CureJM Grant Recipient:

Dr. Younghun Han, Baylor College of Medicine TX

Lay Summary

Juvenile dermatomyositis (JDM) is a rare autoimmune disorder that causes skin rash, muscle inflammation, and weakness affecting about four in one million children. While the cause is unknown, females are affected about twice as often as males. Although the condition is rare, rheumatologists studying the disease have been highly collaborative in conducting research projects to better understand the genetic and environmental factors that influence its development.

Through the application of genome-wide association studies "GWAS," our team has examined genetic structures to identify "comorbid" conditions. Comorbid refers to when one patient has two or more different diseases or medical conditions. We are applying a multi-trait joint analysis of these GWAS structures to provide a framework to help usher in new or repurposed drugs. An in-silico network analysis of the GWAS structures that give rise to disease-associated proteins will create a link to drugs that can target these disease-specific proteins. Our site has curated the world's largest collection of genetic results from studying participants with JDM and other myositis conditions. We will use this bank and additional data on other genetically influenced factors to expand our knowledge of the causation of JDM and how these factors may impact future treatments. In this project, the combination of multifactorial and polygenic traits associated with juvenile dermatomyositis will help provide insights and biological understanding from the JDM GWAS results.

Key People

Dr. Younghun Han

I am an Assistant Professor of the Section of Epidemiology and Population Science in the Department of Medicine and Institute for Clinical and Translational Research at the Baylor College of Medicine. I have more than 15 years of experience conducting case-control and family-based studies on various diseases in large genomic and genetic groups. My research projects have focused on identifying specific locations on genes that influence susceptibility to complex diseases such as liver cancer, lung cancer, glioma, and other rare diseases. Through the application of GWAS methods, I have extensively examined the shared genetic structures among numerous polygenic traits to identify genetic comorbid conditions using multi-trait joint analysis. I am also working with promising candidates for drug repurposing by making associations between drugs and presumed disease-associated proteins.

Impact of Cure JM Funding

The Cure JM Foundation research grant will allow my group to apply our knowledge of rare disease GWAS associations to JDM. We have vast experience in the area of genetics and rare diseases, and applying this knowledge will lead to new insights related to understanding JDM and its risk factors. We also hope to uncover potential new targets for JDM drug research and repurposing.