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Taxonomic Relationships among the Clostridia

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Clostridia are prokaryotic bacteria belonging to the phylum Firmicutes, the Gram-positive (mostly), low G + C bacteria that currently contains three classes, "*Bacilli*", "*Clostridia*", and "*Erysipelotrichia*". The class "*Clostridia*" contains the order *Clostridiales*, within which the family *Clostridiaceae* contains 13 genera distributed among three paraphyletic clusters and a fourth clade represented by a single genus. The first clostridial cluster contains the genus *Clostridium* and four other genera. The genus *Clostridium* has been extensively restructured, with many species moved to other genera, but it remains phylogenetically heterogenous. The genus currently contains 204 validly described species (http://www.bacterio.net), of which approximately half are genuinely *Clostridium*.

The main pathogenic clostridial species, *Clostridium botulinum*, *Clostridium chauvoei*, *Clostridium haemolyticum*, *Clostridium novyi*, *Clostridium perfringens*, *Clostridium septicum*, and *Clostridium tetani*, clearly belong to the genus *Clostridium* because they share common ancestry with the type species *Clostridium butyricum*. These species belong to the phylogenetic group described by Collins *et al*. (1994) as "cluster I", and are *Clostridium* sensu stricto. The taxonomy of *C. botulinum* is unique since it is currently defined as *C. botulinum* only by the ability to produce one or more botulinum toxins; however, strains that can do this belong to at least four *Clostridium* species. This situation is complex and taxonomically confusing, since strains of other species, such as *C. butyricum* which may produce botulinum toxin and cause human botulism, have been given their own species designation (that is, not *C. botulinum*). To compound the inconsistency around species designation in the taxonomy of *Clostridium*, *C. novyi* type A and *Clostridium haemolyticum* belong to the same genospecies as *C. botulinum* group III (the agents of animal botulism). Many *Clostridium* species which do not belong to this genus sensu stricto, as defined by the type species *C. butyricum*, are distributed among the genera of *Clostridiaceae* but are described as "incertae sedis". These fall into different phylogenetic clusters throughout the low G +C Gram-positive phylum,

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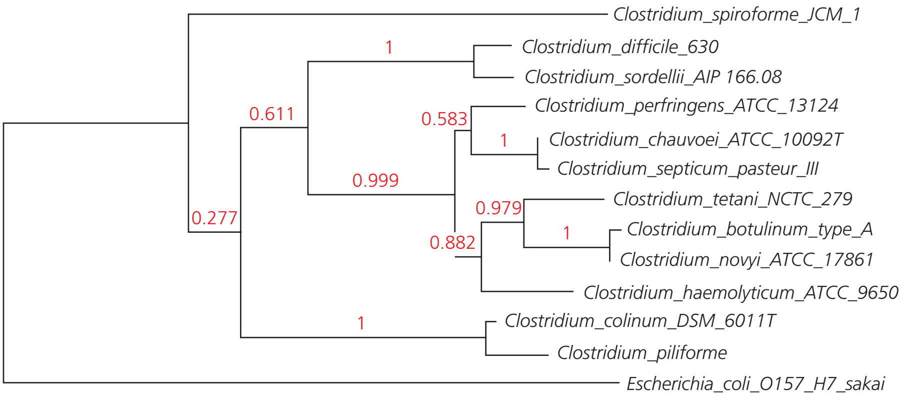

Figure 1.1 Phylogenetic tree displaying the relationship between *Clostridium* species. *Escherichia coli* from the *Enterobacteriaceae* family was used as an out group. The phylogenetic tree was constructed using the "One Click" mode with default settings in the Phylogeny.fr platform (http://phylogeny.lirmm.fr/phylo_cgi/index.cgi). The numbers above the branches are tree support values generated by PhyML using the aLRT statistical test.

and belong to distinct 16S rRNA gene-sequence-based clusters that represent different genera and different families. For example, *Clostridium difficile* and *Clostridium sordellii* fall into cluster XIa ("*Peptostreptococcaceae*"), *Clostridium colinum* falls into cluster XIVb ("*Lachnospiraceae*"), and *Clostridium spiroforme* falls into cluster XVIII, a new family. Figure 1.1 shows these relationships based on 16S rRNA sequences.

Interestingly, the genus *Sarcina* falls within the genus *Clostridium* sensu stricto, and indeed should have taxonomic preference as the genus name. This taxonomic precedence, as well as the genus attribution of the non-*Clostridium* sensu stricto animal and human pathogens currently assigned the genus name *Clostridium*, seems unlikely to change in the near future because of the chaos and the potential hazard that such otherwise justified genus name changes would engender. Future taxonomic classification based on whole-genome sequencing may help to resolve some of the complexity of clostridial classification.

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