EDITORIAL

# What's new in genetics in June 2022?



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In recent years there have been tremendous advances in genomic technologies, with resultant increases in the utilisation of these in Clinical Genetic practice. Despite this, there is no uniform, international pattern of genetic healthcare provision—in some countries there are formal training programmes for Physicians in Clinical (Medical) Genetics and for the training of Genetic Counsellors. This has clear potential to limit the access to Clinical Genetic testing and the benefits for patients and families. To help standardise training, an ad hoc committee of the European Society of Human Genetics has documented proposed training standards for relevant professionals and for all European Union member states to recognise the various types of genetic health professionals [1].

Equity of access to genetic tests and genetic healthcare advice has long been recognised as problematic. Best et al. report a systematic review to identify factors which reduce access to clinical genetics services, depending upon geographical location [2]. Such factors include service model designs, logistical issues and workforce capacity. Possible strategies to improve things could include better use of 'virtual' clinics and increased workforce capacity.

This month we present a series of papers characterising novel disease genes or unusual presentations of known genes. Rofes et al. revisit the phenotypic effects of mosaic *PTEN* variants; with a report of a patient who presented with a phenotype resembling Peutz–Jeghers syndrome [3]. Zhou et al. describe bi-allelic variants in *TCTE1* as a cause of male infertility [4]. Despite only reporting a single case, the clear overlaps between the patient and a *TCTE1* null mouse support the clinical relevance of the genetic variant. Kang et al describe an adult with an atypical presentation of Alexander disease; and provide evidence for pathogenicity of in frame deletions affecting *GFAP* [5]. We rarely accept case reports in the *European Journal of Human Genetics*; we require a high degree of novelty or extensive functional work to add to our understanding of phenotypes and variant interpretation.

Given the sheer scale of human genome variation, identifying causal variants is challenging. Identifying novel genes in undiagnosed patients ('gene hunting') is the core mission of many geneticists. Protasova presents a novel method to identify variants in biologically relevant genes, by using analysis of spatial and temporal expression of paralogs [6]. They present the use of this method to identify novel genes in childhood ataxia. Over 5% of our genome is composed of segmental duplications. These predispose to chromosome rearrangements and are difficult to map with whole-genome sequencing. Nicolle et al report the use of optical genome mapping to overcome this and define 16p13.11 triplication syndrome [7]. Once variants are identified, functional studies are often needed to confirm pathogenicity. In Boring-Opitz syndrome, DNA methylation studies on peripheral blood are reported as aiding classification of relevant genetic variants [8]. Classically, Clinical Geneticists make diagnoses by recognising facial dysmorphology. The work of Rouxel et al. shows that computerised analysis of facial images can distinguish between 2 genotypes of Kabuki syndrome [9]. Could this be yet another tool to distinguish pathogenic from non-pathogenic variants?

Non-invasive prenatal testing for genomic conditions is a contentious issue. Perrot and Horn review the literature to describe how reproductive autonomy is understood and implemented in different European countries [10]. Garcia et al describe a study showing that women do not view utilisation of non-invasive prenatal testing as an obligation of responsible motherhood - one reason being that foetal anomaly scans can provide information on actionable anomalies [11]. In keeping with this, a Dutch study reports that women do not, in the majority of cases, feel pressured into using non-invasive prenatal testing [12]. An expert comment on these issues is also provided by Ruth Horn [13].

Genomics also aids our understanding of health and disease at the population level. Khan et al characterise migration patterns in the Kho population; identifying possible regions of positive genomic selection [14]. Laville presents a novel method for quantifying gene-lifestyle interactions in human diseases [15]. Mendelian randomisation has emerged as a powerful technique—de Leeuw provides a helpful review of the field [16].

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AMcN conceived and wrote this editorial.

## COMPETING INTERESTS

The author declares no competing interests.

## ADDITIONAL INFORMATION

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