# Title of the publication

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Abbreviations: SAM, self-assembled monolayer; OTS, octadecyltrichlorosilane

## Introduction

Studying the essentiality of genes helps with identifying the fundamental processes necessary for cell viability [1]. So far, scientists have studied the essential genes in organisms from different domains of life [2]. The results have led to new insights for developing new antibiotics that target essential genes of pathogenic bacteria [3, 4] and synthesising new genomes [5, 6]. Researchers have used different methods for studying the essentility of genes in prokaryotes. Baba et al. [7] have made a library of single gene deletions using phage lambda Red recombination system to screen essential genes while another group have used antisense RNA knockdowns for this purpose [8]. Another method that is widely used due to its simplicity and accuracy is transposon mutagenesis along with high-throughput sequencing [9, 10, 11, 12, 13, 14, 15]. In this method, pools of single insertion mutants are constructed using transposon mutagenesis and the effect of each mutation on the survival of mutants is evaluated by sequencing the survivors [16]. This can lead to the identification of essential genes.

Although the essentiality of genes has been studied in a variety of organisms, there is still room to study the evolutionary conservation of essentiality. Barquist et al. [17] have used transposon-directed insertion-site sequencing to study the differentiation of the essentiality of genes in *Salmonella* serovars Typhi and Typhimurium which has led to divergence in their pathogenecity and host ranges. We extend this research by studying 12 bacterial strains. These include *Salmonella* enterica subsp. enterica serovar Typhi str. Ty2, *Salmonella* enterica subsp. enterica serovar Enteritidis str. P125109, *Salmonella* enterica subsp. enterica serovar Typhimurium str. SL1344, *Salmonella* enterica subsp. enterica serovar Typhimurium str. A130, *Salmonella* enterica subsp. enterica serovar Typhimurium str. D23580, *Escherichia* coli UPEC ST131, *Escherichia* coli ETEC CS17, *Escherichia* coli ETEC H10407, *Citrobacter* rodentium ICC168, *Klebsiella* pneumoniae RH201207, *Klebsiella* pneumoniae subsp. pneumoniae Ecl8, and *Enterobacter* cloacae subsp. cloacae NCTC 9394. All these strains are selected from Enterobacteriaceae family.

Enterobacteriaceae is a family that includes bacteria with different host ranges and pathogenecity found in soil, water, plants, animals and humans [18]. In humans, various strains from this family can cause diarrhoea, septicaemia, urinary tract infection, meningitis, respiratory disease, and wound and burn infection [18]. Besides, they can infect poultry and livestocks and cause financial losses for farmers [18]. Here, we perform a transposon-directed insertion-site sequencing experiment to study the conservation of essentiality in strains from 5 different species in this family.

## Results

We have studied the essentiality of genes in 12 strains from Enterobacteriaceae family. The species are depicted in Fig .

## Discussion

## Materials and Methods

**ACKNOWLEDGMENTS.**

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**Reserved for Publication Footnotes**

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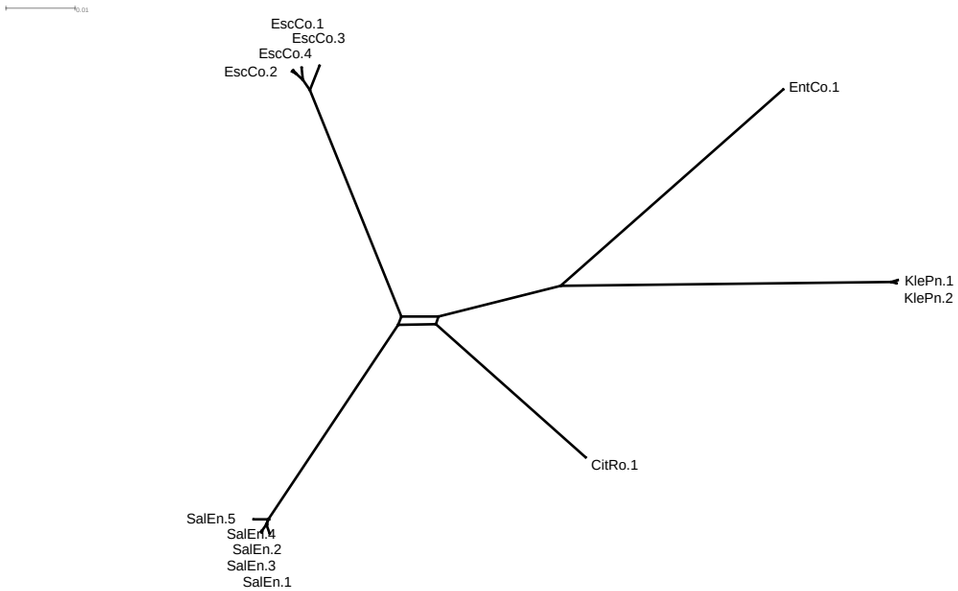


**Fig. 1.** Species tree. How is it made?