NamesforLife Release 20190402

During March 2019, there were a total of 183 changes in the taxonomy of prokaryotes with validly published names, as compared to **NamesforLife Release 20190226**. These changes include 111 novel taxa (one new subspecies, 89 species, 6 genera and one family), 1 species reduced to the rank of subspecies, and 17 new combinations, 36 transfers of taxa and 18 changes in the preferred names appearing in the NamesforLife condensed taxonomy.

NamesforLife maintains and distributes two views of the monthly state of prokaryotic taxonomy, based on recent updates of the published record and supporting data. The taxonomies are purely hierarchical, and based on the validly published names (those which conform to the principles and rules set forth in the *International Code of Nomenclature of Prokaryotes*) appearing in the *International Journal of Systematic and Evolutionary Microbiology*. These taxonomies represent a consensus view of experts who apply a contemporary method of classification including phylogenetic analysis of the small ribosomal subunit (16S rRNA gene), pairwise comparison of genome sequences and phenotypic properties.

Table 1. A summary of the current state of taxonomy of prokaryotes with validly published names.

	Complete Taxonomy[a]	Condensed Taxonomy[b]	HQ16S[c]	Genomes (type)[d]	Genomes (non-type)[e]	Genomes (combined)
Phyla	49	40	40	39	35	39
Classes	161	97	99	90	75	91
Orders	388	245	245	215	170	219
Families	801	567	566	476	360	499
Genera	3,484	3,000	2,984	2,003	1,107	2,195
Species/Subsp.	26,279	16,082	15,963	7,308	4,203	9,093

[a] The *Complete Taxonomy* includes all published synonyms, homonyms and names that may be considered illegitimate, rejected, orthographically or grammatically incorrect or not validly published for a documented reason. It is used to establish nomenclatural accuracy and determining the correct current state of a name and to correctly interpreting the names appearing in older literature. It also includes a growing subset of published *Candidatus* taxa.

[b] The *Condensed Taxonomy* is a view of the current state of prokaryotic taxonomy and nomenclature that leverages features of the NamesforLife Information Architecture. Each species/subspecies is uniquely represented in a single point in the hierarchy, based on its most recent validly published name or revision in its circumscription or properties. Mapping to earlier states and all associated data and literature is addressed using NamesforLife DOIs.

[c] The *HQ16S* data sets consists of curated, high-quality 16S rRNA gene sequences used in the published descriptions of type strains of species/subspecies of bacteria and archaea with validly published names. Linking to verified deposits of viable type material in over 125 culture collections as well as earlier synonyms, the *HQ16S* dataset allows for accurate identification and naming of > 98% of bacteria and archaea with validly published names.

[d-e] NamesforLife genome sequence data is a continuously updated version of publicly available prokaryotic genome assemblies. **Release 20190402** contains 194,720 records including 9,046 assemblies that are verified as sourced from 7,321 type strains with validly published names. Four hundred and eighty-seven type strain genome records were re-annotated to reflect the most recent changes in nomenclature. An additional 148,891 assemblies could be associated with 9,093 taxa with validly published names at varying levels of taxonomic resolution. This includes 31,703 records in which the nomenclature had been previously re-annotated. Of the remaining sequence records, 5,080 were identified as *Candidatus* taxa and could be placed into 473 discrete "groups". The remaining 31,703 sequences were associated with names that have no standing in the nomenclature of prokaryotes.

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