

## THE ALL-SPECIES LIVING TREE PROJECT RELEASE LTPs123, September 2015

The SSU ribosomal sequence database of type strains has been updated with the new species validly published in the IJSEM journal up to May 2015 [issue 65(Pt\_05)]. This current release is available online at <http://www.arb-silva.de/projects/living-tree/>.

As a result of this last upgrade, the current ARB databases contains a total of 11,939 (SSU) and 792 (LSU) sequences belonging to various type strains and all sequences can be found in SILVA's SSURef123 and LSURef102. Please read the summary below concerning changes of the current release.

### Changes in the SSU dataset

Three species already included in previous LTP releases have now a better quality sequence (new acc). Issues 65(Pt\_01) to 65(Pt\_05) were tracked in order to build a list of new validly published species with their corresponding type strain SSU sequence. Out of more than 320 new entries listed, 20 were new combinations of species already present in the tree which names only needed to be updated (new name) ([table1.pdf](#)). Ten names have been permanently deleted from the database.

In total, 383 new distinct species and nine sequence substitutions have been added into the database and genealogical tree. A manual cross-check was undertaken between the sequence-associated information provided by SILVA and the effective publication or validation in IJSEM. Overall, 80.68% of the sequences carried outdated information on their species name ([table2.pdf](#)). Consequently, the corrected and/or updated species name now appears in the ARB database in the field called "fullname\_ltp".

### 23S rRNA-based All-Species Living Tree

The present size increase of the LSURef SILVA database demands an update of the LTP\_LSU dataset. This dataset has not been updated since the release LTP\_s102. An update is being prepared but has not an estimated date of release.

### SSU-tree

The LTP\_s121 dataset was used as the reference for the automatic alignment of the new 386 sequences using the SINA aligner (<http://www.arb-silva.de/>) followed by a manual curation of misplaced bases. The sequences were inserted in the LTP\_s121 tree using the parsimony tool implemented in the ARB software package (<http://www.arb-home.de/>).

### Orphan species.

During this update 13 new "orphan" species have been identified, and four former orphan species now are represented by an SSU sequence. As a result, the LTP has 27 orphan species in the current release.

## Detected orphan species:

Name	SSU sequence status.
<i>Actinobaculum massiliense</i>	Lost pure culture
<i>Alkalinema</i> (genus)	Cyanobacteria. 16S partial sequence
<i>Bacillus oryzaecorticis</i>	1109 bp
<i>Bacillus subtilis</i> subsp. <i>inaquosorum</i>	1168 bp
<i>Bartonella rochalimae</i>	1171 bp
<i>Borrelia bavaricus</i>	No 16S seq. Available
<i>Borrelia kurtenbachii</i>	No 16S seq. Available
<i>Bradyrhizobium cytisi</i>	vector contamination
<i>Bradyrhizobium neotropale</i>	748 bp
<i>Bradyrhizobium rifense</i>	vector contamination
<i>Chromobacterium piscinae</i>	1140 bp
<i>Citrobacter pasteurii</i>	No 16S seq. Available
<i>Desulfobulbus desulfuricans</i> subsp. <i>desulfurians</i>	poor quality
<i>Desulfobulbus marinus</i>	poor quality
<i>Dyadobacter jiangsuensis</i>	Not freely published (requested to author).
<i>Edwardsiella piscicida</i>	704 bp
<i>Geobacillus galactosidasius</i>	ambiguous
<i>Micromonospora haikouensis</i>	1108 bp
<i>Mycobacterium minnesotense</i>	862 bp
<i>Pantanalinema</i> (genus)	Cyanobacteria. 16S partial sequence
<i>Pararhodobacter aggregans</i>	1195 bp
<i>Rhodobacter ovatus</i>	1135 bp
<i>Siccibacter colletis</i>	No 16S seq. Available
<i>Streptomyces rosealbus</i>	ambiguous
<i>Streptomyces sundarbensensis</i>	bad quality
<i>Sulfuriferula multivorans</i>	No 16S seq. Available
<i>Vibrio inhibens</i>	No 16S seq. Available

## Partial 16S rRNA sequences in LTP.

Solid phylogenetic analyses should not include sequences which length is **shorter than 1300 nucleotides**. These sequences are recommended to be included by parsimony onto a pre-fixed topology. This release includes 77 sequences of such length (between 1200 and 1300 nucleotides) and they are highlighted in red color (**ARB\_color = 1**).

## Taxonomy disclaimer

Former releases inherited taxonomy paths from LPSN (<http://www.bacterio.net/-classifphyla.html>) . Since the release s119 this is not possible for all entries because the LPSN archive is under development and the taxonomy files are not fully updated. Hence, the fields **tax\_ltp** and **hi\_tax\_ltp** have been built manually upon visual inspection of the Living-Tree and scrutinisation of original articles where new species were published. Although these fields were built carefully, users are warned that disagreement between LTP taxonomy fields and official classifications can occur.

## Supplementary files

[LTPs123\\_description\\_of\\_fields.pdf](#): description of fields introduced by the Living Tree Project.

[fasta\\_LTPs123.eft](#): export filter to extract data from LTP-ARB databases.

[LTPs123\\_SSU.arb](#): ARB database.

[LTPs123\\_SSU.csv](#): CSV database: acc, start and stop positions plus all LTP fields.

[LTPs123\\_SSU.aligned.fasta](#): multifasta alignments of type strains. The headers of the sequences accordingly stand for the following information: accession number, start and stop position, length, type of sequence, fullname\_ltp, hi\_tax\_ltp.

[LTPs123\\_SSU.compressed.fasta](#): multifasta datasets of unaligned type strain sequences. The headers of the sequences accordingly stand for the following information: accession number, start and stop position, length, type of sequence, fullname\_ltp, hi\_tax\_ltp.

[LTPs123\\_SSU\\_tree.pdf](#): the complete All-Species Living Tree as a .pdf file.

[LTPs123\\_SSU\\_tree\\_overview.pdf](#): an overview of the tree in .pdf format.

[LTPs123\\_SSU\\_tree.newick](#): the complete tree in newick format.

[Table1\\_LTPs123\\_SSU.pdf](#): list of changes applied since the former release LTPs121, including: insertions, deletions and modifications.

[Table2\\_LTPs123\\_SSU.pdf](#): outdatings found in the species name of the new SSU entries.

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## Contact us

Thank you for all the requests and comments received to date regarding any aspect of the All-Species Living Tree Project. The additional input from the scientific community is helping us to develop our product throughout the updates. Therefore, please do not hesitate to contact us at [living-tree@arb-silva.de](mailto:living-tree@arb-silva.de).