Collaborative Study Using Medidata Rave Omics Leads to Discovery of Potential Biomarkers for Early Response to Treatment in Castleman Disease

- New research presented at the 61st Annual Meeting of the American Society of Hematology
- Medidata, a Dassault Systèmes company, is collaborating with the Castleman Disease Collaborative Network to advance personalized medicine for this life-threatening disorder
- Identifying indicators of early treatment response is essential in diseases with sudden, rapid onset

NEW YORK – Dec 9, 2019 – The first use of serum proteomics data to identify early indicators of response to treatment in a rare, hyperinflammatory, lymphoproliferative disorder (Idiopathic Multicentric Castleman disease) was presented at the 61st Annual Meeting of the American Society of Hematology. The Castleman Disease Collaborative Network (CDCN) and Medidata's Rave Omics team used machine learning to identify a protein biomarker that could be used to measure the likelihood of response soon after beginning therapy.

Idiopathic Multicentric Castleman Disease (iMCD) is a rare, difficult to diagnose, life-threatening disorder. Orphan diseases, like iMCD, are often poorly understood with limited treatment options and data for physicians to select the most appropriate therapy for patients. The CDCN advances research programs to understand the etiology of the disease, develop better diagnostic methods, identify patients who will respond to approved therapy, and find novel drug targets to develop new therapies.

"This collaborative study using Medidata Rave Omics signals a real advance in our efforts to personalize treatment for Castleman disease," said Dr. David Fajgenbaum, co-founder and executive director of the CDCN. "Early testing to predict treatment response to siltuximab (the only FDA-approved drug for iMCD) is urgently needed to inform clinicians about the likelihood of patient response to therapy, adjust treatments if needed, and identify novel therapeutic targets for siltuximab non-responders."

Earlier, more precise indicators of response to therapy are critical for timely treatment administration, especially in diseases with sudden and severe onset. This collaboration on the "Quantitative Changes in Serum Proteins Including CXCL13 Are Early Indicators of Response to Anti-IL6 Therapy in Idiopathic Multicentric Castleman Disease" revealed these key insights:

- Proteins that change significantly in responders, but remain abnormal in non-responders, warrant further investigation as potential early indicators of treatment response or as candidate therapeutic targets for drug development
- The biomarker, CXCL13, was among the proteins found to be significantly different in responders vs. non-responders. CXCL13 was recently found to be the most elevated cytokine (cell signalling protein) in iMCD flares
- Quantifying levels of CXCL13 and other serum proteins may lead to the development of a more continuous scale of response rather than traditional outcome measures, which could help fine-tune therapeutic interventions

"We are proud to be a part of this vital effort with CDCN to discover new ways to empower researchers and patients. Medidata's Rave Omics is helping to make precision medicine a reality," said Glen de Vries, co-CEO and co-founder, Medidata. "Using our machine learning algorithms to streamline the integration and analysis of translational data will help accelerate the discovery of novel biomarkers and drug targets."

Medidata's Rave Omics solution is part of the company's Acorn AI portfolio. Acorn AI combines data, technology and deep expertise to help life sciences clients deliver actionable insights across the entire continuum, from accelerating breakthrough innovation to optimizing study execution and commercial success, as well as demonstrating the value of therapies.

About Medidata

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