EDITORIAL

Why don't we all use genomic testing?

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Genomic testing is vital for the diagnosis of many rare conditions. However, globally, there is not equity of access to such technologies. Lack of funding is a major barrier. However, Mordaunt et al. found that even when fully funded, uptake of genome sequencing for intellectual disability was less than expected [1]. They suggest that allowing mainstream clinicians to order testing may increase uptake. Strnadová et al interviewed adults with intellectual disability, and found that the informed consent process was a barrier to test uptake [2].

It is recognised that sharing genetic information within families is challenging. To have a genetic test for a condition you are at risk of, you have to first be informed of that risk. Ballard et al undertook a systematic review to identify interventions that may help increase this information sharing [3]. The review did not identify any consistently successful intervention for this persistent issue.

DNA methylation analysis is playing a role clinically in assessing variants of uncertain significance. Currently, episignature classifiers have been trained on pathogenic variants of large effect. Here, episignatures of mosaic variants and hypomorphic variants were studied [4]. Lee et al report the methylation episignature of HNRNPU variants, potentially providing a clinically useful episignature [5].

Clinical descriptions of rare conditions are key to assisting diagnosis and management. Engel et al describes a large series of individuals with BRAT1 variants [6]. They confirm 2 broad phenotypes; one with potential early lethality. There is no diagnostic facial dysmorphism. Traditionally, facial dysmorphism has played a key role in diagnosis of genetic conditions. Bannister et al demonstrated that computerised 3D facial phenotyping is superior to 2D phenotyping in this regard [7]. Vincent and Graham describe phenotypic variability in CREBBP [8]. Villavicencio Gonzalez and Dhindsa comment on the discovery of STX1A variants in a novel developmental disorder [9].

Genome sequencing has an increasing role in diagnosis of common diseases. In this issue, EMQN recommendations for diagnosis of inherited cardiac conditions are presented [10]. This suggests use of a multidisciplinary team. Genes to be included on panels for given conditions are specified. Reporting of variants should follow local practice. Pulmonary fibrosis is not typically a genetic condition. Vibert et al identified that people with Lynch syndrome, and more aggressive cancer phenotypes, have additional variants in other cancer genes [11]. Desroziers et al identified novel, biallelic variants in SFTPB, which affect splicing, in 2 adults with pulmonary fibrosis [12]. A Dutch guideline demonstrates the potential role of genotyping in irinotecan dosing [13]. These papers highlight again the role of genomics in both adult and paediatric medicine.

Will Artificial Intelligence (AI) help solve the current issues in medical genomics? Duong and Solomon identify that ChatGPT performs as well as human respondents to certain genomics questions. But they conclude it still has some way to go before being reliable enough for clinical practice.

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