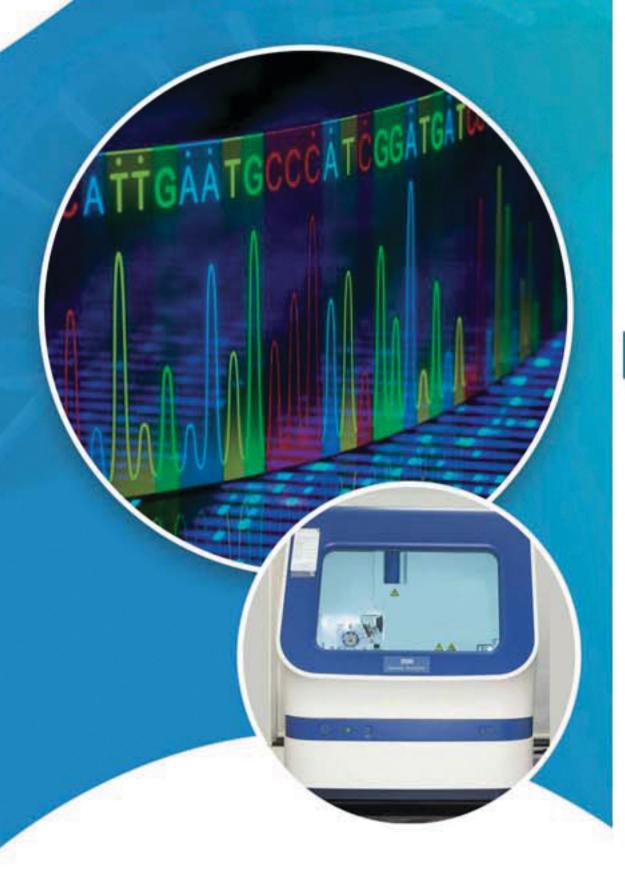


SANGER SEQUENCING





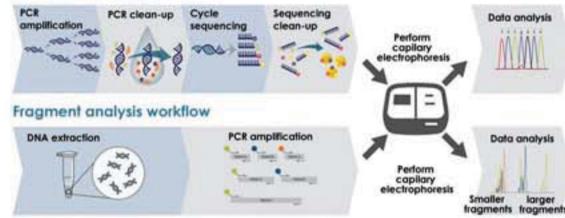


Greenarray Sanger sequencing services provide high-quality results, industry-leading customer service at competitive prices with fast turnaround time. We are well-equipped to handle DNA sequencing from different sample types. Our mission is to eliminate bottlenecks, improve productivity, advance your research progress and accuracy in diagnostics.

SANGER SEQUENCING

Greenarray accepts a variety of different templates to use as starting material for Sanger sequencing reactions.

Sanger sequencing workflow



- Gold standard for detecting repeat sequences, copy number variation and single nucleotide changes.
- · Cheap, fast, easy workflow
- Get longer read length (up to 1,200bp)
- Data analysis is easy & quick.

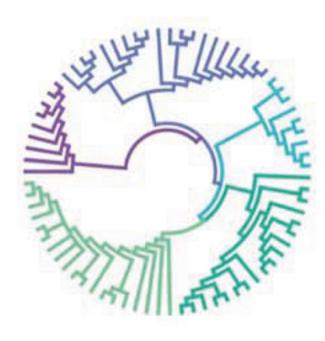






Ribosomal RNA (rRNA) gene sequence of bacteria is one of the most reliable molecular methods of microbial identification. Greenarray offers this sequencing service for identifying bacterial and archaeal species with the help of universal 16S rRNA primers.

18S rRNA gene sequencing



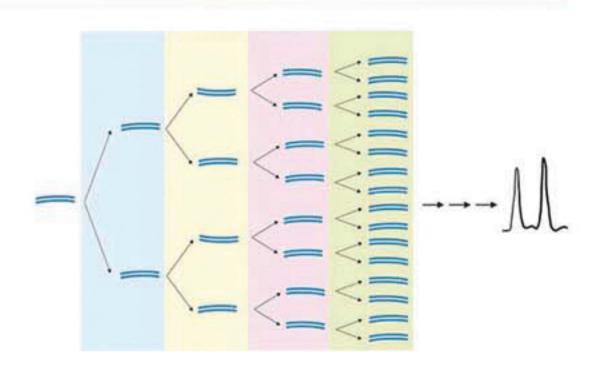
18S rRNA gene has conserved and variable regions and widely used in molecular analysis to reconstruct the evolutionary history of organisms, especially in vertebrates, as its slow evolutionary rate makes it suitable for phylogenetic studies.







Quantitative fluorescent polymerase chain reaction (QF-PCR)



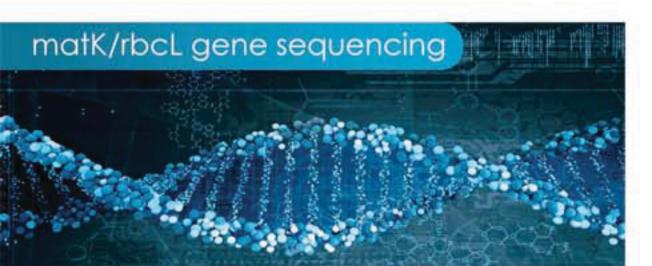
Quantitative fluorescent polymerase chain reaction (QF-PCR) provides a targeted and rapid diagnosis of chromosomal abnormalities. It has the advantages over the cytogenetics of being faster with the results appearing within 24-48 hours.





The nuclear ribosomal internal transcribed spacer (ITS) region is the most commonly chosen genetic marker for the molecular identification of fungi in environmental sequencing and molecular ecology studies.

Fungal ITS Sequencing



rbcL and matK are the core chloroplast genes of plant species. rbcL genes are used for phylogenetic analysis within family and subclass of angiosperm. matK is a single-copy and one of the fastest evolving genes used for systematic and evolutionary studies of plants.

COI gene sequencing

The most broadly used barcode marker for animal identification is mitochondrial cytochrome c oxidase subunit I (COI), which is highly conserved across species employing oxidative phosphorylation for metabolism. COI-based DNA barcoding can delimit diverse animal species, indicating the high rates of sequence change at species level and constraints on intraspecific divergence in COI sequence (a 658-bp region of COI gene).





Targeted gene sequencing are useful tools for analysing specific mutations in the gene of interest. Identifying heterozygous base positions or small insertions or deletions in genomic DNA is often employed to locate mutations or polymorphisms in diploid organisms.

Targeted gene sequencing may contain set of genes or single gene regions that have known or suspected associations with the disease or phenotype under study.

Fragment Analysis (Microsatellite)

Microsatellite markers are co-dominant, polymorphic DNA loci containing repeated nucleotide sequences, typically with 2 to 10 nucleotides per repeated unit.

The number of nucleotides in the repeated unit is the same for the majority of the repeats within an individual microsatellite locus, but the number of repeats for a specific locus may differ, resulting in alleles of varying length, which can be analysed with fragment analysis by capillary electrophoresis.

About Greenarray

Greenarray is a molecular diagnostic laboratory. We offer diagnosis of infectious diseases, genetic testing and healthcare information to improve health and wellness. Our goal is to provide high quality affordable and accessible services.



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