Streptomyces coelicolor

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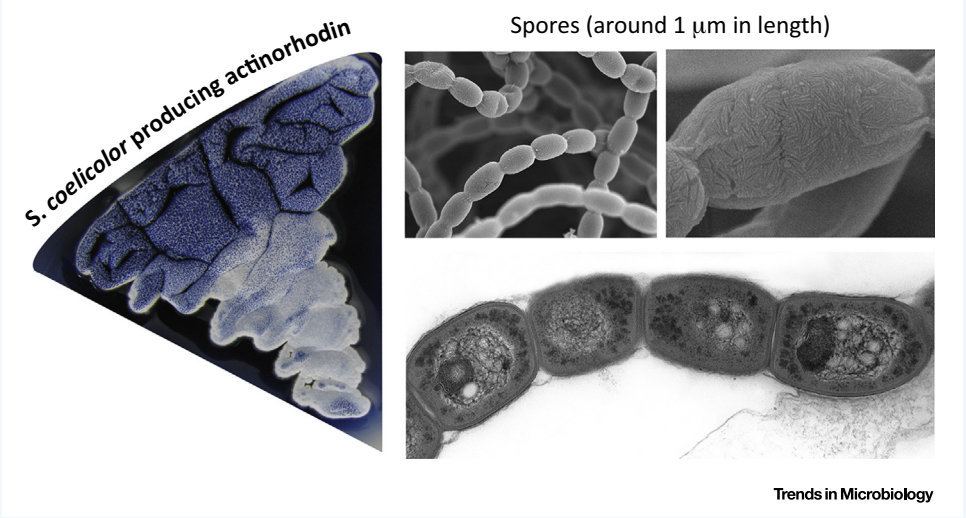
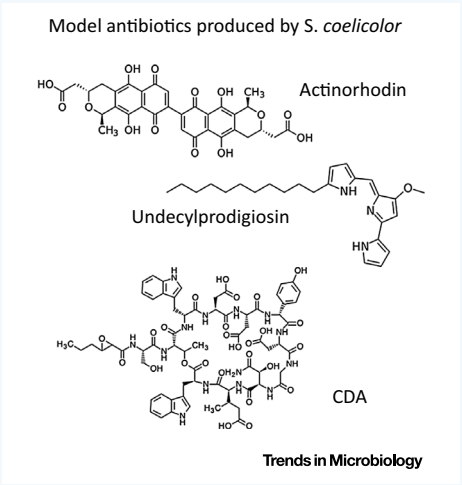


Streptomyces coelicolor A3(2) is amongst the best studied representatives of the genus *Streptomyces*, which is the largest genus within the Actinobacteria. Streptomycetes have a remarkably complex developmental life cycle and the capacity to produce a plethora of natural products. Whilst referred to as *S. coelicolor* A3(2), this strain is more closely related to *Streptomyces violaceoruber* ISP5049 than to the type strain for the species, *S. coelicolor* Müller. However, the name was maintained as it had become the workhorse for genetics and a model for development and antibiotic production. Streptomycetes are multicellular mycelial bacteria that grow as vegetative hyphae, which are compartmentalized via cross-walls. Reproduction occurs when specialized aerial hyphae differentiate into chains of spores. Streptomycetes produce around half of the clinically used antibiotics and other pharmaceutically useful natural products such as anthelmintics, anticancer agents, and immunosuppressives.



TAXONOMY AND CLASSIFICATION:
KINGDOM: Bacteria
PHYLUM: Actinobacteria
ORDER: Actinomycetales
SUBORDER: Streptomicineae
FAMILY: Streptomycetaceae
GENUS: *Streptomyces*
SPECIES: *Streptomyces coelicolor*
Filamentous Gram-positive sporulating bacteria

KEY FACTS:
Single 8.2 Mbp chromosome, with a G +C content of 72%.

The genome is linear and has a centrally located origin of replication. The ends of the chromosome carry terminal inverted repeats with covalently linked proteins that protect the free 5′ ends.

The genome of *S. coelicolor* A3(2) encodes 7825 proteins, more than the eukaryote *Saccharomyces cerevisiae*.

S. coelicolor A3(2) is capable of undergoing the loss of more than 1 Mbp of its genome at either chromosome end.

Professor Sir David Hopwood chose *S. coelicolor* because he felt that its pigments would form ideal markers for genetics experiments, long before it was known that they were antibiotics.

Prior to genome sequencing, *S. coelicolor* A3(2) was known to produce the red-pigmented prodiginine antibiotic, undecylprodigiosin, the blue-pigmented polyketide actinorhodin, and the nonribosomal peptide calcium-dependent antibiotic CDA.

Genome sequencing revealed the presence of at least 18 further biosynthetic gene clusters (BGCs) for specialized metabolites, many of which are not expressed under standard laboratory conditions.

S. coelicolor was the first organism to grow in the absence of its cell-division machinery.

S. coelicolor is a model organism for the study of morphological development of Actinobacteria. Its *bld* and *whi* mutants, which fail to produce either aerial hyphae or spores, respectively, are used to understand the regulatory networks that control sporulation.

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  https://doi.org/10.1016/j.tim.2018.12.008

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