EDITORIAL

Artificial intelligence – the next generation of sequencing?

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Many of us recognise that genomic testing is becoming increasingly complex. One proposed solution to this is genomics multidisciplinary team meetings (MDTs), in which clinicians and laboratory staff jointly consider evidence for variant pathogenicity. A systematic review found that this approach yields a 6–25% increase in diagnoses [1]. The MDT was found to be very effective in resolving uncertain variants and increasing the speed of genomic reporting. This MDT approach was broadly acceptable to a range of specialisms.

Some clinical presentations, such as epilepsy or intellectual disability, are well accepted indications for exome or genome testing. Other clinical presentations are less well studied. Meng et al. identify severe childhood speech disorders as another indication for exome or genome testing [2]. A discrete choice experiment indicated high potential test uptake from the Australian public for this indication.

It has long been recognised that sharing genetic information within families is challenging. Nääs et al. report a qualitative study of people with cancer gene variants perceptions and practices of informing relatives [3]. Patients in the trial reported variable practice in contacting relatives – for example some only informed close relatives while others discussed their test results with multiple distant relatives. Some perceived it as their duty to inform their relatives while others felt that a direct approach from clinicians was more appropriate. These findings have implications for clinical practice.

As ever, in this month's EJHG, we present a range of papers updating and expanding phenotypes of rare conditions. Veyt et al. report a new series of NROB1 (DAX1) in which duplications were detected prenatally in phenotypically normal males [4]. There was an association with male reduced fertility in a single individual. Hoogenboom et al. report a person with a PUF60 pathogenic variant who manifested a DNA methylation profile more in keeping with Cornelia de Lange syndrome [5]. Dong et al. report an association of GJA8 gene variants with familial acorea–microphthalmia–cataract syndrome [6]. This is the first gene established as a potential cause of acorea (absent pupil). Cascajo-Almenara et al. report a potential benefit from coenzyme Q10 treatment in people with neurological disease associated with GEMIN5 variants [7]. Of course a genomics diagnosis does not always bring complete certainty. Raspa et al. report a qualitative interview study of parents of children diagnosed with severe combined immunodeficiency [8]. Parents reported multiple types of uncertainty post-diagnosis. Such as uncertainty of survival of the patient or what treatment option would be best.

Machine learning and artificial intelligence – and their potential to improve healthcare – are hot topics at present. Caniza et al. present LanDis [9]. This is a freely available resource that allows exploration of the interactome in relationship to heritable diseases. Duong and Solomon explore the ability of a large-language model to answer genetics questions (compared to a human) [10]. When answering 85 multiple choice questions, ChatGPT did not perform any differently to a human respondent. A statistical analysis of the EUROCAT congenital anomalies databases identified six potential new associations (anomalies occurring in a pair), the aetiology of which warrants further investigations [11].

How does the media portray genetic testing in imagery? Horton et al. analysed stock images relating to genetic – almost all focussed on technical aspects and only one alluded to communication of results [12]. The authors conclude this may contribute to the public thinking that genetic testing can be more informative and definitive than it usually is.

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