Vibrio cholerae

Vibrio cholerae is a Gram-negative, comma-shaped bacterium. The bacterium's natural habitat is brackish or saltwater. Some strains of *V. cholerae* cause the disease cholera. *V. cholerae* is a facultative anaerobe[1] and has a flagellum at one cell pole as well as pili. *V. cholerae* can undergo respiratory and fermentative metabolism. When ingested, *V. cholerae* can cause diarrhea and vomiting in a host within several hours to 2-3 days of ingestion. *V. cholerae* was first isolated as the cause of cholera by Italian anatomist Filippo Pacini in 1854,[2] but his discovery was not widely known until Robert Koch, working independently 30 years later, publicized the knowledge and the means of fighting the disease.[3][4]

1 Characteristics

V. cholerae is Gram-negative and comma-shaped. Initial isolates are slightly curved, whereas they can appear as straight rods upon laboratory culturing. The bacterium has a flagellum at one cell pole as well as pili. *V. cholerae* is a facultative anaerobe, and can undergo respiratory and fermentative metabolism.[1]

2 Pathogenesis

V. cholerae pathogenicity genes code for proteins directly or indirectly involved in the virulence of the bacteria. During infection, *V. cholerae* secretes cholera toxin, a protein that causes profuse, watery diarrhea,[known as Rice-water Stool]. Colonization of the small intestine also requires the toxin coregulated pilus (TCP), a thin, flexible, filamentous appendage on the surface of bacterial cells. *V. cholerae* can cause syndromes ranging from asymptomatic to cholera gravis.[4] In endemic areas, 75% of cases are asymptomatic, 20% are mild to moderate, and 2-5% are severe forms such as cholera gravis.[4] Symptoms include abrupt onset of watery diarrhea (a grey and cloudy liquid), occasional vomiting, and abdominal cramps.[1][4] Dehydration ensues, with symptoms and signs such as thirst, dry mucous membranes, decreased skin turgor, sunken eyes, hypotension, weak or absent radial pulse, tachycardia, tachypnea, hoarse voice, oliguria, cramps, renal failure, seizures, somnolence, coma, and death.[1] Death due to dehydration can occur in a few hours to days in untreated children. The disease is also particularly dangerous for pregnant women and their fetuses during late pregnancy, as it may cause premature labor and fetal death.[4][5][6] In cases of cholera gravis involving severe dehydration, up to 60% of patients can die; however, less than 1% of cases treated with rehydration therapy are fatal. The disease typically lasts 4–6 days.[4][7] Worldwide, diarrhoeal disease, caused by cholera and many other pathogens, is the second-leading cause of death for children under the age of 5 and at least 120,000 deaths are estimated to be caused by cholera each year.[8][9] In 2002, the WHO deemed that the case fatality ratio for cholera was about 3.95%.[4]

3 Genome

V. cholerae has two circular chromosomes, together totalling 4 million base pairs of DNA sequence and 3,885 predicted genes.[10] The genes for cholera toxin are carried by CTXphi (CTXφ), a temperate bacteriophage inserted into the *V. cholerae* genome. CTXφ can transmit cholera toxin genes from one *V. cholerae* strain to another, one form of horizontal gene transfer. The genes for toxin coregulated pilus are coded by the VPI pathogenicity island (VPI). The entire genome of the virulent strain *V. cholerae* El Tor N16961 has been sequenced,[1] and contains two circular chromosomes.[4] Chromosome 1 has 2,961,149 base pairs with 2,770 open reading frames (ORF's) and chromosome 2 has 1,072,315 base pairs, 1,115 ORF's. The larger first chromosome contains the crucial genes for toxicity, regulation of toxicity, and important cellular functions, such as transcription and translation.[1]

The second chromosome is determined to be different from a plasmid or megaplasmid due to the inclusion of housekeeping and other essential genes in the genome, including essential genes for metabolism, heat-shock proteins, and 16S rRNA genes, which are ribosomal subunit genes used to track evolutionary relationships between bacteria. Also relevant in determining if the replicon is a chromosome is whether it represents a significant percentage of the genome, and chromosome 2 is 40% by size of the entire genome. And, unlike plasmids, chromosomes are not self-transmissible.[4] However, the second chromosome may have once been a megaplasmid because it contains some genes usually found on plasmids.[1]

V. cholerae contains a genomic island of pathogenicity and is lysogenized with phage DNA. That means that the genes of a virus were integrated into the bacterial genome and made the bacteria pathogenic. The molecular pathway involved in expression of virulence is discussed in the

pathology and current research sections below.

3.1 Bacteriophage CTXφ

CTXφ (also called CTXphi) is a filamentous phage that contains the genes for cholera toxin. Infectious CTXφ particles are produced when *V. cholerae* infects humans. Phage particles are secreted from bacterial cells without lysis. When CTXφ infects *V. cholerae* cells, it integrates into specific sites on either chromosome. These sites often contain tandem arrays of integrated CTXφ prophage. In addition to the *ctxA* and *ctxB* genes encoding cholera toxin, CTXφ contains eight genes involved in phage reproduction, packaging, secretion, integration, and regulation. The CTXφ genome is 6.9 kb long.[11]

3.2 *Vibrio* pathogenicity island

The *Vibrio* pathogenicity island (VPI) contains genes primarily involved in the production of toxin coregulated pilus (TCP). It is a large genetic element (about 40 kb) flanked by two repetitive regions (*att*-like sites), resembling a phage genome in structure. The VPI contains two gene clusters, the TCP cluster, and the ACF cluster, along with several other genes. The *acf* cluster is composed of four genes: *acfABCD*. The *tcp* cluster is composed of 15 genes: *tcpABCDEFHIJPQRST* and regulatory gene *toxT*.

4 Ecology and epidemiology

The main reservoirs of *V. cholerae* are people and aquatic sources such as brackish water and estuaries, often in association with copepods or other zooplankton, shellfish, and aquatic plants.[12]

Cholera infections are most commonly acquired from drinking water in which *V. cholerae* is found naturally or into which it has been introduced from the feces of an infected person. Other common vehicles include contaminated fish and shellfish, produce, or leftover cooked grains that have not been properly reheated. Transmission from person to person, even to health care workers during epidemics, is rarely documented. *V. cholerae* thrives in a aquatic environment, particularly in surface water. The primary connection between humans and pathogenic strains is through water, particularly in economically reduced areas that do not have good water purification systems.[9]

Nonpathogenic strains are also present in water ecologies. The wide variety of strains of pathogenic and nonpathogenic strains that c-exist in aquatic environments are thought to allow for so many genetic varieties. Gene transfer is fairly common amongst bacteria, and recombination of different *V. cholerae* genes can lead to new virulent strains.[13]

5 Diversity and evolution

Two serogroups of *V. cholerae*, O1 and O139, cause outbreaks of cholera. O1 causes the majority of outbreaks, while O139 – first identified in Bangladesh in 1992 – is confined to Southeast Asia. Many other serogroups of *V. cholerae*, with or without the cholera toxin gene (including the nontoxigenic strains of the O1 and O139 serogroups), can cause a cholera-like illness. Only toxigenic strains of serogroups O1 and O139 have caused widespread epidemics.

V. cholerae O1 has two biotypes, classical and El Tor, and each biotype has two distinct serotypes, Inaba and Ogawa. The symptoms of infection are indistinguishable, although more people infected with the El Tor biotype remain asymptomatic or have only a mild illness. In recent years, infections with the classical biotype of *V. cholerae* O1 have become rare and are limited to parts of Bangladesh and India.[14] Recently, new variant strains have been detected in several parts of Asia and Africa. Observations suggest these strains cause more severe cholera with higher case fatality rates.

6 Gallery

- *Vibrio cholerae* bacteria
- Diagram of the bacterium, *V. cholerae*

7 See also

- Drinking water
- Haiti cholera outbreak

8 References

[1] "Laboratory Methods for the Diagnosis of Vibrio cholerae" (PDF). Centre for Disease Control. Retrieved 29 October 2013.

[2] See:

- Filippo Pacini (1854) "Osservazioni microscopiche e deduzioni patologiche sul cholera asiatico" (Microscopic observations and pathological deductions on Asiatic cholera), *Gazzetta Medica Italiana: Toscana*, 2nd series, **4** (50) : 397-401 ; **4** (51) : 405-412. The term "vibrio cholera" appears on page 411.
- Reprinted (more legibly) as a pamphlet.

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9 External links

- Copepods and cholera in untreated water
- Vibrio cholerae El Tor N16961 Genome Page
- Patho-Genes Homepage

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