STATION 1 (Welcome)

WELCOME TO THE CBEC TINY THINGS TOUR (STATION 1)

This tour is designed to acquaint CBEC visitors with the amazingly diverse array of organisms here that are not typically noticed, mainly because they're too small to be seen without either very careful observation or the aid of a magnifier (either a handheld device or a microscope).

The tour will discuss representatives of the six kingdoms of living things (Bacteria, Archaea, Fungi, Plants, Protists, and Animals), as well as viruses. In addition to brief discussions of the particular organisms themselves, we'll consider the role that these organisms play in their immediate environment, their effect on the larger biosphere, and their ability to teach us about the past and the future.

Taking the Tour:

To take the tour, visitors may use the Tiny Things Tour map, where the 14 stations are indicated with red numbers. The map should be used in conjunction with the printable list of stations. The list has the GPS coordinates for each station, along with QR codes that provide links to the web pages that describe each station. The GPS coordinates, as well as a simple description of each location are included on each station's web page. If visitors haven't brought along a mobile device (to view the web pages), they can print a copy of the tour pages by clicking this **link**. A guided version of the Tiny Things Tour is scheduled on a regular basis. Check the CBEC schedule for upcoming guided tours.

Each web page includes a photo of the representative organism, it's common name and scientific name, a description of the station location (including its GPS location), and a description of the organism and its environment. Organism names are linked to the Encyclopedia of Life website, so that visitors can learn more about its taxonomy and various other details. The pages also include additional links and references for interested visitors (under the "Learn More" and "Notes & References" headings). Each page includes an icon, described below, that will let visitors know the range of sizes of the organism under discussion. A glossary is provided to help with words that may be unfamiliar. Linked terms are indicated by a bold, italicized font. Although the tour stations are numbered, there is no need to visit them sequentially. Check out as many or as few stations as you have time for, and in whatever order you like.

An eye icon indicates that the representative organism may be seen without the aid of a magnifier

A magnifying glass icon indicates that the representative organism typically requires a handheld magnifier to observe

A microscope icon indicates that the representative organism cannot be seen without the aid of a microscope

Tour Links:

Tour Map

List of Stations (with locations and links to web pages)

Start the Tour (Go to Station 2)

Printable (PDF) Tour Pages

Learn More:

Microbiology of Wetlands

Chesapeake Bay Microorganisms: Keys to Understanding the Ecosystem

https://www.chesapeakebay.net/discover/field-guide

Notes & References:

Bodelier P, Dedysh S. (2013) *Microbiology of wetlands*. Front Microbiol. 4:79

photo attribution: copepod – http://eol.org/pages/2625033/overview (distributable under Creative Commons license)

STATION 2

INSECT PATHOGENS OF PLANTS
SYCAMORE LACE BUG

Station Location: CBEC Visitor Center, GPS coordinates: 38°56’51.33”N, 76°13’14.54”W
[Go to List of Tour Stations] [Back to Tour Home Page (Station 1)] [Forward to Station 3]

Taxonomy

- Domain: Eukarya
- Kingdom: Animalia
- Phylum: Arthropoda
- Class: Insecta
- Order: Hemiptera
- Family: Tingidae
- Genus/Species: Corythucha ciliata

The term “**pathogen**” generally means that the organism in question can cause disease in a host. The degree of damage that is caused by the pathogen is referred to as the pathogen’s “**virulence**.” Of the various organisms that you’ll learn about on this tour, only two are generally considered pathogens, the bacterium *Vibrio vulnificus* (Station 8), and the subject of this station, the Sycamore Lace Bug, a “true bug” of the order Hemiptera. Only a tiny fraction of viruses and small organisms (bacteria, protozoa, insects, etc.) are considered pathogens. The vast majority of small organisms are not associated with plant or animal diseases, and many are beneficial to their **host**.

Sycamore Lace Bugs belong to the family Tingidae, a group of insects commonly called "lace bugs", because the insect's **pronotum** and fore wings have a lacy appearance. Lace bugs are considered "**host specific**", because they are adapted to live in a very specific environmental niche, i.e. their "host". Although the Sycamore Lace Bug may live on other species of the Sycamore genus (Platanus), the main host is the American Sycamore (*Platanus occidentalis*). The insect is native to North America, but has spread to Europe and Asia, since the 1960s. Sycamore Lace Bugs are considered to "**parasites**" of sycamore trees. Parasites are organisms that derive their nutrients from their host, at the host's expense. Successful parasites are thought to be those that can live in this manner, without killing their host. Sycamore Lace Bugs do not typically kill their host tree, although the host sycamore may die if, in addition to a lace bug infestation, it also suffers from other stress factors (repeated dry years, etc.).

Learn More:

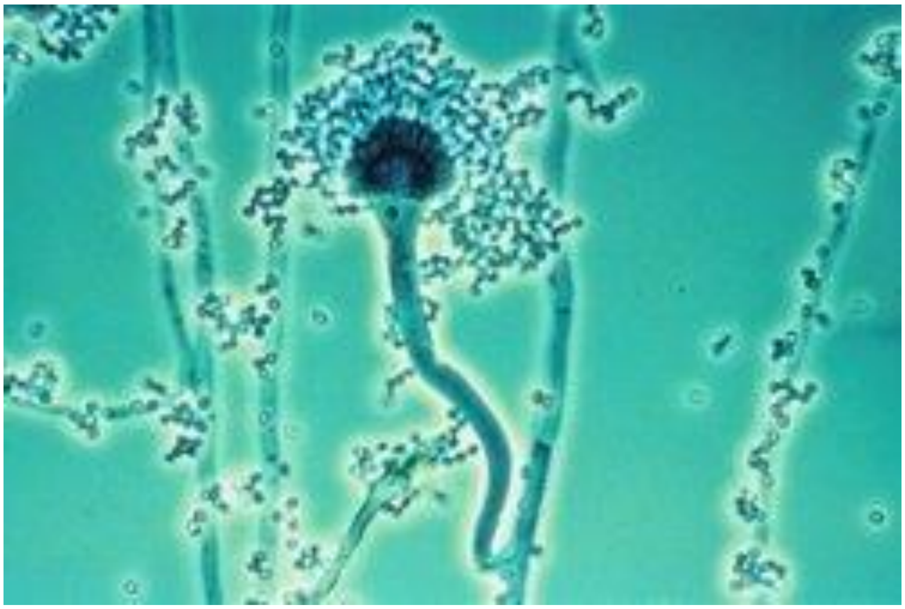
UF/IAFS: Featured Creatures – Sycamore Lace Bug

Notes & References:

photo attribution: http://eol.org/pages/612339/overview (distributable under Creative Commons License)

STATION 3

FILAMENTOUS FUNGI – SAV SYMBIONTS
ASPERGILLUS VERSICOLOR



Station Location: Marshy Creek Pier, GPS coordinates: 38°57’09.85”N, 76°13’45.44”W
[Go to List of Tour Stations] [Back to Station 2] [Forward to Station 4]

Taxonomy

- Domain: Eukaryota
- Kingdom: Fungi
- Division: Ascomycota
- Class: Eurotiomycetes
- Order: Eurotiales
- Family: Trichocomaceae
- Genus/Species: representative organism – Aspergillus versicolor

Symbionts are organisms that live in a close biological relationship with one another. The symbiotic relationship can be beneficial to both partners (**mutualism**), beneficial to only one of the partners (**commensalism**), or detrimental to one of the partners (parasitism). The association of fungi with vascular plants, such as crop plants and trees, is an example of a mutually beneficial symbiosis (with some exceptions). This relationship is called a **mycorrhizal** symbiosis, and this symbiosis is generally beneficial to the plant partner by increasing nutrient absorption and decreasing the effects of toxins and pathogens. The relationship has been well studied in terrestrial plants, but it's important to know that the health of submerged aquatic plants (SAV) may also depend on such mycorrhizal associations. The SAV beds that you can see from the pier are a complex association of the vascular plants with a wide variety of microorganisms, including many that are beneficial to the continuing health of the visible plants.

Learn More:

Surprising spectra of root-associated fungi in submerged aquatic plants

AM fungal communities inhabiting the roots of submerged aquatic plant Lobelia dortmanna are diverse and include a high proportion of novel taxa.

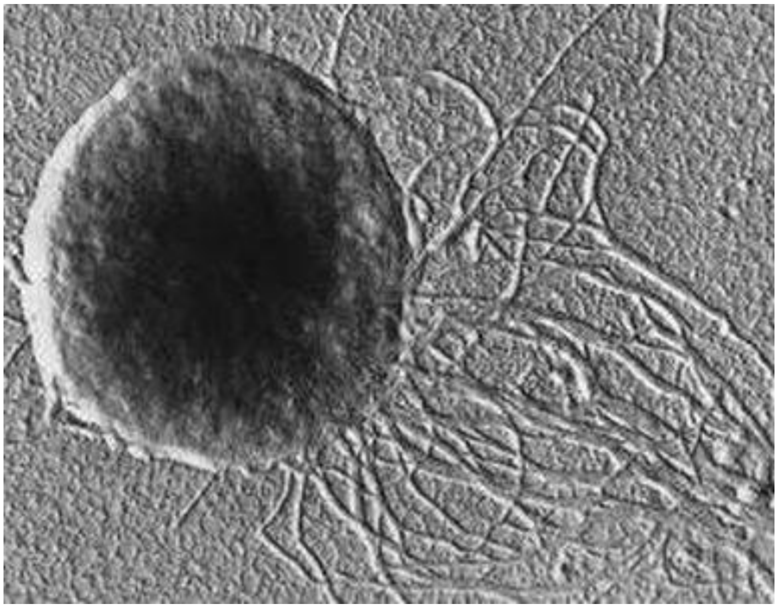
The New York Botanical Garden: Hidden Partners: Mycorrhizal Fungi and Plants

Notes & References:

photo attribution: https://en.wikipedia.org/wiki/Aspergillus_fumigatus (distributable under Creative Commons License)

STATION 4

METHANOGENS – VISITORS FROM THE DEEP BIOSPHERE 
EXAMPLE ORGANISM: *METHANOCOCCUS MARIPALUDIS*



Station Location: Marshy Creek Pier, GPS coordinates: 38°57’09.85”N, 76°13’45.44”W
[Go to List of Tour Stations] [Back to Station 3] [Forward to Station 5]

Taxonomy:

- Domain: Archaea
- Kingdom: Euryarchaeota
- Phylum: Euryarchaeota
- Class: Methanococci
- Order: Methanococcales
- Family: Methanococcaceae
- Genus/Species: representative organism – Methanococcus maripaludis

During your tour, you may notice what appears to be an oil slick on the surface of the water. If the oily sheen is easily dispersed, it’s likely that the chemical you’re observing is methane released by an ancient variety of **prokaryotes** called **archaebacteria.** The archaebacteria (Archaea is one of the three recognized domains of living things) were once thought to be comprised only of “extremophiles” (organisms living in extreme environments), but are now know to be widely dispersed, living in environments that include marshlands like the Chesapeake Bay estuary, and in the human microbiome. Archaebacteria resemble bacteria in their morphology and cellular biology, but have genetic mechanisms and metabolic pathways that are like those seen in **eukaryotes**. Some evidence suggests that the Archaea were the first living things to evolve, possibly as early as 3.5 billion years ago.

Although the Archaea are difficult to study by routine microbiological techniques (culture, etc.), investigation of their chemical components (e.g. nucleic acids) can tell us much about the evolution of life, and about changes to specific environments over time. Bolide impacts, such as the event that shaped the lower Chesapeake approximately 35 million years ago, may have released microorganisms that were inhabitants of the "deep biosphere", including the methanogens that produce oily patches on the surface of the bay, as described above. Some researchers have speculated that the greatest extinction event in the Earth's history (the Great Permian Extinction, approximately 250 million years ago) resulted from high levels of atmospheric methane, following such bolide impacts, the increased vulcanism that resulted from those impacts, and the sudden increase in activity by methanogens.

Learn More:

The deep biosphere in terrestrial sediments in the chesapeake Bay area, Virginia, USA

The origin and emergence of life under impact bombardment

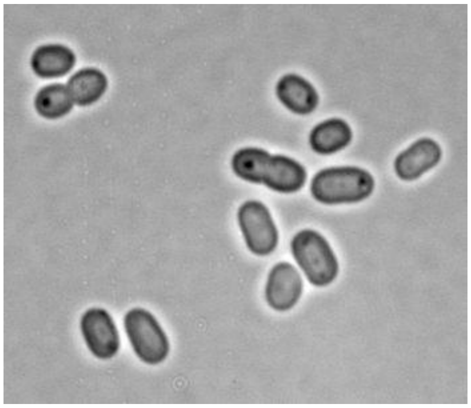
Chesapeake Bay Impact Crater

Notes & References:

Image source: http://www.bact.wisc.edu/Bact303/Methanococcus.jpeg

STATION 5

BACTERIAL PLANKTON – SIGNIFICANT CONTRIBUTORS TO CHLOROPHYLL PRODUCTION
EXAMPLE ORGANISM: SYNECHOCCUS SPECIES



Station Location: Marshy Creek Pier, GPS coordinates: 38°57'09.85"N, 76°13'45.44"W
[Go to List of Tour Stations] [Back to Station 4] [Forward to Station 6]

Taxonomy

- Domain: Bacteria
- Kingdom: Bacteria
- Phylum: Cyanobacteria
- Class: Cyanophyceae
- Order: Synechococcales
- Family: Synechococcaceae
- Genus/Species: representative organism – Synechococcus species

Most visitors to CBEC will know that chlorophyll-producing organisms are the basis of the food web, and that without them, no other living organism would exist. These primary producers are able to convert light energy into biomass, and that biomass is essential to organisms without that capability. Photosynthetic organisms are also critical for climate control and oxygen production. Many if not most people tend to visualize large vascular plants when they think of photosynthesis, but over 40% of the Earth's photosynthetic production is performed by phytoplankton, which are single-celled algae (eukaryotic) and bacteria (prokaryotic).

Chlorophyll-producing bacteria are called cyanobacteria. Cyanobacteria are among the first living organisms to occur on Earth, having evolved approximately 3.5 billion years ago. Mats of cyanobacteria are the oldest known fossils. Chloroplasts, the organelles responsible for photosynthesis in algae and green plants, are thought to be endosymbionts, i.e. photosynthetic bacteria evolved as organelles within eukaryotic cells.

Members of the genus Synechococcus are some of the most prolific and important constituents of bacterial phytoplankton in oceans and estuaries, particularly in temperate and tropical waters. They have been measured in concentrations exceeding one million cells per milliliter. Another group of cyanobacteria that is significant in terms of chorophyll production (possibly even more significant than Synechococcus) is the genus Prochlorococcus. The two genera are similar, but Prochlorococcus is smaller and has evolved a unique light-harvesting complex, employing different pigments than other photosynthetic organisms.

Learn More:

Fundamentals of Environmental Measurements: Algae, Phytoplankton, and Chlorophyll

Introduction to Cyanobacteria: Architects of Earth's Atmosphere

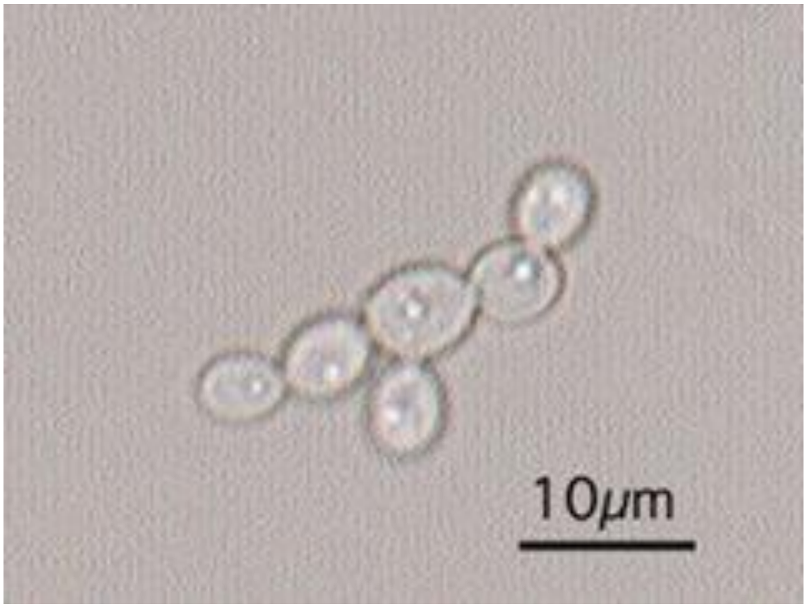
The Origin of Mitochondria and Chloroplasts

Notes & References:

Photo attribution: https://en.wikipedia.org/wiki/Synechococcus (distributable under Creative Commons license)

STATION 6

YEAST – COMMON INHABITANTS OF THE PHYLLOSPHERE
EXAMPLE ORGANISM: CANDIDA SPECIES



Station Location: Lake Knapp Pavilion, GPS coordinates: 38°57’07.91”N, 76°14’00.83”W
[Go to List of Tour Stations] [Back to Station 5] [Forward to Station 7]

Taxonomy

- Domain: Eukaryota
- Kingdom: Fungi
- Division: Ascomycota
- Class: Saccharomycetes
- Order: Saccharomycetales
- Family: Saccharomycetaceae
- Genus/Species: representative organism – Candida species

The above-ground parts of plants are normally colonized by a wide variety of bacteria, fungi, algae, and protists. This collection of microorganisms is termed the “phyllosphere.” Understanding of the phyllosphere includes studies of the individual microbes present on particular plants, the interaction of the various species inhabiting those particular plants, and similar studies regarding the effects of the phyllosphere on groups of plants. Specific plants and plant communities may have unique phyllosphere profiles (i.e. specific associations of particular microbes). Such studies are important both scientifically and economically, since microbial interactions with other microbes and with their host, can have significant impacts on plant health. Understanding of the phyllosphere has lagged behind our understanding of the rhizosphere (the relationship of microbial communities with subterranean plant surfaces).

While some microbial colonists on plant surfaces may be beneficial or pathogenic to the host, it is thought that the majority of inhabitants of the phyllosphere have little or no effect on the plant. The resident microbes, however, may have antagonistic or supportive roles among themselves.

Although quantitative studies have indicated that bacteria are the predominant microbial inhabitants of above-ground plant surfaces, fungi are typically also present in impressive numbers. The Kingdom Fungi is generally divided, morphologically, into filamentous fungi (molds, mushrooms, etc.) and the single-celled organisms called yeasts. Most identified fungal plant pathogens ("phytopathogens") are filamentous (basidiomycetes and ascomycetes). Recently, yeast species have been identified that are antagonistic toward these fungal pathogens. This research may be an example of how phyllosphere research may be useful in improving plant health.

Learn More:

Microbiology of the Phyllosphere

Each tree species has unique bacterial identity, microbiome research shows

Phyllosphere yeasts rapidly break down biodegradable plastics

The plant microbiome explored: implications for experimental botany

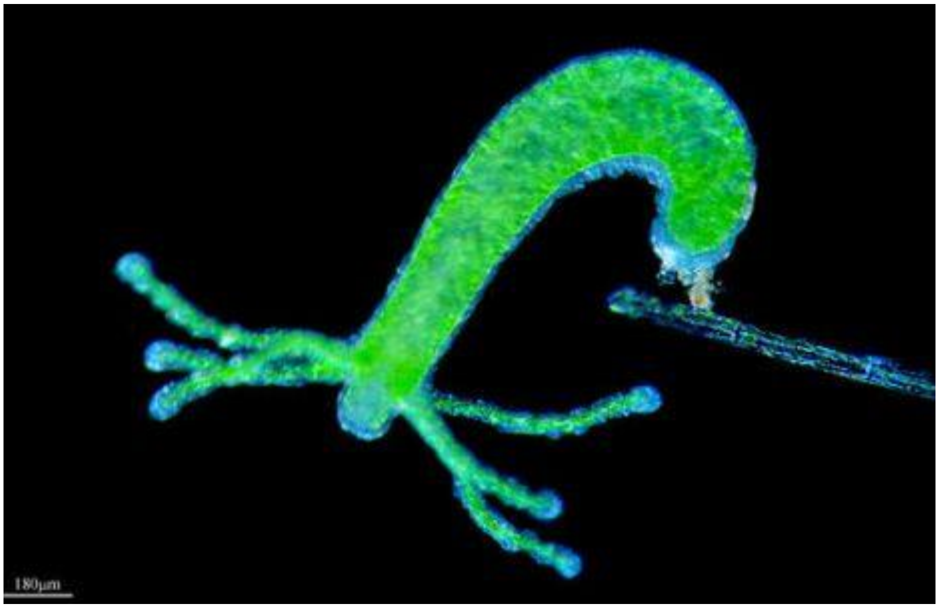
Review: Utilization of antagonistic yeasts to manage postharvest fungal diseases of fruit.

Notes & References:

Photo attribution: http://eol.org/pages/1013921/media (distributable under Creative Commons license)

STATION 7

INDICATOR OF BENTHIC HEALTH
HYDRA SPECIES



Station Location: Lake Knapp Pavilion, GPS coordinates: 38°57’07.91”N, 76°14’00.83”W
[Go to List of Tour Stations] [Back to Station 6] [Forward to Station 8]

Taxonomy

- Domain: Eukarya
- Kingdom: Animalia
- Phylum: Cnidaria
- Class: Hydrozoa
- Order: Anthoathecata
- Family: Hydridae
- Genus/Species: Hydra species

“**Benthos**” is a term used to describe the community of organisms that live in close association with the bottom of bodies of water (e.g. seabeds). These organisms can be further classified according to their **trophic** status as “phytobenthos” (primary producers) and “zoobenthos” (consumers), or by their size, where macrobenthos includes organisms 1 mm or larger, meiobenthos includes organisms less than 1 mm and greater than 0.1 mm, and microbenthos, organisms 0.1 mm or less. Finally, benthic organisms may be described by where they live, in relation to the aquatic floor, i.e endobenthos (organisms that live in the sediment), epibenthos (organisms that live on top of the sediment), and hyperbenthos (organisms that live just above the sediment). The example organism in this tour, Hydra species, are members of the macrobenthos (growing up to 10 mm in size).

Scientists use surveys of benthic populations to determine the health of the associated body of water. The types and numbers of organisms that form the benthos are reliable indicators of the effects of pollution and other environmental stresses. A program named "Chesapeake Bay Long-Term Benthic Monitoring and Assessment Program in Maryland" was established in 1984. It's run by a private contractor, in coordination with the Maryland Department of Natural Resources and the U.S. EPA Chesapeake Bay Program. This program has two components, including "a fixed-site monitoring sampling effort directed at identifying trends in benthic condition, and a probability-based sampling effort intended to estimate the area of the Maryland Chesapeake Bay with benthic communities meeting and failing to meet the Chesapeake Bay Program's Benthic Community Restoration Goals (i.e. the "state of the bay")."[1] The program monitors a large number and variety of benthic species[1].

Hydra species are among the organisms monitored in the study described above. Hydra species can usually be seen with the naked eye, but a magnifying loupe is usually useful for visualizing them. Hydra, like jellyfish, are members of the phylum Cnidaria, a group of primitive invertebrates that are characterized by a radially symmetrical body plan and stinging cells called nematocysts. Hydra are freshwater invertebrates that are common in temperate and tropical waters. They live attached to aquatic vegetation or other submerged material. They eat organisms that pass within range of their stinging tentacles. Hydra are of particular scientific interest because they apparently do not age and have what is described as an unlimited lifespan.

Learn More:

Society for Freshwater Science: What Is The Benthos?

PBS NatureWorks: Benthos

Chesapeake Bay Benthic Monitoring Program

Chesapeake Bay Program: Life at the Bottom

Northern State University: The Natural Source – Hydra

Introduction to Cnidaria

Notes & References:

Photo attribution: http://eol.org/pages/99065/overview (distributable under Creative Commons license)

[1]Chesapeake Bay Benthic Monitoring Program: Reports and Other Documents

STATION 8

INDICATORS OF ESTUARINE OXYGENATION
COPEPODS

Station Location: wetlands near Hog Bay, GPS Coordinates: 38°57’08.84”N, 76°14’05.64”W
[Go to List of Tour Stations] [Back to Station 7] [Forward to Station 9]

Taxonomy

- Domain: Eukarya
- Kingdom: Animalia
- Division: Arthropoda
- Class: Hexanauplia
- Subclass: Copepoda

Organisms that live in estuaries such as the Chesapeake Bay require adequate levels of dissolved oxygen in their aquatic habitat. The requirements vary depending on the organism and on their specific **niche**. In the Chesapeake Bay, aquatic animals require a range of 1-6 mg/L of dissolved oxygen. Oxygen sources for aquatic environments include atmospheric oxygen that diffuses into the water, and oxygen produced by photosynthetic organisms. Decomposers (fungi, bacteria, etc.) deplete oxygen by using it in their **metabolic** processes. When substances that act as nutrients for the decomposers (e.g. sewage, fertilizers, etc.) become more concentrated, oxygen depletion can occur, resulting in “dead zones”, oxygen levels may be dangerously low (**hypoxia**) or absent entirely (**anoxia**). Over the last few decades, scientists have tracked dead zones in the Chesapeake Bay.

The effect of these dead zones on aquatic life and on the general health of the Bay can be analyzed by determining changes in the numbers of organisms such as zooplankton, and by correlating these numbers with corresponding changes in oxygenation. Researchers have used relative copepod abundance, as well as their relative vertical position in the aquatic environment, in this sort of analysis.[1] Such studies have indicated that this indicator reliably corresponds with changes in oxygenation, and may predict more general changes on the estuarine environment.

Copepods are multi-celled (**metazoan**) animals that are abundant in all aquatic environments around the world. They range in size from approximately 0.2 mm in length to almost 10 mm, with an average length of approximately 1-2 mm. As such, at least a magnifying loupe is generally required to visualize them. They are **crustaceans**, and may be "free-living, symbiotic, or internal or external parasites on almost every phylum of animals in water".[2] The subclass Copepoda is incredibly diverse, with about 21,000 described species. Paleontologists have discovered copepod fossils dating to the Cambrian period (about 541-485 million years ago). Free-living (non-parasitic) copepods tend to be **planktonic**, but some may be **benthic**. Some researchers have stated that copepods may represent the largest animal biomass on Earth[3], and as such, represent a significant layer of the global energy web and carbon cycle.

Learn More:

Chesapeake Bay Program: Dissolved Oxygen

Copepods and hypoxia in Chesapeake Bay: abundance, vertical position and non-predatory mortality

NOAA Ocean Service Education: Monitoring Estuaries – Dissolve Oxygen

Chesapeake Bay Foundation: Dead Zones

University of Maryland Center for Environmental Science: Ecocheck – Summer Bay Forecast (Dissolved Oxygen)

[2]Smithsonian National Museum of Natural History – The World of Copepods

Notes & References:

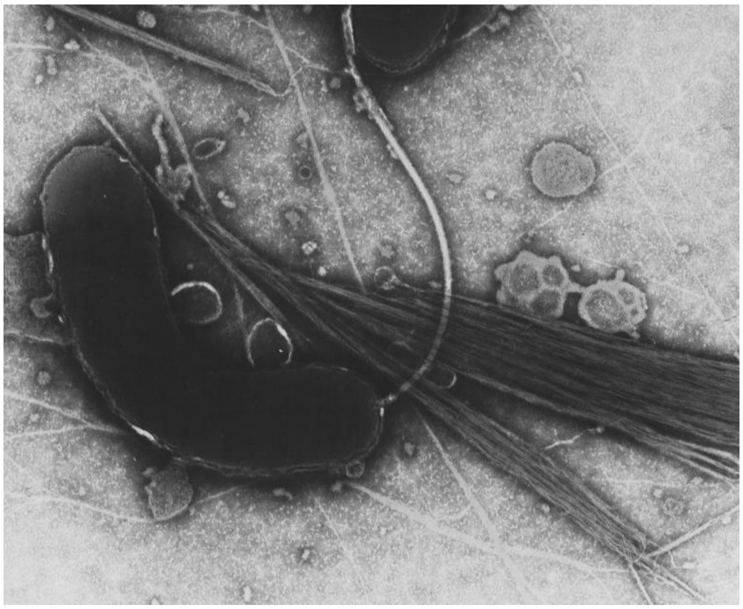
[1]David T. Elliott, James J. Pierson, Michael R. Roman; Copepods and hypoxia in Chesapeake Bay: abundance, vertical position and non-predatory mortality, Journal of Plankton Research, Volume 35, Issue 5, 1 September 2013, Pages 1027–1034, https://doi.org/10.1093/plankt/fbt049

[3]Johannes Dürbaum; Thorsten Künnemann (November 5, 1997). "Biology of Copepods: An Introduction". Carl von Ossietzky University of Oldenburg. Archived from the original on May 26, 2010. Retrieved December 8, 2009.

Photo attribution: http://eol.org/pages/2625033/overview (distributable under Creative Commons license)

STATION 9

BACTERIAL PATHOGENS OF HUMANS
VIBRIO VULNIFICUS



Station Location: Hog Bay, GPS Coordinates: 38°57’07.02”N, 76°14’09.32”W
[Go to List of Tour Stations] [Back to Station 8] [Forward to Station 10]

Taxonomy

- Domain: Bacteria
- Kingdom: Bacteria
- Phylum: Proteobacteria
- Class: Gammaproteobacteria
- Order: Vibronales
- Family: Vibrionaceae
- Genus/Species: Vibrio vulnificus

Some estimates suggest that there are as many as ten times the number of bacterial cells in the human body as there are human cells.[1] Without these organisms, human life would not be possible, since the human **microbiota** contribute in numerous, essential ways to our life processes. It’s important to keep this in mind, when considering the relatively small number of bacteria that are pathogenic to humans.

Bacteria, particularly human pathogens, are frequently divided into two main groups, based on their staining characteristics. These groups are called “Gram-positive” and “Gram-negative”, terms named for the Danish microbiologist who developed the staining technique. The color of the organism, following staining (violet for Gram-positive organisms, reddish pink for Gram-positive organisms), reflects a distinct difference in the type of cell wall that encloses the bacterium in question, and a separate evolutionary development of the two types of microbes. Other general ways of describing bacteria include their type of motility (or lack of motility), their atmospheric requirements (e.g. whether oxygen is required or toxic), their morphology (e.g. shape and size), their rate of growth (i.e. some bacteria reproduce in minutes, while others take weeks or longer), and their metabolic chemistry (what type of compounds are metabolized, and what sort of waste products are produced). The genus Vibrio includes several important human pathogens, *V. cholerae* (the causative agent of cholera), *V. vulnificus, V, parahaemolyticus,* and *V. alginolyticus. Vibrio* species are Gram-negative, motile, rod-shaped bacteria. The *Vibrio* species that cause infections in the U.S. (all of those listed, except *V. cholerae*), are halophilic organisms (salt-loving) and are typically found in warm, coastal waters.

Vibriosis (infection caused by non-cholera *Vibrio* species) occurs in approximately 80,000 Americans each year, with about 100 deaths reported. Infections involving *V. vulnificus* are particularly concerning, since the **morbidity** and **mortality** associated with these infections is quite high (approximately 25% of *V. vulnificus* infections result in death). The principle types of infections caused by *V. vulnificus* are acute gastroenteritis (normally associated with consumption of contaminated shellfish), necrotizing ("flesh-eating") wound infections (usually caused by infection of a previously-existing wound to contaminated water), and invasive septicemia (also associated with consumption of contaminated shellfish). The CDC reports that approximately 80% of the reported cases of vibriosis occur between May and October, when coastal water temperatures are warmer. Evidence suggests that as global temperatures have risen and the warm season is extended, the bacterial load of *Vibrio* species in shellfish has increased. A recent journal article reports that "a warming trend in sea surface temperature is strongly associated with spread of vibrios, an important group of marine prokaryotes, and emergence of human diseases caused by these pathogens".[2]

Learn More:

American Society for Microbiology – Infection and Immunity: Vibrio vulnificus, Disease and Pathogenesis

US FDA – Vibrio vulnificus Health Education Kit Fact Sheet

CDC – Vibrio Species Causing Vibriosis

Chesapeake Bay Program: Five Facts About Vibrio

Vibrio vulnificus: From Oyster Colonist to Human Pathogen

Notes & References:

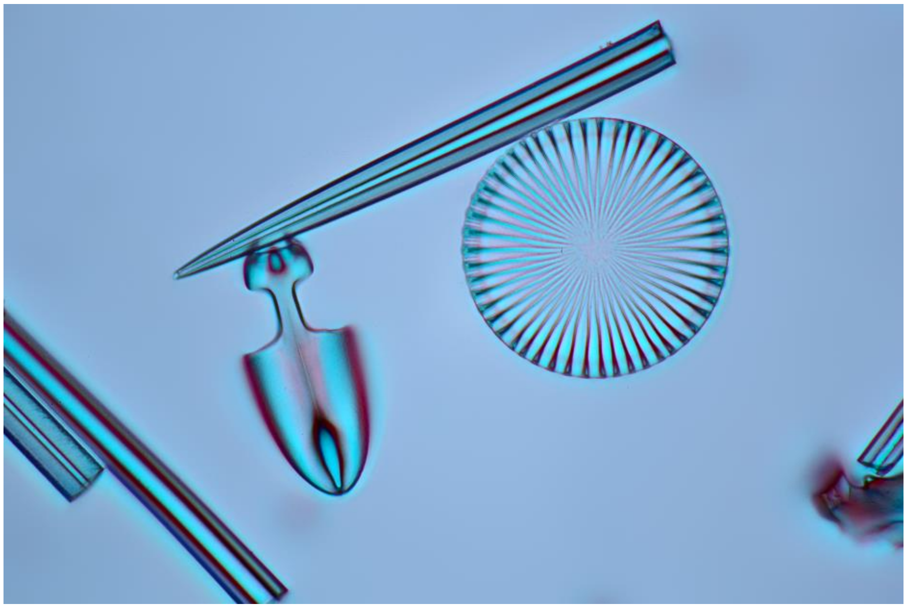
[1]American Academy of Microbiology FAQ: Human Microbiome January 2014

[2]Vezzulli L, Grande C, et al. "Climate influence on Vibrio and associated human diseases during the past half-century in the coastal North Atlantic". PNAS, Vol 113 No 34, Aug 23, 2016.

Photo
attribution: https://commons.wikimedia.org/wiki/Category:Vibrio_cholerae#/media/File:Vibrio_cholerae.jpg (distributable under Creative Commons license)

STATION 10

ALGAE AT THE BASE OF THE FOOD CHAIN
DIATOMS



Station Location: Hog Bay, GPS Coordinates: 38°57'07.02"N, 76°14'09.32"W
[Go to List of Tour Stations] [Back to Station 9] [Forward to Station 11]

Taxonomy

- Domain: Eukaryota
- Kingdom: Protista
- Superphylum: Heterokonta
- Phylum: Ochrophyta
- Class: Bacillariophyceae

The food chain is the hierarchical sequence of organisms through which food and energy are stored and transmitted. The chain is hierarchical in the sense that at each level of the chain (or pyramid), the transfer and storage of energy is less efficient than at the level preceding it. These "trophic levels" are defined by the number of energy transfers that separate them from other levels. At the base of this food pyramid are the primary producers. Primary producers (**autotrophs**) are organisms capable of storing energy in organic molecules (most commonly through photosynthesis by "photoautotrophs"). Aquatic, unicellular algae (microalgae) represent a large proportion of the Earth's population of photoautotrophs. In addition to being a significant part of the food chain, microalgae also produce approximately half of atmospheric oxygen.[1]

Microalgae thrive in every type of global aquatic environment. They are an incredibly diverse group of organisms, with the estimated number of species ranging from 200,000 to 800,000.[2] Microalgae produce a wide variety of chemical products that are essential to other aquatic organisms. Omega-3 fatty acids (the significant component of "fish oil" products that are marketed for human consumption) are produced by microalgae, which are then consumed by fish (fish do not produce omega-3 fatty acids).

The single-celled algae called diatoms form a large part of global phytoplankton, and are an essential part of the food chain. There are an estimated 100,000 species of diatoms, organized into approximately 200 genera. Their photosynthetic activity is responsible for "an estimated 45% of the total oceanic primary production of organic material".[3] Paleontologists believe that diatoms evolved during the Triassic Period, with their earliest fossil records traced to the early Jurassic (approximately 185 million years ago). A striking characteristic of the diatoms is their silicon cell wall, which is called a frustule. The frustule is composed of silica, is covered with a layer of carbohydrate material, and organized in two overlapping parts, called thecae. The inner theca (the hypotheca) is overlapped by an outer theca (the epitheca). This morphology can be visualized a box with a lid. The shapes of the frustule vary depending on the niche occupied by the particular species of diatoms (e.g. some are boat-shaped, which allows easier movement in water columns).

Learn More:

Tree of Life Web Project: Diatoms

Diatoms of the United States: What Are Diatoms?

NOAA – National Ocean Service: What Are Phytoplankton?

Woods Hole Oceanographic Institution: Phytoplankton

The Khan Academy: Food Chains and Food Webs

Notes & References:

[1]http://www.abc.net.au/radionational/programs/scienceshow/microscopic-algae-produce-half-the-oxygen-we-breathe/5041338

[2]Starckx, Senne (31 October 2012) A place in the sun – Algae is the crop of the future, according to researchers in Geel Flanders Today, Retrieved 8 December 2012

[3]Yool, Andrew; Tyrrell, Toby (2003). "Role of diatoms in regulating the ocean's silicon cycle". Global Biogeochemical Cycles. 17 (4): n/a. Bibcode:2003GBioC..17.1103Y

Photo attribution: https://commons.wikimedia.org/wiki/File:Rheinberg_2_diatom.jpg (distributable under Creative Commons license)

STATION 11

SOIL PROTOZOA – ENSURING HEALTHY SOIL
CERCOMONAS SPECIES

Station Location: intersection of Beach and Fox Pass Trails, GPS Coordinates: 38°56’52.81”N, 76°13’54.35”W

[Go to List of Tour Stations] [Back to Station 10] [Forward to Station 12]

Taxonomy

- Domain: Eukaryota
- Kingdom: Protista
- Phylum: Cercozoa
- Class: Sarcomonadea
- Order: Cercomoadida
- Family: Cercomonadidae
- Genus/Species: Cercomonas species

Taxonomy, the branch of science dedicated to classification of organisms, continues to evolve, and is now greatly influenced by molecular techniques that allow taxonomists to group organisms according to their genetic and evolutionary relatedness. While this has complicated the more general taxonomic groupings, most biologists still think in terms of the six (or five) Kingdoms of living things, when discussing the principle organizational aspects of living things. In this scheme, the Kingdom protista is comprised of "organisms which are unicellular or unicellular-colonial and which form no tissues".[1] The protists are commonly subdivided into photosynthetic organisms, and the heterotrophic (non-photosynthetic) protists, which have been termed protozoa. The protozoa include ciliates (Ciliophora), flagellates (Mastigophora), and amoeba (Sarcodina), terms that describe the organism's type of motility.

Protozoans play a significant role in ensuring the health of soil. Soil protozoa add nitrogen to the soil by consuming bacteria and releasing the nitrogen from that metabolic process as ammonia, frequently near plant roots that require nitrogen for growth. Microbiologists have demonstrated that soil protozoa are particularly active in the **rhizosphere**. Soil protozoa also control overgrowth of soil bacteria and microalgae, by consuming as many as 5 million bacteria per day. Keeping bacterial populations in check also acts to ensure the health of those microbial populations, by limiting overpopulation and competitive stresses. Specific types of protozoans (e.g. flagellates vs ciliates) vary depending on the microenvironment and niche.

Cercomonads are small flagellates that are common in the soil. They have two flagella that are used for motility and consume bacteria by forming a pseudopod to capture prey.

Learn More:

USDA National Resources Conservation Service: Soil Protozoa

Smithsonian.com: Soil Has a Microbiome, Too

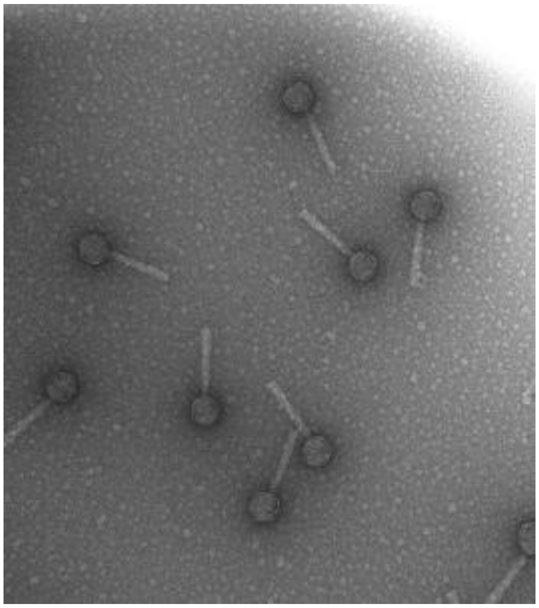
Notes & References:

[1]Whittaker, R. H. (1969). "New Concepts of Kingdoms of Organisms". Science. 163 (3863): 150–60. doi:10.1126/science.163.3863.150. PMID 5762760

Photo attribution: https://en.wikipedia.org/wiki/Cercomonadida#/media/File:Cercomonas_sp.jpg (distributable under Creative Commons license)

STATION 12

WETLAND VIRUSES & THEIR IMPORTANCE



Station Location: Outdoor Exhibit Area Trail, GPS Coordinates: 38°56’50.62”N, 76°13’51.63”W
[Go to List of Tour Stations] [Back to Station 11] [Forward to Station 13]

Virus Classification

- Group: Group I (dsDNA)
- Order: Caudovirales
- Family: Myoviridae
- Subfamily: Tevenvirinae
- Genus: T4virus
- Species: representative organism – Enterobacteria phage T4

Viruses are infectious agents that are only able to replicate inside a living organism. They typically consist only of a nucleic acid molecule (either DNA or RNA) and a protein coat (which is sometimes covered by a lipid envelope). When viral particles exist outside of a living cell, they are called virions. Viruses infect every type of organism. As with other microbes, the vast majority of viruses are not pathogenic to humans (or to other host organisms), although viruses are rarely discussed except in that context. Recent estimates suggest that there are approximately 10^{31} virus particles in the oceans. Based on such astronomical numbers, attempts to estimate the total number of viral species on Earth, or even those that inhabit living organisms, is a speculative effort. Although the icon associated with this station is a microscope, viruses cannot be visualized with “normal” light microscopy. Viruses range in size from 20 to 400 nanometer (a nanometer is equal to 10^{-9} meters), so special techniques (e.g. electron microscopy) is required in order to view virons or the viruses infecting cells.

Microbiologists have estimated the distribution of viruses in the Chesapeake Bay. In a 1991 study, results of such a study indicated that the number of viruses in the Bay "ranged between 2.6 x 10(6) and 1.4 x 10(8) viruses ml-1 with a mean of 2.5 x 10(7) viruses ml-1", with significant increases in numbers during the summer months.[1] One of the researchers' conclusions, following this study, was that "The high virus counts obtained in this study suggest that viruses may be an important factor affecting bacterial populations in the Chesapeake Bay, with implications for gene transfer in natural aquatic bacterial populations and release of genetically engineered microorganisms to estuarine and coastal environments."

Although many viruses identified in estuarine environments, such as the Chesapeake Bay, represent disease threats to other organisms that live or interact with the waters of the estuary, there are also viruses present in such environments that are known to be beneficial, or may prove to be so, with additional research. One example of this is the recent discovery of a virus (OMKO1) in a Connecticut pond that may prove useful in treating infections by multi-drug resistant bacteria, which currently pose an increasingly significant threat to humans.[2] This virus acts on the human pathogen, *Pseudomonas aeruginosa*, by effectively allowing antibacterial compounds to more easily enter the bacterium. The study is also significant because it represents the advancement of the therapeutic alternative known as "phage therapy" (bacteriophages are types of viruses).[3]

Learn More:

Applied and Environmental Microbiology: Distribution of Viruses in the Chesapeake Bay

How Many Viruses on Earth?

All the Virology on the WWW

An Infinity of Viruses

Notes & References:

[1]Wommack KE, Hill RT, et al. "Distribution of viruses in the Chesapeake Bay." Appl Environ Microbiol 1992 Sep; 58(9): 2965–2970.

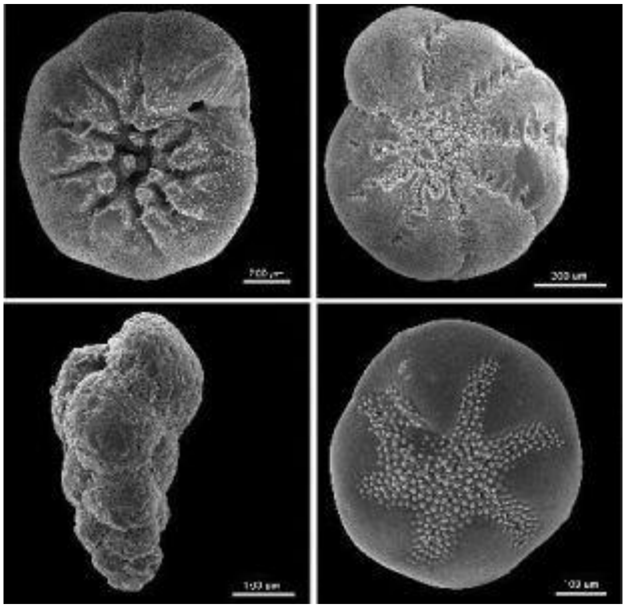
[2]Virus discovered in pond can help kill antibiotic-resistant superbugs

[3]Nature: Scientific Reports – Phage selection restores antibiotic sensitivity in MDR Pseudomonas aeruginosa

Photo attribution: https://commons.wikimedia.org/wiki/File:Bacteriophage_P2.jpg (distributable under Creative Commons license)

STATION 13

LIVING PROTOZOANS & MICROFOSSILS
FORAMINIFERA



Station Location: Outdoor Exhibit Area Trail, GPS Coordinates: 38°56'50.62"N, 76°13'51.63"W
[Go to List of Tour Stations] [Back to Station 12] [Foward to Station 14]

Taxonomy

- Domain: Eukaryota
- Kingdom: Protista
- Phylum: Retaria
- Subphylum: Foraminifera

Forams are amoeboid protists that are commonly classified in the phylum Retaria, subphylum Foraminfera, although the taxonomy of the forams is complicated and fluid. Forams are typically shelled, and the shells are called "tests". The tests are typically chambered, with openings connecting the chambers. The Foraminfera are grouped according to their types of shells which are usually composed of calcite formed in various manners. The shells may also be composed of whatever material is nearby (these are called "agglutinated" structures). While many of the Foraminfera are small (approximately 0.1 mm), some species can grow to 20 centimeters long. The larger species often "farm" single-celled algae withing their shells. Most species, though, consume bacteria and phytoplankton, using cellular extensions called reticulopodia to capture their prey. Reticulopodia also assist their motility. There are over 10,000 identified species of living forams, most of which are **benthic**. Forams are an important source of food for other aquatic organisms, including snails and fish. They are found in every type of aqueous environment, and are extremely abundant in certain locales, existing in concentrations in the tens of thousands per square foot of ocean bottom.

In addition to the estimated 10,000 living species of forams, paleobiologists have identified over 40,000 foram species in the fossil record. Foraminifera probably evolved during the Cambrian Period (541-485 **mya**), with an abundance of well-characterized fossils existing from all of the periods of the Paleozoic and Cenozoic Eras. This record has been extremely important for paleontology, since it provides a reliable means of determining the geologic age of the matrix in which they're found, and for constructing evolutionary timelines for organisms living during these ancient periods.

Learn More:

UMCP Berkeley: Introduction to the Foraminifera

World Foraminifera Database

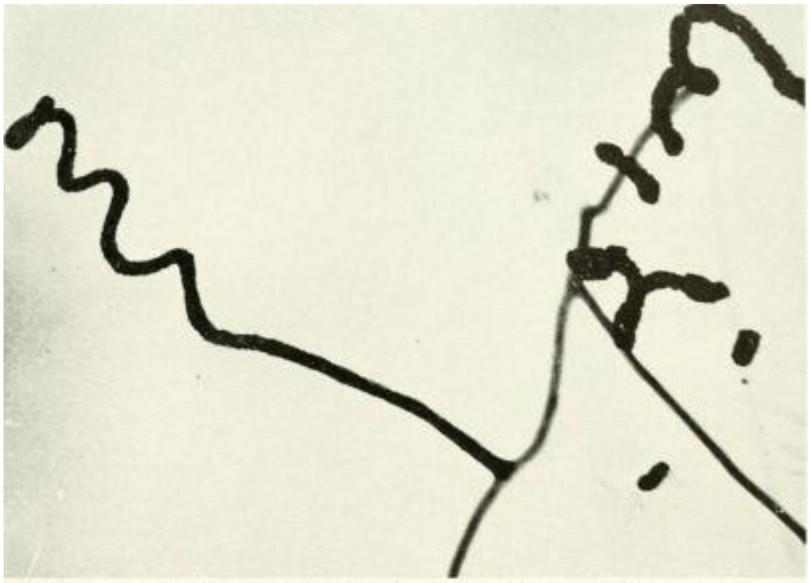
INTRODUCTION: Foraminiferal repopulation of the Late Eocene Chesapeake Bay Impact Crater

Notes & References:

Photo attribution: https://commons.wikimedia.org/wiki/File:Benthic_foraminifera.jpg (distributable under Creative Commons license)

STATION 14

THE SOIL FOOD WEB – ACTINOMYCETES



:E 37. Sporophores of *S. diastaticus*. × 4,500, showing uniform density over whole surfac

Station Location: west side of Outdoor Exhibit Area Trail, GPS: 38°56’51.69”N, 76°13’48.45”W
[Go to List of Tour Stations] [Back to Station 13] [Return to Tour Welcome Page (Station 1)]

Taxonomy

- Domain: Bacteria
- Kingdom: Bacteria
- Phylum: Actinobacteria
- Class: Actinobacteria
- Order: Actinomycetales
- Family: Actinomycetaceae
- Genus/Species: representative organism – Actinomyces species

The term “actinomycete” is a non-taxonomic term that’s used to describe a large group of bacteria with similar characteristics that are generally members of the order Actinomycetales. Members of the group have similar cell walls, and tend to form threadlike strands that grow as mycelia, often with aerial hyphae. These characteristics are similar to those of fungi, but actinomycetes are prokaryotic (fungi are eukaryotic) and are generally much smaller than fungi. Actinomycetes are just one group of the bacterial biomass in the soil. Estimates are that a teaspoon of productive soil typically contains between 1 million and 1 billion bacteria. [1]

Soil bacteria are essential to the nutrient cycle, which ensures that various minerals and nutrients are recycled and made available for living organisms. The actinomycetes contribute to this cycle by decomposing certain biologically produced materials (e.g. chitin and cellulose) that are hard for other soil microorganisms to catabolize. Actinomycetes typically perform this decomposition activity in soils with a high (basic) pH. Fungi perform a similar function, typically in soil with a low (acidic) pH.

If you're visiting this station on a spring or autumn day, or following a rain storm, you may notice the characteristic aroma of "turned earth". Actinomycetes are principally responsible for that smell. That "earth scent" has been termed "petrichor" and is associated with the release of a chemical called geosmin from soil actinomycetes. Human noses are exquisitely sensitive to geosmin and are able to detect it at concentrations as low as 5 parts per trillion. [2] Scientists have investigated the role of geosmin in human evolution. [3]

Actinomycetes are also important as the source of life-saving antibiotics. The first drug active against the bacterium that causes tuberculosis (*Mycobacterium tuberculosis*) was purified from the actinomycete *Streptomyces griseus* by the soil microbiologist Selman Waksman (a discovery which earned him the 1952 Nobel Prize in Medicine). Actinomycetes are the source of many other antibiotics, and may represent a source of future therapies against drug-resistant pathogens.

Learn More:

Aroma Chemistry: The Aroma of Rain

The Living Soil: Soil Bacteria

The White Plague in the City of Angels – Scientific Discovery of Streptomycin, 1946

Antimicrobials from Actinomycetes – Back to the Future

Notes & References:

[1] USDA Natural Resources Service: Soils

[2] Wikipedia: Geosmin

[3] Smithsonian Magazine On-line: "What Makes Rain Smell So Good?"

photo attribution: Actinomycete – Wikimedia Commons