Rockefeller University Scientist Uses Bionano Saphyr to Analyze Genomes of Patients and Animals Susceptible to COVID-19

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Using Bionano data in comparative genomics analysis of patients with severe disease and animals that are susceptible to SARS-CoV-2 against patients and animals resistant to disease may reveal biomarkers for COVID-19 risk and how to treat it

SAN DIEGO, Oct. 26, 2020 (GLOBE NEWSWIRE) -- Bionano Genomics, Inc. (Nasdaq: BNGO) announced today that Dr. Erich Jarvis, a Howard Hughes Medical Institute investigator at the Rockefeller University and Chair of the Vertebrate Genome Project (VGP), is bringing his expertise in comparative genomics to the COVID-19 Host Genome SV Consortium as a co-principal investigator. The consortium, founded by Dr. Ravindra Kolhe at Augusta University, is centered around the analysis with Saphyr of structural variants (SVs) in the human genome that predispose to or protect against COVID-19. Identifying such variants in the genome can lead to the development of novel drugs, the repurposing of existing drugs for COVID-19, the development of targeted vaccines and importantly, the identification of risk markers that allow better triaging of patients who need certain treatment or early access to vaccines.

Dr. Jarvis brings to the consortium a unique and powerful approach to understanding host response genetics called comparative genomics, in which genomes of different species with and without certain traits are compared to reveal the variants responsible for the traits of interest. In the case of COVID-19 response, the genomes of animals that are believed to be sensitive to SARS-CoV-2 infection will be compared to genomes of species presumed to be immune to infection or disease. The non-human animal species that were susceptible to SARS-CoV-2 infection to be included in the study are the Chinese horseshoe bat, a natural reservoir for the virus; the Chinese pangolin, an alternative reservoir; the clouded leopard, an animal that tested positive for SARS-CoV-2 infection in the Bronx Zoo; and four domestic species that are believed to be vulnerable: the sheep, Arabian camel, horse and Chinese hamster. For the human arm of the study, the Jarvis team will analyze the genomes of ten patients who were hospitalized and/or died from COVID-19. The genomes of ten individuals who did not get sick after exposure will function as controls along with those of more than one hundred vertebrate species assembled by the VGP and presumed to be resistant to infection.

Analysis by comparative genomics requires complete genome assemblies for the species to be analyzed, and those assemblies have to be as accurate and complete as possible. The genome assembly team of the VGP has developed and optimized a pipeline utilizing long-read sequencing, Bionano optical maps, and a method called Hi-C to build reference-quality genomes.

Data generated with Bionano's Saphyr system are essential for these assemblies because Bionano data provide a level of structural accuracy required to achieve complete and accurate assemblies, as was demonstrated in a previously announced publication that showed Saphyr's contribution to the first ever telomere-to-telomere assembly of a complete human X chromosome.

Typical genome analysis studies use short-read sequencing technologies and have limits because they miss rare variants, cannot analyze parts of the genome that are absent from the reference and they suffer from incorrect alignments to structural variants and incomplete assemblies with gaps in important regions, such as complex, repetitive immune genes. Long-read sequencing data combined with structural variation data generated by Saphyr can build the high-quality genomes needed for the VGP, and provide the genome structural variation data needed to investigate the COVID-19 response across species. The comparative genomics approach to studying the various animal species and human patient genomes allows for a detailed characterization of conserved genetic elements, and may identify elements crucial to vulnerability or protection from infection. Dr. Jarvis and the VGP intend to include further focus on the ACE2 gene, which enables the virus to infect the cell, the MHC region that plays a crucial part in the immune response to the virus and analyze the rest of the genome as well. Many immune gene regions have been incompletely assembled in most draft genomes, making it impossible to do this type of comparative genomics analysis until complete reference quality genomes are available for each species. The high-quality genomes are the only available method to analyze point-mutations and structural variations together.

Erik Holmlin, PhD, CEO of Bionano Genomics added: "The SARS-CoV-2 pandemic has turned the world on its side this year, leading to a concerted global effort by researchers to better understand how to properly combat this pandemic and who is most at risk of developing severe COVID-19. We believe the most effective way to develop and steer effective treatment is to better understand the genomic basis for COVID-19 susceptibility. This belief in part prompted the creation of the COVID-19 Host Genome SV Consortium, which brought scientists and clinicians together, using Saphyr as the core technology to find the structural variants that predispose to or protect against disease. We recently announced a publication by the VGP that deemed Bionano's optical mapping technology an essential component to building complete reference-quality genomes, and we are excited to once again be a part of this innovative and globally important research effort, which could lead to better treatment and better selection of patients who need certain treatment or vaccines the most."

About Bionano Genomics

Bionano is a genome analysis company providing tools and services based on its Saphyr system to scientists and clinicians conducting genetic research and patient testing, and providing diagnostic testing for those with autism spectrum disorder (ASD) and other neurodevelopmental disabilities through its Lineagen business. Bionano's Saphyr system is a platform for ultra-sensitive and ultra-specific structural variation detection that enables researchers and clinicians to accelerate the search for new diagnostics and therapeutic targets and to streamline the study of changes in chromosomes, which is known as cytogenetics. The Saphyr system is comprised of an instrument, chip consumables, reagents and a suite of data analysis tools, and genome analysis services to provide access to data generated by the Saphyr system for researchers who prefer not to adopt the Saphyr system in their labs. Lineagen has been providing genetic testing services to families and their healthcare providers for over nine years and has performed over 65,000 tests for those with neurodevelopmental concerns. For more information, visit www.bionanogenomics.com or www.lineagen.com.

Forward-Looking Statements

This press release contains forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995. Words such as "may," "will," "expect," "plan," "anticipate," "estimate," "intend" and similar expressions (as well as other words or expressions referencing future events,

conditions or circumstances) convey uncertainty of future events or outcomes and are intended to identify these forward-looking statements. Forward-looking statements include statements regarding our intentions, beliefs, projections, outlook, analyses or current expectations concerning, among other things, the expected scope of the consortium's research, including the anticipated contribution of Dr. Jarvis and his team; the contribution of Bionano's technology to the development or repurposing of drugs, improved treatment methods or vaccines for COVID-19 and the identification of related risk markers; Bionano's expected contribution to the generation of high-quality, complete reference genomes; Saphyr's capabilities in comparison to other genome analysis technologies; and the advancement of strategic objectives by the consortium, the VGP or Bionano. Each of these forward-looking statements involves risks and uncertainties. Actual results or developments may differ materially from those projected or implied in these forward-looking statements. Factors that may cause such a difference include the risks and uncertainties associated with: the impact of the COVID-19 pandemic on our business and the global economy; general market conditions; changes in the competitive landscape and the introduction of competitive products; changes in our strategic and commercial plans; our ability to obtain sufficient financing to fund our strategic plans and commercialization efforts; the loss of key members of management and our commercial team; and the risks and uncertainties associated with our business and financial condition in general, including the risks and uncertainties described in our filings with the Securities and Exchange Commission, including, without limitation, our Annual Report on Form 10-K for the year ended December 31, 2019 and in other filings subsequently made by us with the Securities and Exchange Commission. All forward-looking statements contained in this press release speak only as of the date on which they were made and are based on management's assumptions and estimates as of such date. We do not undertake any obligation to publicly update any forward-looking statements, whether as a result of the receipt of new information, the occurrence of future events or otherwise.

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