

Closing the diagnostic gap in rare genetic conditions

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Abstract

The diagnosis of rare genetic diseases has seen a leap in recent years thanks to technological advances in next generation sequencing. Government and private initiatives facilitate the adoption of such technologies both in clinical and research settings, which has advanced our understanding of rare genetic conditions. However, the diagnostic yield (30-60%) reflects the need for further approaches to address this diagnostic gap. Lack of diagnosis is problematic at all levels and is mainly translated into missed opportunities of coordinated care and potential therapies. Therefore, despite the promising achievements in both diagnosis methodologies and novel therapies, many patients remain undiagnosed. To address this unmet clinical need, we put together a framework that can easily be adopted in clinical and research settings to narrow the diagnostic gap. This diagnostic gap workflow is a multidisciplinary approach based on data sharing, data mining, functional work and up to date biobase. Here we explain the diagnostic gap workflow, and give an example of how it has led to improved diagnostic rate in a number of critically ill infants who remained without a diagnosis despite having had whole genome sequencing. We propose this workflow can seamlessly be implemented without the need for sophisticated infrastructure.

Biography

Lamia Mestek Boukhibar a BScHons degree in molecular genetics from King's College London (2007) and completed her DPhil in genetics at Oxford University in 2010. She has held several postdoctoral positions at University College London and Imperial College where she worked on several basic research projects addressing the genetics of healthy ageing, and the genetics of biological robustness. Lamia then moved from basic to translational research in 2016 when she joined the Great Ormond Street Institute of Child Health and Great Ormond Street Hospital. Lamia put her experience in genetics and genomics to address unmet clinical needs where she led the research side of developing a robust workflow to offer rapid whole genome sequencing for critically ill infants with a suspected rare genetic condition. She has now focused her interest in addressing yet another unmet clinical need which is the diagnostic odyssey. She has implemented simple yet effective workflow to close the diagnostic gap. She published in several peer reviewed journals and was invited to several national and international conferences and seminars.

Publications

1. Bi-allelic Variants in TKFC Encoding Triokinase/FMN Cyclase Are Associated with Cataracts and Multisystem Disease, January 2020 *The American Journal of Human Genetics* 106(2)
2. Sotos Syndrome Presenting with Neonatal Hyperinsulinaemic Hypoglycaemia, Extensive Thrombosis, and Multisystem Involvement, March 2019 *Hormon Research in Pediatrics* 92(1):1-7, DOI:10.1159/000496545
3. Making a rapid genetic diagnosis in a neonate with anuric renal failure, October 2018



[5th Annual Summit on Rare Diseases and Orphan Drugs](#) | March 18, 2021

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