A Biotechnology.

A&A Bio is also taking part in Virus-X, along with ArcticZymes, a Tromsø, Norway-based subsidiary of Biotec Pharmacon, that sells cold-adapted enzymes for molecular research and diagnostics prospected from the marine Arctic. ArcticZymes announced earlier this month that it would receive €460,000 over the next four years as part of its participation in Virus-X.

Jethro Holter, ArcticZymes' managing director, told GenomeWeb that Virus-X will play a "significant part" in broadening the company's discovery pipeline. He said that any molecular enzymes yielded will not only complement ArcticZymes existing portfolio, but "enable its commercial partners in the development of next-generation molecular tool and diagnostics."

"We are focusing on extreme biotopes ... mainly in Norway and Iceland," said Ævarsson of Virus-X. "We expect the corresponding viruses that we isolate from the geothermal ecosystems as well as the gene products to be thermostable and active as higher temperatures," he added.

Virus-X is particularly interested in proteins that participate in the processing of nucleic acids, such as nucleases, polymerases, ligases, and helicases, which it believes may "be of great utility" for in vitro applications. However, the isolation and sequencing of the viral metagenomic material and extracting of the viral sequences will be "far from trivial," Ævarsson claimed.

That should entail the development of novel sequencing approaches as the project proceeds. "The genetic material of viruses may, for example, have modifications that make the use of traditional sequencing techniques difficult," Ævarsson said. "Part of the project is to look into the specific problems of this kind and possible solutions."

To reach its goals, Virus-X will call on the expertise of investigators from Icelandic biotech firm Matis; Saromics Biostructures and Lund University in Sweden; the University of Bergen in Norway; the University of Durham in the UK; Dutch biotech company Bio-Product; the University of Gdansk in Poland; the Max Planck Institute, the University of Stuttgart, and the University of Bielefeld in Germany; and Institut Pasteur and Université Blaise Pascal in France. Each participating company and institution in Virus-X will seek to explore the diversity of selected viruses using its own skill set.

For example, François Enault, a researcher at Université Blaise Pascal focused on the environmental analysis of virus genomes and metagenomes, told GenomeWeb that his goal in the project is to "explore the composition and dynamics of microbial and viral communities in a wide range of environments," especially extreme environments like those in Iceland and Norway.

"Extreme biotopes are indeed understudied and harbor a vast and almost unknown pool of viral genomes and proteins," Enault said. "The development of different in silico methodologies and their application to the metagenomes obtained in the project should help in understanding the relations between viruses and their hosts," he said. The data produced will also help to link these microbial and viral communities to environmental conditions and enable researchers to see if conditions can be used to predict the composition of biological communities, Enault added.

In addition to sequencing and understanding microbial ecosystems, bioinformatics will also be a focus within Virus-X. "The genetic divergence of viral genes makes annotation of these genes extremely difficult, which makes the development of new bioinformatics tools one of the main technology development issues in the project," Ævarsson commented.

One investigator tasked with accomplishing this is Johannes Söding, part of the quantitative and computational biology group at the Max-Planck Institute for Biophysical Chemistry in Göttingen.

"Bioinformatics plays an important role in this project as viral protein sequences are often so strongly diverged that search techniques such as BLAST usually cannot find homologous proteins," Söding said. He said his lab will develop a computational analysis pipeline for homology-based function and structure prediction to prioritize candidate proteins for analysis.

These activities will all take place under the Virus-X umbrella. By March 31, 2020, when the project ends, Ævarsson said that Virus-X will have generated "very valuable sequence," as well as 3D structure and biochemical data, including characterizations of structure-function relationships in diverse protein families, including proteins that have an unknown function today.

The consortium also expects to have developed new enzyme products, new bioinformatics tools, and improved protein structure determination services for the European scientific community.

"We also expect to improve our understanding of microbial communities, including those in extreme biotopes, and gain better insight into the functional dynamics of those ecosystems including host-virus interactions," Ævarsson said.