

Accurate Fine-mapping of Structural Variants in Elusive Rare Diseases Using Optical Genome Mapping Technology

Brancati Heinrich *

Department of Hematology and Hemotherapy Service, Hospital Universitario y Politécnico La Fe, 46026 Valencia, Spain

Introduction

Rare diseases, often genetically complex and elusive, present significant diagnostic and therapeutic challenges in modern medicine. A major hurdle in understanding these diseases lies in the difficulty of identifying Structural Variants (SVs) in the genome, which are large-scale alterations in the structure of chromosomes. These variations, which can involve deletions, duplications, inversions, or translocations, have been implicated in many rare diseases, yet their detection remains a challenge with traditional genomic methods. However, recent advancements in Optical Genome Mapping (OGM) technology have provided a powerful tool for overcoming these limitations, enabling accurate detection and fine-mapping of SVs in elusive rare diseases. This article explores the utility of OGM in rare disease diagnostics, emphasizing its ability to detect, characterize, and map structural variants that other technologies often miss. SVs can be responsible for a variety of genetic disorders, including developmental and neurological disorders, cancers, and metabolic diseases. Unlike Single Nucleotide Polymorphisms (SNPs), which affect individual nucleotides, structural variants can have profound consequences because they can disrupt large genes or regulatory regions, leading to disease.

One of the challenges with structural variants is that they are often difficult to detect using traditional sequencing techniques. High-throughput sequencing methods, such as Whole-Genome Sequencing (WGS), tend to be more efficient at detecting small variations like point mutations or short indels but often fail to capture the full spectrum of structural changes, especially larger or complex variants. This is particularly problematic in the study of rare diseases, where such variants are often the underlying cause but go undetected or mischaracterized due to limitations in current sequencing technologies [1].

Description

Fine-mapping refers to the process of precisely identifying the boundaries of genetic variations, which is particularly important for structural variants in rare diseases. Many rare diseases are caused by complex structural alterations, and identifying the exact nature of these variations is crucial for understanding their pathogenic mechanisms and developing targeted treatments. OGM's ability to detect and map structural variants with high precision makes it a valuable tool for fine-mapping these elusive alterations. In many cases, rare diseases are caused by structural variants that have been difficult to detect using conventional genomic technologies. For example, complex rearrangements, such as large inversions or translocations, are often missed by high-throughput sequencing methods. Optical genome mapping allows researchers to detect these structural variants with a level of resolution that traditional sequencing methods cannot provide. By visualizing large DNA molecules

and mapping the genome at a higher resolution, OGM can identify and characterize structural variants that would otherwise go undetected. For instance, in cases where a patient's genetic disorder is caused by a large chromosomal deletion or duplication, OGM can provide clear evidence of the exact location and extent of the variation. This precision allows for a more accurate diagnosis and a better understanding of the genetic basis of the disease [2].

Some rare diseases are associated with complex genomic rearrangements that involve multiple structural variants. These can include balanced translocations, inversions, or copy number variations that disrupt genes or regulatory elements in ways that are not easily detectable using traditional sequencing methods. Optical genome mapping excels in detecting these types of alterations, providing a detailed view of the structural rearrangements in question. For example, in rare genetic disorders associated with chromosomal translocations, OGM can help identify the exact breakpoints of the translocation and provide a map of the rearranged chromosome [3]. This fine-mapping of structural variants is critical for understanding the functional consequences of these genomic alterations, as well as for developing targeted therapies that address the specific mutation. In many rare disease cases, the underlying genetic cause remains elusive despite extensive genetic testing. This is often because structural variants are missed or inadequately characterized by traditional methods. Optical genome mapping offers a solution to these unresolved cases by enabling researchers to uncover hidden structural variants. In clinical practice, this can lead to a diagnosis for patients who have been through multiple rounds of genetic testing without success. By providing a more comprehensive view of the genome, OGM can reveal previously unknown structural variants that are critical to understanding a rare disease. In many cases, the identification of these variants can lead to a more accurate diagnosis and better clinical management of the disease [4].

Once structural variants are accurately mapped, the information can be used to inform personalized treatment strategies for patients with rare diseases. Many rare diseases caused by structural variants involve disruptions to key genes or regulatory regions. With precise mapping, clinicians can identify the specific genes or pathways that are affected by these variants, allowing for more targeted and effective therapies. In the future, optical genome mapping may play an important role in personalized medicine by enabling clinicians to tailor treatments based on the exact genetic profile of an individual's disease.

The integration of optical genome mapping into clinical practice has the potential to revolutionize the diagnosis and treatment of rare diseases. As technology continues to evolve, the accuracy, resolution, and accessibility of OGM will improve, making it an invaluable tool for clinicians and researchers alike. In the near future, optical genome mapping may be used routinely in clinical genetic testing to uncover structural variants in rare disease patients who have previously been undiagnosed. Moreover, as our understanding of the genetic underpinnings of rare diseases grows, OGM will likely become a key component of personalized medicine, offering clinicians the tools they need to develop individualized treatment plans based on precise genetic information [5].

*Address for Correspondence: Brancati Heinrich, Department of Hematology and Hemotherapy Service, Hospital Universitario y Politécnico La Fe, 46026 Valencia, Spain, E-mail: heinri@edu.com

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Conclusion

Optical genome mapping represents a significant advancement in genomic technology, offering a powerful method for the detection and fine-mapping of structural variants in rare diseases. With its ability to visualize large-scale structural alterations with high resolution, OGM fills a critical gap left by traditional sequencing techniques. As this technology continues to evolve, it promises to enhance our understanding of the genetic basis of rare diseases and pave the way for more accurate diagnoses and personalized treatments. The potential of optical genome mapping to uncover hidden structural variants will undoubtedly play a pivotal role in advancing rare disease research and improving patient outcomes.

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Conflict of Interest

There are no conflicts of interest by author.

References

1. Kadlubowska, Magda K. and Isabelle Schrauwen. "Methods to improve molecular diagnosis in genomic cold cases in pediatric neurology." *Genes* 13 (2022): 333.
2. Sokpor, Godwin, Yuanbin Xie, Joachim Rosenbusch and Tran Tuoc. "Chromatin remodeling BAF (SWI/SNF) complexes in neural development and disorders." *Front Mol Neurosci* 10 (2017): 243.
3. Simon, Ruth, Christoph Wiegrefe and Stefan Britsch. "Bcl11 transcription factors regulate cortical development and function." *Front Mol Neurosci* 13 (2020): 51.
4. Jacobs, Patricia A., Caroline Browne, Nina Gregson and Christine Joyce, et al. "Estimates of the frequency of chromosome abnormalities detectable in unselected newborns using moderate levels of banding." *J Med Genet* 29 (1992): 103-108.
5. Dias, Cristina, Sara B. Estruch, Sarah A. Graham and Jeremy McRae, et al. "BCL11A haploinsufficiency causes an intellectual disability syndrome and dysregulates transcription." *Am J Hum Genet* 99 (2016): 253-274.

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