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Review Article

ESCHERICHIA COLI AS A MODEL ORGANISM

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Escherichia coli, the enteric bacterium, is an ever-present constituent of all human beings and form a fraction of the normal flora of gut. It is debatably the most finely understood and extensively studied free-living organism on our planet. *Escherichia coli* is well acknowledged by the shortened name of *E. coli*. This article has introduced *E. coli* as a model organism in the biological study and also its several applications which have spawned from research of *E. coli*. *E. coli* is the first choice for researchers to investigate numerous basic biological processes which are essential for life and is the most extensively used organism in molecular genetics. The reason of widespread use of *E. coli* for study purpose is the ease of its maintenance and breeding in a laboratory environment plus its meticulous experimental advantages. As compared to other living organisms more is known about *E. coli* because of its simple nutritional requirements, rapid growth rate and most important it's well established genetics. Rate of cell division of *E. coli* is average of once in every 30 min, thus enabling quick environmental adaptation. This fast division rate of *E. coli* has helped in evolutionary experiments which are conducted in the laboratories.

Keywords: *Escherichia coli*, Model, Organism, Research, Field

INTRODUCTION

Escherichia coli is a Gram-negative, non sporulating and facultative anaerobic rod. It is about 2.0 micrometers (μm) in length and its diameter is 0.25-1.0 μm as shown in Figure 1 (Kubitschek, 1990). Those strains which have flagella are motile. Structurally flagella have peritrichous arrangement (Darnton *et al.*, 2007). 37°C (98.6°F) is the optimal temperature for multiplication of *E. coli* but few of the laboratory strains can grow up to 49°C (120°F) of temperature (Fotadar, 2005). Multiplication can be driven by utilizing a large number of redox pairs involving 'reduction' of substrates like oxygen, fumarate, trimethylamine N-oxide and dimethyl sulfoxide plus 'oxidation' of substances like formic acid, pyruvic acid, amino acid and hydrogen (Ingledew and Poole, 1984).

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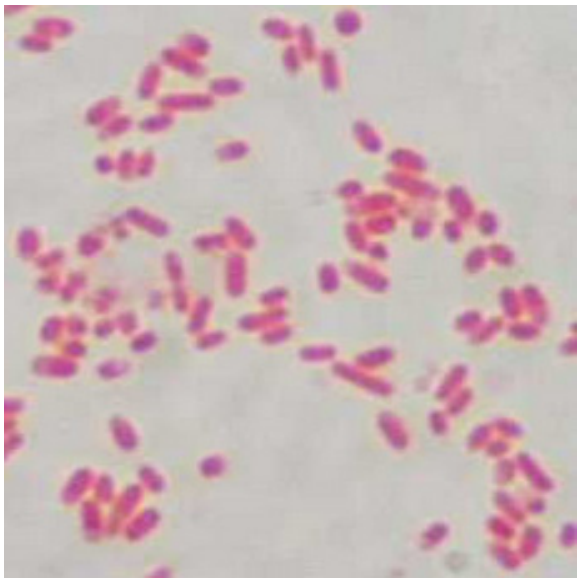
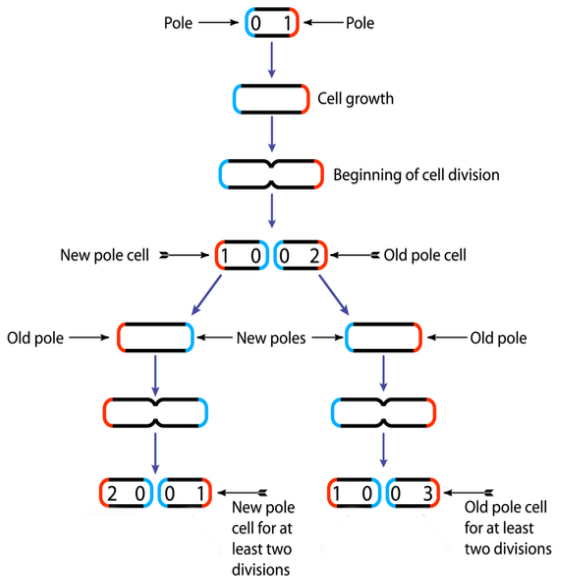
Figure 1: *Escherichia coli*



LIFE CYCLE OF *ESCHERICHIA COLI*

In life cycle of *Escherichia coli,* there is division of one cell into two daughter cells. This process is known as binary fission (Figure 2). Under circumstances when no mutation occurs, the daughter cells are identical genetically to the parent cell. Thus there is "local doubling" of the *E. coli* population. However, it is not necessary that both daughter cells survive but *E. coli* population undergoes exponential growth, if the numbers of surviving daughter cells exceed unity on an average (Zwietering *et al*., 1990).

Figure 2: Life Cycle of *Escherichia coli*



ESCHERICHIA COLI TRANSMISSION

Escherichia coli is found commonly in the distal part of intestine in warm-blooded organisms (endotherms) (Vogt and Dippold, 2005). They constitute about 0.1% of normal flora of gut (Eckburg *et al*., 2005). Major route of transmission for *E. coli* is oro-fecal after which bacterial pathogenic strains cause disease. *E. coli* cells can only survive outside the body for a limited period of time so they can be considered as ideal indicator organisms in order to test samples from environment for fecal contamination (Thompson and Andrea, 2007). However, research work carried out in this regard has showed that environmental samples may have *E. coli* strains that can survive for relatively long period of time even outside the host (Ishii and Sadowsky, 2008).

ESCHERICHIA GENERA HISTORY

A German pediatrician named odor *Escherichia* in 1885 discovered *E. coli* in the feces of healthy individuals and named it Bacterium *coli* because of the fact it is found in the colon. Early prokaryotic classification placed Bacterium *coli* in a genera based on their motility and shape. Afterwards Ernst Haeckel's bacterial classification placed bacteria in the Monera kingdom (Escherich, 1885). In 1895 Migula reclassified

bacteria in the genus *Escherichia* which was named so after its discoverer (Castellani, 1919). This genus belongs to the bacterial group formally called "coliforms" which are member of the "the enterics" known as Enterobacteriaceae family (George and Garrity, 2005).

ESCHERICHIA COLI PHENOTYPIC DIVERSITY

Escherichia coli includes a vast population of bacteria that demonstrate a very high degree of both phenotypic and genetic diversity. Taxonomic reclassification is required after looking at the genomic sequencing of a great number of isolates of the *E. coli* and also related bacteria (Krieg and Holt, 1984). *E. coli* is still one of the most varied bacterial specie and only about 20% of the genome seems to be common in all strains (Lukjancenko *et al*., 2010).

As a matter of fact, the members of *Shigella genus* (*S. flexneri, S. dysenteriae, S. sonnei and S. boydii*) must be classified as strains of *E. coli* from the evolutionary point of view. This phenomenon is termed as taxa in disguise. In the same way, other *E. coli* strains (e.g., the *K*-12 strain commonly used in recombinant DNA work) are very different, thus they warrant reclassification (Lan and Reeves, 2002).

A specie subgroup, which has distinctive characteristics thus distinguishing it from other, is called a strain. One can find these minute characteristic differences only at the molecular level which are responsible for changes in the lifecycle or physiology of the bacterium as for example, a strain may attain the ability to use a unique carbon source, take upon particular ecological niche, resist antimicrobial agents or gain pathogenic capacity. However, strains of *E. coli* are usually host-specific thus making it easy to determine the source of fecal contamination in samples obtained from environment. A good example is that if researchers know that which *E. coli* strains are present in a sample of water, it will allow them to hypothesize that whether the contamination has its origin from a human or some other mammal and even from a bird (Thompson and Andrea, 2007).

On the bases of evolutionary relatedness, there is a common subdivision system of *E. coli* known as serotype. Serotype is based on antigens of surface (i.e., O-antigen which is a part of lipopolysaccharide layer, K-antigen, H: flagellin and capsule for example O157:H7) (Orskov *et al*., 1977). However it is common to quote only the serogroup that is the O-antigen. Presently upto 190 serogroups are known till date. The common strain of laboratory is non type able because it has a mutation which prevents the formation of an O-antigen (Stenutz *et al*., 2006).

New strains of *E. coli* evolved like all life forms, i.e., through the natural biological processes of horizontal gene transfer, gene duplication and mutation. About 18% laboratory strain MG1655 genome was acquired horizontally from *Salmonella* divergence (Lawrence and Ochman, 1998). All *E. coli* strains are derived from either *E. coli* B or *E. coli* K-12 strains. In microbiology, few strains developed traits which can be harmful to a animal host (Nataro and Kaper, 1998). O157:H7 is a more virulent strain which causes serious illness and even death in immunocompromised persons, the elderly people and the very young (Hudault *et al*., 2001).

ESCHERICHIA COLI STRAINS

Many of the *E. coli* strains have been

characterized and isolated. Most of the strains of *E. coli* which are commonly used in the research work are derived from Clifton's K-12 strain (λ^+ F^+ ; O16) and to a lesser extent from *Bacillus coli* strain (B strain; O7) (Brzuszkiewicz *et al*., 2011).

DNA SEQUENCE OF *ESCHERICHIA COLI*

About 60 genomic sequences of *Shigella* and *Escherichia* species are available which have complete genomic sequences. A significant amount of diversity is seen when these sequences are compared. Over 20% of each genome represents those sequences which are present in each isolates and about 80% of genome can differ among the isolates (Lukjancenko *et al*., 2010). An individual genome consists about 4,000 to 5,500 genes, however there are more than 16,000 gene sequences in *E. coli* strains (the pan-genome). This fact reveals that a large variety of component genes exist which have been interpreted and about two-thirds of pan-genome of the *E. coli* originated in other species by horizontal gene transfer process (Zhaxybayeva and Doolittle, 2011).

ESCHERICHIA COLI PROTEINS

Many *E. coli* proteins have been isolated and studied. A 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 that time (Arifuzzaman *et al*., 2006). But another study found 5,993 interactions between proteins of the same *E. coli* strain though this data showed little overlap with that of the above data (Hu *et al*., 2009).

ESCHERICHIA COLI AS A MODEL ORGANISM

In a laboratory setting, the *E. coli* can be grown inexpensively and easily. *E. coli* has been widely studied for about 60 years. It is the most extensively investigated prokaryotic model organism and considered to be very important species in biotechnology and microbiology (Fang *et al*., 2002).

NONPATHOGENIC *ESCHERICHIA COLI* ADVANTAGES

Nonpathogenic strains of *Escherichia coli* serve as probiotic agents in the field of medicine especially to treat various diseases of gastrointestinal tract (Grozdanov *et al*., 2004) which include inflammatory bowel disease (Kamada *et al*., 2005).

ROLE OF *ESCHERICHIA COLI* IN RESEARCH FIELD

E. coli holds an important position in industrial microbiology and modern biological engineering because of its easy manipulation and also long history of its laboratory cultures (Lee, 1996). The research work of Herbert Boyer and Stanley Norman Cohen regarding use of restriction enzymes and plasmids in order to create recombinant DNA by *E. coli* became the base of biotechnology (Russo, 2003).

E. coli is considered to be a very flexible host for the heterologous proteins production (Cornelis, 2000). Recombinant protein production involves various protein expressions in *E. coli*. Plasmids have been used to introduce genes into the microbes by researchers which have lead to high level of protein expression. Such proteins can be produced by the fermentation process in

the industries at mass level. A very useful and important application of recombinant DNA technology was production of human insulin by *E. coli* manipulation (Tof and Ilanit, 1994).

Many folded forms of proteins have been successful in expressing them in *E. coli* which was previously thought to be difficult and even impossible. A good example is that proteins which have multiple disulphide bonds may have the ability to be produced in periplasmic space or in cytoplasm of those mutants having sufficiently oxidizing agent in order to allow the formation of disulphide-bonds (Bessette *et al*., 1999). On the other hand proteins that need post-translational modification glycosylation for function or stability use the system of N-linked glycosylation which is found in *Campylobacter jejuni* engineered into *E. coli* for their expression (Huang *et al*., 2012).

E. coli cells in modified form have been used in the development of vaccine, bioremediation, biofuels production (Summers and Rebecca, 2013) and formation of immobilized enzymes (Nic, 2013).

In microbiology studies, *E. coli* is widely used as a model organism. Unlike wild type strains, cultivated strains (e.g., *E. coli* K12) used in the laboratories are well-adapted to the lab environment and cannot survive in intestine. Many laboratory strains have lost their ability of biofilms formation. By this way wild type strains are protected from antibodies and also other chemical attacks, however, this requires expenditure of large number of material resources and energy (Fux *et al*., 2005).

E. coli was used as a model bacterium in order to describe bacterial conjugation (Lederberg *et al*., 1946) and it is still the primary model to study this process. *E. coli* has helped in understanding phage genetics (Benzer, 1961).

CONCLUSION

Escherichia coli is a natural mammalian gut bacteria used as a model organism for scientific research. *E. coli* is a single-celled organism that can be manipulated and killed with no ethical concerns. It has a rapid growth rate and is very easy to culture in laboratory. The *E. coli* can survive in uneven growth conditions including uneven temperatures, oxygen content, and nutrient availability. Most strains of *E. coli* are harmless, posing no threat to the scientists that use them. Finally, and most importantly, *E. coli* genetics are well-studied and can be manipulated easily. Genetic engineering using tools like conjugation and transduction allow scientists to genetically engineer *E. coli* strains to better understand genetic processes and test new ideas.

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