

Presentation title: Technologies: classical and next-gen approaches

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Abstract

For most of the 35 years since its invention, the dye-terminator or Sanger method has been the dominant approach for DNA sequencing, and current capillary electrophoresis platforms using this technique are still considered the gold standard in terms of both read length and sequencing accuracy.

The commercial launch of the first massively parallel pyro-sequencing platform in 2005 ushered in the new era of high throughput genomic analysis now referred to as next-generation sequencing (NGS). Several NGS technologies are now available, generating four to five orders of magnitude more sequence at several thousand fold reduction in cost per base than the best Sanger methods. These platforms are currently being utilised for everything from re-sequencing of candidate genes or entire genomes to expression profiling and endless applications in-between.

In the relatively short time frame since 2005, NGS has fundamentally altered genomics research and allowed investigators to conduct experiments that were previously not technically or financially viable. The various technologies that constitute this new paradigm continue to evolve as well as further improvements in technology robustness and process streamlining enabling high-quality genomic data to be generated routinely in short timeframes.

This presentation will describe fundamental principles and technologies behind Sanger and next-generation sequencing. The different sequencing chemistries and engineering configurations will be outlined as well as the advantages and disadvantages of different applications on each commercially available NGS platform.