



MICROBIAL SOLUTIONS

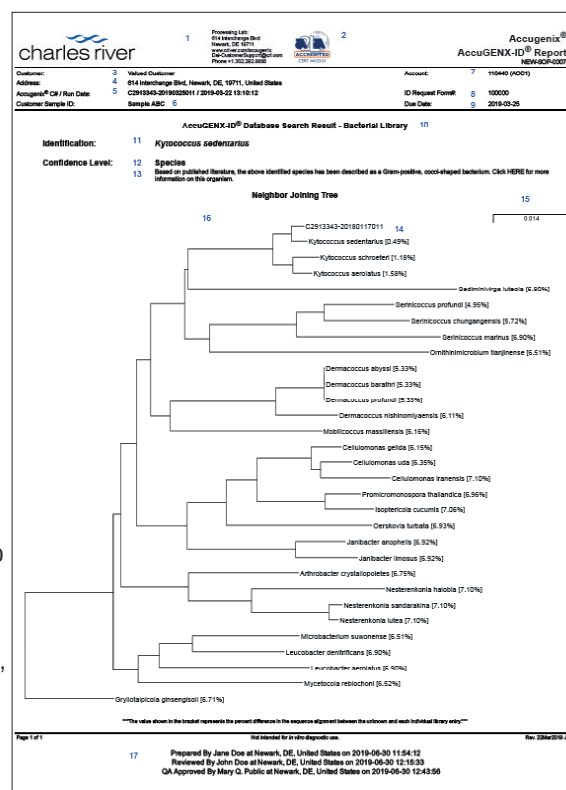
AccuGENX-ID® Identification Report Guide for BacSeq and FunITS

Interpretation

Sample C2913343- 20190325011 has a closest match of *Kytococcus sedentarius* and links directly to it in the Neighbor Joining Tree. The sample and its closest match have 0.49% difference in sequence in the first 500 base-pair region of the 16S gene. The identification result is *Kytococcus sedentarius*, with a Species level of confidence.

Section Descriptions

1. Lab where your sample was processed.
2. A2LA logo with Processing Lab ISO 17025 accreditation certificate number.
3. Your company name.
4. "Ship To" address from your Identification Request Form.
5. Unique sample code (C#) assigned by Charles River, followed by the date and time the data was generated.
6. Your sample ID, as provided on the Identification Request Form.
7. Your six-digit Account #, followed by a four-digit alpha numeric code in parenthesis.
8. Each Identification Request Form received with samples has a unique number.
9. The due date of your Identification Report.
10. Name of the microbial organism reference library used to identify this sample.
11. Final identification result.
12. Confidence level of the identification (Species, Species*, Genus, Family, Order, Class or No Match [for fungi only: the organism was sequenced successfully, but no taxonomic classification could be confidently made based on our current ITS2 fungal library]).
13. Descriptive information about the identified species (only for Species-level identifications).
14. The result of the alignment represents the percent genetic difference, or # of nucleotide differences, between the unknown sample sequence and the library entry sequence.



15. The % value is the length of the line next to it; similar to a legend on a map, it provides a horizontal distance scale for the Neighbor Joining Tree. The % value is somewhat arbitrary but falls between the % differences of the 1st and 10th closest matches.
16. Neighbor Joining Tree – visually represents the genetic differences between your isolate and its 30 closest matches.
17. Electronic signatures in compliance with FDA regulation 21 CFR Part 11.

Methods

Charles River AccuGENX-ID® identifies microorganisms through comparative sequencing of the 16S ribosomal RNA (rRNA) gene in bacteria and the ITS2 region in fungi. The DNA sequence is assessed for quality, assembled, and compared to the validated Accugenix® library. A phylogenetic tree is interpreted by trained data analysts in order to make the identification. Our microbial phylogeneticists use a combination of the genetic variability, branching order of the neighbor joining tree, and knowledge of the interspecies variation when interpreting the reports and assigning the taxonomic confidence level. Occasionally, there are organisms that are too closely related and have a high degree of conservation in the ribosomal RNA regions such that 16S or ITS2 sequencing is not able to separate them (our “Species*” confidence level, which indicates that “*The unknown matches two or more closely related species”).

The proprietary methods employed by Charles River compare sample sequences against full-coverage proprietary libraries, result in conclusive data interpretation, and an identification with assigned confidence levels based on phylogenetic analyses. Utilizing these scientifically proven methods, and validated, continuously curated, proprietary libraries provide the most accurate microbial identifications.