Materials and Methods

Titles: Comprehensive Genome Annotation

To effectively identify the genes associated with key chromosomal genome characteristics, particularly those linked to antimicrobial resistance and mobile genetic elements, we conducted a thorough functional genome annotation of the assembled contigs across all samples. This annotation was accomplished using the PATRIC (v3.46.3) annotation pipeline, focusing specifically on bacterial genomes as our primary taxonomic target.

Our methodology involved meticulous processing of the assembled contigs through a dedicated pipeline, ensuring that each contig received a unique genome identifier. This structured approach not only facilitated precise genetic classification but also enabled us to highlight genes of particular interest that are essential for understanding the complexities of antibiotic resistance and the dynamics of mobile genetic elements within the bacterial populations under study.

Characterization and Analysis of Comparative Antimicrobial Resistance

The resistome profiles of the Escherichia coli genome sequence dataset (strain MOD1 – EC4326 & SCHI0016.S.230) were extensively analyzed using advanced methodologies such as BLASTP and k-Mer-based detection. This in-depth analysis aimed to identify and quantify various elements associated with antibiotic resistance and virulence factors. Furthermore, it involved the systematic classification of identified Antibiotic Resistance Genes (ARGs) into distinct mechanistic categories. The use of BV-BRC BLASTs was pivotal in this process, allowing for a comprehensive examination of all genes, including those integrated within the genomic structure, in relation to specialized gene repositories within BV-BRC.

Results

Title: Chromosomal Sequence Properties

Genome Information/Chromosomal Sequence Properties

The chromosomal properties for the 2 of genome sequences range in different sizes from and the annotation process for each isolate **as shown in Table 1**, reported S1, and S2, isolate annotation to predict 5,518, and 4,749 coding sequences (CDSs). The Genome Length are 5,319,590 Bp and 4,879,867 Bp and their GC content to be 50.28%, 50.70%. respectively. In contrast, the total CDS in the S1 has the largest Genome Length and coding sequence but lesser percentage GC content when compared to the other genome. The chromosomal properties of all 2 isolates to the collected genomes from the NCBI database showed close relativity when compared to each other.

Table 1: Chromosomal Genome Properties of Escherichia Coli

Sample ID	Genome Length (Bp)	Contigs	Contig N50	Plasmids	GC contents	CDS	Functional Proteins	Hypothetical proteins	RNA genes	CRISPR genes	pGfam domains
E-1	5,319,590	243	146,357	0	50.28	5,518	4,873	645	94	4	5,387
E-2	4,879,867	45	359,891	0	50.70	4,749	4,315	434	74	0	4,663