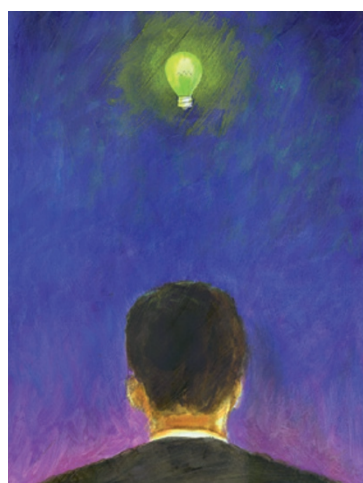


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This issue of *Nature Reviews Microbiology* is a Focus issue on Next-Generation Sequencing. For a Focus issue, it is obviously good to pick a ‘hot topic’, but from the perspective of presenting a collection of articles on a specific theme, it is also good if that theme is of interest to readers from different research areas. Next-generation sequencing certainly fits the bill. No collection of articles on this topic would be complete without an overview of the technologies themselves, and indeed, many such overviews have already been published. Here, we present something a little different in the Progress article from Mark Pallen, Nick Loman and colleagues. The authors not only provide a snapshot of the high-throughput sequencing platforms that are currently available, but also cover the whole process, from sample preparation to data analysis and storage, including a sobering assessment of the add-on costs of setting up a sequencing facility for microbial applications. With the technology introduced, the Review articles then look at three very different applications. Jeff Gordon and colleagues present one of the first comprehensive overviews of the virome (the phage populations associated with the microbiota in the human gut), discussing the insights into phage diversity that have been facilitated by next-generation sequencing and, in an interesting twist, setting these insights in the context of the potential for revitalizing phage therapy. Jörg Vogel and colleagues then take us into the realms of a gedankenexperiment — a hypothetical or thought experiment — with their assessment of how close we are to being able to carry out dual RNA-seq (that is, being able to analyse gene expression changes in a pathogen and its host simultaneously); in their view, such experiments are now technically feasible and will become the gold standard for host–pathogen transcriptomics in the future. Over the past decade, single-cell whole-genome sequencing has steadily been gaining acceptance, and some of the most recent applications of this exciting technology are reviewed by Roger Lasken. Last, one of the most high-profile applications of next-generation sequencing has been in the analysis of the human microbiome. One of the main conclusions of the analysis conducted by the Meta-HIT consortium was the stratification of the microbiota into three distinct enterotypes. In a Comment article, Paul O’Toole and colleagues look at this stratification and assess how it has held up to closer scrutiny. These articles represent just a few examples of the ways in which next-generation sequencing is changing the face of microbiology as we know it. We hope you enjoy the issue — let us know what you think on Twitter: [@NatureRevMicro](https://twitter.com/NatureRevMicro).