
Genomic analysis report

Archive_test

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Anses

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Test report addressed to

XXXXXXXXXXXXXXXXXX

Request	
Archive name	Archive_test
Number of analyzed strains	2
Unanalyzed strains	NA
Date of analysis	2020-06-22
LSA-INS-1477 Sequencing method using Starflow	

1 Results

1.1 Request

<i>Strains ID requester</i>	<i>Context of Isolation requester</i>	<i>Date of analysis</i>
<i>05CEB51</i>	<i>Food</i>	2020-06-22
<i>05CEB52</i>	<i>Milk</i>	2020-06-22

1.2 Quality report

<i>Strains ID requester</i>	<i>Number of contigs</i>	<i>N50</i>	<i>Closest reference genome</i>
<i>05CEB51</i>	5	2786542	Staphylococcus_aureus_AJ_938182
<i>05CEB52</i>	2	2586542	Staphylococcus_aureus_CP_000703

1.3 Identification and typing strains

<i>Strains ID requester</i>	<i>Species</i>	<i>Sequence Type</i>
<i>05CEB51</i>	<i>aureus</i>	5
<i>05CEB52</i>	<i>aureus</i>	2

1.4 Enterotoxin detected

<i>Strain ID requester</i>	<i>Enterotoxins detected</i>
<i>05CEB51</i>	seu(2), sex(2), seg(1), sec(1), seo(19), sen(1), sem(1), sel(1), sei(1), seh(1)
<i>05CEB52</i>	seo(99), sen(1)

**in red, are indicated enterotoxin coding gene for which a new variant was identified.*

1.5 Strain clustering

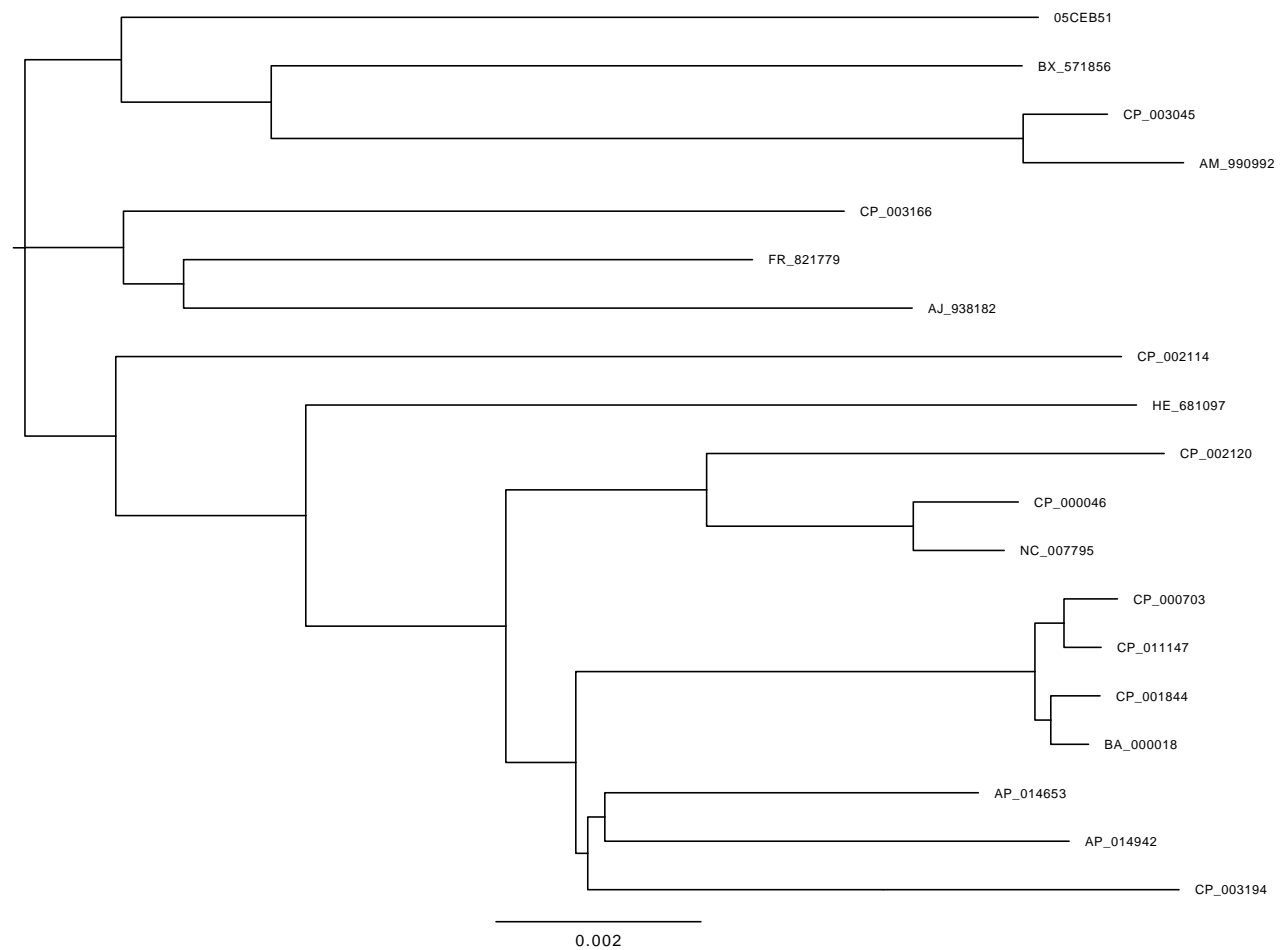


Figure 1: Phylogeny relatedness between reference genome of Staphylococcus sp. and genomes from this study. This phylogeny was obtained using Neighbor joining algorithm and based on distance matrix from k-mer analysis implemented in Fastosh.

2 Complementary informations

The parameters to evaluate quality of reads and assembly are presented in the quast report available in result archive. The thresholds used for assembly are presented in Anses internal method LSA-INS-1477 and the recommandations of quality parameters are described in guidance document XXX.

Report automatically edited, the 2020-06-22.

The test report only concerns the item analyzed, as received. This test report may only be copied in the form of a complete photographic facsimile. The laboratory can not be held responsible for any errors concerning the information provided by the requester of the analyses (information indicated in *Italics*).

It includes X annex(s)

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Validated by Deborah MERDA, LRUE project leader, *Staphylococcus* team.