

common genetic diseases, such as cardiomyopathy and congenital deafness. In cancer testing, gene panels are being widely adopted to perform detailed tumor profiling. Each tumor has a unique set of somatic mutations, and these assays aim to detect as many treatable or prognostic mutations as possible to offer individually tailored patient care. Currently available panels vary widely in size, from a few dozen genes up to nearly a thousand. For cancer, targeted testing allows for high-depth sequencing at low cost, helpful for detecting clinically relevant mutations present at low allelic percentage due to tumor or sample heterogeneity.

- **Whole exome sequencing (WES).** Exome sequencing is really just a type of targeted sequencing. It uses hundreds of thousands of custom probes to pull out the roughly 1.5% of the genome that consists of protein-encoding exons. At a time when whole genome sequencing is still costly, WES enables a broad survey for protein coding mutations (which are responsible for as much as 80% of Mendelian disease) at significantly reduced cost. This has led to some wonderful success stories, allowing physicians to deliver answers and even therapies for children with orphan diseases who had suffered through prolonged and unsuccessful diagnostic odysseys. WES is also used in oncology to perform a very broad analysis, mostly in the research setting but also in some clinical laboratories.
- **Whole genome sequencing (WGS).** Whole genome sequencing is the most comprehensive type of DNA analysis that can be performed on an individual. However, current costs and informatic challenges still preclude its routine use in clinical practice. Indications for use in medical genetics are mostly limited to cases where exome sequencing has failed to provide an answer but the clinical suspicion of genetic disease remains high. For cancer applications, WGS is the only NGS application that can detect novel structural rearrangements (e.g., insertions, deletions, translocations) that may be clinically relevant. Because of associated costs, WGS is generally performed to lower sequencing depth than either targeted panels or exomes, and may suffer from a lack of statistical power to detect low percentage mutations in heterogeneous tumor samples.

The choice of approach is mainly a function of sequencing cost and interpretive workload. Interpreting NGS clinical assays can be laborious, with considerable effort required to research the potential relevance of novel, suspicious variants. These interpretive challenges should lessen over time with improvements to variant databases.

Future Applications

Because NGS can be used to detect genetic anomalies of essentially any size scale, from SNPs to very large rearrangements and even aneuploidy, almost all of today's genetic diagnostic tests could in principle be supplanted by NGS. This includes RNA analysis, because NGS-based analysis of the transcriptome (RNA-seq) is straightforward. As costs continue to drop, it is reasonable to expect NGS to occupy an increasingly prominent place in the diagnostics lab. Additionally, NGS holds promise for application into novel areas, including microbiome analysis and blood screening for early markers of diseases,

including cancer. Continuing technologic advances may even extend the applications further. Already third generation (or "single molecule" or "next next generation") technologies are emerging that can rapidly sequence single molecules in parallel without the need for focal amplification, and these could soon have an impact in the clinical laboratory.

Acknowledgment

The assistance of Jeremy Segal, MD PhD, Assistant Director, Division of Genomic and Molecular Pathology, University of Chicago in the revision of the section on molecular diagnosis is greatly appreciated.

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