



an Open Access Journal by MDPI

Genomic Analysis of Common Disease

Guest Editor:

Dr. Golder N. Wilson

Department of Pediatrics, Texas
Tech University Health Sciences
Center, Lubbock, and
KinderGenome Genetics Private
Practice, 5347 W Mockingbird,
Dallas, TX 75209, USA

Deadline for manuscript
submissions:

31 July 2024

Message from the Guest Editor

The ability of NextGen or massive parallel sequencing technology to screen all genes in the human genome for mutations is changing the reductive one disease–one responsible gene paradigm to one of multifactorial causation. A combined genomic analysis of microarray and whole exome sequencing can define the respective duplication/deficiency of chromosome regions and of gene sequence alterations, the former being common in patients with intellectual disability, and the latter being common in diseases affecting older children and adults. This Special Issue will begin with a brief introduction of genomics and an article contrasting its results when applied to patients with increased joint laxity. Patients with developmental disability and joint laxity from hypotonia of surrounding muscles will have a mixture of copy number and sequence variants, and those with laxity from dysplastic connective tissue in Ehlers–Danlos syndrome will have sequence variants in a different but overlapping network of genes. Accompanying articles that describe DNA results from genomic analysis of other common conditions ranging from cardiovascular diseases to cancer will be explored as well.



mdpi.com/si/179370

Special Issue