

# Eureka Genomics Plays Key Role in Identification of Viral Strains Involved in an Emerging Disease Afflicting Syrah Grapevines in California

Hercules, CA—July 9, 2009—Eureka Genomics, an industry leader in advanced bioinformatics analysis of next generation sequencing data, announced today that it played a key role in the characterization of a previously undefined viral syndrome that is threatening California vineyards—and has baffled scientists for nearly 20 years.

This disease, known as “Syrah Decline,” is a growing concern to the multi-million dollar Syrah segment of the California wine industry. A related disease has been on the rise in French vineyards as well. Up until now, the pathogenicity, histological, graft incompatibility and genetic studies did not produce any conclusive results or insights into the cause of this syndrome.

This investigation into the decline of Syrah grapevines is led by Dr. Adib Rowhani of the University of California, Davis, as part of the university’s ongoing research into California grape production and vineyard management. Eureka Genomics will continue to be involved in the project.

The study was based on Eureka Genomics’ proprietary next-generation sequencing data analysis technology. Researchers at U. C. Davis isolated total RNA from both diseased and unaffected grapevines. An Illumina Genome Analyzer was used to generate sequencing reads. Dr. Viacheslav Fofanov, Director of Bioinformatics at Eureka Genomics, then compared 5.3 million short reads from the infected vine against 2.3 million short reads from the unaffected reference plant.

Sequences unique to the diseased sample were assembled, and using the BLAST search algorithm, homologous sequences were identified by comparison of the assembled contigs to the GenBank database. These identified sequences were sorted into pathogen and parasite classes. Among the viral species identified, a mixed infection of *Grapevine rupestris stem-pitting-associated 1 virus* strains was described as containing at least two novel members.

“The resolution of this mixture of closely-related sequence reads into a collection of viral strains is groundbreaking research,” said Dr. Maher Al Rwahnih, senior research scientist on the project at U. C. Davis. “We knew viral identification was possible with long reads, but to de-convolute a viral mixture from short reads is truly remarkable. The cost effectiveness of the short read approach will completely change how novel disease agents are identified and characterized. Ultimately, this research will be of great practical benefit to the California wine industry.”

“Our powerful algorithms and advanced Next Generation Bioinformatics Service played a key role in the discovery of the new viral strains,” said Dr. Heather Koshinsky, Chief Scientific Officer at Eureka Genomics. “It allowed this very talented group of researchers to undertake otherwise time- and cost-prohibitive computations. The success of the project on Syrah Decline highlights the utility of our technology in the identification of heretofore

unknown pathogens. This technology has considerable application in human disease, agriculture, and cleantech. Emerging challenges in those areas previously thought to be economically intractable can now be managed within the Eureka Genomics pipeline, leading to approaches that will scale out to become routine procedures.”

**About Eureka Genomics Corporation.**

Partnering with companies that offer complementary services, Eureka Genomics focuses on next generation sequencing applications in concert with its proprietary Next Generation Bioinformatics Service to develop improved diagnostics, therapeutics and vaccines. Eureka Genomics is planning to open bioinformatics service centers in four countries. More information can be obtained through [www.eurekagenomics.com](http://www.eurekagenomics.com) or by contacting Didier Perez, COO, at [Didier@eurekagenomics.com](mailto:Didier@eurekagenomics.com) or by calling (415) 269 0666.