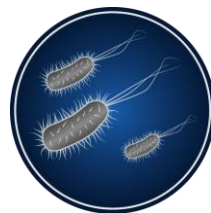


Evaluation, Validation and Implementation of Alternative and Rapid Microbiological Methods

Genetic-based Technologies

Michael J. Miller, Ph.D.



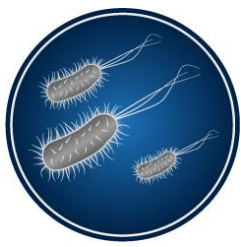
MICROBIOLOGY
CONSULTANTS, LLC



Genetic-based Technologies

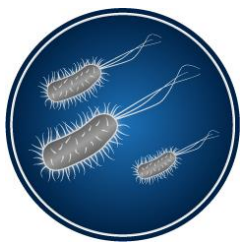
- Are now recognized as providing superior results when compared with other classical microbiology methods
- Detection of specific microorganisms
- Microbial identification
- Strain differentiation
- Estimation of viable cell count





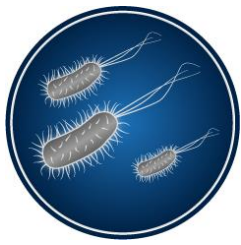
Genetic-based Technologies

- Regulatory agencies and the compendia have acknowledged the strength in these technologies
 - The FDA aseptic processing guidance recommends the use of rapid genotypic methods for microbial ID and investigations into failures (e.g., sterility test; media fill contamination)
 - Ph. Eur. and JP recommend PCR for mycoplasma
 - JP has a chapter on using DNA sequencing for microbial ID
 - The Australian Therapeutic Goods Administration (TGA) requires that a sensitive method of microbial identification, such as molecular typing techniques using RNA/DNA homology, is utilized when the identification of an isolate is used to invalidate a sterility test



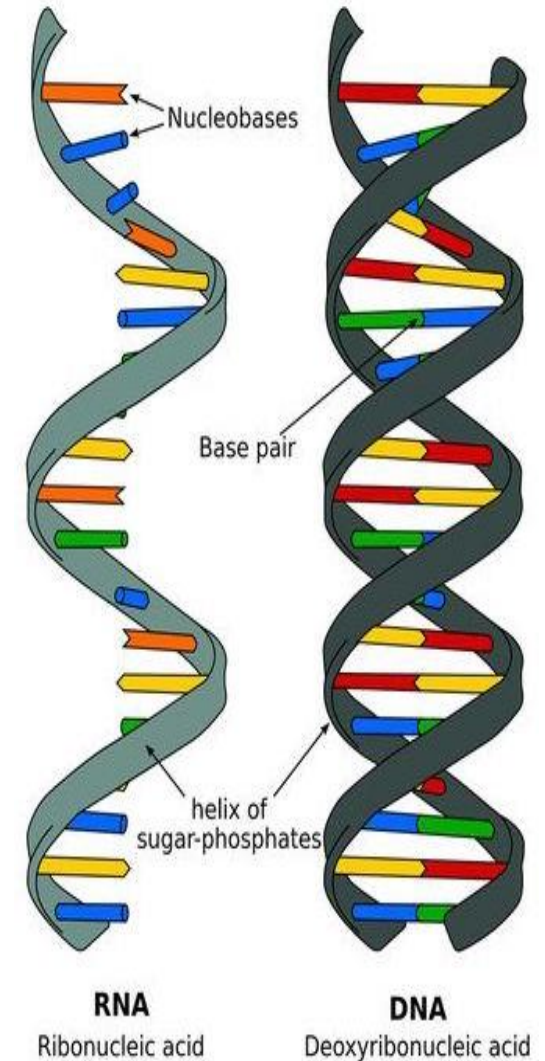
Scientific Principles

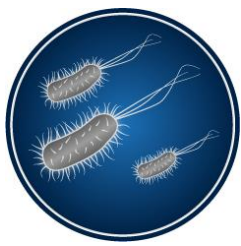
- Amplification and detection of target DNA or RNA sequences using polymerase chain reaction (PCR)
 - Quantitative (q) PCR (quantitate the PCR amplicons)
 - Reverse transcriptase (RT) PCR
 - Transcription Mediated Amplification (TMA) and Nucleic Acid Sequence Based Amplification (NASBA)
- Fragmentation of DNA sequences that encode for the rRNA operon (Ribotyping)
- Gene sequencing
- Applications include the detection of specific organisms in a sample, the identification of a microbial isolate, and an estimation of viable cell count



Review: DNA and RNA

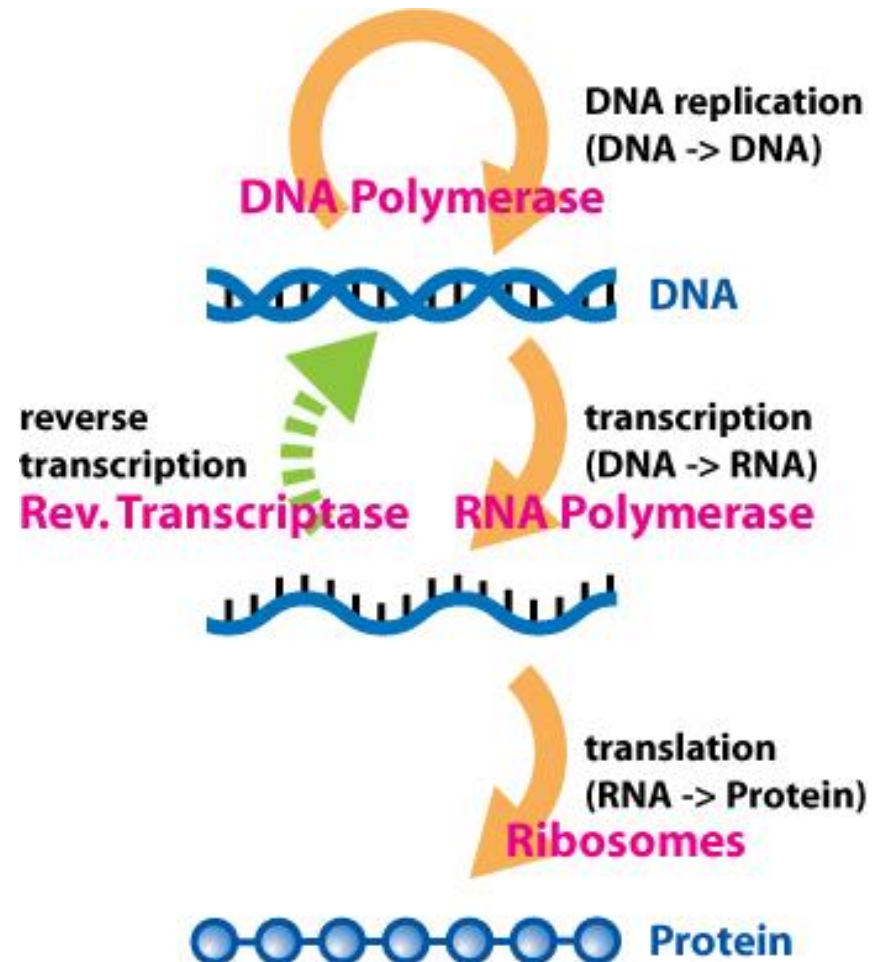
	Deoxyribonucleic acid DNA	Ribonucleic acid RNA
Function	Genetic information storage	Converts DNA genetic information into proteins mRNA, tRNA and rRNA
Configuration	Double Stranded	Single Stranded
# Copies	1 - few	1000's of rRNA
Sugar	Deoxyribose	Ribose
Bases	Adenine, Guanine, Cytosine, Thymine	Adenine, Guanine, Cytosine, Uracil





Review: DNA and RNA

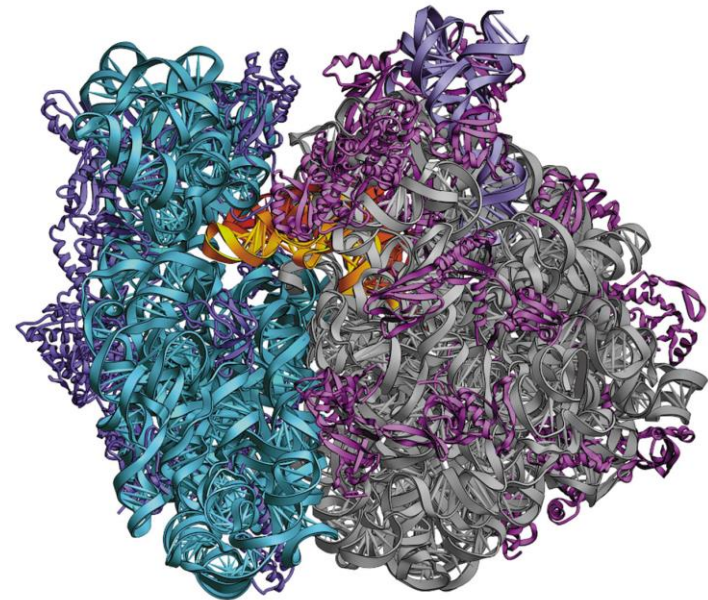
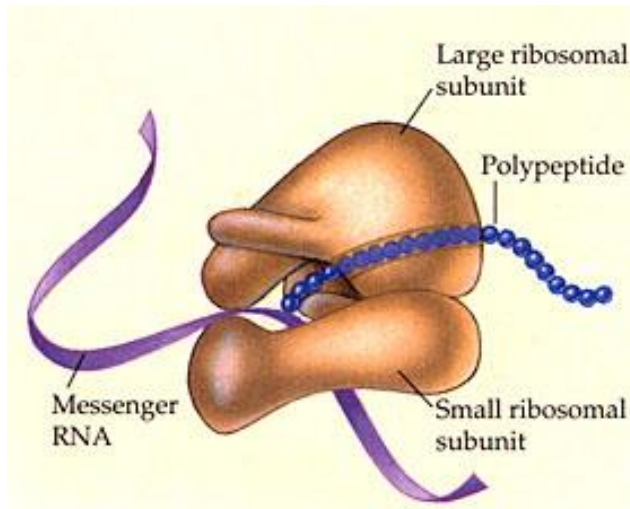
- DNA can replicate to form new DNA during cell division
- RNA is transcribed from DNA
- RNA is translated into proteins within ribosomes





Review: Ribosomes

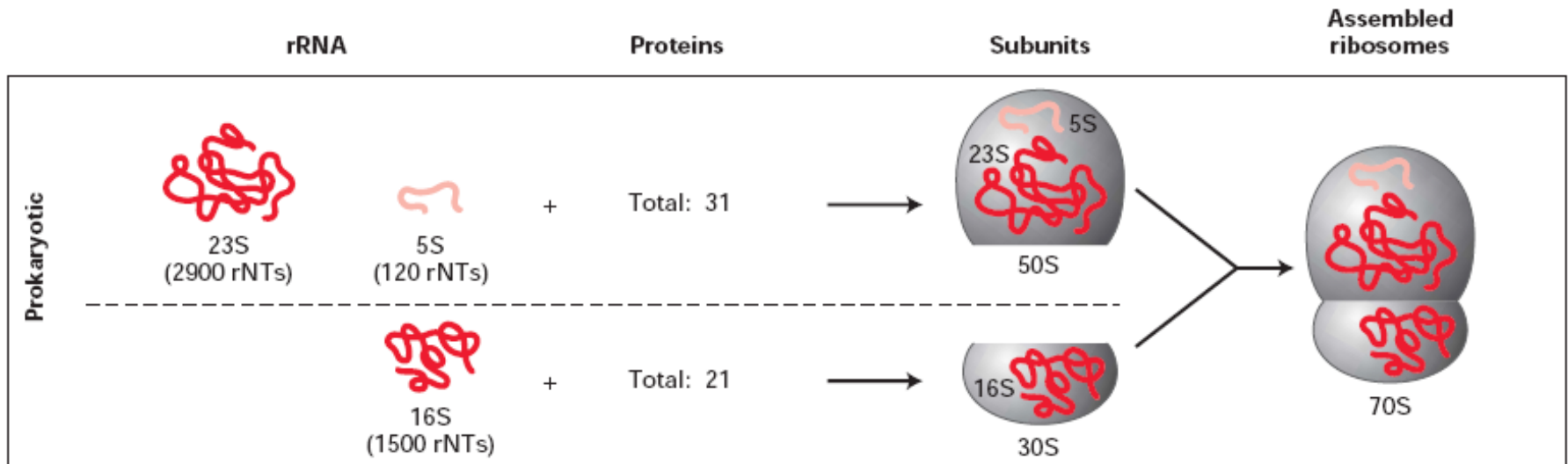
- Ribosome structure and ribosomal RNA (rRNA)
 - DNA sequences encode for rRNA





Review: Ribosomes

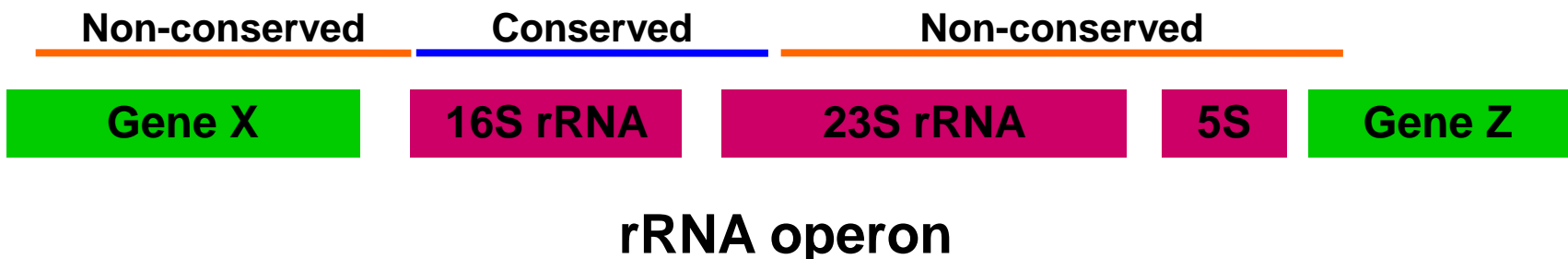
- Ribosome subunits and rRNA

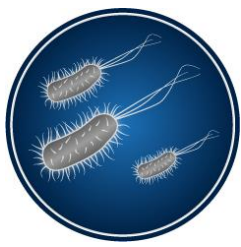




Review: rRNA

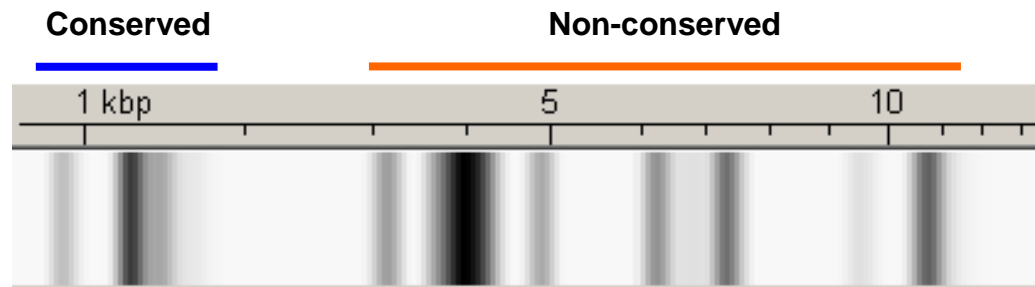
- rRNA fragments are highly conserved at the genus and species level (16S sequence)
 - Correct RNA structure is critical for ribosome function
 - Bergey's Manual of Systemic Bacteriology now uses 16S rDNA sequences as the standard for taxonomic classification of bacteria
- Non-conserved fragments (spacer and flanking regions of the 16S sequence) can be used to differentiate strains within a particular species

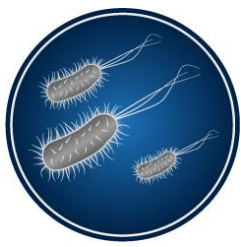




16S rRNA Ribotyping

- Bacterial DNA is extracted from a cell and cut into fragments
- The fragments are hybridized with a DNA probe (derived from 16S rRNA operon and spacer/flanking regions)
- The probe has a detection marker (e.g., luminescent)
- The fragments can be viewed as banding patterns and compared with an identification database

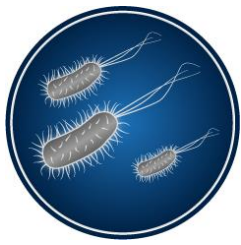




Hygiene RiboPrinter

- Automated ribotyping system for microbial identification and strain tracking (original developed by Dupont Qualicon)

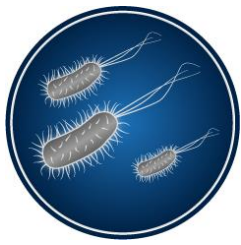




Hygiene RiboPrinter

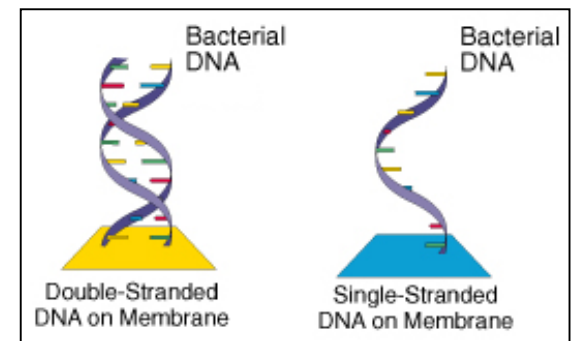
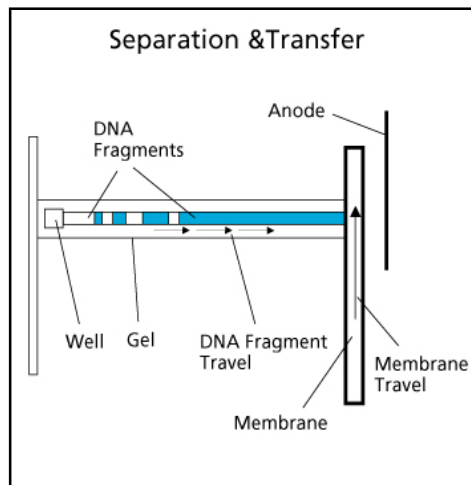
- Dilute pure colony sample in buffer
- Pre-process samples: heat inactivation/add lysing agent
- DNA is extracted and cut into fragments by a restriction enzyme (e.g., EcoRI, PvuII)

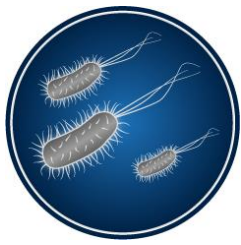




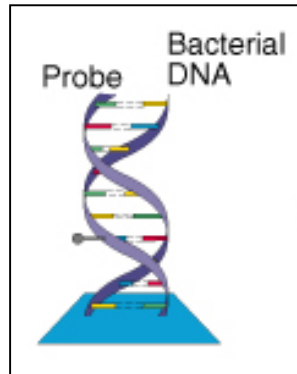
Hygiene RiboPrinter

- Fragments are separated according to size by gel electrophoresis, transferred and immobilized on a moving nylon membrane (automated Southern blot)
- The immobilized double-stranded DNA is denatured to single-stranded DNA

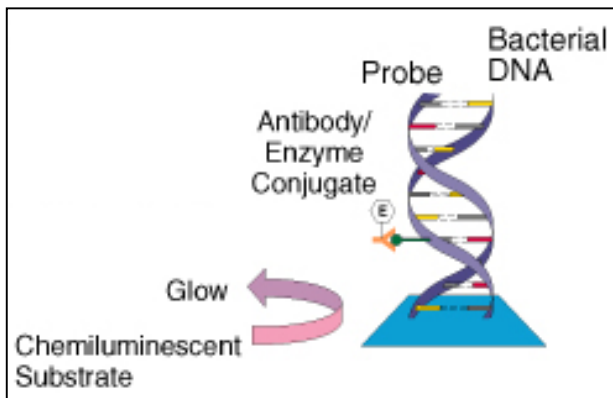




Hygiene RiboPrinter



The membrane is hybridized with the DNA probe (derived from *E. coli* rRNA operon; contains sequences encoding for 16S rRNA, 23S rRNA, 5S rRNA, and spacer region including Glu-tRNA)



An antibody-enzyme conjugate is bound to the probe and a chemiluminescent agent is added



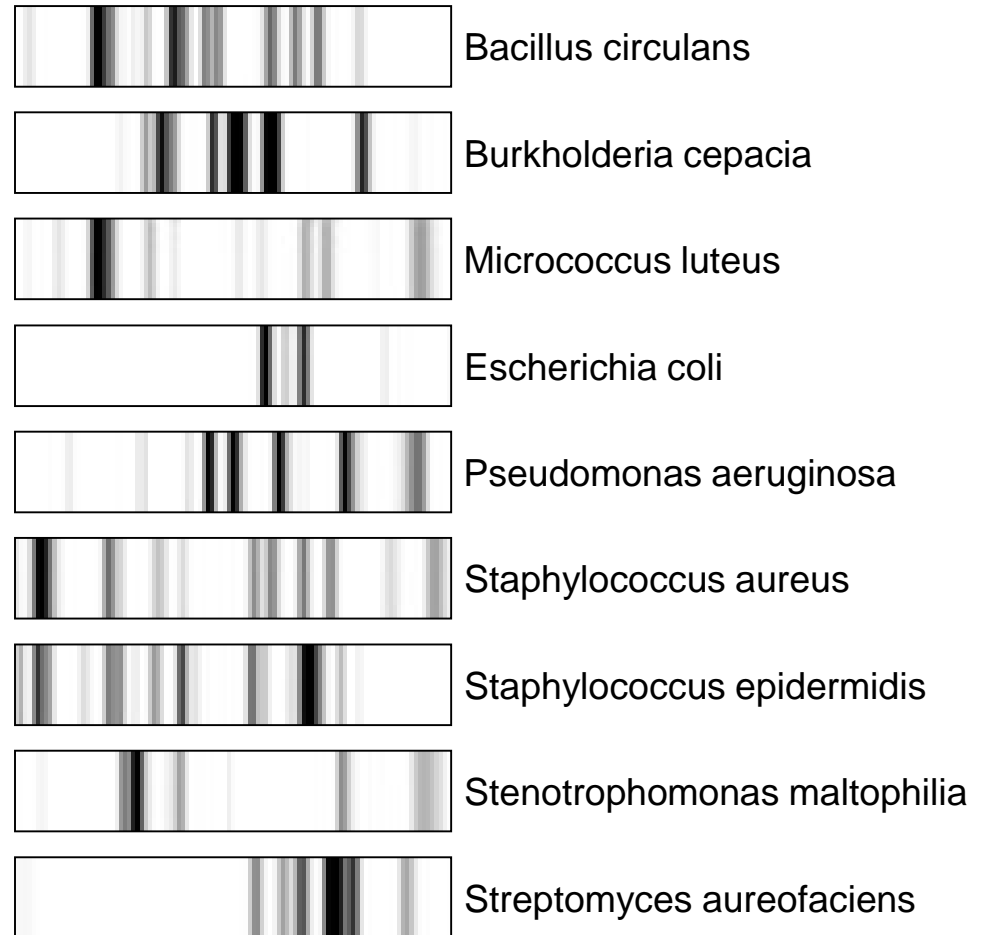
Hygiena RiboPrinter

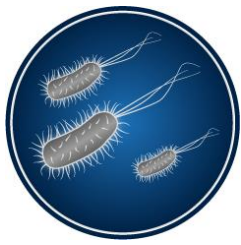
- Light emitted by the fragments are captured by a digitizing camera and stored as image data in the computer
- The software creates the RiboPrint pattern, which is then compared with patterns stored in the system database and the bacterium is identified
- System is fully automated; up to 32 ID' s per 24 hours



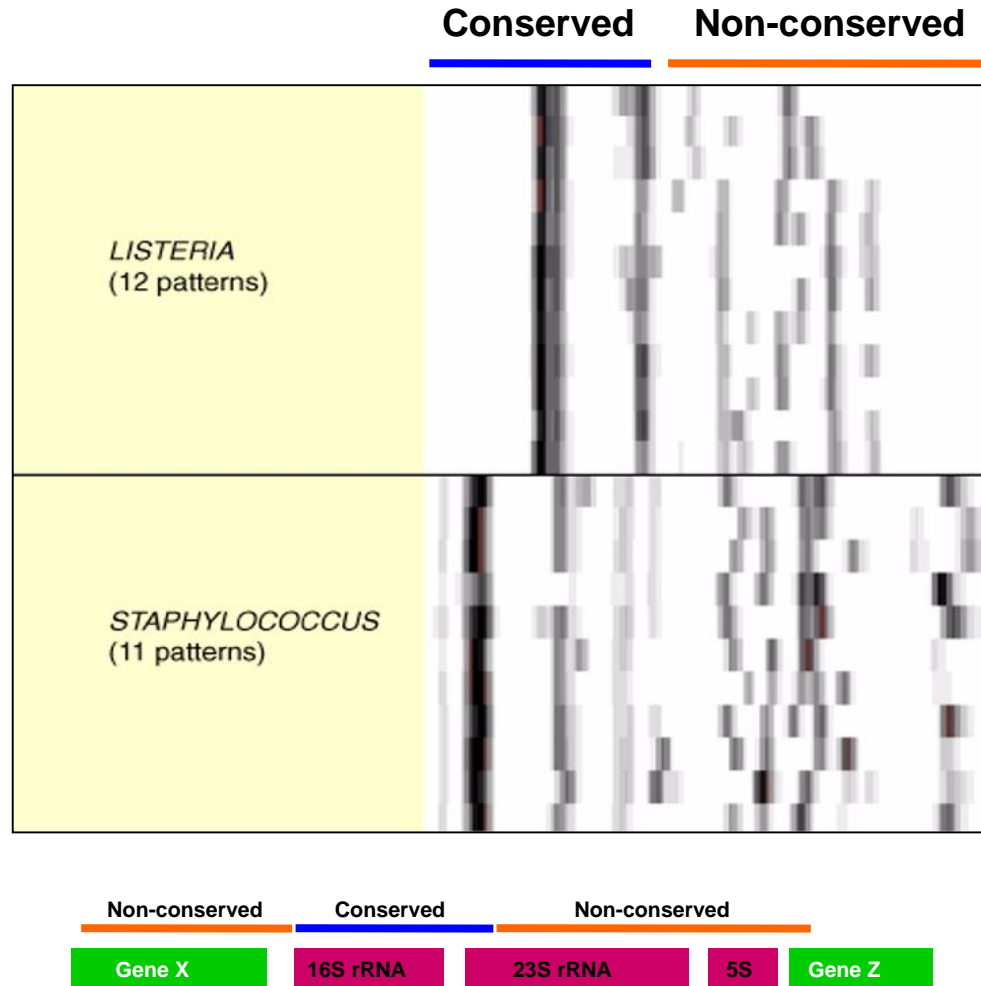
Hygiene RiboPrinter

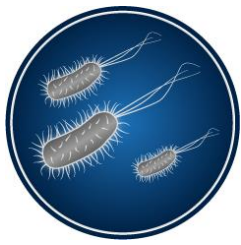
- Current database contains more than 6900 patterns
- 219 bacterial genera
- 1440 species



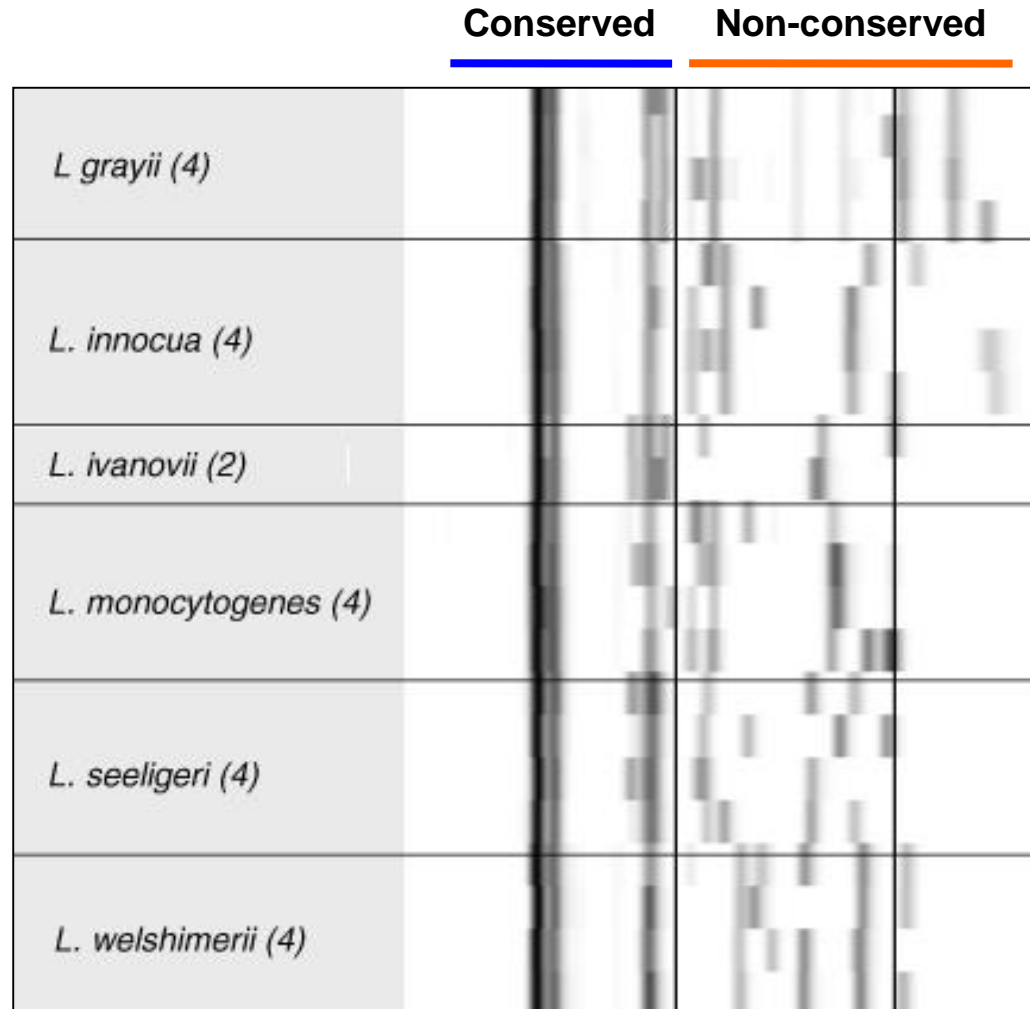


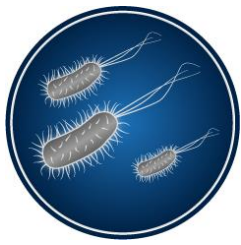
Hygiena RiboPrinter





Hygiene RiboPrinter





Case Study

- Sterility test positive investigation, samples sent to lab

Vitek Identification

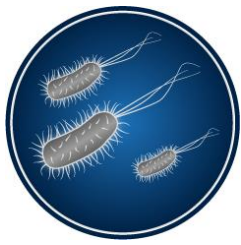
S. epidermidis (finished product)

S. epidermidis (raw material)

S. epidermidis (personnel gloves)

RiboPrinter Pattern





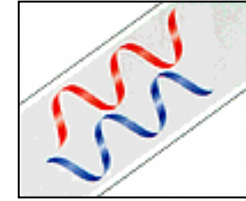
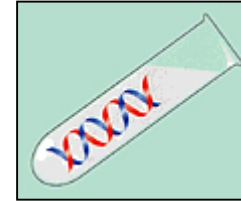
Review: PCR

- Polymerase Chain Reaction (PCR)
- Small fragments of DNA (primers) are used to find a specific sequence (target) on a sample of DNA
- A heat stable enzyme (e.g., *Taq* DNA polymerase) makes millions of copies of the target sequence, which can be easily detected
- We will explore different types of PCR processes
 - Real-time, quantitative PCR
 - Reverse transcriptase PCR
 - Rep-PCR: typing of non-coding repetitive DNA sequences



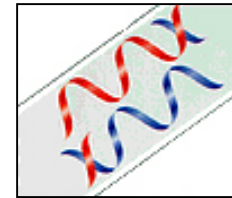
Review: PCR

DNA is extracted and heated to separate the double strands



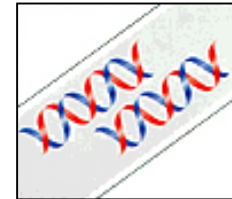
Heat to
90° C

DNA primers (short, synthetic sequences) are added, which bind to unique target sequences on the template DNA, if they are present



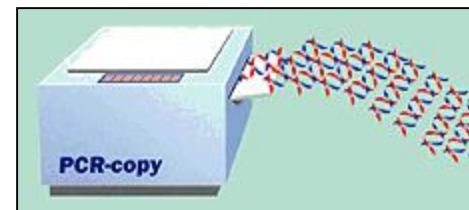
Lower
heat to
55° C

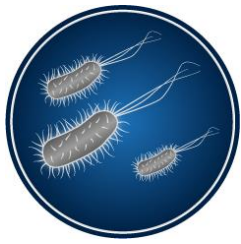
Heat-stable DNA polymerase and nucleotide bases (A,T,G,C) are added. The primer is elongated, producing two new complete copies of the template DNA strands



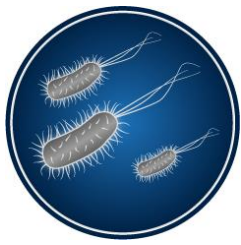
Raise
heat to
70° C

The process is repeated, resulting in millions of copies of the target DNA



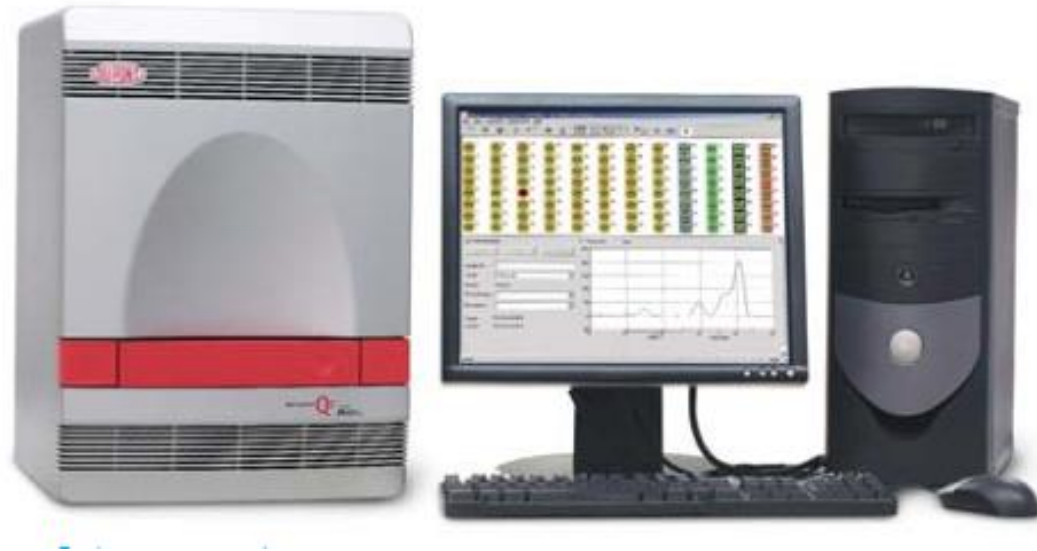


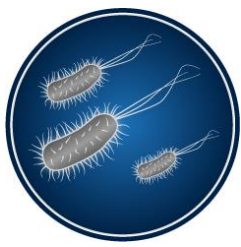
PCR Video



Hygiena BAX System Q7

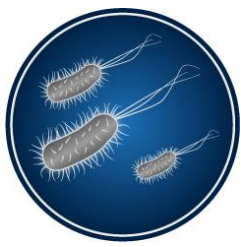
- Automated real-time, quantitative PCR and probe-based detection





Hygiena BAX System Q7

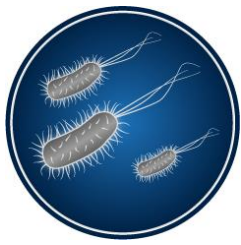
- DNA amplification is measured as it occurs, allowing the detection of sequence-specific PCR copies as they accumulate in "real time"
- The test sample is enriched in media to provide enough DNA for analysis and to eliminate false positives from dead cells or residual DNA
- Two types of assays:
 - Intercalating dye (SYBR Green) chemistry
 - Taqman probe-based chemistry that allows more than one detection event



Hygiena BAX System Q7

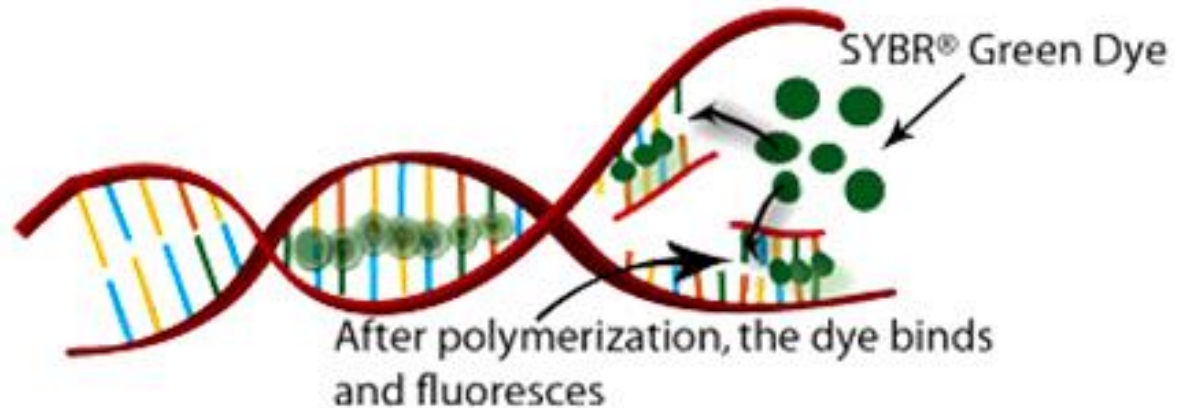
- Enriched samples are heated in a lysis reagent solution to rupture the bacterial cell wall and release DNA
- PCR reaction tubes contain tablets that are hydrated with the test samples
- The tablets contain intercalating dye or probes, along with all the reagents, enzymes and primers needed for the PCR reaction
- The primers match a unique genetic region of the target's DNA





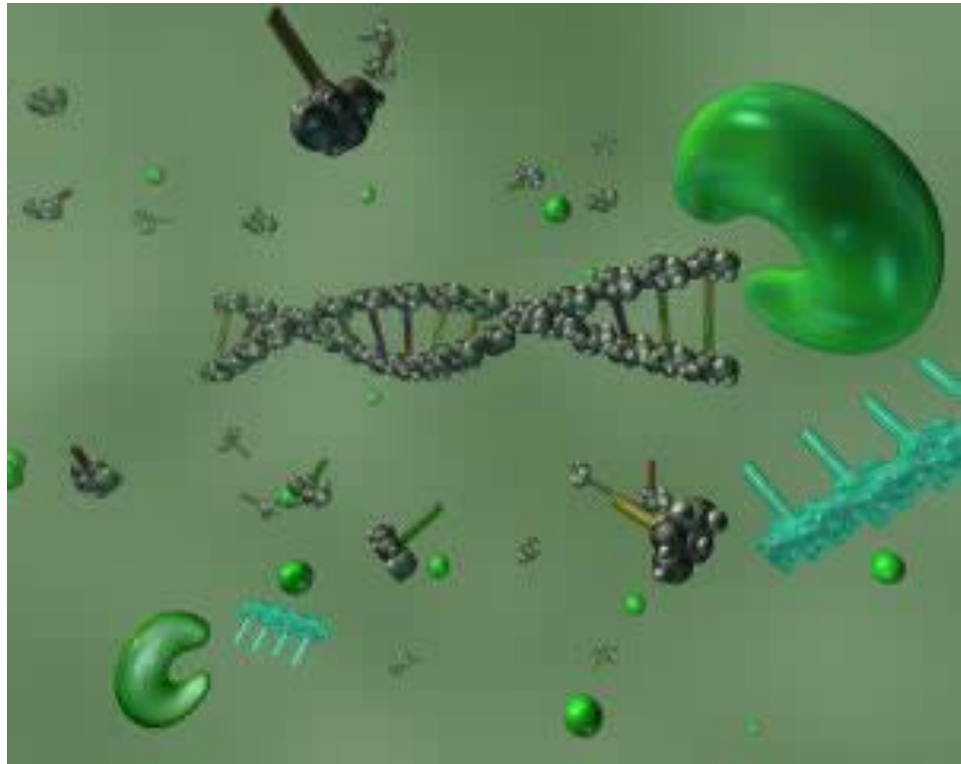
Intercalating Dye SYBR Green Assay

- During PCR, SYBR Green dye binds to a newly synthesized double-stranded DNA
- The bound dye emits a fluorescent signal when excited by light
- Each PCR cycle will result in an increase in fluorescence
- Plot the fluorescence in real time. No DNA target = no fluorescence





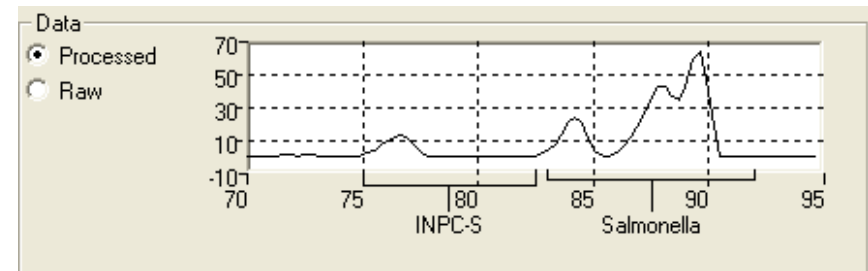
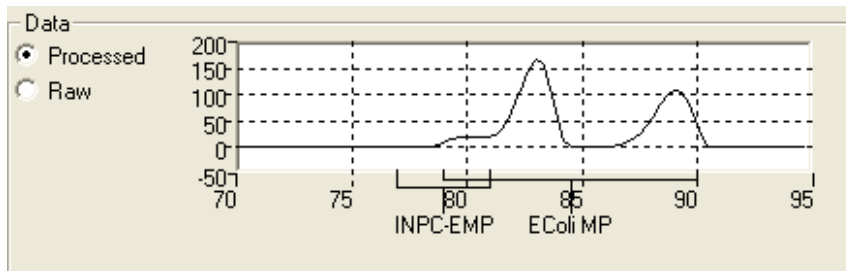
Intercalating Dye SYBR Green Assay

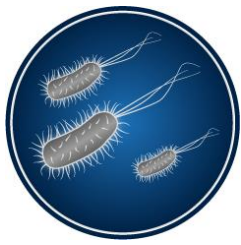




Intercalating Dye SYBR Green Assay

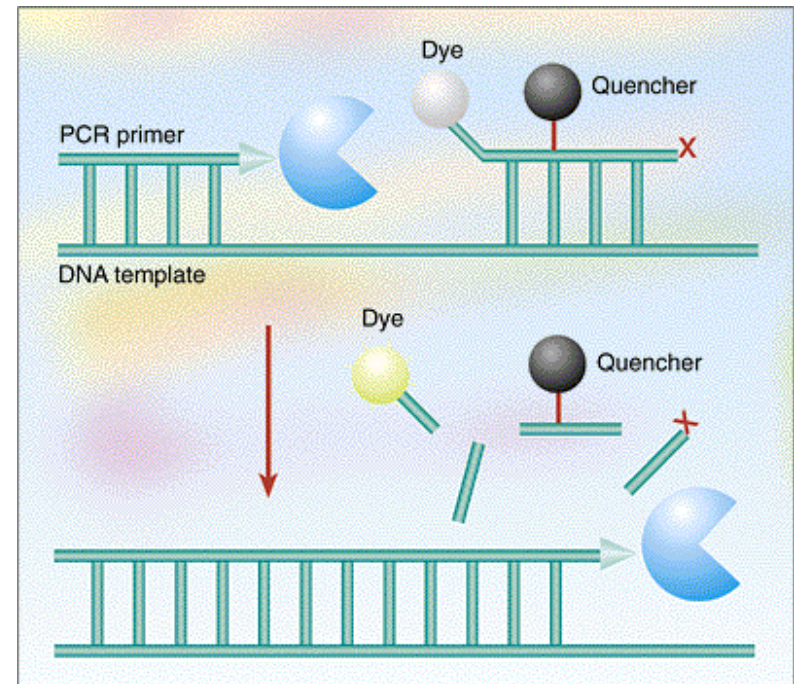
- After PCR detection, we will generate a melting curve
- Excite the dye to produce a fluorescence baseline signal
- The temperature is slowly raised to denature the DNA, releasing the dye and lowering the fluorescent signal
- Change in fluorescence is plotted against temperature
- Each target organism generates its own melting curve

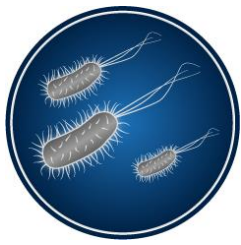




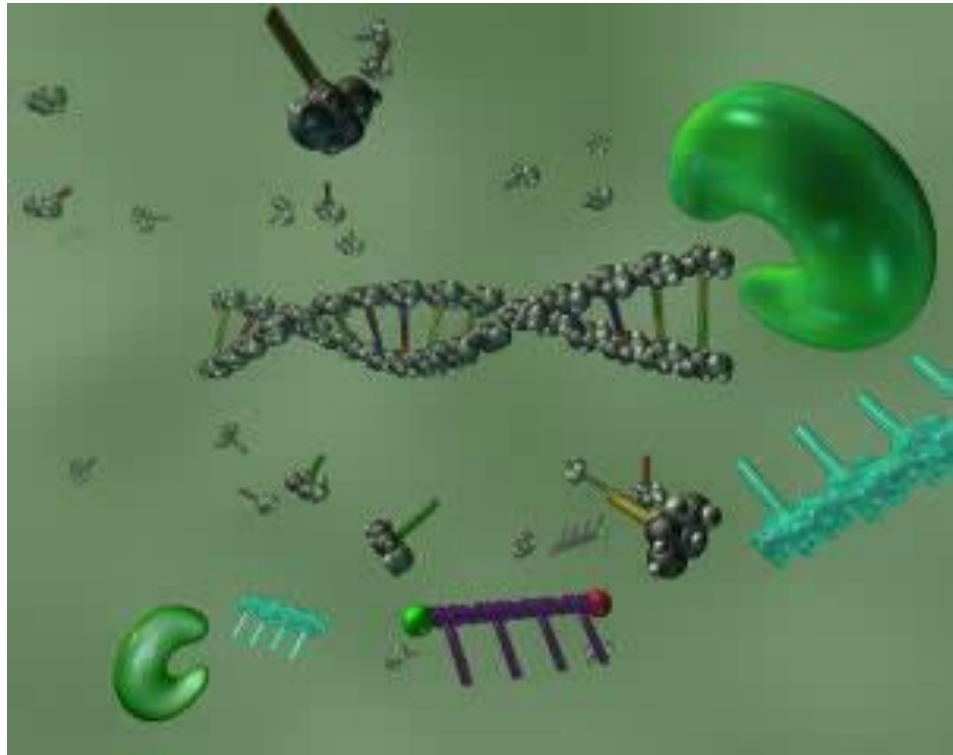
Taqman Probe-based Assay

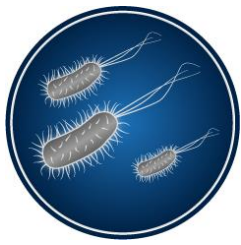
- During PCR, at the same time primers bind to a target sequence, a Taqman probe binds to another region of the target sequence
- The probe contains a fluorescent reporter dye at one end and a quencher dye at the other end. There is no fluorescence.
- As Taq polymerase extends the primer, the probe is cleaved, releasing the reporter dye and increasing the fluorescence signal
- Each PCR cycle increases the level of fluorescence





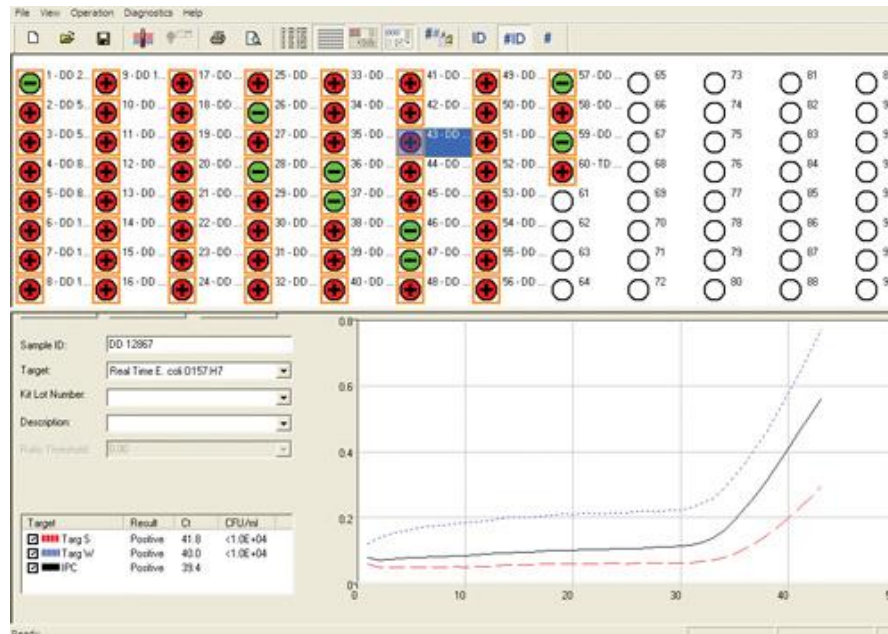
Taqman Probe-based Assay

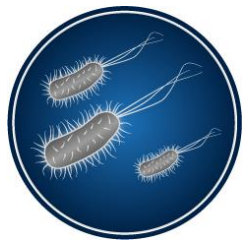




Hygiena BAX System Q7

- Continuous wavelength detection allows the use of multiple dyes (and probes) in a single reaction and in real time
 - *Salmonella*, *S. aureus*, *Vibrio*, *Shigella*, *Listeria monocytogenes*, *Campylobacter jejuni/coli*, *E. coli* O157:H7, Cronobacter (*Enterobacter sakazakii*), yeast and mold





Biotecon Diagnostics microproof Hygiene Screening System

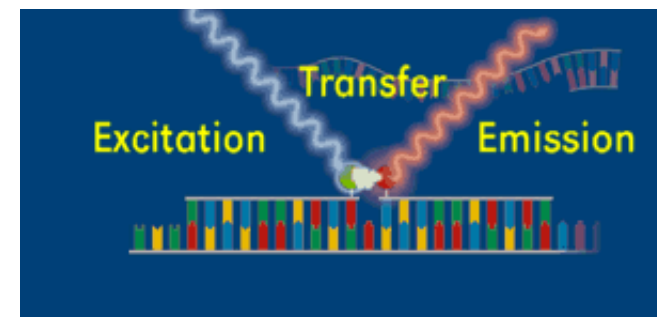
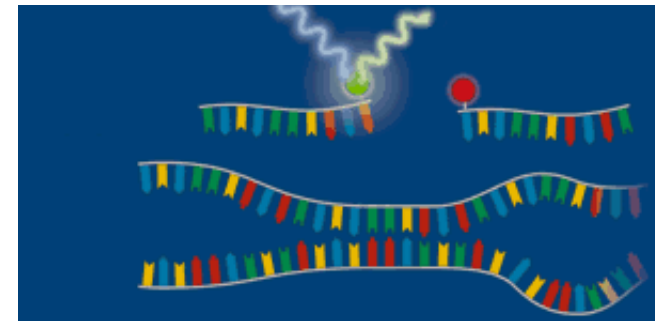
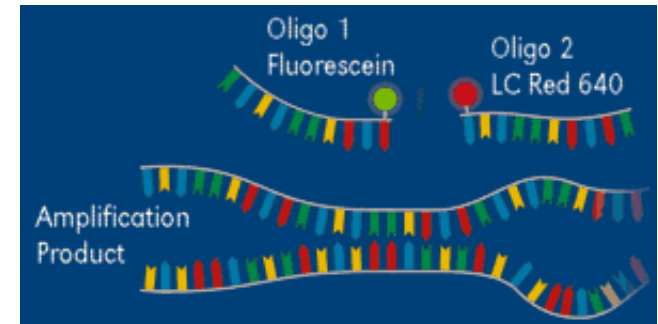
- PCR-based technology for the detection of microorganisms belonging to the genera *Corynebacterium*, *Staphylococcus*, *Micrococcus*
- PCR amplification in the Roche LightCycler
- Simultaneous detection within 90 minutes
- Start with an isolated colony





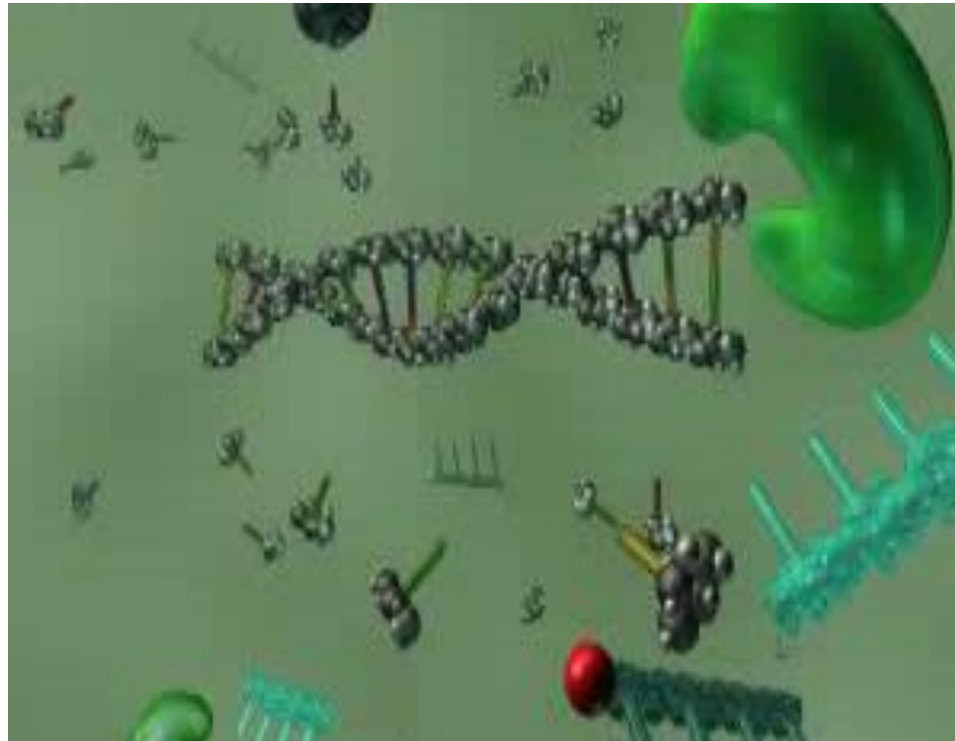
Biotecon Diagnostics Hygiene Screening System

- FRET probes to detect amplification
- Fluorescence resonance energy transfer (FRET) occurs between excited states of two dyes
- The donor dye is excited by a light source
- When the dyes are close to each other, excitation is transferred from the donor dye to the acceptor dye
- The acceptor dye emits light of a different wavelength; this is detected





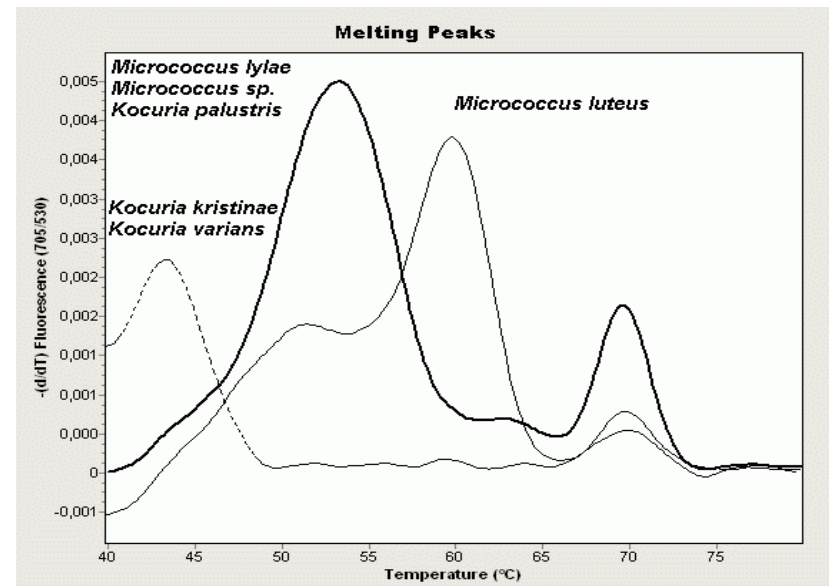
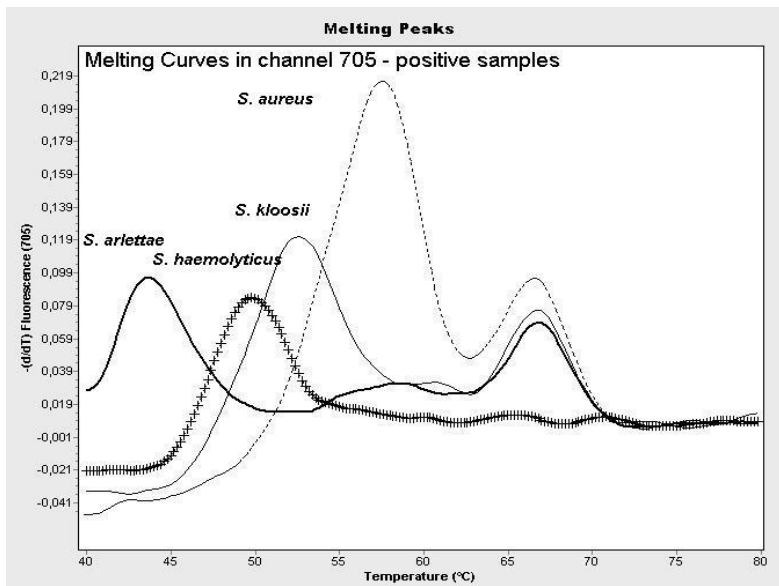
FRET Probe





Biotecon Diagnostics Hygiene Screening System

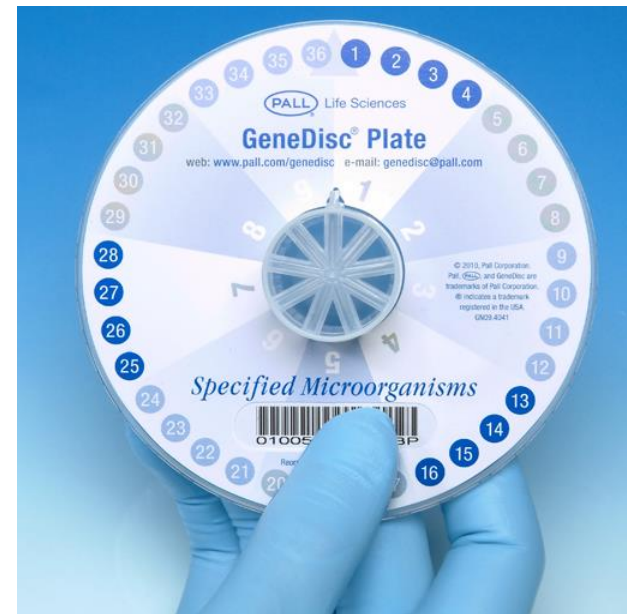
- Melting curves and melting peaks are used to differentiate and identify some organisms to the species level

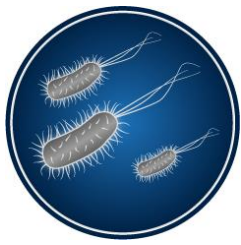




Pall GeneDisc

- Quantitative (q)PCR to simultaneously detect multiple organisms in the same sample
- Different primers and probes/dyes for each DNA sequence is in the outside edge of the disc
- Taqman probe technology

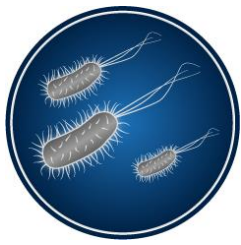




Pall GeneDisc

- Samples are filtered, media is added to the filter cartridge and the membrane is incubated for 6-16 hours
- The membrane is removed and placed in a lysis tube. Organisms on the membrane are lysed (sonicated for 8 min) and heated (100° C for 19 min) to release the DNA

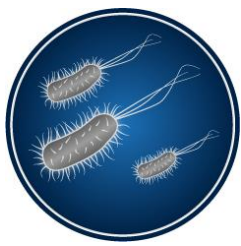




Pall GeneDisc

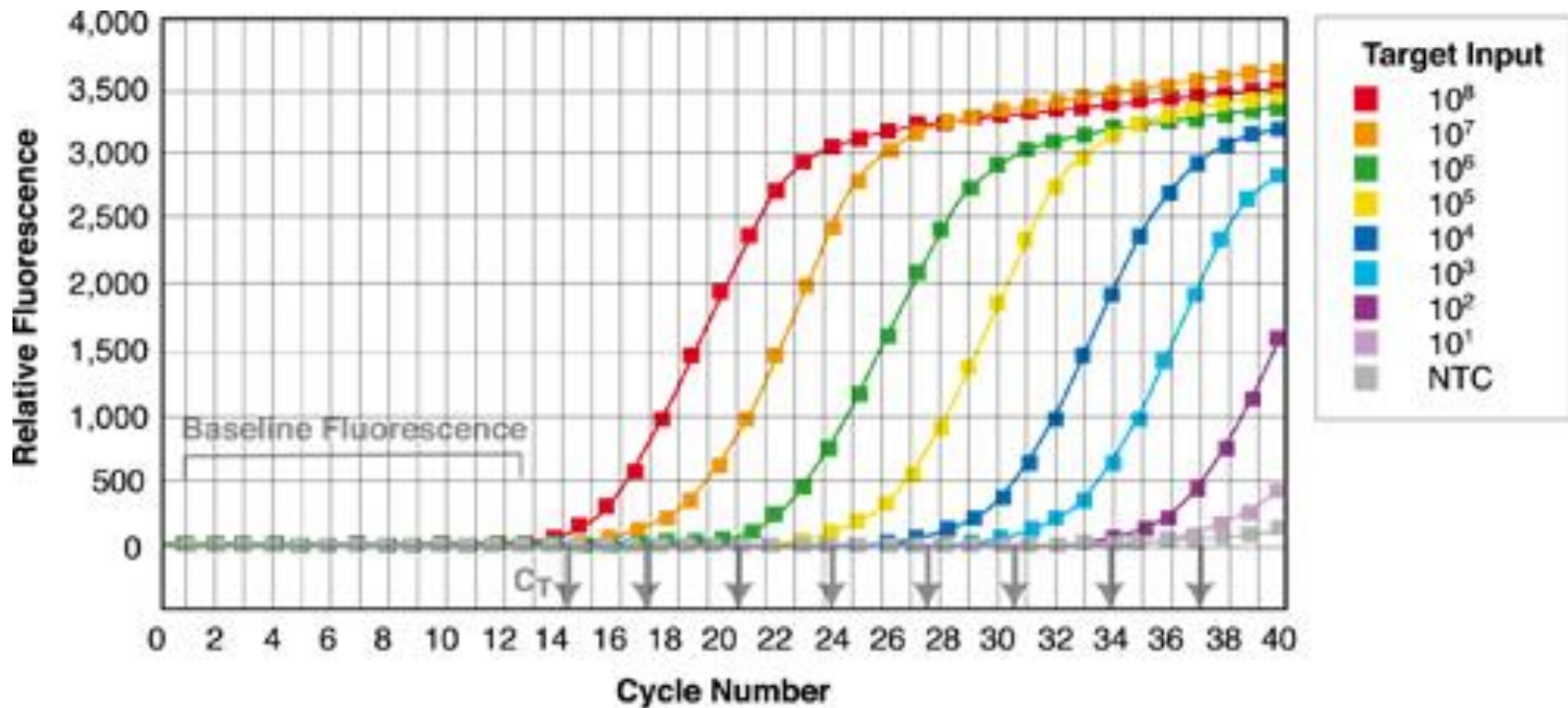
- The purified DNA and a Master Mix (polymerase and deoxynucleotides) are added to the upper hub of a GeneDisc plate
- The plate is inserted into the instrument, and the disk rotates through 4 different heating and cooling sections during the PCR amplification and detection process

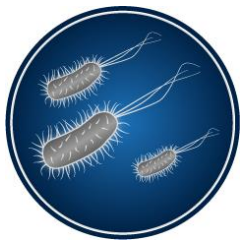




Pall GeneDisc

- Fluorescent signals increase during amplification





Pall GeneDisc Software Display

GeneDisc Cyclor Analysis Records Admin Maintenance ?

Analysis report

GeneDisc® Specified Microorganisms 06

Operator name	cour tneyn
Result file name	PV_2010_08_17_10h32min41.xls
Analysis date and time	17/08/10 10h43m48s
Barcodes	DY0Z12610325BP / 002012010SR004
Serial number	111775001

Alarms : No alarm

Notes : [View](#)

S1 S2 S3 S4 S5 S6

Sector 6 : "SPC 5 undiluted repeat"

Target	PCR result (GU/Vol. filt)	External standard	Blank
Salmonell.	Absence : < 190.00		Absence
E coli	Absence : < 190.00		Absence
C albicans	Presence : 4.2e+02		Presence
P aerugin	Presence : 1.7e+03		Presence
S aureus	Presence : 1.6e+03		Presence
A niger	Absence : < 190.00		Absence

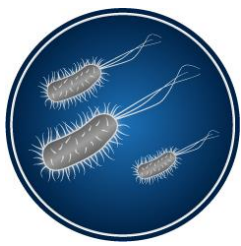
Life Sciences V2.10.8

[Standard curves](#) [Advanced report](#) [End](#)



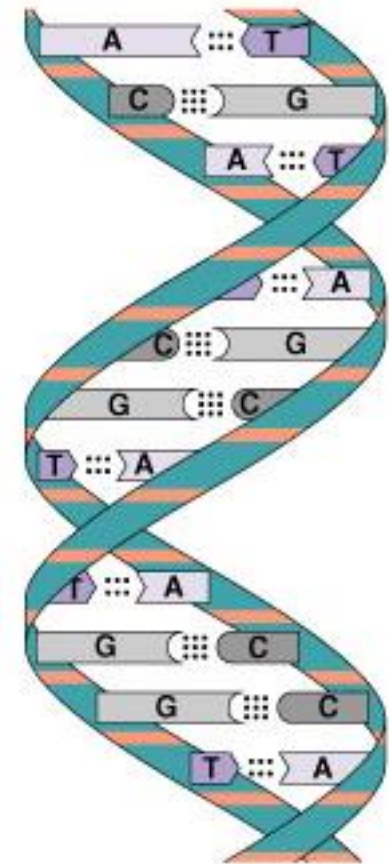
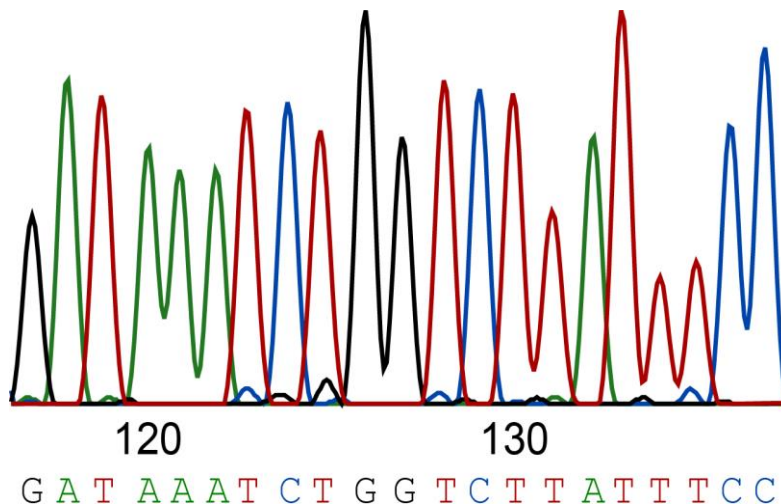
Pall GeneDisc

- Up to 6, 9 or 12 test samples may be assayed per disc
 - Depends on plate/application; includes positive and negative controls
 - 8 modular system units have the capability of testing up to 96 samples per run (~1 hour)
- Plate for Compendial Specified Microorganisms:
 - *Escherichia coli*, *Salmonella spp.*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Candida albicans*, *Aspergillus brasiliensis* (*A. niger*)
- Food Testing
 - STEC, non-STECS and *E. coli* O157, *Salmonella*, *Listeria*
- Environmental
 - *Legionella*, *Pseudomonas*, *Enterococcus*, *Cyanobacteria*, *E. coli*



Gene Sequencing

- The process of recording the exact sequence of nucleotides in a section of an organism's DNA
- DNA sequences can be used for microbial identification





Gene Sequencing

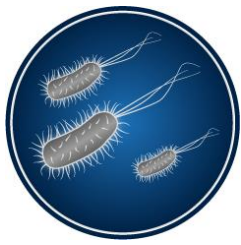
- Methods have simplified over the years!





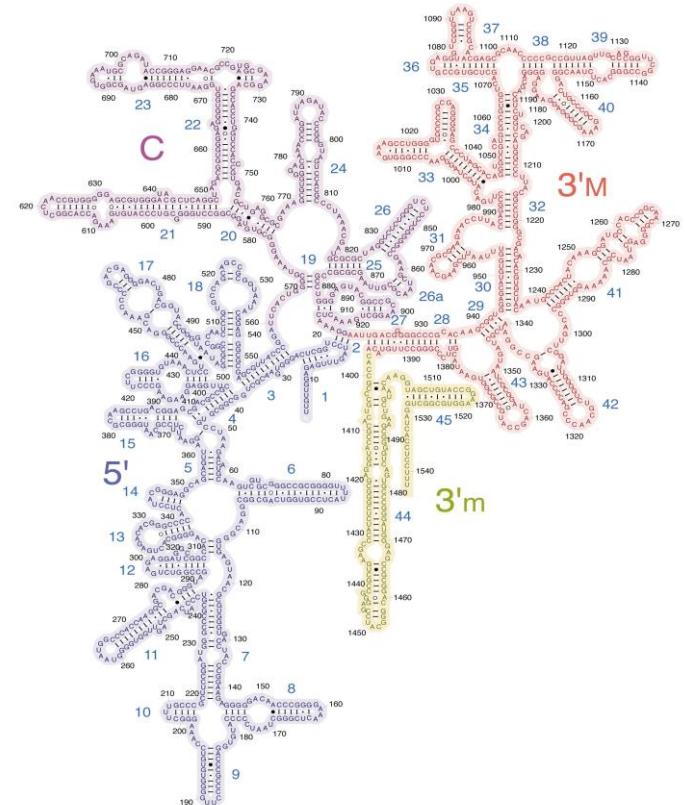
Thermo Fisher MicroSEQ

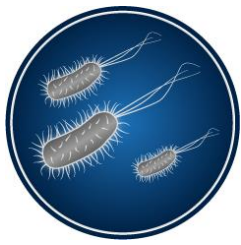




Thermo Fisher MicroSEQ

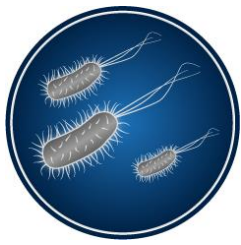
- Sequencing the first 500 base pairs of 16S rRNA gene for bacteria and the D2 region of large-subunit rRNA gene for fungi
 - Universal among bacteria and fungi
 - Functionally conserved
 - Provides a high level of discrimination
 - Stable, not influenced by environmental conditions
 - Can sequence the entire 16S gene for greater bacterial differentiation (1500 bps)





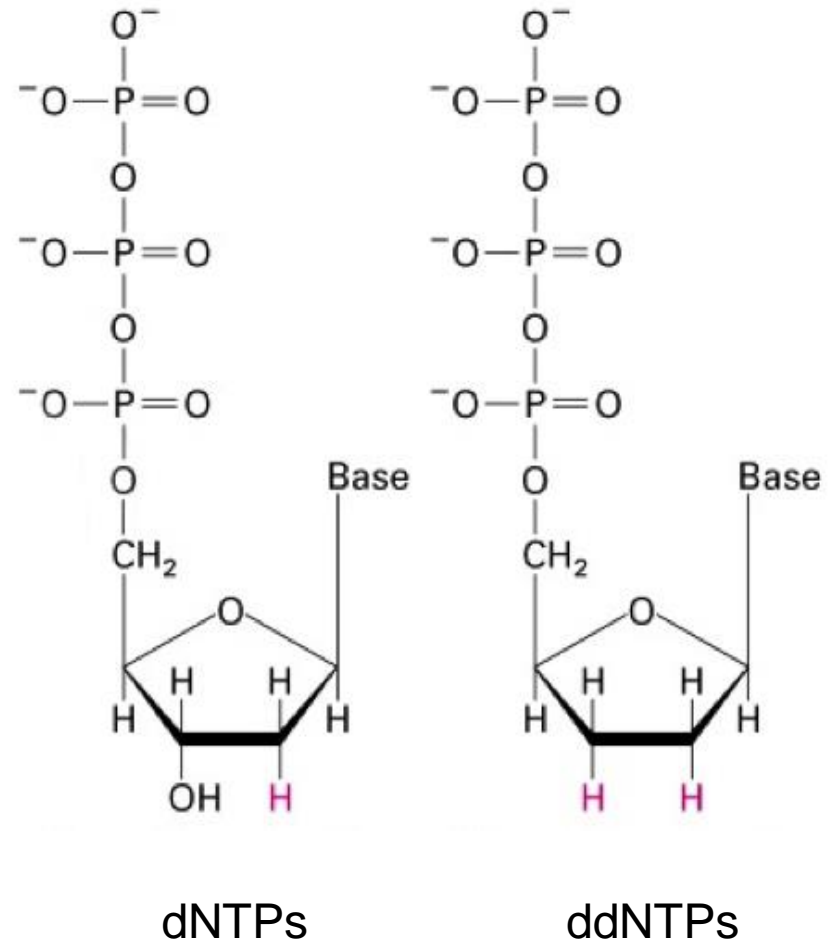
Thermo Fisher MicroSEQ

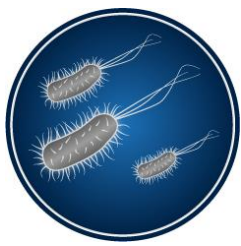
- Start with a loopful of cells from a plate or pure culture
- Extract DNA
- For bacteria, add primer for 16S rDNA and amplify DNA by PCR in a thermal cycler
- Perform cycle sequencing
 - Primers direct the sequencing of the forward or reverse reaction for each of the DNA strands
- Use a mixture of standard deoxyribonucleotides (dA, dT, dC, dG) and dideoxyribonucleotides (ddNTP)



Thermo Fisher MicroSEQ

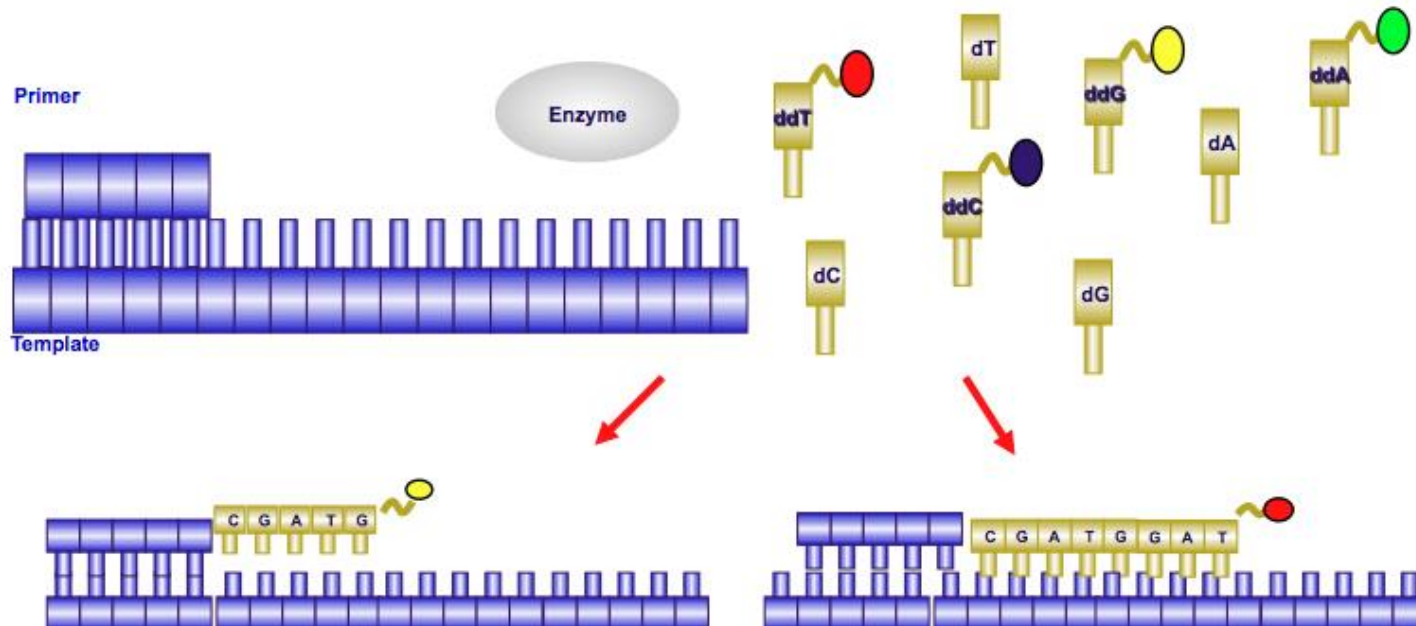
- ddNTPs lack a 3'-hydroxyl (-OH) group on their deoxyribose sugar
- Once a ddNTP is incorporated during sequencing, DNA elongation is terminated





Thermo Fisher MicroSEQ

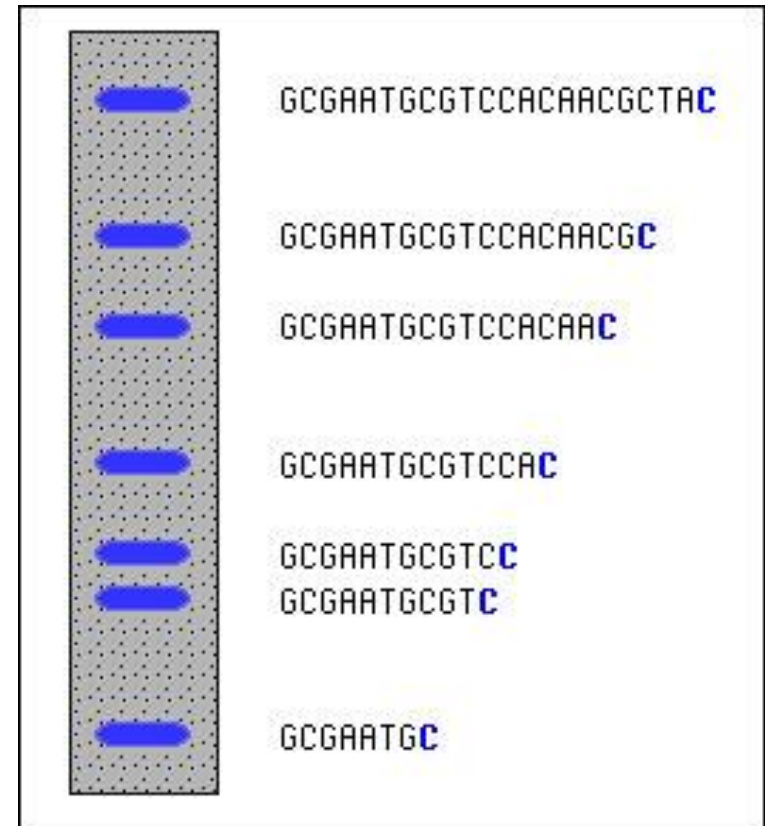
- Each ddNTP is also labeled with a different fluorescent dye
- The terminating DNA strand extensions result in DNA fragments of varying length and ending in a different dye

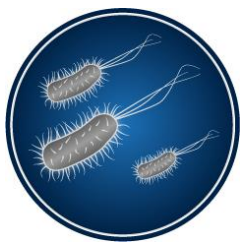




Thermo Fisher MicroSEQ

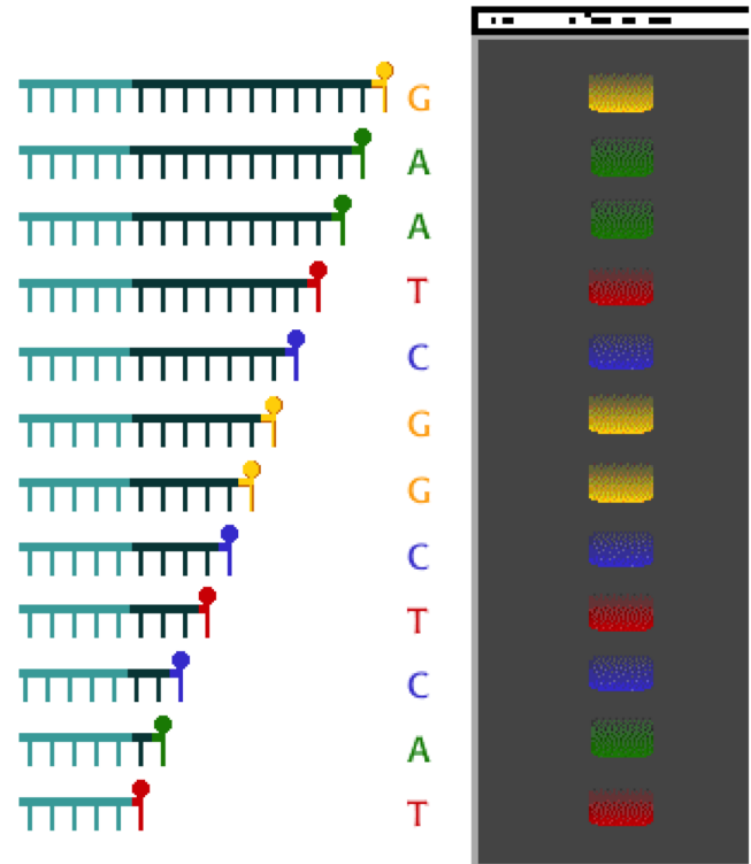
- The following illustrates different lengths of DNA all ending in a cytosine dideoxynucleotide
- Now we have to do the same with the other three nucleotides





Thermo Fisher MicroSEQ

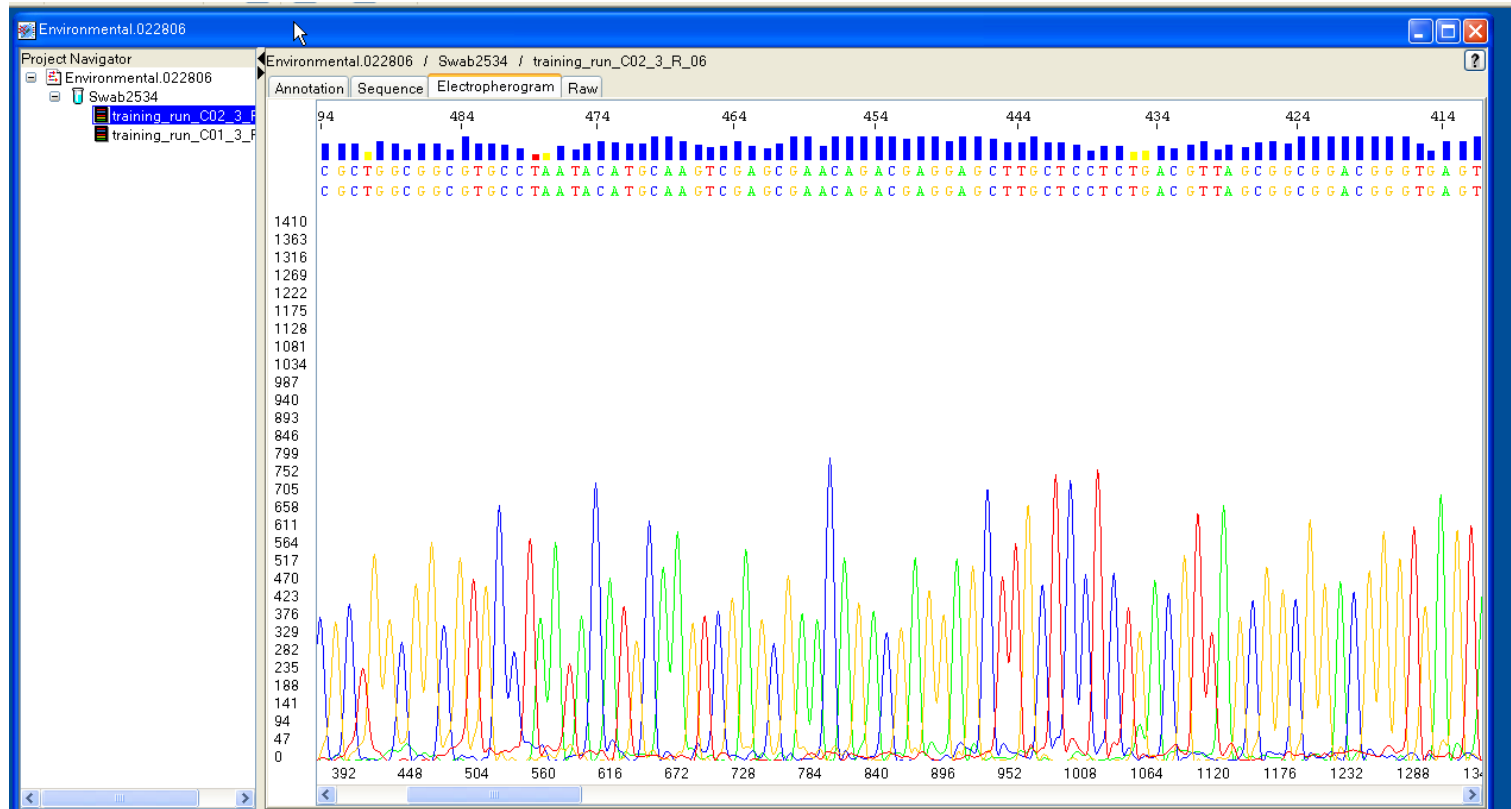
- A genetic analyzer separates all DNA fragments using capillary electrophoresis and a laser detects the last nucleotide in each fragment via fluorescence of the dye at the end
- Fragments are arranged by size and this represents a DNA sequence in the correct order





Thermo Fisher MicroSEQ

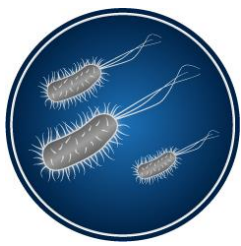
- The sequence is compared with a database or library and the best match for a microbial ID is provided





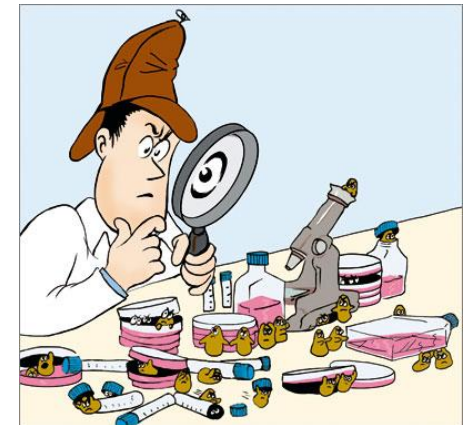
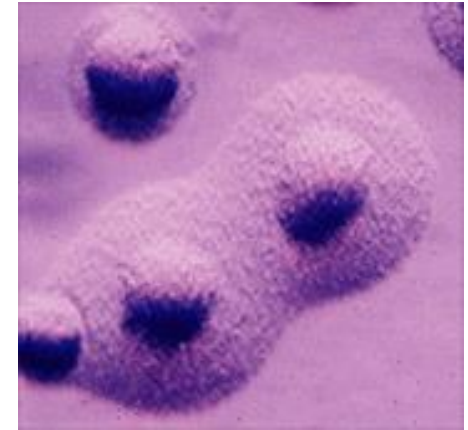
Thermo Fisher MicroSEQ

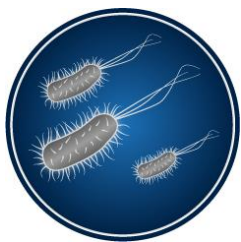
- 80 IDs/day
- Higher throughput if using greater capacity capillary analyzers
- Database
 - > 1800 bacteria
 - > 90 Mycoplasma
 - > 1100 yeast and mold



Mycoplasma Detection RMMs

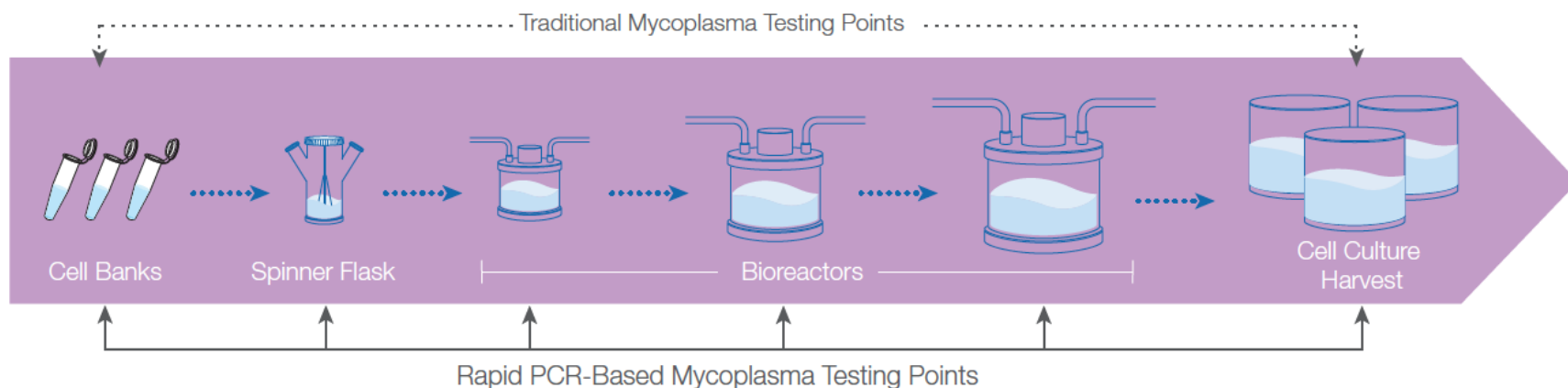
- The current Mycoplasma test is a 28-day culture test
- In 2007, the Ph. Eur. accepted nucleic acid tests (real-time PCR) as an alternative to traditional Mycoplasma detection (after validation)
- JP has a similar chapter
- RMMs utilizing nucleic-acid amplification techniques can now detect Mycoplasma within hours

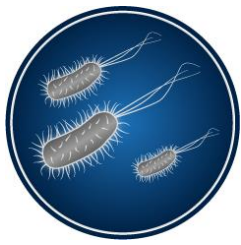




Mycoplasma Detection RMMs

- Rapid PCR-based testing for Mycoplasma can now be conducted throughout the cell culture manufacturing process, from inoculation through harvest
- Thermo Fisher MycoSEQ, **EMD Millipore MilliPROBE**, Greiner Bio-One CytoCheck, Roche MycoTool

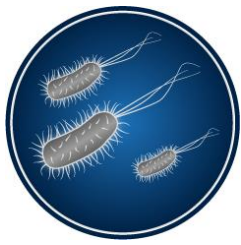




Thermo Fisher MycoSEQ

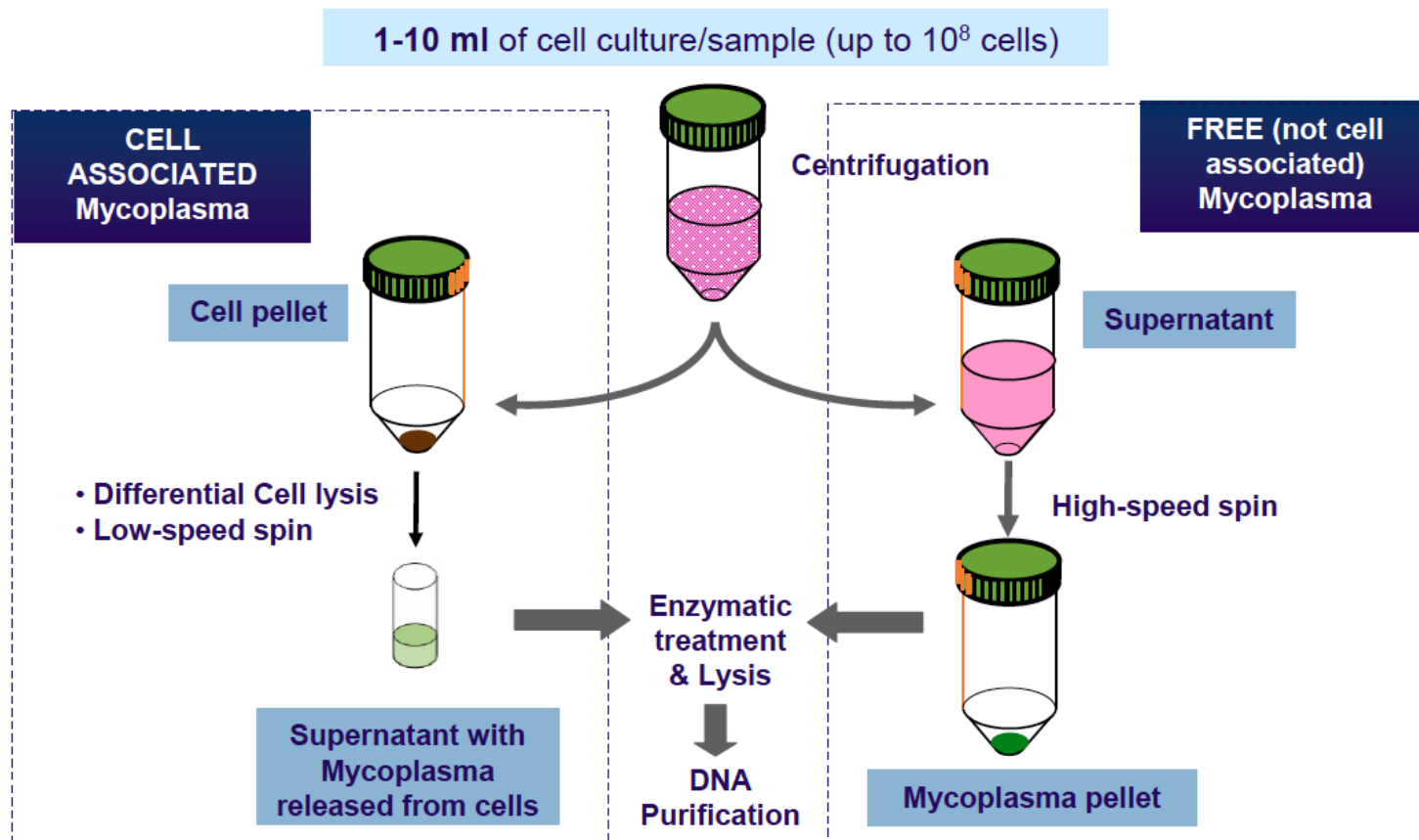
- Detection of greater than 90 Mycoplasma species, while excluding species closely related at the genetic level
- Limit of detection has been demonstrated as low as 1 CFU or copy equivalent per ml of test sample as compared with culture method
 - Amgen required a 7-day enrichment in liquid medium to eliminate interference from their commercial protein product
- SYBR Green probe
- Time-to-results <5 hr

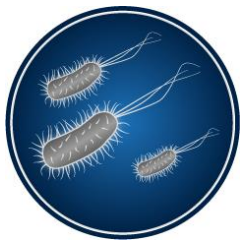




Thermo Fisher MycoSEQ

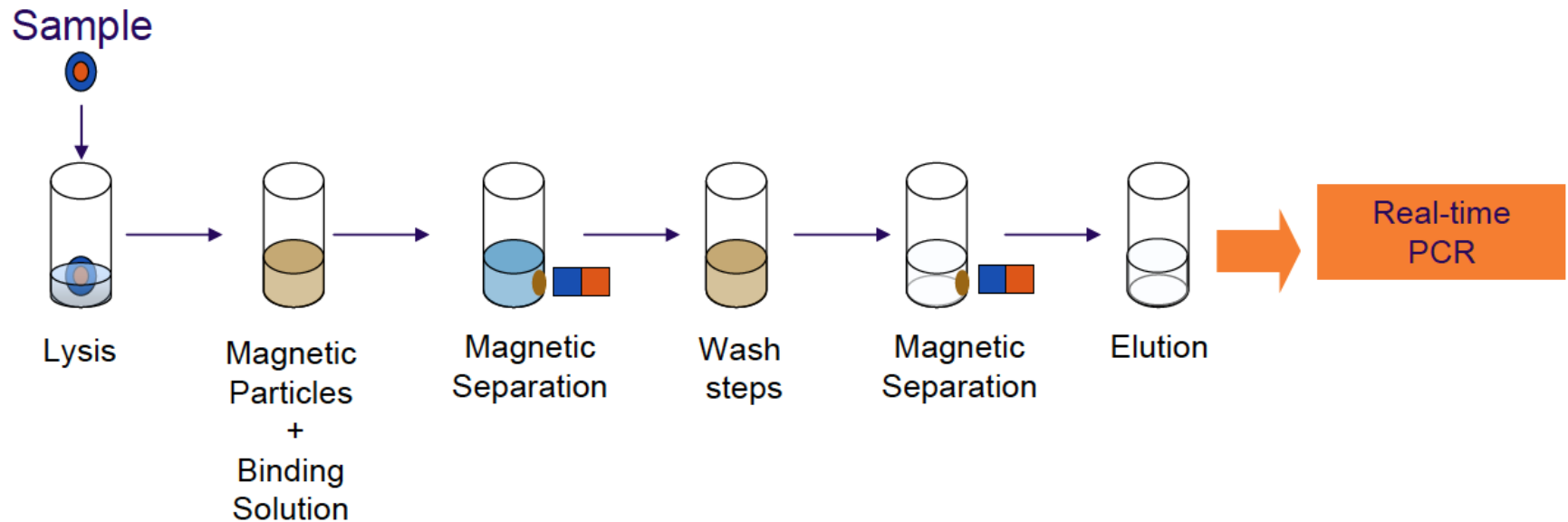
- Sample preparation

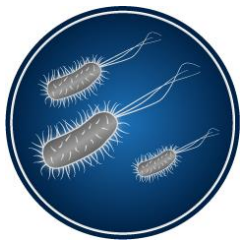




Thermo Fisher MycoSEQ

- DNA purification





Thermo Fisher MycoSEQ

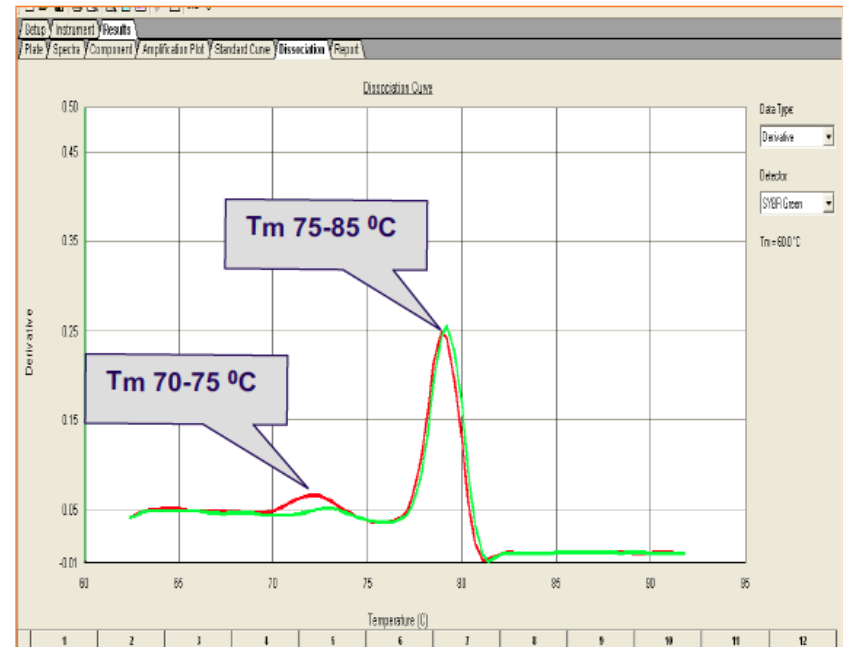
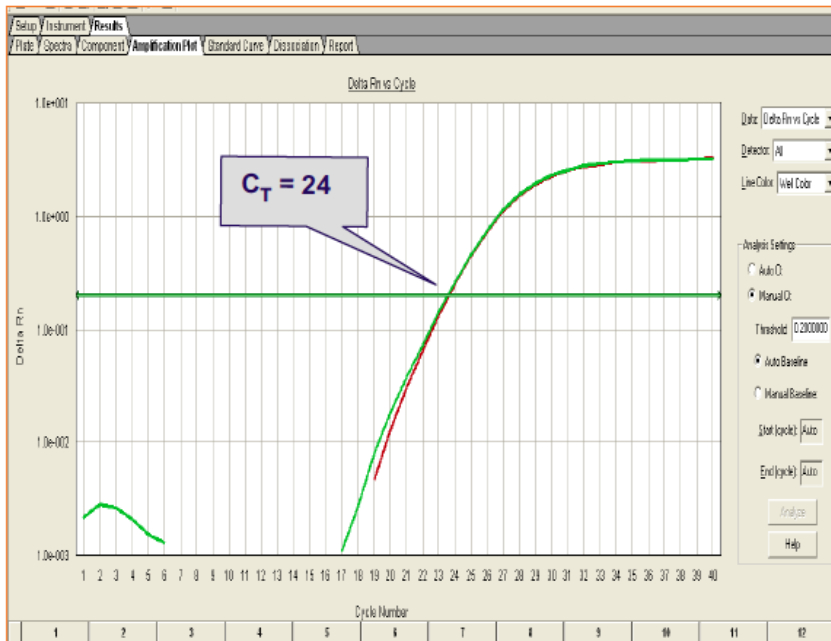
- AutoMate Express™ Nucleic Acid Extraction System
- Up to 13 samples per run
- Purification time ≤ 1 hr





Thermo Fisher MycoSEQ

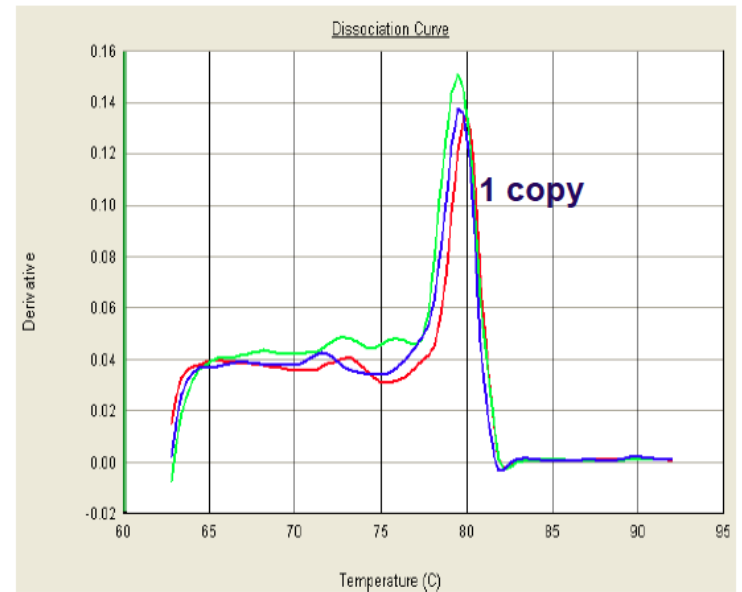
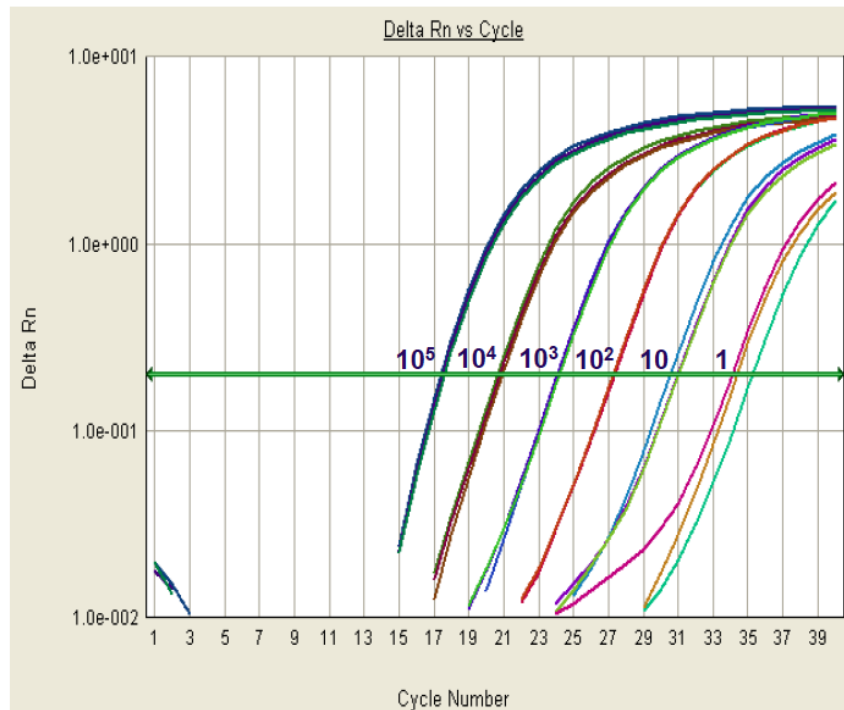
- Detection via real-time PCR and DNA melting curve analysis

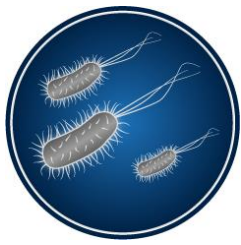




Thermo Fisher MycoSEQ

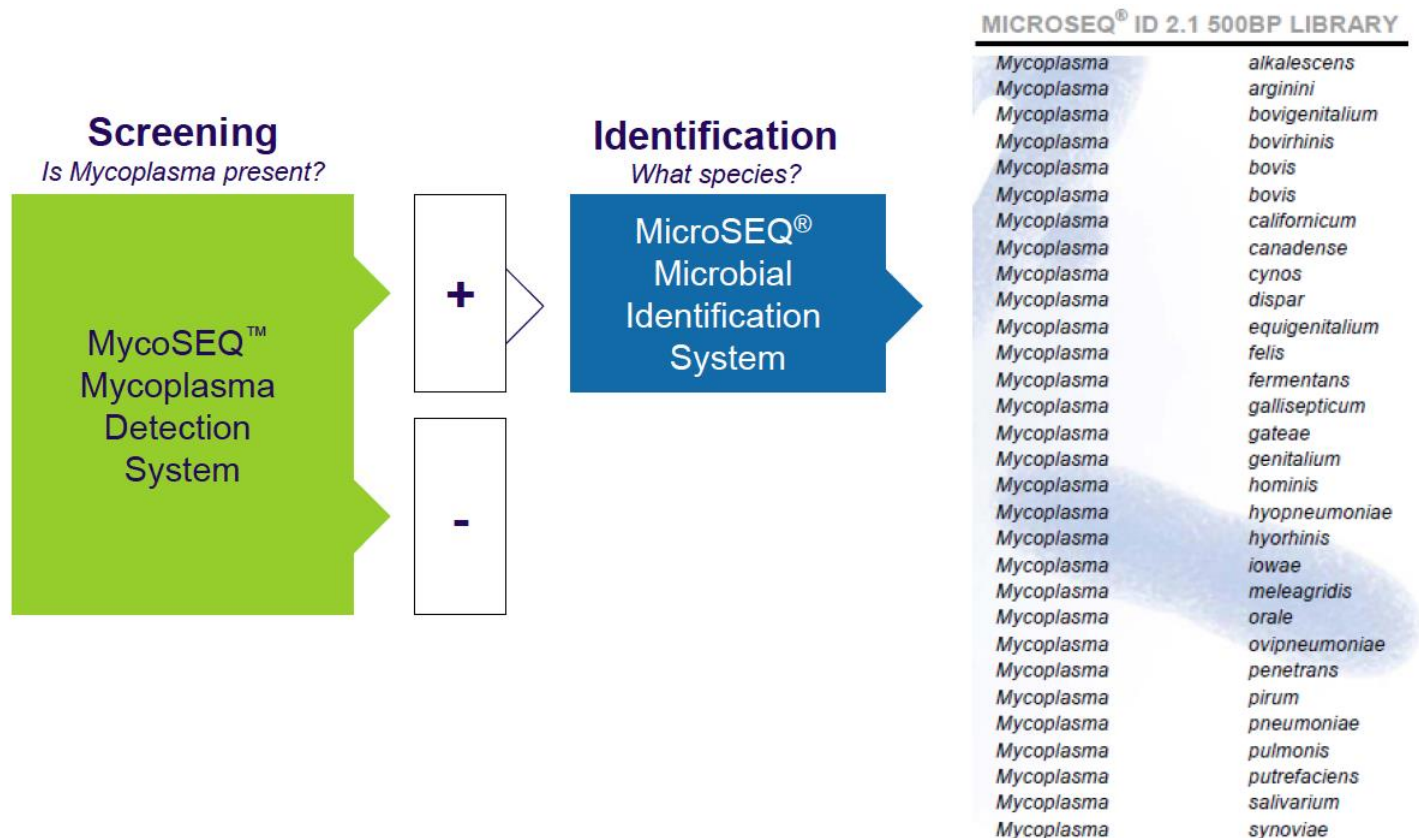
- Assay Sensitivity (example *Mycoplasma arginini*)

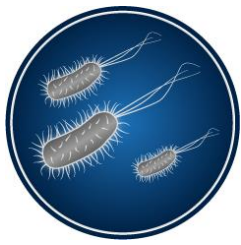




Thermo Fisher MycoSEQ

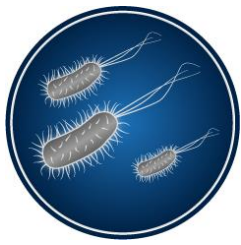
- If a positive result is obtained, can use MicroSEQ to ID





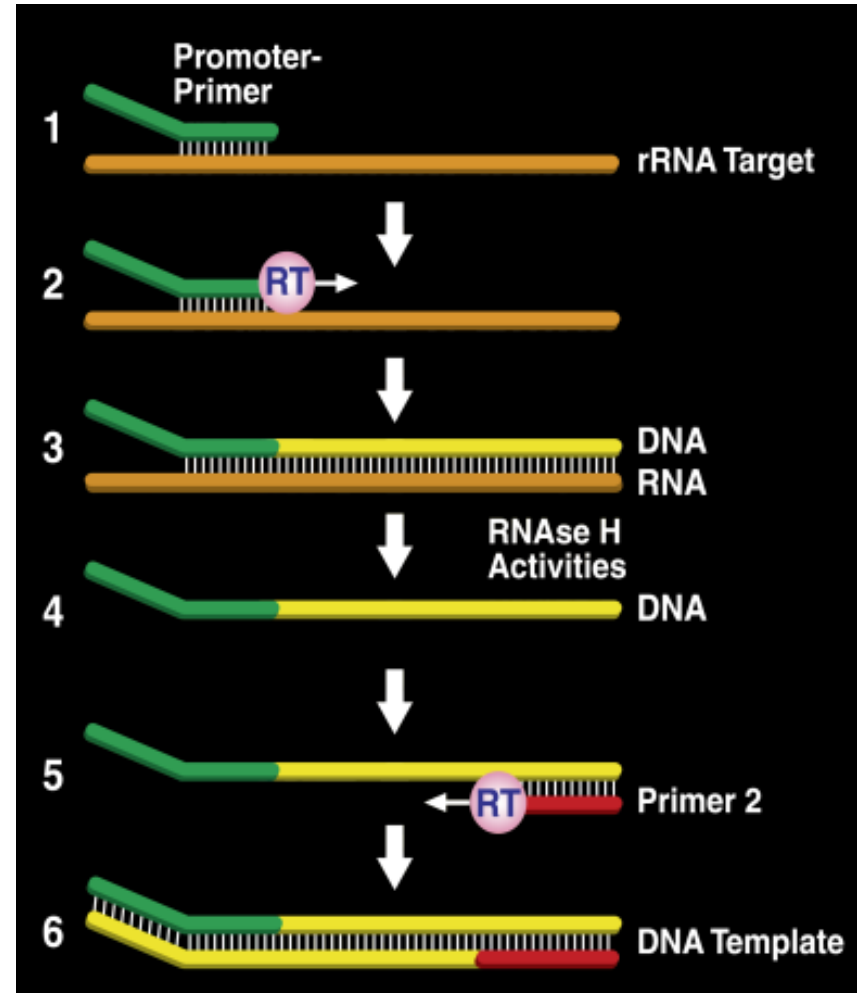
Transcription-Mediated Amplification

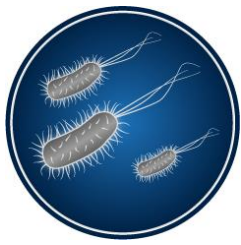
- Real-Time Transcription Mediated Amplification (TMA) is now being used for Mycoplasma testing
- Targets ribosomal RNA
- RNA is a better marker of cellular viability
- RNA is not as stable outside of the cell as DNA
- Less risk of detecting DNA from non-viable cells or contamination from residual DNA in the sample and/or the work environment



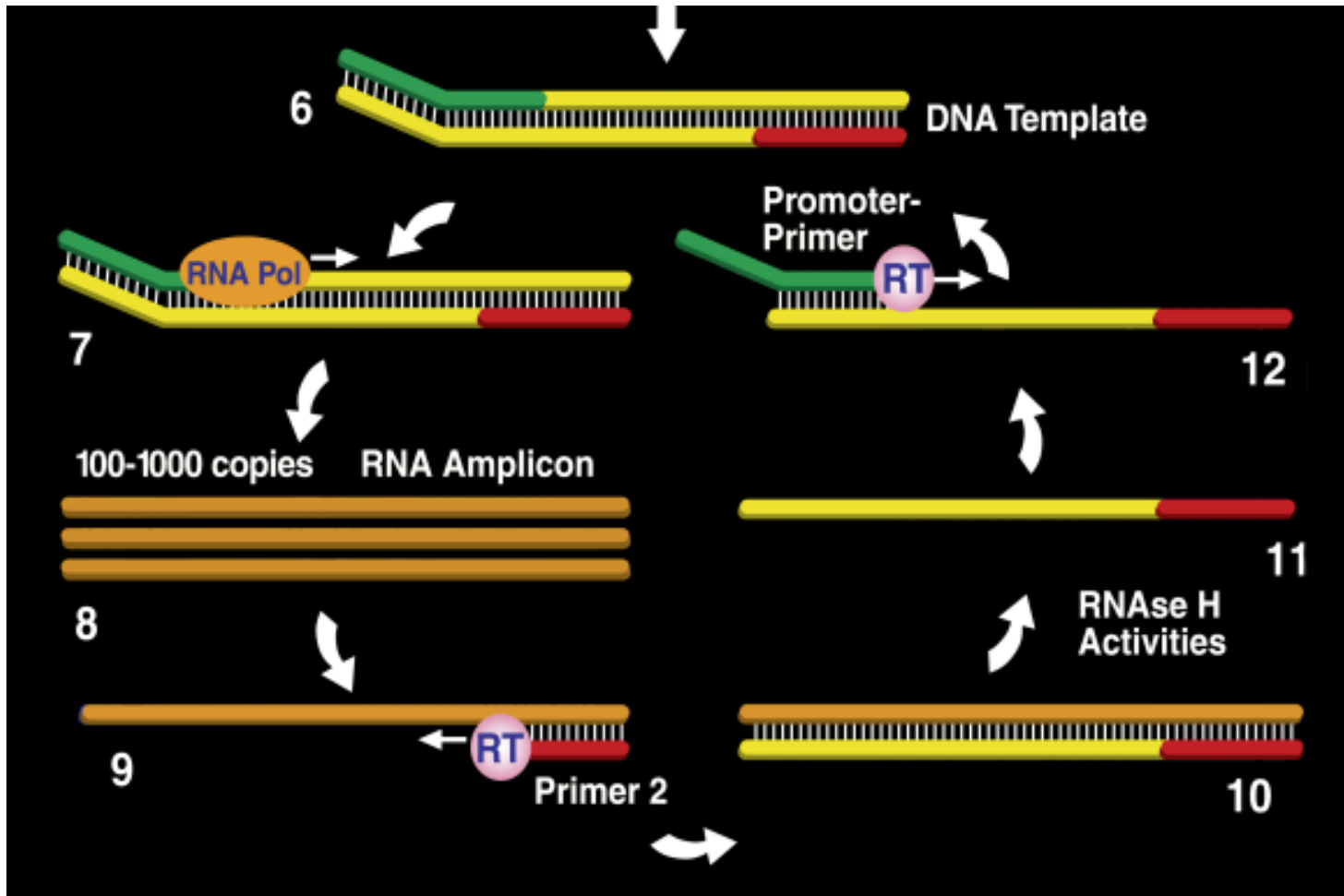
Transcription-Mediated Amplification

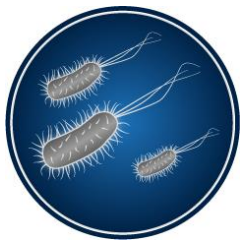
- Primer binds to RNA sequence
- Reverse transcriptase (RT) synthesizes complementary DNA
- RT mimics RNase H activity and removes the single-strand RNA
- Second primer binds to remaining cDNA strand
- RT synthesizes second cDNA strand
- RNA polymerase makes millions of copies of RNA and the process is repeated (next slide)



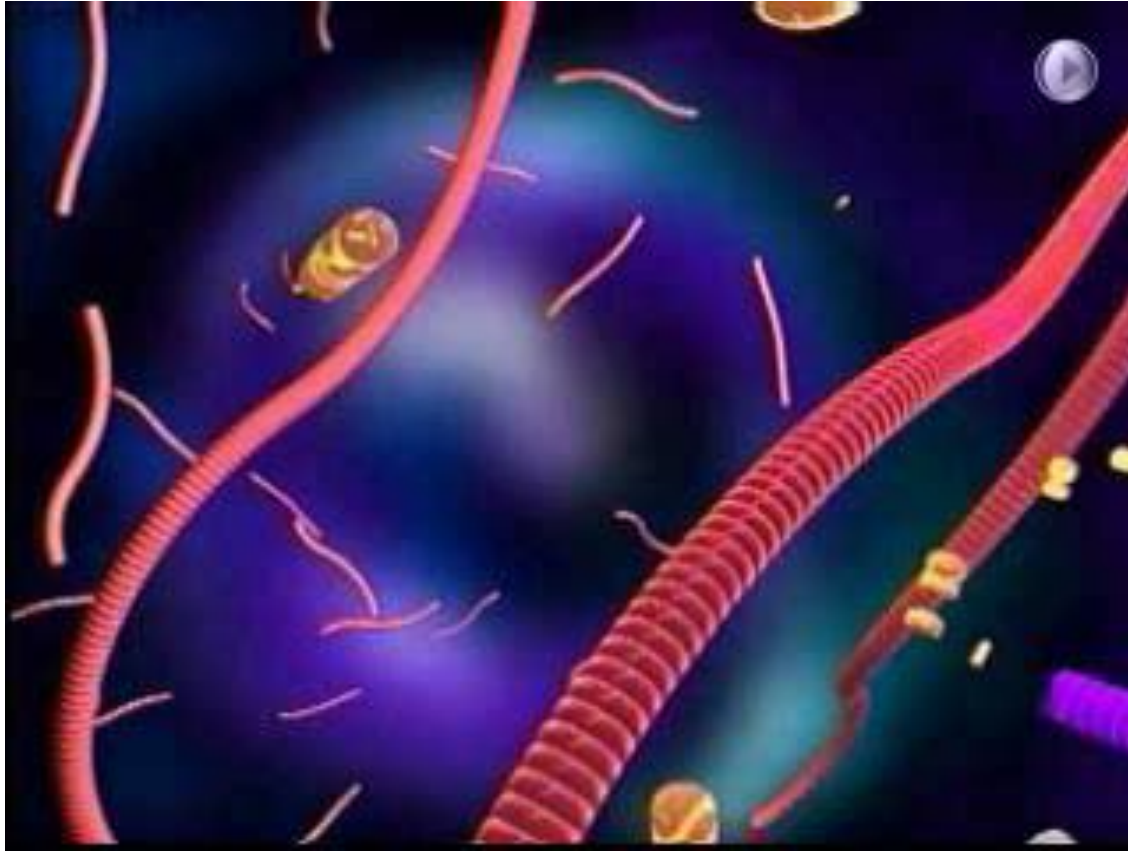


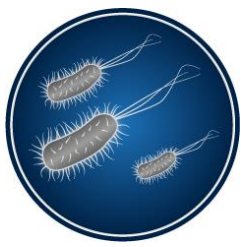
Transcription-Mediated Amplification





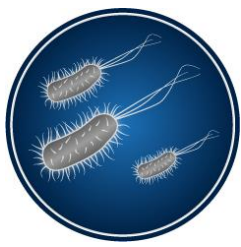
Transcription-Mediated Amplification





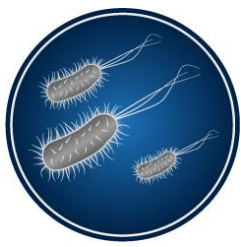
TMA Advantages Over PCR

- Easy to use; single tube format with no washing steps
- Isothermic reaction (e.g., 42°C); no need for a thermocycler
- Enzymes are less sensitive to interference
- Less risk of false positives from other organisms, nonviable cells or residual DNA
- Targets 1000's of RNA copies per cell vs. 1 DNA target
- Produces 100-1000 RNA copies per cycle compared with two DNA copies per cycle (10 billion fold increase of copies within 15-30 min)



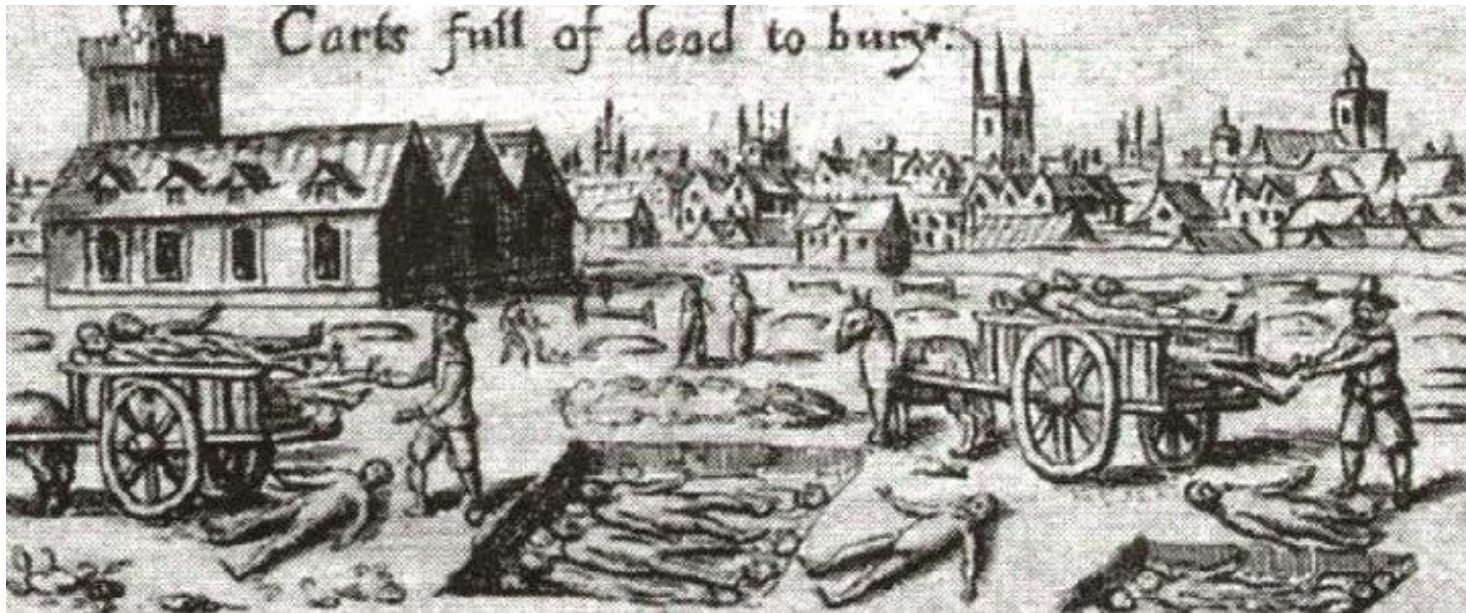
TMA vs. NASBA

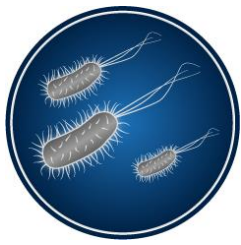
- TMA (transcription-mediated amplification)
 - Uses reverse transcriptase (RT) with RNase *activity* and RNA polymerase
- NASBA (nucleic acid sequence-based amplification)
 - Uses reverse transcriptase (RT), RNA polymerase, and RNase H added to the reaction mixture



Final Note

- 1665-1666: The Great Plague of London (100,000 dead)
- We always assumed this was caused by *Yersinia pestis*





Final Note

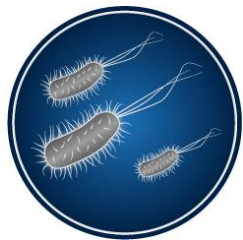
- 2016: London Underground extension; human remains were excavated from a supposed “plague pit”
- Confirmed *Y. pestis* using nucleic acid amplification



3000+
skeletons to be
excavated by
Crossrail

60
archaeologists
working on the site

1
known Roman
road running
through the site



The End of Genetic-based RMMs

