

## Phylogenomics of the phylum Ciliophora

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The phylum Ciliophora is a diverse and evolutionarily cohesive lineage. Recently, phylogenomic analyses have been used to examine relationships within and among ciliate classes. However, not all classes were represented in these analyses, thus their deep phylogenetic relationships between remain unclear. Here, we expanded taxon sampling and generated a dataset that includes representative taxa from all ciliate classes (except Ciliacotrichea). The new dataset contains genomic and transcriptomic data from over 60 ciliate species, 12 of which are newly sequenced. We determined which lineages use non-canonical genetic codes and used this information to correctly predict protein sequences. We constructed a supermatrix of over 250 genes. The subphyla Postciliodesmatophora and Intramacronucleata are recovered. Within the Intramacronucleata, two robust superclades are formed: the Spirotrichea, Armophorea, Litostomatea (SAL) and the Colpodea, Oligohymenophorea, Nassophorea, Plagiopylea, Prostomatea, Phyllopharyngea (CON3P).