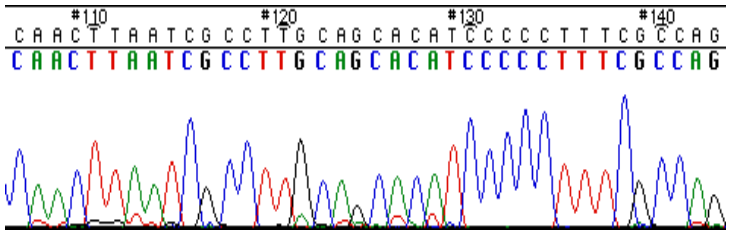
Sanger Sequencing

Why/When: *Sequencing is performed for a variety of reasons:*

1. ***To identify organisms isolated from clinical or environmental samples that cannot be distinguished by other methods.*** Pure isolates from the General Microbiology, TB/Mycology, and/or Environmental Microbiology sections are sequenced to provide genus or species - level identifications. On occasion, we are unable to identify the organism because a) it has never been sequenced, or b) the sequence is 99-100% similar to too many other genera. BSB sections use sequencing as part of their routine testing algorithm.

2. ***To sequence regions that allow strain differentiation within a particular virus type.*** The Virology/Serology Section provides Norovirus and Enterovirus positive samples to the MB section to determine the strain of Norovirus or the type of Enterovirus by sequencing. Rabies virus may also be submitted to determine the specific type. Norovirus results are submitted to the CaliciNet database maintained by the Centers for Disease Control & Prevention in Atlanta, GA.

Sanger Sequencing *allows us to examine the bases that make up portions of the genome of different pathogens. The whole genome is composed of only A, T, G, and Cs as seen below. It is beautifully simple and exact.*

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>dbj|AB685427.1| Rhodococcus corynebacterioides gene for 16S ribosomal RNA,
Identities = 460/460 (100%), Gaps = 0/460 (0%)
Query 1    GGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGGCCCTTCGGGGTA  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 2  GGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGGCCCTTCGGGGTA  61


>gb|AY438619.1| Nocardia corynebacterioides NRRL 21057 16S ribosomal RNA gene,
Identities = 460/460 (100%), Gaps = 0/460 (0%)
Query  1   GGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGGCCCTTCGGGGTA  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1   GGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGGCCCTTCGGGGTA  60
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