COMPLEX GENOMIC REARRANGEMENTS AND RARE DISEASES

In the past, several Mendelian genetic diseases have been identified because the gene in question was interrupted due to a chromosomal breakpoint. Recent developments in sequencing and mapping technologies have provided several new tools for analyzing complex genomic rearrangements, which can harbor the etiology of rare diseases.
A publication by Schuy et al.[1] (Trends in Genet) specifically analyzes the relationship between rare diseases and complex genomic rearrangements (CGRs), defined as "structural variants (SV) that host more than one breakpoint junction and / or comprise structures consisting of several of a SV in cis ". CGRs "also include structural rearrangements that have at least three cytogenetically visible breakpoints." The paper lists pros and cons of different technological approaches, aimed at implementation in a clinical cytogenomics laboratory. It also critically analyzes the data available in the literature. The article appears to be a further step in the trend "from cytogenetics to cytogenomics" that A. Lindstrand, the leader of the group, undertook in 2019 (Genome Medicine[2]).

1 https://www.cell.com/trends/genetics/fulltext/S0168-9525(22)00145-7?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0168952522001457%3Fshowall%3Dtrue
2 https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-019-0675-1