

Biolog Lab Services Report Interpretation Guide – DNA Sequencing

Top ten matches to the Biolog DNA database

16S DNA: 504 base pairs			
D16M3 DNA Match Report - LIBRARY USED			
Match	%Diff	Length	Library Entry Name
1	.20	504	Micrococcus-luteus
2	2.17	505	Micrococcus-lylae-R2855
3	2.38	503	Micrococcus-antarcticus
4	2.58	503	Micrococcus-lylae-T
5	2.97	503	Pseudarthrobacter-phenanthrenivorans-R1257
6	2.97	504	Glutamicibacter-nicotianae
7	3.16	504	Arthrobacter-oryzae-T
8	3.17	503	Pseudarthrobacter-phenanthrenivorans-T
9	3.17	504	Arthrobacter-pascens/ramosus
10	3.37	505	Arthrobacter-woluwensis

KEY: % Genetic Difference, Size of DNA Sequence, Database Entries

Genetic relationships are expressed in the form of Percent Genetic Differences (%GD). This is calculated as the percentage of positions that differ when two sequences are aligned with minimal sequence gaps.

A species level match may be assigned if the %GD between the unknown and the closest match is less than the approximate average %GD between species within that genetic family, which is usually 1%.

We utilize phylogenetic trees to approximate the average inter-species %GD and have found, through our 10+ years of database building experience, that it ranges from 0.5% to 3.0%, with an average of about 1%.

Thus, we will assign a species level match only if the %GD between the unknown and a database entry is less than 3% and is less than the average %GD between species related to it.

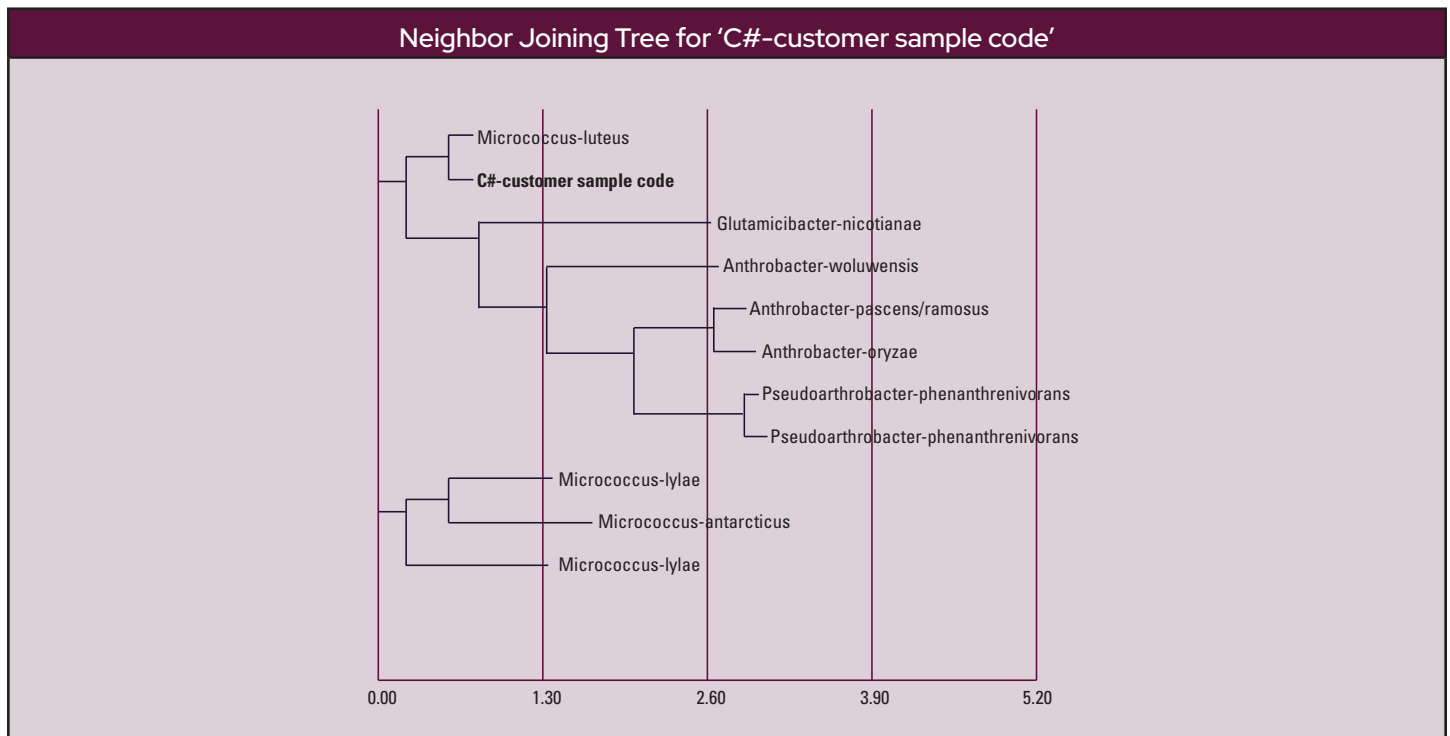
A genus level match will be assigned when the sequence does not meet the requirements for a species level match, but still clusters within the branching of a well-defined genus.

Concise Alignment

Concise Alignment with <i>Micrococcus-luteus</i>	
Sample:	(373) C
LibEnt 1:	(373) A

The concise alignment displays differences in the library sequence vs that of the customer sample. The number indicates the position in the sequence at which the difference starts. In this sample, the only difference between the sample and the library entry is at position 373; the sample contains a "C", whereas the library sequence has an "A" at this position.

Neighbor Joining Tree



The neighbor-joining tree displays the inter-species relationships between the top ten matches and the unknown. Distances can be calculated by summing the horizontal distances. For examples, the estimated %GD between *M. luteus* and *M. lylae* is the sum of segments A, B, and C.

Taxonomy

We strive to keep pace with the ever-changing current taxonomy with respect to naming organisms within our database. We use multiple taxonomic resources to check current names and changes frequently. If there is a name change or an organism that has a basonym or synonym that will better explain the results, we will note that on the report.

References

Montgomery, S. O., S. Anderson, M. G. Waddington, J. G. Bartell, G. Nunn, and Foxall, P. 1999. Variation in Bacterial Interspecific Distances – New Rules for interpretation of 16S rDNA Sequences? Abstract, 1999 International Union of Microbiological Societies Meeting, Sydney.

Palys, T., L.K. Nakamura, and F. M. Cohan. 1997. Diversity in the Bacterial World: the Role of DNA Sequence Data. IJSB. 47:1145-1156.

Further Reading

16S Microbial Identification System Evaluation Papers

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Patel, J. B., D.G.B. Leonard, X. Pan, J. M. Musser, R. E. Bergman and I. Nachamkin. 2000. Sequence-Based Identification of Mycobacterium Species Using the MicroSeq 500 16S rDNA Bacterial Identification System. J. Clin. Micro. 38:246-251.

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