

## Microbiology Of Comand

Bacteria (Order)	%
actinomycetales	23.83899138
clostridiales	13.36919014
gemmatimonadales	10.98837546
bacillales	8.00994737
sphaerobacterales	6.74435641
xanthomonadales	4.90717714
bacteroidetes order ii. incertae sedis	3.52977464
chromatiales	3.18277331
sphingobacterales	2.17454167
thermomicribiales	1.54319203
acidimicrobiales	1.33884680
anaerolineales	1.12968211
cytophagales	1.08630694
pseudomonadales	0.86075608
acidithiobacillales	1.04582345
phycisphaerales	0.81448923
thermoanaerobacterales	0.81256145
rhodocyclales	0.59183005
rhodospirillales	0.44724616
desulfuromonadales	0.41158213
thermodesulfobacterales	0.36049583
planctomycetales	0.35953193
chloroflexales	0.31326509
rubrobacterales	0.29591502
burkholderiales	0.27181771
thermales	0.26410657
flavobacterales	0.26314268
chlorobiales	0.23229811
sphingomonadales	0.20723691
thermoleophilales	0.20627301
ignavibacterales	0.20434523
verrucomicrobiales	0.16386174
enterobacterales	0.16193395
desulfovibrionales	0.15229503
nitriliruptorales	0.14747557
opituales	0.10795597
solirubrobacterales	0.07711141
holophagales	0.06843637
thermolithobacterales	0.06361691
methylophilales	0.05976134

bdellovibrionales	0.05879745
candidatus brocadiales	0.03566403
bacteroidales	0.03277235
bacteria	0.03277235
rickettsiales	0.02506121
methylococcales	0.01927785
lactobacillales	0.01542228
syntrophobacterales	0.01349450
natranaerobiales	0.01253060
acidobacteria	0.01060282
desulfobacterales	0.00963893
chlamydiales	0.00867503
chroococcales	0.00867503
legionellales	0.00771114
spartobacteria	0.00674725
vibrionales	0.00674725
thiotrichales	0.00674725
desulfurellales	0.00578336
hydrogenophilales	0.00578336
thermoflexales	0.00481946
dehalococcoidia	0.00289168
nitrospirales	0.00289168
oscillatoriales	0.00289168
deinococcales	0.00192779
solibacterales	0.00192779
gloeobacterales	0.00096389
acholeplasmatales	0.00096389
fibrobacterales	0.00096389
magnetococcales	0.00674725
spirochaetales	0.00385557
gaiellales	0.00385557
firmicutes	0.00289168
prochlorales	0.00192779
aquificales	0.00192779

**Actinomycetes** are of great benefit and populate the soil and outer surfaces of plant roots, driving off parasitic fungi and other soil-borne pathogens. The area, which includes the root zone and the soil closely associated with it, is known as the "Rhizosphere". These rhizosphere - inhabiting bacteria are antagonistic to plant-parasitic nematodes and inhibit egg hatch and/or penetration of roots.

The mechanisms by which antagonistic bacteria inhibit plant-parasitic nematodes include:

1. Production of antibiotics that kill nematode eggs
2. Degradation of the root exudates that the nematode relies on for location and to stimulate egg hatch
3. Induction of systemic acquired resistance (SAR).

Pasteuria spp. are endospore-forming Actinomycetes, which are parasites of invertebrates, including nematodes. Spores of these species adhere to the cuticle of the host nematodes that encounter them while moving through the soil. The bacteria's life cycle occurs within the nematode - from spores to bacteria to spores again. The bacteria multiply within the nematode eventually causing death.

Fungi (Class)	%
eurotiomycetes	41.38796895
sordariomycetes	36.45840537
orbiliomycetes	13.10352814
basidiomycota	6.29687818
agaricomycetes	0.87692196
pezizomycetes	0.80855623
dothideomycetes	0.70337819
leotiomycetes	0.47067176
glomeromycetes	0.19786620
agaricostilbomycetes	0.13081520
eukaryota	0.10517805
tremellomycetes	0.10320596
saccharomycetes	0.05784793
mortierellomycotina	0.04009913
anthozoa	0.03615495
insecta	0.03484023
aconoidasida	0.02235033
microbotryomycetes	0.01380462
chytridiomycetes	0.01248989
mucoromycotina	0.01183253
bryopsida	0.00854572
liliopsida	0.00788835
bivalvia	0.00723099
ichthyosporea	0.00723099
dinophyceae	0.00460154
cryptomycota	0.00460154
basidiobolomycetes	0.00460154
ascomycota	0.00328681
coniocybomycetes	0.00328681
hydrozoa	0.00328681
exobasidiomycetes	0.00262945
blastocladiomycetes	0.00262945
coccidia	0.00197209
xanthophyceae	0.00197209
lecanoromycetes	0.00131473
chlorophyceae	0.00065736
cystobasidiomycetes	0.00065736

**Orbiliomycetes** are a class of fungi in the Ascomycota. It includes the single order Orbiliales, which in turn includes the single family Orbiliaceae.

The Orbiliaceae are a family of saprobic sac fungi in the order Orbiliales. The family contains 288 species in 12 genera. Members of this family have a widespread distribution, but are more prevalent in temperate regions. Some species in the **Orbiliaceae** are carnivorous fungi, and have evolved a number of specialized mechanisms to trap nematodes.

This family is well known for its many nematophagous species. Shortly after coming into contact with its prey, fungal mycelia penetrate the nematode and spontaneously differentiate into functional structures, known as traps, which will ultimately digest the nematode's internal contents. There are 5 types of trap mechanisms recognized in this family:

- Adhesive network: the most common trap, formed by hyphal outgrowths that recurve into themselves to form nematode-trapping loops.
- Adhesive knob: a roughly spherical cell, attached to the hyphae either directly or on an erect stalk. Adhesive knobs are typically closely spaced along a section of hyphae.
- Nonconstricting rings: always found with the adhesive network traps, and formed from thickening hyphae that curve and fuse to the supporting stalk.
- Adhesive column: a layer of cells on a hyphae with an adhesive surface.

Constricting rings: these are rings of hyphae that swell rapidly inwards upon contact with the nematode, quickly (in 1–2 seconds) "lassoing" the victim.

Most **trapping fungi** can proliferate in soil in the absence of nematodes, meaning a resident population can exist even after nematodes have been killed off. Therefore, future infestations can be prevented.

*Through the utilization of DNA extraction techniques and gene-sequencing, we are aware that Comand contains several thousand species of bacteria and fungi and that these populations can be influenced through various production and re-inoculation techniques*