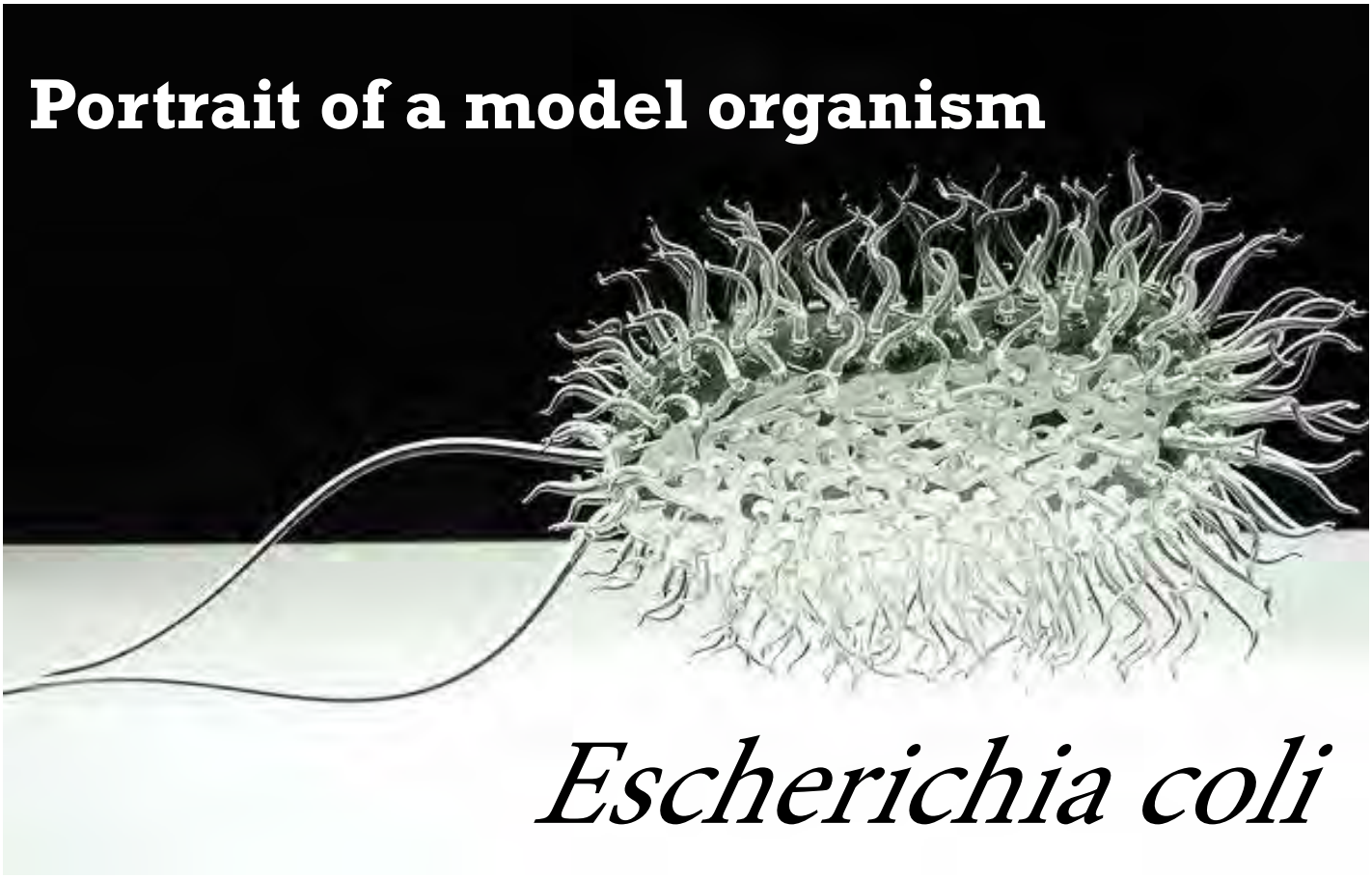
Portrait of a model organism



Escherichia coli

E.coli is a Gram-negative, Facultative anaerobic organism, Bacillus (shape) rod-shaped, spore forming bacterium that is commonly found in the lower gastrointestinal tract of warm-blooded organisms (endotherms). Morphologically cells are typically rod-shaped, and are about 2.0 microns (μm) long and 0.5 μm in diameter, with a cell volume of 0.6–0.7 $(\mu m)^3$.

History

The genera Escherichia and Salmonella diverged around 10^2 million years ago (credibility interval: 57–176 mya), which coincides with the divergence of their hosts: the former being found in mammals and the latter in birds and reptiles. This was followed by a split of the escherichian ancestor into five species (E. albertii, E. coli, E. fergusonii, E. hermannii and E. vulneris.) ago.

In 1885, a German pediatrician, Theodor Escherich, discovered this organism in the feces of healthy individuals and called it Bacterium coli commune due to the fact it is found in the colon and early classifications of Prokaryotes placed these in a handful of genera based on their shape and motility (at that time Ernst Haeckel's classification of Bacteria in the kingdom Monera was in place).

Habitat

It can live on a wide variety of substrates. *E.coli*uses mixed-acid fermentation in anaerobic conditions, producing lactic acidlactate, succinate, ethanol, acetate and carbon dioxide. Since many pathways in mixed-acid fermentation produce hydrogen gas, these pathways require the levels of hydrogen to be low, as is the case when *E. coli*lives together with hydrogen-consuming organisms, such as methanogens or sulphate-reducing bacteria.Optimal growth of *E.coli*occurs at 37 °C (98.6 °F) but some laboratory strains can multiply at temperatures of up to 49 °C (120.2 °F).

Growth can be driven by aerobic respirationaerobic or anaerobic respiration, using a large variety of redoxredox pairs, including the oxidation of pyruvic acid, formic acid, hydrogen and amino acids, and the reduction of substrates such as oxygen, nitrate, fumarate, dimethyl sulfoxide and trimethylamine N-oxide.

E.coli epidemic

Escherichia coli is a common inhabitant of the intestinal tract of man and warm-blooded animals. Most strains of *E.coli* are harmless and are a part of the normal intestinal microflora. These strains serve a useful function in the body by suppressing the growth of harmful bacteria and by synthesizing appreciable amounts of vitamins.

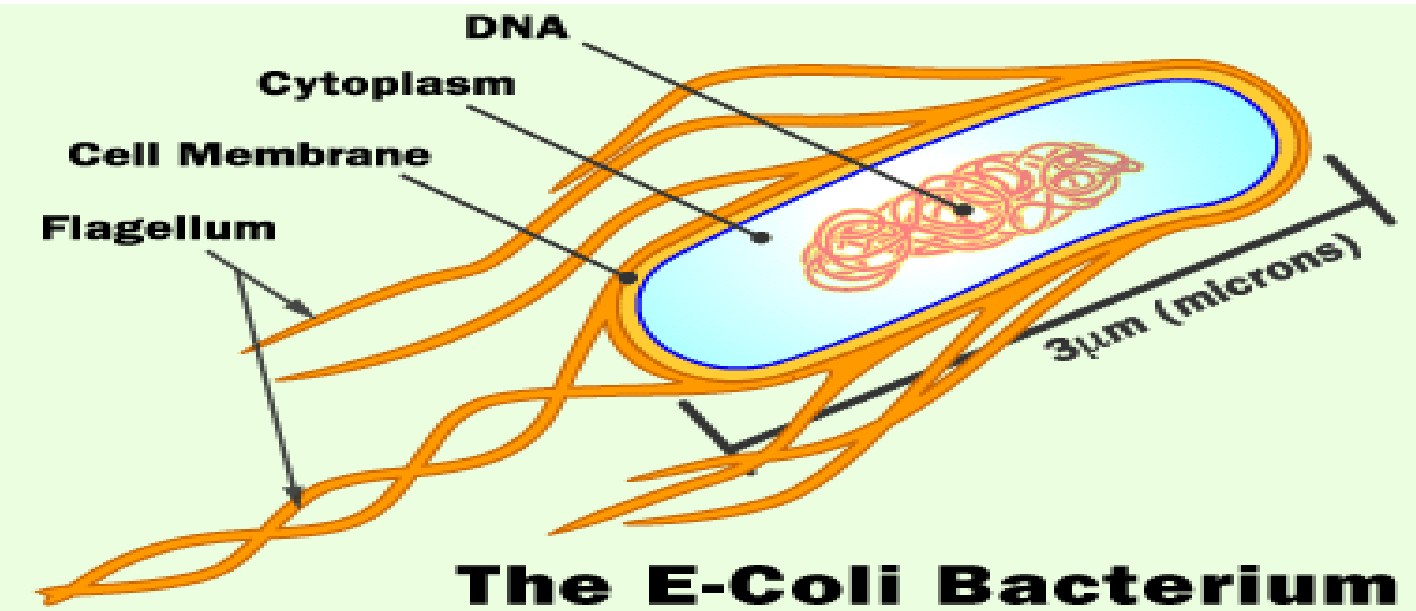
However, within the species, there are 4 strains or categories that cause diarrheal illnesses or disease. These 4 categories are:

Enteropathogenic *E.coli* causes severe diarrhea in infants that can last for over 2 weeks and results in death if dehydration is severe. In adults, the illness is characterized by severe diarrhea, nausea, vomiting, abdominal cramps, headache, fever, and chills. The time for onset of the illness is 17 to 72 hours; the duration of the illness is 6 hours to 3 days. This strain has caused illness to develop in people when it was transmitted in fecally contaminated water and a coffee substitute.

Enteroinvasive *E.coli* is similar to shigellosis and is caused by bacterial penetration and destruction of intestinal mucosa. Symptoms include: chills, fever, headache, muscle pain, abdominal cramps, and profuse diarrhea. The illness occurs 8 to 24 hours after ingestion of food or water containing this organism. The ingestion of a large number of cells (104 to 105 cells) is required to cause the illness.

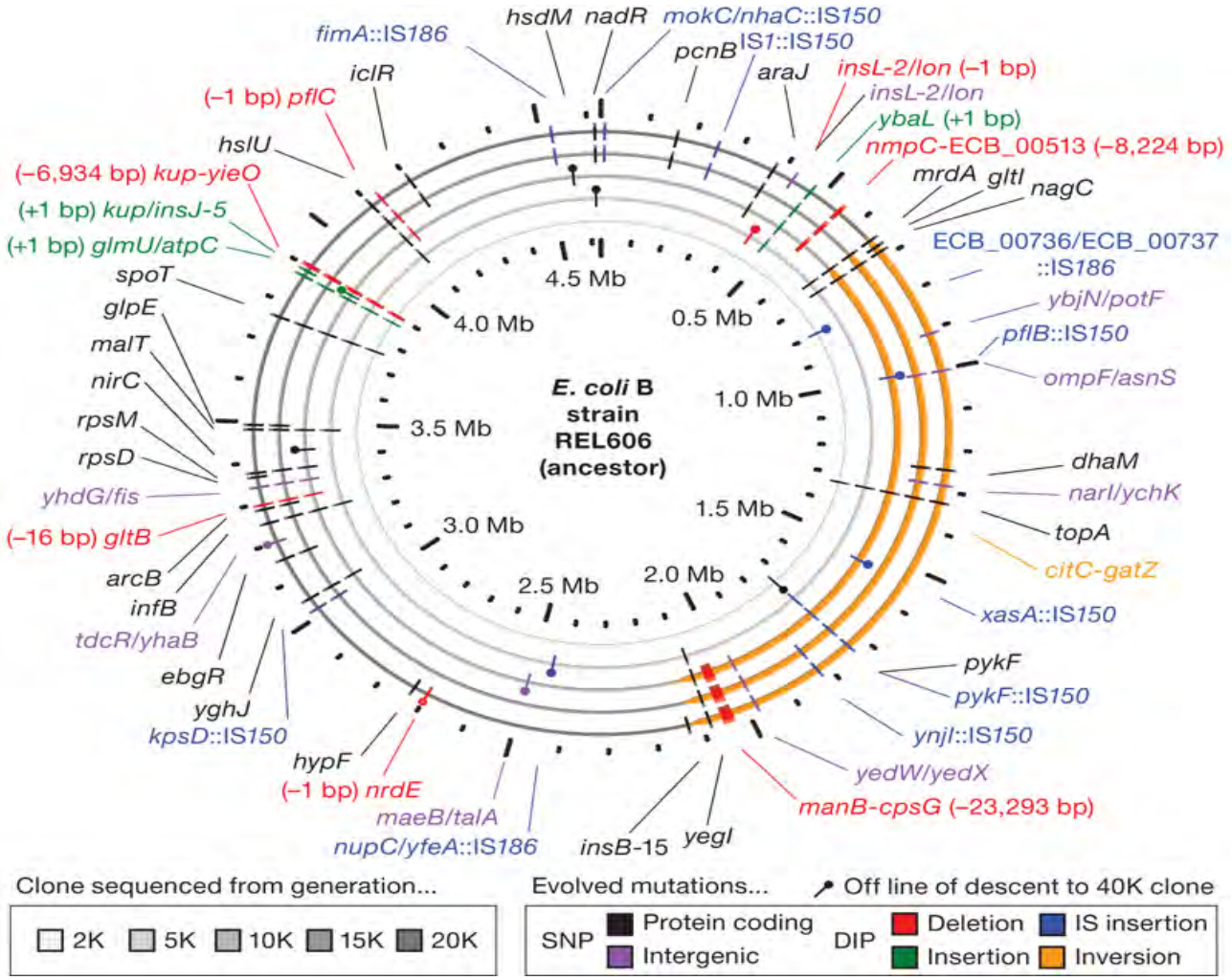
Enterotoxigenic *E.coli* include strains that produce enterotoxins when the organisms multiply in the intestine. These strains are commonly responsible for "traveler's diarrhea". They have been responsible for illness in India, in U.S. soldiers in Vietnam, and in travelers in Mexico. This is a problem for travelers from developed countries with good hygiene who visit countries with poor hygiene standards.
The illness is characterized by severe diarrhea, which may lead to dehydration. The diarrhea may last up to 19 days. Usually there is no fever. The onset of the illness can occur 8 to 44 hours after ingestion. Infective dose, as determined by a human study, is 108 to 1010 microorganisms.

Enterohemorrhagic *E.coli* (*E.coli*O157:H7) is characterized by severe abdominal cramps usually, but not always, followed by bloody diarrhea (hemorrhagic colitis). Some individuals exhibit only watery diarrhea. Vomiting may occur but there is usually little or no fever. The incubation period is usually about 3 to 9 days. This microorganism can also cause hemolytic uremic syndrome in children. This is the leading cause of kidney failure in children, which often requires dialysis and may ultimately lead to death. Other manifestations of illness due to this microorganism include a central nervous system involvement in which patients develop blood clots in the brain and death frequently results.



Genomics

The first complete DNA sequence of an *E.coli* genome (laboratory strain K-12 derivative MG1655) was published in 1997. It was found to be a circular DNA molecule 4.6 million base pairs in length, containing 4288 annotated protein-coding genes (organized into 2584 operons), seven ribosomal RNA (rRNA) operons, and 86 transfer RNA (tRNA) genes. Despite having been the subject of intensive genetic analysis for approximately 40 years, a large number of these genes were previously unknown. The coding density was found to be very high, with a mean distance between genes of only 118 base pairs. The genome was observed to contain a significant number of transposons/transposable genetic elements, repeat elements, cryptic prophages, and bacteriophage remnants. Today, over 60 complete genomic sequences of Escherichia and Shigella species are available. Comparison of these sequences shows a remarkable amount of diversity; only about 20% of each genome represents sequences present in every one of the isolates, while approximately 80% of each genome can vary among isolates. Each individual genome contains between 4,000 and 5,500 genes, but the total number of different genes among all of the sequenced *E.coli*strains (the pan-genome) exceeds 16,000. This very large variety of component genes has been interpreted to mean that two-thirds of the *E.coli*pangenome originated in other species and arrived through the process of horizontal gene transfer.



Proteomics

Full sets of *E.coli* proteins and their interactions have also been isolated and studied. A 2006 study purified 4,339 proteins from cultures of strain K-12 and found interacting partners for 2,667 proteins, many of which had unknown functions at the time. A 2009 study found 5,993 interactions between proteins of the same *E.coli* strain though this data showed little overlap with that of the 2006 publication.

Role of E.coli in biotechnology

Because of its long history of laboratory culture and ease of manipulation, E. colialso plays an important role in modern biological engineering and industrial microbiology. The work of Stanley Norman Cohen and Herbert Boyer in E. coli, using plasmids and restriction enzymes to create recombinant DNA, became a foundation of biotechnology. *E.coli*is a very versatile host for the production of heterologous proteins, and various Protein expression (biotechnology)protein expression systems have been developed which allow the production of recombinant proteins in E. coli. Researchers can introduce genes into the microbes using plasmids which permit high level expression of protein, and such protein may be mass-produced in industrial fermentation processes.

One of the first useful applications of recombinant DNA technology was the manipulation of *E.coli*to produce human insulin. Modified *E.coli*cells have been used in vaccine development, bioremediation, production of biofuels

E.coli is frequently used as a model organism in microbiology studies.

In 1946, Joshua Lederberg and Edward Tatum first described the phenomenon known as bacterial conjugation using *E.coli* as a model bacterium, and it remains the primary model to study conjugation.
E.coli was an integral part of the first experiments to understand phage genetics, and early researchers, such as Seymour Benzer, used *E.coli* and phage T4 to understand the topography of gene structure.

E.coli was one of the first organisms to have its genome sequenced; the complete genome of *E.coli* K12 was published by Science in 1997.

The long-term evolution experiments using *E. coli,* begun by Richard Lenski in 1988, have allowed direct observation of major evolutionary shifts in the laboratory. In this experiment, one population of *E.coli*unexpectedly evolved the ability to aerobically metabolize citrate, which is extremely rare in *E. coli.* As the inability to grow aerobically is normally used as a diagnostic criterion with which to differentiate *E.coli* from other, closely related bacteria, such as Salmonella, this innovation may mark a speciation event observed in the lab. By evaluating the possible combination of nanotechnologies with landscape ecology, complex habitat landscapes can be generated with details at the nanoscale. On such synthetic ecosystems, evolutionary experiments with *E.coli* have been performed to study the spatial biophysics of adaptation in an island biogeography on-chip.