Escherichia coli

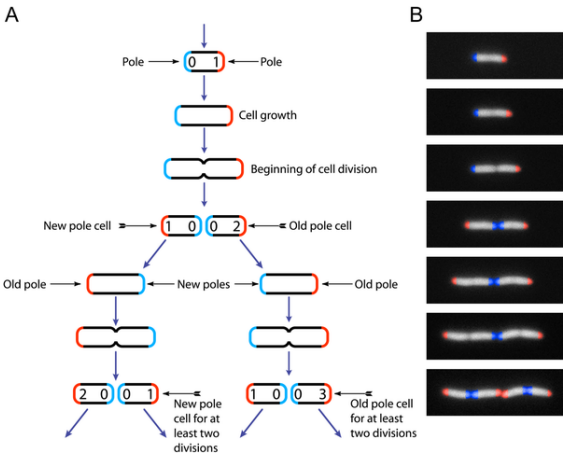
"E. coli" redirects here. For the protozoan commensal, see Entamoeba coli.
This article is about Escherichia coli as a species. For E. coli in medicine, see Pathogenic Escherichia coli. For E. coli in molecular biology, see Escherichia coli (molecular biology).

Escherichia coli (/ˌɛʃɪˈrɪkiə ˈkoʊlaɪ/;[1] also known as ***E. coli***) is a Gram-negative, facultatively anaerobic, rod-shaped bacterium of the genus *Escherichia* that is commonly found in the lower intestine of warm-blooded organisms (endotherms).[2] Most *E. coli* strains are harmless, but some serotypes can cause serious food poisoning in their hosts, and are occasionally responsible for product recalls due to food contamination.[3][4] The harmless strains are part of the normal flora of the gut, and can benefit their hosts by producing vitamin K_2,[5] and preventing colonization of the intestine with pathogenic bacteria.[6][7] *E. coli* is expelled into the environment within fecal matter. The bacterium grows massively in fresh fecal matter under aerobic conditions for 3 days, but its numbers decline slowly afterwards.[8]

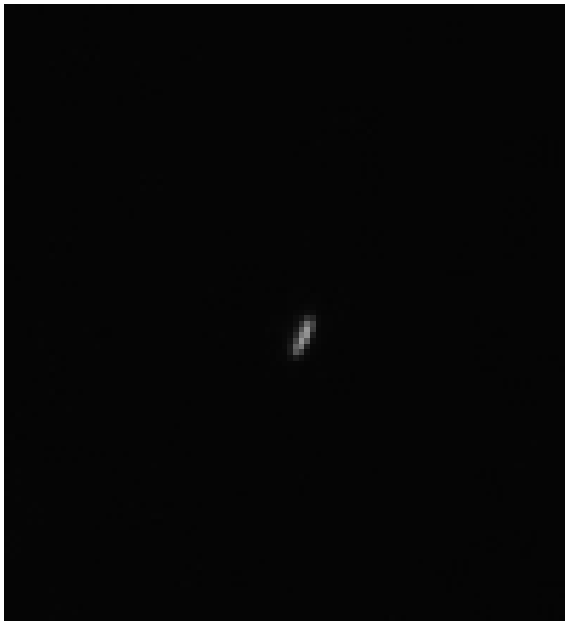
E. coli and other facultative anaerobes constitute about 0.1% of gut flora,[9] and fecal–oral transmission is the major route through which pathogenic strains of the bacterium cause disease. Cells are able to survive outside the body for a limited amount of time, which makes them potential indicator organisms to test environmental samples for fecal contamination.[10][11] A growing body of research, though, has examined environmentally persistent *E. coli* which can survive for extended periods outside of a host.[12]

The bacterium can be grown and cultured easily and inexpensively in a laboratory setting, and has been intensively investigated for over 60 years. *E. coli* is a chemoheterotroph whose chemically defined medium must include a source of carbon and energy. Organic growth factors included in chemically defined medium used to grow *E. coli* includes glucose, ammonium phosphate, mono basic, sodium chloride, magnesium sulfate, potassium phosphate, dibasic, and water. The exact chemical composition is known for media that is considered chemically defined medium.[13] *E. coli* is the most widely studied prokaryotic model organism, and an important species in the fields of biotechnology and microbiology, where it has served as the host organism for the majority of work with recombinant DNA. Under favorable conditions, it takes only 20 minutes to reproduce.[14]

1 Biology and biochemistry



Model of successive binary fission in E. coli



A colony of E. coli *growing*

1.1 Type and morphology

E. coli is a Gram-negative, facultative anaerobic (that makes ATP by aerobic respiration if oxygen is present, but is capable of switching to fermentation or anaerobic respiration if oxygen is absent) and nonsporulating

bacterium.[15] Cells are typically rod-shaped, and are about 2.0 micrometers (μm) long and 0.25–1.0 μm in diameter, with a cell volume of 0.6–0.7 μm^3.[16][17][18]

E. coli stains Gram-negative because its cell wall is composed of a thin peptidoglycan layer and an outer membrane. During the staining process, E. coli picks up the color of the counterstain safranin and stains pink. The outer membrane surrounding the cell wall provides a barrier to certain antibiotics such that E. coli is not damaged by penicillin.[13]

Strains that possess flagella are motile. The flagella have a peritrichous arrangement.[19]

1.2 Metabolism

E. coli can live on a wide variety of substrates and uses mixed-acid fermentation in anaerobic conditions, producing lactate, 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.[20]

1.3 Culture growth

Optimum 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).[21] Growth can be driven by aerobic or anaerobic respiration, using a large variety of redox 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.[22] E. coli is classified as a facultative anaerobe. It uses oxygen when it is present and available. It can however, continue to grow in the absence of oxygen using fermentation or anaerobic respiration. The ability to be able to continue growing in the absence of oxygen is an advantage to bacteria because their survival is increased in environments where water predominates.[13]

1.4 Cell cycle

Main article: Cell cycle

The bacterial cell cycle is divided into three stages. The B period occurs between the completion of cell division and the beginning of DNA replication. The C period encompasses the time it takes to replicate the chromosomal DNA. The D period refers to the stage between the conclusion of DNA replication and the end of cell division.[23] The doubling rate of *E. coli* is higher when more nutrients are available. However, the length of the C and D periods do not change, even when the doubling time becomes less than the sum of the C and D periods. At the fastest growth rates, replication begins before the previous round of replication has completed, resulting in multiple replication forks along the DNA and overlapping cell cycles.[24]

Unlike eukaryotes, prokaryotes do not rely upon either changes in gene expression[25] or changes in protein synthesis[26] to control the cell cycle. This probably explains why they do not have similar proteins to those used by eukaryotes to control their cell cycle, such as cdk1. This has led to research on what the control mechanism is in prokaryotes. Recent evidence suggests that it may be membrane- or lipid-based.[27]

1.5 Genetic adaptation

E. coli and related bacteria possess the ability to transfer DNA via bacterial conjugation or transduction, which allows genetic material to spread horizontally through an existing population. The process of transduction, which uses the bacterial virus called a bacteriophage,[28] is where the spread of the gene encoding for the Shiga toxin from the *Shigella* bacteria to *E. coli* helped produce *E. coli* O157:H7, the Shiga toxin producing strain of *E. coli.*

2 Diversity

Escherichia coli encompasses an enormous population of bacteria that exhibit a very high degree of both genetic and phenotypic diversity. Genome sequencing of a large number of isolates of *E. coli* and related bacteria shows that a taxonomic reclassification would be desirable. However, this has not been done, largely due to its medical importance,[29] and *E. coli* remains one of the most diverse bacterial species: only 20% of the genes in a typical *E. coli* genome is shared among all strains.[30]

In fact, from the evolutionary point of view, the members of genus *Shigella* (*S. dysenteriae*, *S. flexneri*, *S. boydii*, and *S. sonnei*) should be classified as *E. coli* strains, a phenomenon termed taxa in disguise.[31] Similarly, other strains of *E. coli* (e.g. the K-12 strain commonly used in recombinant DNA work) are sufficiently different that they would merit reclassification.

A strain is a subgroup within the species that has unique characteristics that distinguish it from other strains. These differences are often detectable only at the molecular level; however, they may result in changes to the physiology or lifecycle of the bacterium. For example, a strain may gain pathogenic capacity, the ability to use a unique carbon source, the ability to take upon a particular ecological niche, or the ability to resist antimicrobial agents. Different strains of *E. coli* are often host-specific, making it possible to determine the source of fecal contamination in environmental samples.[10][11] For exam-

ple, knowing which *E. coli* strains are present in a water sample allows researchers to make assumptions about whether the contamination originated from a human, another mammal, or a bird.

2.1 Serotypes

Main article: Pathogenic Escherichia coli § Serotypes

A common subdivision system of *E. coli*, but not based on evolutionary relatedness, is by serotype, which is based on major surface antigens (O antigen: part of lipopolysaccharide layer; H: flagellin; K antigen: capsule), e.g. O157:H7).[32] It is, however, common to cite only the serogroup, i.e. the O-antigen. At present, about 190 serogroups are known.[33] The common laboratory strain has a mutation that prevents the formation of an O-antigen and is thus not typeable.

2.2 Genome plasticity and evolution

Like all lifeforms, new strains of *E. coli* evolve through the natural biological processes of mutation, gene duplication, and horizontal gene transfer; in particular, 18% of the genome of the laboratory strain MG1655 was horizontally acquired since the divergence from *Salmonella*.[34] *E. coli* K-12 and *E. coli* B strains are the most frequently used varieties for laboratory purposes. Some strains develop traits that can be harmful to a host animal. These virulent strains typically cause a bout of diarrhea that is unpleasant in healthy adults and is often lethal to children in the developing world.[35] More virulent strains, such as O157:H7, cause serious illness or death in the elderly, the very young, or the immunocompromised.[35][36]

The genera *Escherichia* and *Salmonella* diverged around 102 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.[37] This was followed by a split of the escherichian ancestor into five species (*E. albertii*, *E. coli*, *E. fergusonii*, *E. hermannii*, and *E. vulneris*). The last *E. coli* ancestor split between 20 and 30 million years ago.[38]

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.[39] 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 laboratory.

2.3 Neotype strain

E. coli is the type species of the genus (*Escherichia*) and in turn *Escherichia* is the type genus of the family Enterobacteriaceae, where the family name does not stem from the genus *Enterobacter* + “i” (sic.) + "aceae", but from “enterobacterium” + “aceae” (enterobacterium being not a genus, but an alternative trivial name to enteric bacterium).[40][41][42]

The original strain described by Escherich is believed to be lost, consequently a new type strain (neotype) was chosen as a representative: the neotype strain is U5/41^{T},[43] also known under the deposit names DSM 30083,[44] ATCC 11775,[45] and NCTC 9001,[46] which is pathogenic to chickens and has an O1:K1:H7 serotype.[47] However, in most studies, either O157:H7, K-12 MG1655, or K-12 W3110 were used as a representative *E. coli*. The genome of the type strain has only lately been sequenced.<ref name=doi:10.1186/1944-32

2.4 Phylogeny of *E. coli* strains

A large number of strains belonging to this species have been isolated and characterised. In addition to serotype (*vide supra*), they can be classified according to their phylogeny, i.e. the inferred evolutionary history, as shown below where the species is divided into six groups.[48][49] Particularly the use of whole genome sequences yields highly supported phylogenies. Based on such data, five subspecies of *E. coli* were distinguished.[43]

The link between phylogenetic distance (“relatedness”) and pathology is small,[43] *e.g.* the O157:H7 serotype strains, which form a clade (“an exclusive group”)—group E below—are all enterohaemorragic strains (EHEC), but not all EHEC strains are closely related. In fact, four different species of *Shigella* are nested among *E. coli* strains (*vide supra*), while *E. albertii* and *E. fergusonii* are outside of this group. Indeed, all *Shigella* species were placed within a single subspecies of *E. coli* in a phylogenomic study that included the type strain,[43] and for this reason an according reclassification is difficult. All commonly used research strains of *E. coli* belong to group A and are derived mainly from Clifton’s K-12 strain (λ^{+} F^{+}; O16) and to a lesser degree from d'Herelle's *Bacillus coli* strain (B strain)(O7).

3 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 about 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 transposable genetic elements, repeat elements, cryptic prophages, and bacteriophage remnants.[50]

Today, several hundred complete genomic sequences of *Escherichia* and *Shigella* species are available. The genome sequence of the type strain of *E. coli* has been added to this collection not before 2014.[43] 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 around 80% of each genome can vary among isolates.[30] 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 pangenome) 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.[51]

4 Gene nomenclature

Genes in *E. coli* are usually named by 4-letter acronyms that derive from their function (when known). For instance, recA is named after its role in homologous recombination plus the letter A. Functionally related genes are named recB, recC, recD etc. The proteins are named by uppercase acronyms, e.g. RecA, RecB, etc. When the genome of *E. coli* was sequenced, all genes were numbered (more or less) in their order on the genome and abbreviated by b numbers, such as b2819 (=recD) etc. The "b" names were created after Fred Blattner who led the genome sequence effort.[52] Another numbering system was introduced with the sequence of another *E. coli* strain, W3110, which was sequenced in Japan and hence uses numbers starting by JW... (Japanese W3110), e.g. JW2787 (= recD).[53] Hence, recD = b2819 = JW2787. Note, however, that most databases have their own numbering system, e.g. the EcoGene database[54] uses EG10826 for recD. Finally, ECK numbers are specifically used for alleles in the MG1655 strain of *E. coli* K-12.[54] Complete lists of genes and their synonyms can be obtained from databases such as EcoGene or Uniprot.

5 Proteomics

5.1 Proteome

Several studies have investigated the proteome of *E. coli*. By 2006, 1,627 (38%) of the 4,237 open reading frames (ORFs) had been identified experimentally.[55]

5.2 Interactome

The interactome of *E. coli* has been studied by affinity purification and mass spectrometry (AP/MS) and by analyzing the binary interactions among its proteins.

Protein complexes. 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.[56] A 2009 study found 5,993 interactions between proteins of the same *E. coli* strain, though these data showed little overlap with those of the 2006 publication.[57]

Binary interactions. Rajagopala *et al.* (2014) have carried out systematic yeast two-hybrid screens with most *E. coli* proteins, and found a total of 2,234 protein-protein interactions.[58] This study also integrated genetic interactions and protein structures and mapped 458 interactions within 227 protein complexes.

6 Normal microbiota

E. coli belongs to a group of bacteria informally known as coliforms that are found in the gastrointestinal tract of warm-blooded animals.[40] *E. coli* normally colonizes an infant's gastrointestinal tract within 40 hours of birth, arriving with food or water or from the individuals handling the child. In the bowel, *E. coli* adheres to the mucus of the large intestine. It is the primary facultative anaerobe of the human gastrointestinal tract.[59] (Facultative anaerobes are organisms that can grow in either the presence or absence of oxygen.) As long as these bacteria do not acquire genetic elements encoding for virulence factors, they remain benign commensals.[60]

6.1 Therapeutic use

Nonpathogenic *E. coli* strain Nissle 1917, also known as Mutaflor, and *E. coli* O83:K24:H31 (known as Colinfant[61]) are used as probiotic agents in medicine, mainly for the treatment of various gastroenterological diseases,[62] including inflammatory bowel disease.[63]

7 Role in disease

Main article: Pathogenic Escherichia coli

Most *E. coli* strains do not cause disease,[64] but virulent strains can cause gastroenteritis, urinary tract infections, and neonatal meningitis. It can also be characterized by severe abdominal cramps, diarrhea that typically turns bloody within 24 hours, and sometimes fever. In rarer cases, virulent strains are also responsible for bowel necrosis (tissue death) and perforation without progress-

ing to hemolytic-uremic syndrome, peritonitis, mastitis, septicemia, and Gram-negative pneumonia.[59]

There is one strain, *E.coli* #0157:H7, that produces a toxin called the Shiga toxin (classified as a bioterrorist agent). This toxin causes premature destruction of the red blood cells which then clog the body's filtering system, the kidneys, causing hemolytic-uremic syndrome (HUS). This in turn causes strokes due to small clots of blood which lodge in capillaries in the brain. This causes the body parts controlled by this region of the brain not to work properly. In addition, this strain causes the buildup of fluid (since the kidneys do not work) leading to edema around the lungs and legs and arms. This increase in fluid buildup especially around the lungs impedes the functioning of the heart, causing an increase in blood pressure.[65][66][67][68]

Uropathogenic *E. coli* (UPEC) is one of the main causes of urinary tract infections.[69] It is part of the normal flora in the gut and can be introduced in many ways. In particular for females, the direction of wiping after defecation (wiping back to front) can lead to fecal contamination of the urogenital orifices. Anal intercourse can also introduce this bacterium into the male urethra, and in switching from anal to vaginal intercourse, the male can also introduce UPEC to the female urogenital system.[69] For more information, see the databases at the end of the article or UPEC pathogenicity.

In May 2011, one *E. coli* strain, O104:H4, was the subject of a bacterial outbreak that began in Germany. Certain strains of *E. coli* are a major cause of foodborne illness. The outbreak started when several people in Germany were infected with enterohemorrhagic *E. coli* (EHEC) bacteria, leading to hemolytic-uremic syndrome (HUS), a medical emergency that requires urgent treatment. The outbreak did not only concern Germany, but also 11 other countries, including regions in North America. On 30 June 2011, the German *Bundesinstitut für Risikobewertung (BfR)* (Federal Institute for Risk Assessment, a federal institute within the German Federal Ministry of Food, Agriculture and Consumer Protection) announced that seeds of fenugreek from Egypt were likely the cause of the EHEC outbreak.[70]

7.1 Treatment

The mainstay of treatment is the assessment of dehydration and replacement of fluid and electrolytes. Administration of antibiotics has been shown to shorten the course of illness and duration of excretion of ETEC in adults in endemic areas and in traveller's diarrhoea. The antibiotic used depends upon susceptibility patterns in the particular geographical region. Currently, the antibiotics of choice are fluoroquinolones or azithromycin, with an emerging role for rifaximin. Oral rifaximin, a semisynthetic rifamycin derivative, is an effective and well-tolerated antibacterial for the management of adults with non-invasive traveller's diarrhoea. Rifaximin was significantly more effective than placebo and no less effective than ciprofloxacin in reducing the duration of diarrhoea. While rifaximin is effective in patients with E. coli-predominant traveller's diarrhoea, it appears ineffective in patients infected with inflammatory or invasive enteropathogens.[71]

7.2 Prevention

Antibodies against the LT and major CFs of ETEC provide protection against LT-producing ETEC expressing homologous CFs. Oral inactivated vaccines consisting of toxin antigen and whole cells, i.e. the licensed recombinant cholera B subunit (rCTB)-WC cholera vaccine Dukoral and candidate ETEC vaccines have been developed. In different trials, the rCTB-WC cholera vaccine provided high (85–100%) short-term protection. An oral ETEC vaccine consisting of rCTB and formalininactivated E. coli bacteria expressing major CFs has been shown to be safe, immunogenic and effective against severe diarrhoea in American travellers but not against ETEC diarrhoea in young children in Egypt. A modified ETEC vaccine consisting of recombinant E. coli strains overexpressing the major CFs and a more LT-like hybrid toxoid called LCTBA, have been developed and are being tested.[72] [73]

7.3 Causes and Risk Factors

- Working around livestock
- Consuming unpasteurized dairy product
- Eating undercooked meat
- Drinking impure water

7.4 Prevention Methods

- Wash hands before and after cooking (At least 30 seconds)
- Avoid cross contamination of foods
- Keep food refrigerated or frozen
- Make sure food is kept at appropriate temperature
- Avoid raw meat and poultry
- Do not let food defrost on counter
- Refrigerate left overs

8 Model organism in life science research

Main article: Escherichia coli (molecular biology)

8.1 Role in biotechnology

Because of its long history of laboratory culture and ease of manipulation, *E. coli* plays an important role in modern biological engineering and industrial microbiology.[74] 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.[75]

E. coli is a very versatile host for the production of heterologous proteins,[76] and various 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.[77]

Many proteins previously thought difficult or impossible to be expressed in *E. coli* in folded form have been successfully expressed in *E. coli*. For example, proteins with multiple disulphide bonds may be produced in the periplasmic space or in the cytoplasm of mutants rendered sufficiently oxidizing to allow disulphide-bonds to form,[78] while proteins requiring post-translational modification such as glycosylation for stability or function have been expressed using the N-linked glycosylation system of *Campylobacter jejuni* engineered into *E. coli*.[79][80][81]

Modified *E. coli* cells have been used in vaccine development, bioremediation, production of biofuels,[82] lighting, and production of immobilised enzymes.[76][83]

8.2 Model organism

E. coli is frequently used as a model organism in microbiology studies. Cultivated strains (e.g. *E. coli* K12) are well-adapted to the laboratory environment, and, unlike wild-type strains, have lost their ability to thrive in the intestine. Many laboratory strains lose their ability to form biofilms.[84][85] These features protect wild-type strains from antibodies and other chemical attacks, but require a large expenditure of energy and material resources.

In 1946, Joshua Lederberg and Edward Tatum first described the phenomenon known as bacterial conjugation using *E. coli* as a model bacterium,[86] and it remains the primary model to study conjugation.[87] *E. coli* was an integral part of the first experiments to understand phage genetics,[88] and early researchers, such as Seymour Benzer, used *E. coli* and phage T4 to understand the topography of gene structure.[89] Prior to Benzer's research, it was not known whether the gene was a linear structure, or if it had a branching pattern.[90]

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.[50]

By evaluating the possible combination of nanotechnologies with landscape ecology, complex habitat landscapes can be generated with details at the nanoscale.[91] 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.

Studies are also being performed attempting to program *E. coli* to solve complicated mathematics problems, such as the Hamiltonian path problem.[92]

9 History

In 1885, the German-Austrian pediatrician Theodor Escherich discovered this organism in the feces of healthy individuals. He called it *Bacterium coli commune* because it is found in the colon. 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).[73][93][94]

Bacterium coli was the type species of the now invalid genus *Bacterium* when it was revealed that the former type species ("*Bacterium triloculare*") was missing.[95] Following a revision of *Bacterium*, it was reclassified as *Bacillus coli* by Migula in 1895[96] and later reclassified in the newly created genus *Escherichia*, named after its original discoverer.[97]

10 See also

- Bacteriological water analysis
- Coliform bacteria
- Contamination control
- Dam dcm strain
- Fecal coliforms
- International Code of Nomenclature of Bacteria
- List of bacterial genera named after personal names
- List of strains of Escherichia coli

- Mannan Oligosaccharide based nutritional supplements
- T4 rII system
- 2011 E. coli O104:H4 outbreak

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12 Further reading

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13 External links

- Photo Blog post of Escherichia Coli
- E. coli: Protecting yourself and your family from a sometimes deadly bacterium
- *E. coli* statistics
- Spinach and *E. coli* Outbreak – U.S. FDA
- *E. coli* Outbreak From Fresh Spinach – U.S. CDC
- Current research on *Escherichia coli* at the Norwich Research Park
- E. coli gas production from glucose video demonstration
-

13.1 E. coli databases

- Bacteriome *E. coli* interaction database
- coliBASE (subset of the comparative genomics database xBASE)
- EcoGene (genome database and website dedicated to Escherichia coli K-12 substrain MG1655)
- EcoSal Continually updated Web resource based on the classic ASM Press publication *Escherichia coli and Salmonella: Cellular and Molecular Biology*
- ECODAB The structure of the O-antigens that form the basis of the serological classification of *E. coli*
- Coli Genetic Stock Center Strains and genetic information on *E. coli* K-12
- EcoCyc – literature-based curation of the entire genome, and of transcriptional regulation, transporters, and metabolic pathways
- PortEco (formerly EcoliHub) – NIH-funded comprehensive data resource for *E. coli* K-12 and its phage, plasmids, and mobile genetic elements
- EcoliWiki is the community annotation component of PortEco
- RegulonDB RegulonDB is a model of the complex regulation of transcription initiation or regulatory network of the cell *E. coli* K-12.
- Uropathogenic Escherichia coli (UPEC)

13.2 General databases with E. coli-related information

- 5S rRNA Database Information on nucleotide sequences of 5S rRNAs and their genes
- ACLAME A CLAssification of Mobile genetic Elements
- AlignACE Matrices that search for additional binding sites in the E. coli genomic sequence
- ArrayExpress Database of functional genomics experiments
- ASAP Comprehensive genome information for several enteric bacteria with community annotation
- BioGPS Gene portal hub
- BRENDA Comprehensive Enzyme Information System
- BSGI Bacterial Structural Genomics Initiative
- CATH Protein Structure Classification
- CBS Genome Atlas
- CDD Conserved Domain Database
- CIBEX Center for Information Biology Gene Expression Database
- COGs

14 Text and image sources, contributors, and licenses

14.1 Text

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Intgr, Salvadorjo~enwiki, Imnotminkus, Smithbrenon, Evands, DVdm, Gdrbot, Bgwhite, HoCkEy PUCK, Dj Capricorn, WriterHound, Gwernol, Whosasking, Debivort, Silarius, YurikBot, Ugha, Wavelength, Hairy Dude, NTBot~enwiki, RussBot, Hede2000, Pigman, RadioFan, Gaius Cornelius, Eleassar, Rsrikanth05, RadioKirk, NawlinWiki, Dialectric, Test-tools~enwiki, Grafen, Badagnani, Johann Wolfgang, Trovatore, Clam0p, Terfili, Dogcow, Apokryltaros, Ragesoss, Brian Crawford, Raven4x4x, JHCaufield, IceCreamAntisocial, Ghclark, FF2010, Zzuuzz, Closedmouth, Keymer, D'Agosta, Esprit15d, JoanneB, CWenger, JLaTondre, Katieh5584, Rcharman, Leon2323, DVD R W, CIreland, Bibliomaniac15, Ryūkotsusei, Gvsualan, Veinor, SmackBot, Moeron, KnowledgeOfSelf, Vald, KocjoBot~enwiki, Etherealmuse, Delldot, Ozone77, Jab843, Pedrose, AndrewLeeson, Cacuija, DenGer, Gilliam, Skizzik, Richfife, David.Throop, Tv316, Amatulic, Chris the speller, Bluebot, Simon123, Rkitko, RDBrown, Sirex98, Emt147, Basalisk, DHN-bot~enwiki, Polyhedron, Nintendude, Hgrosser, Scwlong, Newmanbe, Zsinj, NFERD, Can't sleep, clown will eat me, DéRahier, Onorem, Shyne239, Xiner, Rrburke, Goaty, JimHu, Mbertsch, Addshore, Flyguy649, Kingdon, Nakon, Dreadstar, Richard001, Geoffr, Razorhead, Daniel.Cardenas, Vina-iwbot~enwiki, Scharks, Risssa, Pilotguy, Kukini, Fyver528, SashatoBot, Lambiam, Eliyak, GiollaUidir, Rory096, Harryboyles, DO11.10, Kuru, Scientizzle, Gerbennn, Jaganath, Sir Nicholas de Mimsy-Porpington, Steipe, Mgiganteus1, Seb951, Verdant04, Ocatecir, Majorclanger, IronGargoyle, Ben Moore, Blacksmith tb, Nintendonien, JHunterJ, Heartpox~enwiki, Stwalkerster, Kpengboy, Ryulong, Almo~enwiki, Parakkum, Citicat, Andrwsc, Acetylcholine, Belfry, KJS77, Hu12, DeLtA, Vlad788, Paul venter, Kaarel, Wjejskenewr, LCKuhn, Tkasmai, DavidOaks, LadyofShalott, Courcelles, Tawkerbot2, Chris55, LessHeard vanU, DejahThoris, Fvasconcellos, JForget, Philbradley, Eggman64, Ale jrb, Zarex, Agathman, Rawling, 67-21-48-122, NickW557, LittleT889, Moreschi, Casper2k3, Xilog, Yaris678, Cydebot, Nbound, Reywas92, Red Director, Siberian Husky, Weggie, Addhaneshwar, Aristeo, Wikipediarules2221, Amitushtush, Tawkerbot4, Christian75, DumbBOT, Chrislk02, Narayanese, Medvedenko, SpK, Omicronpersei8, RickDC, Thijs!bot, Epbr123, Opabinia regalis, Pajz, Kablammo, Martin Hogbin, N5iln, Andyjsmith, Mojo Hand, Headbomb, Marek69, John254, Horologium, Countmike, Edal, Rhrad, CharlotteWebb, Siegele, CTZMSC3, Blizzard youkai~enwiki, Escarbot, DrMorelos, Dancanm, Mentifisto, Porqin, AntiVandalBot, Majorly, Widefox, Seivad, Seaphoto, Crabula, Jj137, TimVickers, Jademushroom, Cherylyoung, Res2216firestar, JAnDbot, Deflective, Alixandre, Awien, Andonic, Tstrobaugh, Lawilkin, Strafpeloton2, Connormah, Canjth, Bennybp, Bongwarrior, VoABot II, Meredyth, Kuyabribri, EOBeav, Morenna, Lucyin, Freelance Physicist, Sub40Hz, Redwoodseed, Ciar, 28421u2232nfenfcenc, Raveseer, Allstarecho, Asaadi~enwiki, Wpw50, Cpl Syx, Novickas, Dravick, DerHexer, Edward321, Megalodon99, Wi-king, Squidonius, Markco1, Gorton k, Robin S, Gwern, DuncanB, Jackson Peebles, Hdt83, MartinBot, Poeloq, Cjfriedman, Doc Accurate, Jay Litman, Jack007, Cdcdoc, Burnedthru, R'n'B, CommonsDelinker, Admc2006, Fconaway, Wiki Raja, LedgendGamer, Tgeairn, RockMFR, Wlodzimierz, AlphaEta, J.delanoy, Classicalclarinet, Pharaoh of the Wizards, Marcusvra, Trusilver, EscapingLife, Bogey97, Numbo3, Boghog, Uncle Dick, Mike.lifeguard, Sirtrebuchet, WarthogDemon, Danglingdiagnosis, Katalaveno, LordAnubisBOT, Ignatzmice, Theothernextdimension, Mikael Häggström, AntiSpamBot, Chiswick Chap, NewEnglandYankee, Liveste, SJP, Malerin, Mufka, FJPB, Largoplazo, FOTEMEH, Plindenbaum, Schnapster, Desaderal, Pdcook, TigrCmr, Million Moments, YKgm, CA387, Lawrence12345, Erwinser, Deor, Shiggity, ABF, Truehawk, Flyingidiot, Jeff G., Zygomorph, LeilaniLad, Barneca, Soap Poisoning, Philip Trueman, Megdextr, TXiKiBoT, Showjumpersam, Pkarp11, Hqb, Rei-bot, GcSwRhIc, Qxz, Una Smith, Melsaran, 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