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.

Processing Lab:
614 Interchange Blvd
Newark, DE 19711
www.criver.com/accugenix
Del-CustomerSupport@crl.com
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Accugenix®
AccuGENX-ID® Report
NEW-SOP-00071

Customer:	Valued Customer
Address:	614 Interchange Blvd, Newark, DE, 19711, United States
Accugenix® C# / Run Date:	C2913343-20190325011 / 2019-03-22 13:10:12
Customer Sample ID:	Sample ABC
Account:	110440 (ACC1)
ID Request Form#:	100000
Due Date:	2019-03-25

AccuGENX-ID® Database Search Result - Bacterial Library

Identification: *Kytococcus sedentarius*

Confidence Level: **Species**
Based on published literature, the above identified species has been described as a Gram-positive, cocci-shaped bacterium. Click HERE for more information on this organism.

Neighbor Joining Tree

0.014

C2913343-20180117011
Kytococcus sedentarius [0.49%]
Kytococcus schroeteri [1.18%]
Kytococcus aerolatus [1.58%]
Sediminivirga luteola [6.90%]
Serinicoccus profundi [4.95%]
Serinicoccus chungangensis [5.72%]
Serinicoccus marinus [6.90%]
Ornithinimicrobium tianjinense [6.51%]
Dermacoccus abyssi [5.33%]
Dermacoccus barathri [5.33%]
Dermacoccus profundi [5.33%]
Dermacoccus nishinomiyaensis [6.11%]
Mobilicoccus massiliensis [6.16%]
Cellulomonas gelida [6.15%]
Cellulomonas uda [6.35%]
Cellulomonas iranensis [7.10%]
Promicromonospora thailandica [6.96%]
Isoptericola cucumis [7.06%]
Oerskovia turbata [6.93%]
Janibacter anophelis [6.92%]
Janibacter limosus [6.92%]
Arthrobacter crystallopoietes [6.75%]
Nesterenkonia halobia [7.10%]
Nesterenkonia sandarakina [7.10%]
Nesterenkonia lutea [7.10%]
Microbacterium suwonense [6.51%]
Leucobacter denitrificans [6.90%]
Leucobacter aerolatus [6.90%]
Mycetocola reblochoni [6.52%]
Gryllotalpicola ginsengisoli [6.71%]

The value shown in the bracket represents the percent difference in the sequence alignment between the unknown and each individual library entry.

Page 1 of 1   Not intended for in vitro diagnostic use.   Rev. 22Mar2019 JDB

Prepared By Jane Doe at Newark, DE, United States on 2019-06-30 11:54:12
Reviewed By John Doe at Newark, DE, United States on 2019-06-30 12:15:33
QA Approved By Mary Q. Public at Newark, DE, United States on 2019-06-30 12:43:56
This document has been signed electronically by the individual(s) shown above, in compliance with FDA Regulation CFR 21 Part 11.

EVERY STEP OF THE WAY

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 were generated.
6. Your sample ID, as provided on the Identification Request Form.
7. Your six-digit Account Number, 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 [The organism was sequenced successfully, but no taxonomic classification could be confidently made based on our current microbial libraries]).
13. Descriptive information about the identified species (only for Species-level identifications).
14. The value shown in the brackets represents the percent difference in the sequence alignment between the unknown and each library entry.
15. The scale bar represents the number of nucleotide substitutions per site, similar to a legend on a map.
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 microoganisms 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.

Find more information at www.criver.com/microbial-sequencing.

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