EDITORIAL

Genomic medicine goes mainstream

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I believe that we will look back upon 2015 as the year when whole-genome sequencing (WGS) went mainstream, and the concept of genomic medicine started to move into broad practical application. Each human genome is a blueprint, sculpted by millennia of natural selection, and individualised through meiosis. Its decoding will enable formulated health-related decisions that will become an increasing part of our daily existence.

npj Genomic Medicine is a new international, peer-reviewed journal dedicated to publishing the most important scientific advances in genomics as applied to the practice of medicine. As its inaugural editor, my working definition of genomic medicine is as follows: diagnosis, prediction, prognosis, prevention and/or treatment of disease and disorders of the mind and body, using approaches informed or enabled by knowledge of the genome and the molecules it encodes.1 Our goal is to publish outstanding papers that describe genome-related studies of individuals, families or populations in a medical context. We will emphasise the coupling of detailed phenotype and genome sequence, genotypic, or mutational information in delineating the underlying aetiology of disease.

The journal will also welcome detailed case or family reports where n = 1. I can see a time in the near future where such studies of individuals carrying presumed highly penetrant mutations but who are ‘resilient’ for that particular disorder will rival the number of papers describing patients who do succumb to their genetic liability. We will also encourage sharing of ideas, as well as recommendations and/or guidelines of how such data should be used in the clinical management of study subjects and others.

Crystal gazing, based on my own experiences and those of our distinguished Associate Editors, I foresee that in the journal’s first few years, the most impactful areas we hope to publish on will include the following (a few recent studies from the editorial group’s own work are cited for reference): (1) WGS in clinical diagnosis and prognosis;2–7 (2) WGS applied to non-invasive prenatal diagnosis;8,9 (3) WGS characterisation of the ~99% of the genome not readily captured through less comprehensive technologies;10,11 (4) discovery of new regulatory variants related to risk of disease;12–13 (5) new approaches including computational algorithms, population genetics and/or functional experimentation for interpreting data;14–20 (6) databases to allow universal access of massive genomic data sets for research;21 and (7) all of the above integrated and interfaced with ‘smart phone’ technology and other ‘big data’ innovation, which is part of our inevitable future.

As genomic information may inform on past, present and future outcomes of a personal and sensitive nature, it warrants handling, stored, shared and analysed is evolving, falling into the realm of what is now called ‘big science’, something the journal will also cover.

The impact of genomics is now ubiquitous in health research, both basic and clinical, and must be supported by impactful worldwide journal representation. We will wholeheartedly strive to have as many members from as many different countries and backgrounds involved in the different aspects of journal. Diversity drives our genetic history and we believe it is also crucial to the journal’s success. In fact, in agreeing to accept the role of editor, one of my main motivations was to try to use genomic medicine as the medium26 to deliver the message of science to continue to build a global village striving for the optimal health of all of its inhabitants.

COMPETING INTERESTS

The authors declare no conflict of interest.

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REFERENCES

1. Buchanan, J. A. et al. The cycle of genome-directed medicine. Genome Med. 1, 16 (2009).
2. Bell, C. J. et al. Carrier testing for severe childhood recessive diseases by next-generation sequencing. Sci. Transl. Med. 3, 65ra4 (2011).
3. Saunders, C. J. et al. Rapid whole-genome sequencing for genetic disease diagnosis in neonatal intensive care units. Sci. Transl. Med. 4, 154ra135 (2012).
4. Jiang, Y. H. et al. Detection of clinically relevant genetic variants in autism spectrum disorder by whole-genome sequencing. Am. J. Hum. Genet. 93, 249–263 (2013).
5. Chan, K. C. et al. Cancer genome scanning in plasma: detection of tumor-associated copy number aberrations, single-nucleotide variants, and tumor heterogeneity by massively parallel sequencing. Clin. Chem. 59, 211–224 (2013).
6. Yuen, R. K. et al. Whole-genome sequencing of quartet families with autism spectrum disorder. Nat. Med. 21, 185–191 (2015).
7. Miller, N. A. et al. A 26-hour system of highly sensitive whole genome sequencing for emergency management of genetic diseases. Genome Med. 7, 100 (2015).
8. Lo, Y. M. D. et al. Maternal plasma DNA sequencing reveals the genome-wide genetic and mutational profile of the fetus. Sci. Transl. Med. 2, 61ra91 (2010).
9. Chiu, R. W. K. et al. Non-invasive prenatal assessment of trisomy 21 by multiplexed maternal plasma DNA sequencing: large scale validity study. BMJ 342, c7401 (2011).
10. Makrythanasis, P. & Antonarakis, S. E. Pathogenic variants in non-protein-coding sequences. Clin. Genet. 84, 422–428 (2013).
11. Xiong, H. et al. RNA splicing. The human splicing code reveals new insights into the genetic determinants of disease. Science 347, 1254806 (2015).
12. Gutierrez-Arcelus, M et al. Tissue-specific effects of genetic and epigenetic variation on gene regulation and splicing. PLoS Genet. 11, e1004958 (2015).
13. Iskow, R. C. et al. Regulatory element copy number differences shape primate expression profiles. Proc. Natl. Acad. Sci. USA 109, 12656–12661 (2012).
14. Pinto, D et al. Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants. Nat. Biotechnol. 29, 512–520 (2011).
15. Ju, Y. S. et al. Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. Nat. Genet. 43, 745–752 (2011).
16. Letourneau, A et al. Domains of genome-wide gene expression dysregulation in Down’s syndrome. Nature 508, 345–350 (2014).
17. Popadin, K. Y. et al. Gene age predicts the strength of purifying selection acting on gene expression variation in humans. Am. J. Hum. Genet. 95, 660–674 (2014).
18. Uddin, M et al. Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. Nat. Genet. 46, 742–747 (2014).
19. Naseer, M. I. et al. Genome wide analysis of novel copy number variations duplications/deletions of different epileptic patients in Saudi Arabia. BMC Genomics 16(Suppl 1): S10 (2015).
20. Ngeow, J & Eng, C. New genetic and genomic approaches after the genome-wide association study era-back to the future. Gastroenterology 149, 1138–1141 (2015).
21. MacDonald, J. R., Ziman, R, Yuen, R. K., Feuk, L & Scherer, S. W. The database of genomic variants: a curated collection of structural variation in the human genome. Nucleic Acids Res. 42, D986–D992 (2014).
22. Tan, M. H et al. Lifetime cancer risks in individuals with germline PTEN mutations. Clin. Cancer Res. 18, 400–407 (2012).
23. Ali-Khan, S. E., Daar, A. S., Shuman, C, Ray, P. N. & Scherer, S. W. Whole genome scanning: resolving clinical diagnosis and management amidst complex data. Pediatr. Res. 66, 357–363 (2009).
24. Abu-Elmagd, M. et al. Individualized medicine enabled by genomics in Saudi Arabia. BMC Med. Genomics 8(Suppl 1): S3 (2015).
25. Willig, L. K. et al. Whole-genome sequencing for identification of Mendelian disorders in critically ill infants: a retrospective analysis of diagnostic and clinical findings. Lancet Respir. Med. 3, 377–387 (2015).
26. Scherer, S. W. Genomics is the medium for 21st century biology. Genome 55, v (2012).