



## Abstract

The aim of our analysis was to compare the rates of evolution of DNA sequences of genes and intergenic regions. The chromosomes of the related genera of bacteria, *Escherichia coli* K-12, *Salmonella enterica* serovar Typhimurium, and *Citrobacter koseri*, contain extensive regions in which the order of genes of identical. The fact that the gene order is so conserved suggests that both the genes and intergenic spacers were derived by evolution from corresponding sequences in the last common ancestor of the three organisms, and it enabled us to compare the sequence changes in functional genes and in intergenic spacers across the three organisms.

Pairwise comparisons using BLASTN were used to identify regions that had shared genes. ClustalW was then used to identify single base mutations in both genes and inter-gene regions. Mutation frequencies were determined for all paired comparisons. This analysis indicated that the mutation frequencies are significantly higher in intergenic spacers do not have specific sequence-dependent functions, and therefore, they can accumulate mutations more liberally than genes, which are constrained by their function.

## Introduction

Genomes have both useful genetic information and presumed useless inter-gene regions termed as gaps. Gene pairs between organisms can be isolated using a tool called **Basic Local Alignment Search Tool**, commonly referred to as BLAST. *Salmonella Typhimurium* LT2, *Citrobacter Koseri*, and *Escherchia Coli* MG1655 were chosen because Dr. Csonka told me to use them–add real reason later

## Motivation

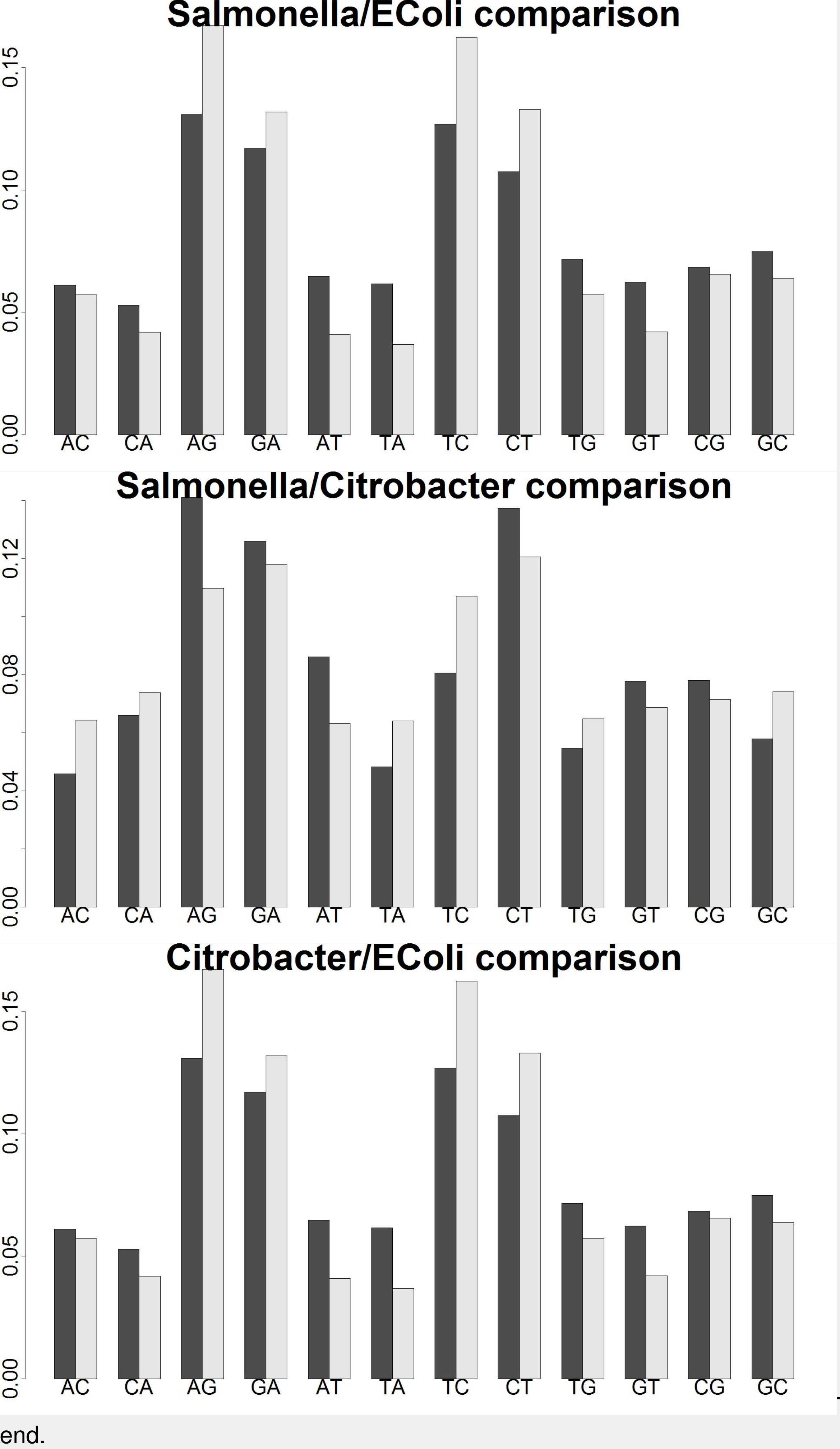
Mutation in genes has a double constraint of DNA’s built in error-handling as well as maintaining function. We suspected that looking at both genes and gaps it could be determined how much similarity there would be in accumulation of mutations at the base level.

## Research Question

**We want to characterize something.** The end.  
TL;DR: Do mutations happen in genes and gaps at the same rate?

## Illustrations

Put some ideas here, to tell about the ideas.



## Example

This just states an example about the research. It might be nice to add a pretty picture here.

## Application

Now I can discuss why that result matters to people.

## Conclusion

Put some concluding remarks here  
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## Acknowledgments

The research of Student Name is supported by NSF grant DMS #1246818. Other thoughts can be placed here.