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Summary

Single- and multilocus sequence typing (S/MLST) is a technique that can be used to distinguish between closely related isolates of a single microbial species by comparing moderately to highly variable DNA sequences. SLST methods involve sequencing one gene that is known to harbor variable DNA sequences, and with MLST, multiple genes of moderate variability are sequenced.

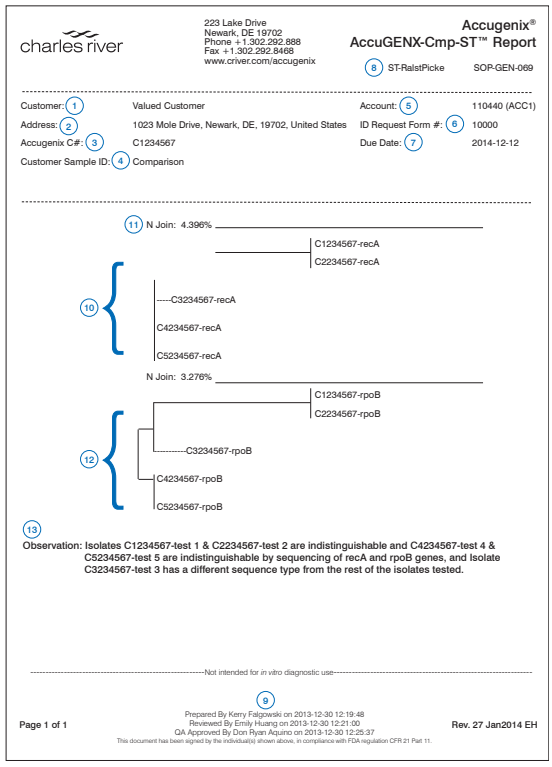
MICROBIAL SOLUTIONS

AccuGENX-ST™ Strain Typing Report Interpretation Guide

Introduction

The gene sequences from each isolate are aligned and compared in a phylogenetic tree (neighbor-joining tree) which shows the amount of conservation and divergence in the DNA of that gene region.

We present the relatedness as a percent difference between the gene sequences. The following example is from samples submitted for strain typing after obtaining a 16S ID of *Ralstonia picketii*. The MLST method for *R. picketii* entails sequencing two protein coding genes. You will receive a comparison report evaluating all the samples which are submitted on an individual Strain Typing Request Form (STRF). The report presents the resulting trees from each of the protein coding genes used for the strain typing. The composition of the trees will depend on the total number of samples that have been submitted for analysis. For example, if two samples are submitted for analysis, the relationship between these two samples will be presented on the comparison report for each gene. If you want to have comparisons made between samples submitted under different request forms, you can request that documentation from your Tech Support Specialist.



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Accugenix®
AccuGENX-Cmp-ST™ Report

(8) ST-RalstPicke SOP-GEN-069

Customer: (1) Valued Customer
Address: (2) 1023 Mole Drive, Newark, DE, 19702, United States
Accugenix C#: (3) C1234567
Customer Sample ID: (4) Comparison
Account: (5) 110440 (ACC1)
ID Request Form #: (6) 10000
Due Date: (7) 2014-12-12

(11) N Join: 4.396%
C1234567-recA
C2234567-recA
(10)
-----C3234567-recA
C4234567-recA
C5234567-recA
N Join: 3.276%
C1234567-rpoB
C2234567-rpoB
(12)
---------C3234567-rpoB
C4234567-rpoB
C5234567-rpoB

(13)
Observation: Isolates C1234567-test 1 & C2234567-test 2 are indistinguishable and C4234567-test 4 & C5234567-test 5 are indistinguishable by sequencing of recA and rpoB genes, and Isolate C3234567-test 3 has a different sequence type from the rest of the isolates tested.

----------Not intended for *in vitro* diagnostic use----------

(9)
Prepared By Kerry Falgowski on 2013-12-30 12:19:48
Reviewed By Emily Huang on 2013-12-30 12:21:00
QA Approved By Don Ryan Aquino on 2013-12-30 12:25:37
This document has been signed by the individual(s) shown above, in compliance with FDA regulation CFR 21 Part 11.

Page 1 of 1 Rev. 27 Jan2014 EH

Section Descriptions

Standard Information

1. Your company name
2. “Ship To” address from your STRF
3. Unique sample code (C#) assigned by Charles River for the strain typing comparison
4. Customer sample ID: Indicates this is a strain typing comparison report
5. Your 6-digit account #, followed by a 4-digit alpha-numeric code in ( )
6. The unique STRF code number
7. The due date of your identification report (Y-M-D)
8. Target species abbreviation for this report’s strain typing analysis
9. Electronic signatures in compliance with FDA regulation 21 CFR Part 11

Phylogenetic (N Join) Trees and Observations

10. Phylogenetic neighbor-joining (N Join) tree for the first gene target, recA, for each isolate submitted on the current STRF. Each C# is followed by the name of the gene sequence under evaluation (e.g., recA or rpoB).
11. The N Join % distance measurement, the percent sequence difference. The length of the line next to this value is proportional to the percentage (similar to a legend on a map) and it provides the horizontal distance scale for the N Join tree.
12. N Join tree for the second gene target (if required for the species being analyzed), rpoB in this case, with the % distance measurement.
13. Observation. Comparisons are made between all the samples submitted on the current STRF only.
    A statement is made as to whether the isolates can be distinguished between, based on the listed genes.

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