Vol. 5 No. 2 (2026)

6838

Pakistan Journal of Medical & Cardiological Review

https://pakjmcr.com/index.php/1/about

Online ISSN 3007-2387

Print ISSN 3007-2379

Ullah, et al - 2026

GENETIC DIVERSITY AND ANTIMICROBIAL SUSCEPTIBILITY OF Morganella morganii BY NEXT GENERATION SEQUENCING

1. **Kaleem Ullah (Corresponding Author)**
Senior lecturer, MLT, Sarhad University, Peshawar.
Email: kaleemullah.siahs@suit.edu.pk
2. **Zainab Liaqat**
Assistant Professor, Sarhad University, Peshawar.
3. Naveed Khan.
MPhil Medical Laboratory Sciences, The University of Haripur.
Email: naveedkhan012017@gmail.com
4. Muhammad Danish
Assistant Professor, MLT, RCAHS, RMI, Peshawar.
Email: muhammad.danish@rmi.edu.pk
5. Shah Quaid
Medical Laboratory Technology, Khyber Medical University, Peshawar.
Email: squaid700@gmail.com
6. Musharaf Humayun shah
Shifa International Hospital, Islamabad.
Email: musharafs584@gmail.com
7. Yaseen Salih
MPhil Scholar, Department of Pharmacy, Abdul Wali Khan University, Mardan.
Email: yaseensalih717@gmail.com
8. Touseef Abid
MLT From NIH, Islamabad.
Email: Touseefabid082@gmail.com
9. Musadiq Khan
Assistant Professor, Rehman Medical Institute, Peshawar.
Email: musadiq.khan@rmi.edu.pk

Vol. 5 No. 2 (2026)

6839

Pakistan Journal of Medical & Cardiological Review

https://pakjmcr.com/index.php/1/about

Online ISSN 3007-2387

Print ISSN 3007-2379

Author Details

Keywords: Morganella morganii, Prevalence, UTI, Antimicrobial Resistance

Received on 15 May 2026
Accepted on 14 June 2026
Published on 30 June 2026

Corresponding E-mails & Authors*:
Kaleem Ullah
Email: kaleemullah.siahs@suit.edu.pk

Abstract

Morganella morganii is one of serious causative agent of urinary tract infection (UTI). Antimicrobial resistance (AMR) poses a serious danger to human health and welfare on global scale and must be addressed on urgent basis. The objective of the current study is to determine the prevalence of *Morganella morganii* in KP Pakistan, identification of antimicrobial resistance genes associated with antimicrobial resistance by next generation sequencing method and evaluation of antibiotics susceptibility against *Morganella morganii* by disc diffusion method. A descriptive crossectional study was conducted at Khyber Teaching Hospital Peshawar Pakistan. Male and female patients of all ages who were infected with *Morganella morganii* were included and antibiotics prophylaxis patients and patients who were unwilling to give sample were excluded from the current study. All the bioinformatics analysis were performed by using different types of Bioinformatic tool such as Trimmomatic, fastqc toolkit, SPAdes, Prokka, CARD, PATRIC and Geneious. Total 200 samples (midstream urine) were collected. Out of 200 urine sample 20 cases of *Morganella morganii* were identified 6 cases in male and 14 cases in female patients. *Morganella morganii* were more prevalent in the females having mean age of 40-60 years and male having mean age of (20-40) years. *Morganella morganii* were sensetive to antibiotics included meropenem (100%) and imipenem (100%) and amikacin (95%) antibiotic while resistant to Co-amoxiclav (100%), cefepime (95%), Ceftazidime (95%), Chloramphenicol (90%) and ampicillin (70%). Using shotgun sequencing 10 important antibiotics resistance genes were identified which includes DHA-27, KpnH, fosA8, gyrB, ArNT, CRP, rsmA, PBP3, qacG and EF-Tu. Phylogenetic analysis of identified strain revealed closely resembled with Morganella morganii Kt 1124991.3 and Morganella sp. GLFB 1326758.3 strains while the important identified antimicrobial resistant genes show similarity with genes identified in Tiawani population. Our study revealed lower prevalence as compared to other UTI causing bacteria in kp. Moreover, shot sequencing revealed that presence of different antibiotics resistant genes in single multiple drug resistant (MDR). This study is conducted in one region and emergence of such MDR strain of *Morganella morganii* is important health issue. Therefore, further studies are required to prevent the spread of antimicrobial resistance genes in *Morganella morganii*.

Introduction:

2. Material and Methodes:

This was descriptive crossectional study was conducted at Khyber Teaching Hospital Peshawar Pakistan. Male and female patients of all ages who were infected with *Morganella morganii* were included and antibiotics prophylaxis patients and patients who were unwilling to give sample were excluded from the current study.Total 200 samples (midstream urine) were collected

Sample Collection and Culture:

Proper inform consent will be taken from the indoor UTI infected patients to give mid-stream urine sample in sterile container. This urine sample was processed for culture within 24 hours at microbiology laboratory. Samples containing bacteria were grown on Cystine Lactose Electrolyte Deficient Agar (CLED Agar) and incubate it over night after overnight incubation at 37℃ the culture plat will observe for growth. After bacterial growth these bacterial colonies of *Morganella morganii* were re-culture on MacConkey agar for furthered differentiation of gram positive and gram-negative bacteria.

2.4 Biochemical Characterization:

After culturing the Bacteria *Morganella morganii* species were confirmed by conventional API20E system (BioMerieux Vitek, Inc.). For this bacterial colonies selected from pure culture were mixed suspension solution provided with API20 Kit. With the help of sterile wire loop or needle bacterial suspension were taken and added into each valve of the API20 Strip fill the well properly. After incubation of 18-20hr at 37 ℃ observe the reaction in each well and note the color change compare the change in the color of each well the chart provided by the manufacture and report the result.

2.5 Culture Preservation:

Bacterial colonies were preserved for DNA extraction in proper preservative media. 1000ml of preservative media was prepared by mixing of 13 g of enrichment agar with 750 ml 70% of Glycerol. 4 ml of preservative was added to each 5ml of eppendorf tube and single colony was preserved in each tube and stored at -20℃.

2.6 Antibiotic Susceptibility Testing:

For antibiotic susceptibility testing Muller Hinton Agar (MHA) were used identify the antibiotic resistance profile as shown in figure 3. Accordingly same bacterial colonies were preserved for DNA extraction proper preservative media. Kirby Baur disc diffusion method was used to perform antibiotic susceptibility testing on colonies according to CLSI guidelines. Resistant, intermediate and susceptible strain of *Morganella morganii* were determined chart by CLSI shown in table no 3. Different antibiotic discs (Oxoid

company) were used in this study which Ceftriaxone (CRO), Ceftazidime (CAZ), Cefepime (FEP), Meropenem (MRP), and Ciprofloxacin (CIP), Amikacin.

2.7 Shotgun Sequencing of Bacterial DNA:

a. DNA Extraction:(Brito et al., 2022)

Extraction of DNA was done manually by using CTab buffer solution.

1. Bacterial colony was picked with the help of sterilized wire loop and mixed with 500 µL lysis buffer (pre-warmed at 60-65°C).
2. 10 µL of Reagent D, 20µl Reagent K & 1.6 µL of MerC Solution was added
3. Sample was incubated at 60-65°C for 1-2 hours for bacterial samples and for tissue incubate over night
4. 700 µL Chlorine Buffer was added in it.
5. Centrifugation was done at 13000 rpm for 10 mins
6. Aqueous layer was collected in new tube and 950 µl of Wash buffer A was added to it
7. Again, centrifugation was done at 13000 rpm for 15 mins.
8. 500 µL of Wash buffer B was added to the pellet and Supernatant was discarded.
9. Centrifuge the pellet at 8000 rpm for 5-10 mins.
10. The supernatant was discarded
11. The pallet was air dried
12. 40-45 µL of Elusion Buffer was added
13. Incubation was done for 10 – 15 min at 60℃ to dissolve the pellet
14. purified extracted sample is stored at -20℃

b. Gel Electrophoresis:

To assess the quality and amount of extracted DNA purified product electrophoresis were run on 1% Agarose gel. 30mL of 1% gel was prepared by adding 0.3g of Agarose in 30mL 1x TBE buffer. Solution was boiled for 1 minute in microwave and cooled down a bit before adding 5 µL ethidium bromide. 2µL PCR purified Samples are then loaded on the gel. The gel electrophoresis condition was 110V with 100A current and 10 Watts.

c. Shotgun Genome Sequencing:

Among 20 isolates of *Morganella morganii* genomic DNA of single MDR strain of *Morganella morganii* were proceed for shotgun genome sequencing. The DNA samples were sheared into 400 to 500 base pair fragments using Covaris M220 Focused Ultrasonicator according to the protocol provided by manufacturer. NEXTflexTM Rapid DNA-Seq Kit (Bio Scientific, Austin Tx, United states) were used for the production of illumina sequencing libraries from fragments. Adopter ligated product were subjected to PCR to make multiple copies. Illumina HiSeq X Ten machine (Illumina, San Diego, CA Korea) were used for paired end Illumina Sequencing.

2.7 Bioinformatic Analysis:

The raw reads produce by HiSeq Illumina sequencing were saved as FASTQ file. Bioinformatic analysis was done by using galaxy platform (Afgan et al., 2018) various tools were used for the analysis of this raw data as shown in table no 2. First of all the low-quality DATA were trimmed with trimmomatic tool (Bolger et al., 2014). The quality of trim data was checked by fastqc toolkit (Cabello-Aguilar et al., 2023). The assembly of good quality reads were performed through spades (Bankevich et al., 2012). Genome was annotated by using prokka (Seemann, 2014). Different kind of antimicrobial resistant determinant were identified in card database (Alcock et al., 2020) . Phylogenetic analysis of identified AMR genes was done by Geneious (Kearse et al., 2012).

Table 2 List of tools used for bioinformatic analysis

Tools	Reference paper
TRIMMOMATIC	(Bolger et al., 2014)
fastqc toolkit	(Cabello-Aguilar et al., 2023)
SPAdes	(Bankevich et al., 2012)
Prokka	(Seemann, 2014)
CARD	(Alcock et al., 2020)
PATRIC	(Olson et al., 2023)
GENEIOUS	(Kearse et al., 2012)

Tools and their reference links used for bioinformatic analysis

3.1 Prevalence of *Morganella morganii* in urine:

Total 200 urine samples were collected from male and female individuals showing clinical sign and symptoms of urinary tract infection who visits Khyber Teaching Hospital Peshawar, Pakistan Out of these 200 urine samples 20(10%) samples have positive growth of *Morganella morganii* as shown in table 3.

Bacteria	Total cases	Positive cases	Negative cases	Percentage
Morganella morganii	200	20	180	10%

Table 3 Total number of *Morganella morganii* cases

a. Gender wise distribution of *Morganella morganii*:

Out of total 140 female urine samples 14 (7%) sample show positive growth of *Morganella morganii* while out of 60 male urine sample 6 (3%) sample show positive growth of *Morganella morganii*. As shown in table no 4.

Gender	Total Cases	Total positive Cases	Total Negative Cases	percentage
Female	140	14	126	7%
Male	60	6	54	3%
Total	200	20	180	10%

Table 4 Total positive and negative cases of *Morganella morganii* in male and female

b. Age wise distribution of *Morganella morganii*:

In the current study both male and female patients were divided into four age groups Group I (1-20 years) Group II (20-40) Group 111 (40-60 years) and Group IV (60-80 years). The highest frequency of *Morganella morganii* were shown in Group III (40-60 years) age groups as mentioned in table no 5.

Group	Age	Age wise M.M Cases
Group I	1-20 Years	2
Group II	20-40 Years	4
Group III	40-60 Years	10

Group IV	60-80 Years	5

Table 5 Number of *Morganella morganii* cases in different age groups

3.2 Susceptible and Resistant Antibiotics Against Morganella morganii in Males and Females:

After confirmation of bacterial growth on MacConkey and cled agar as shown in figure the bacterial isolate were confirmed by analytical profile index (API) kit as shown in figure 1.

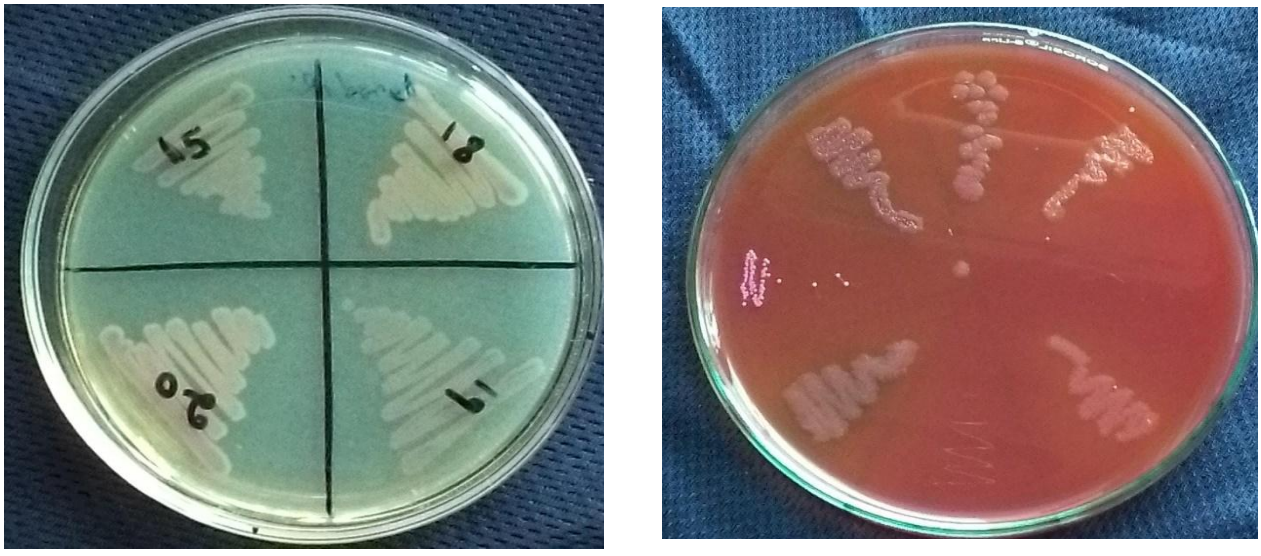


Figure 1 Colonies Morganella morganii on CLED and MacConkey Agar

Figure 2 All the biochemical test for *Morganella morganii* on API Kit.

After confirmation of bacterial isolate were subjected for antibiotic susceptibility test on muller hinton (MHA) agar and standard size of antibiotics disk were apply and report the result as shown in figure 2.
Sixteen different kinds of Antibiotics were Susceptible and resistant in different number of males and females as shown in table no 6.

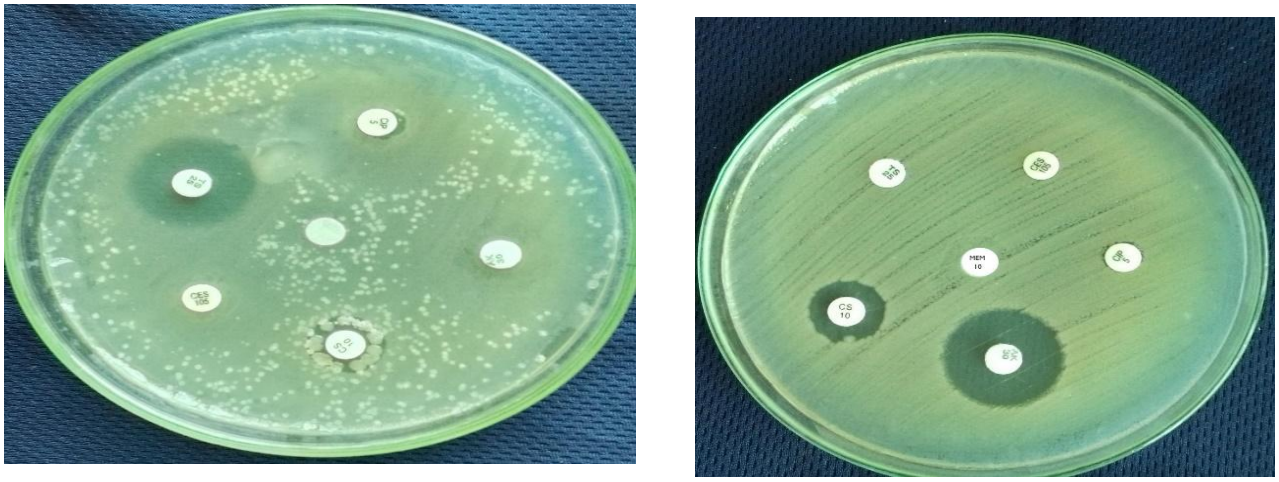


Figure 3 Antibiotics disks on Muller Hinton agar used against *Morganella morganii*

Table 7 Sensitive and Resistant pattern of *Morganella morganii* isolates in males and females (R=resistant, s=sensetive) (M=male, F= female)

Antibiotic	Sensitive (in mm)	Intermediate (in mm)	Resistant (in mm)
Amikacin (30µg)	≥ 17	15-16	≤ 14
Sulbactam (10µg)	≥ 21	16-20	≤ 15
Ciprofloxacin (5µg)	≥ 21	15-16	≤ 20
Gentamicin (10µg)	≥ 15	13-14	≤ 12
Imipenem (10µg)	≥ 16	14-15	≤ 13
Meropenem (10µg)	≥ 23	16-22	≤ 15
Nitrofurantoin (15µg)	≥ 15	14-16	≤ 17

Tigecycline (30µg)	≥ 19	15-11	≤ 14
Pipracillin+tazobactum(15µg)	≥ 18	11-17	≤ 17
Ampicillin(10µg)	≥ 10	NA	≤ 9
Aztreonam (15µg)	≥ 18	19-17	≤ 20
Cefepime (10µg)	≥ 18	14-17	≤ 13
Ceftazidime (10µg)	≥ 19	18-20	≤ 16
Chloramphenicol (10µg)	≥ 23	12-22	≤ 11
Co-amoxiclav (5µg)	≥ 15	NA	≤ 14
Co-trimoxazole (25µg)	≥ 16	11-15	≤ 10

Table 6 show List of Antibiotic their disks content and size of zone of inhibition provided by CLSI

Antibiotic	M	M	M	M	M	M	F	F	F	F	F	F	F	F	F	F	F	F	F	F
Amikacin (3rd generation)	S	S	S	S	S	S	S	R	S	S	S	S	S	S	S	S	S	S	S	S
Sulbactam (3rd generation)	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
Ciprofloxacin (2nd generation)	S	S	S	S	S	S	S	S	S	S	R	S	S	S	S	S	S	S	S	S
Gentamicin (2nd generation)	R	S	S	S	S	S	S	S	S	S	R	S	S	S	S	S	S	S	S	S
Imipenem (1st generation)	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
Meropenem (2nd generation)	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
Nitrofurantoin (3rd generation)	S	S	S	S	R	S	S	R	S	S	S	S	S	S	S	S	S	S	S	S
Tigecycline	R	S	S	S	S	S	S	R	S	S	R	S	S	S	S	S	S	S	S	S
Pipracillin+tazobactum	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
Ampicillin (1st generation)	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	S	S
Aztreonam (3rd generation)	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	S	S	S	S	S
Cefepime (4rt generation)	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	R	R	R	R
Ceftazidime (3rd generation)	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	R	R	R	R
Chloramphenicol (3rd generation)	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	R	R	R	R
Co-amoxiclav (3rd generation)	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
Co-trimoxazole (2nd generation)	R	R	R	R	R	R	R	R	R	R	S	R	S	R	R	R	R	R	R	R

3.3 Prevalence of Resistance and Susceptible Antibiotics Against Morganella *morganii*:

Sixteen different kinds of antibiotics were used against *Morganella morganii* which includes amikacin (30µg), Sulbactam (10µg), ciprofloxacin (5µg), gentamicin (10µg), imipenem (10µg), meropenem (10µg), nitrofurantoin (15µg), tigecycline(30µg), pipracillin+tazobactum (100/15µg), ampicillin (10µg), aztreonam (15µg), cefepime (10µg), Co-trimoxazole (25µg), Co-amoxiclav (5µg), Chloramphenicol (10µg) and Ceftazidime (10µg). The zone of inhibition of these antibiotics were measured and compared with guidelines provided by Clinical and laboratory Standard Institute as shown in table no 6.

Total 20 isolates of *Morganella morganii* were tested against these antibiotics among these all isolates of *Morganella morganii* were at least resistant to one of 16 antibiotics which were tested as shown in table no 9. The most frequently antibiotics to which *M. morganii* were resistant includes Co-amoxiclav (COA) (100%), followed by Cefepime (FEP) (95%), Ceftazidime (CAZ) (95%), Co-trimoxazole (COT) (90%), Ampicillin (AMP) (75%), Aztreonam (ATM) (70%), Tigecycline (TIG) (15%). Isolate of *Morganella morganii* were more susceptible to Amikacin (AMK) (95%), Ciprofloxacin (95%), Sulbactam (95%), Pipracillin+tazobactum (95%), Gentamicin (GIN) (90%), Tigecycline (TIG) (90%) as shown in table no 9. Among these 20 isolates of *Morganella morganii* no isolate was resistant to Meropenem and Imipenem. Furthermore, among these 20 isolates of *Morganella morganii* 1 isolate were found to be MDR that show resistant to all antibiotics except Meropenem and Imipenem which were further processed to whole genome shotgun sequencing as shown in figure 4 and table no 8

		AST Profile	
		Sensetive	Resistant
List of Antibiotic	Amikacin	95%	5%
	Ampicillin	25%	75%
	Aztreonam	30%	70%
	Cefepime	5%	95%
	Ceftazidime	5%	95%
	Chloramphenicol	5%	95%
	Co-amoxiclav	0%	100%

	Co-trimoxazole	10%	90%
	Sulbactam	95%	5%
	Ciprofloxacin	95%	5%
	Gentamicin	90%	10%
	Imipenem	100%	0%
	Meropenem	100%	0%
	Nitrofurantoin	90%	10%
	Tigecycline	85%	15%
	Pipracillin+tazobactum	95%	5%

Table 8 Percentage of Resistant and Sensitive Antibiotics out of total Antibiotic that are apply against Morganella morganii (R=resistant, s=sensetive)

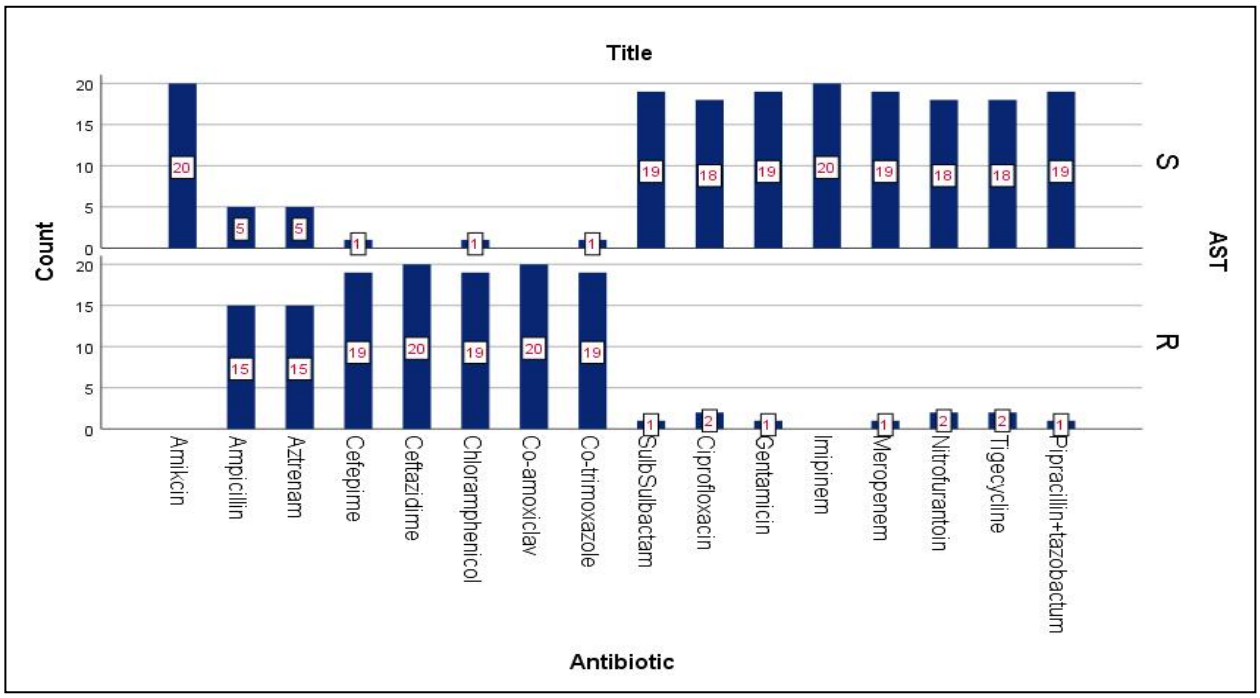


Figure 4 number of antibiotics resistant and Sensetive isolates of *Morganella morganii* (R=resistant, S=sensetive)

3.4 Shotgun Genome Sequencing:

Extracted DNA of bacterial isolate conferred by gel electrophoresis as shown in figure 5.

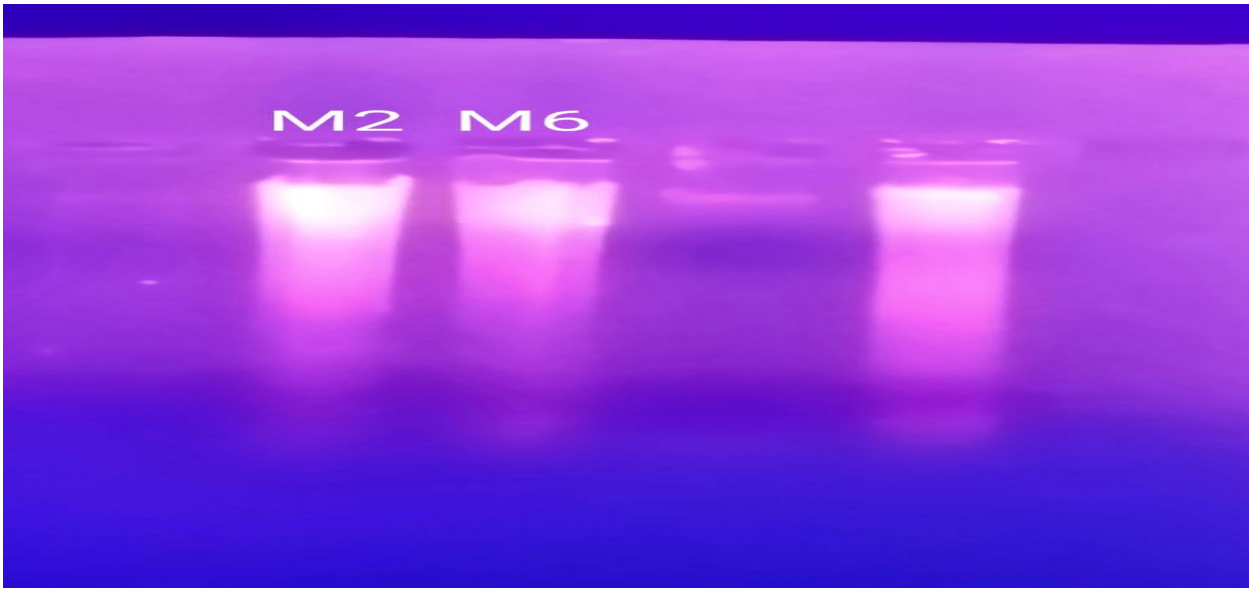


Figure 5 Gel picture of Extracted DNA product

Genomic DNA of single MDR isolate of *Morganella morganii* was sequenced by using illumina miSeq platform using paired end orientation which produced 0.88GB of high-quality data with total 3879337 reads.

a. Trimming:

All the low-quality DATA were trimmed with trimmomatic tool (Bolger et al., 2014). as shown in figure 6 and 7.

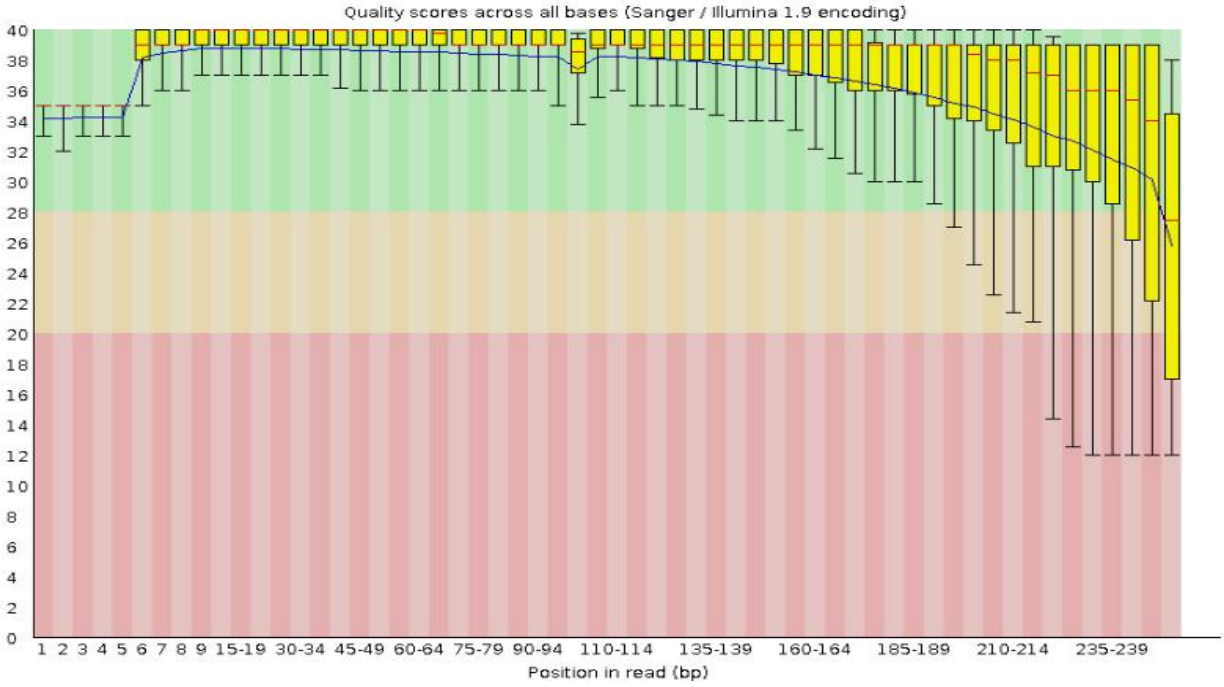


Figure 6 Low-quality data before trimming. Yellow Boxplot that falls under area of pink and purple color area is not good quality sequenced data while the green area is good quality data.

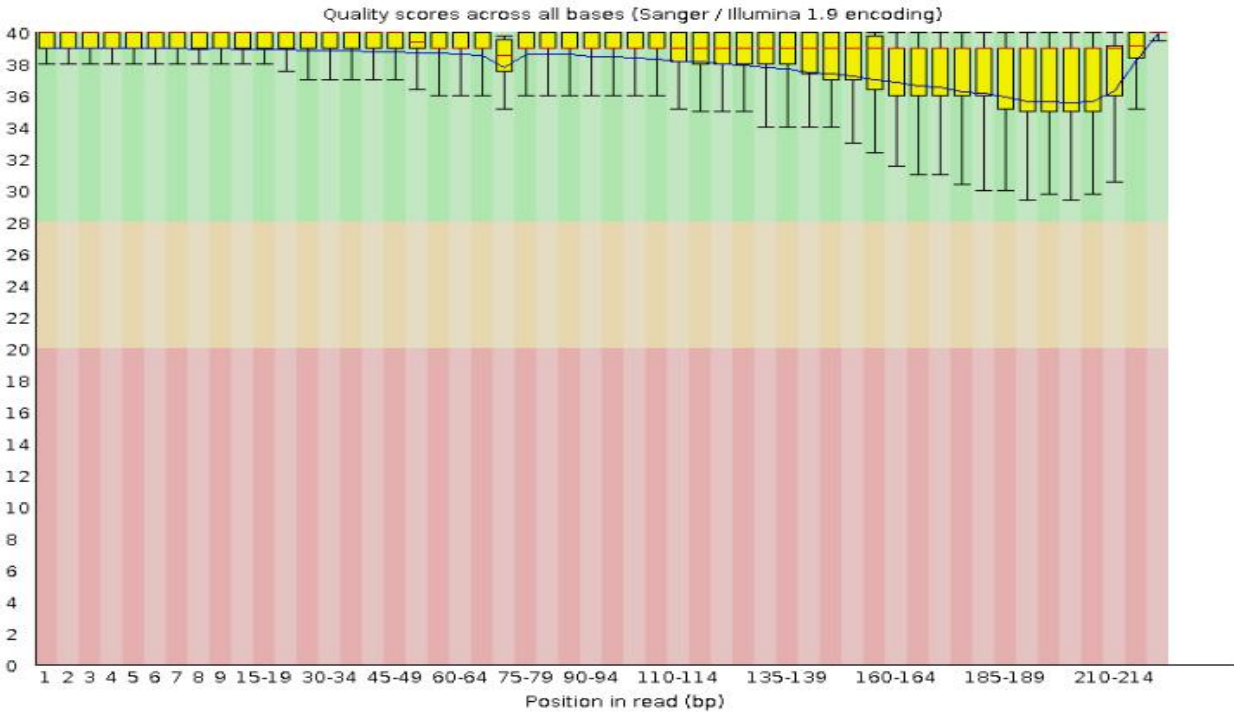


Figure 7 Good quality data after trimming. All yellow color boxplot that falls under the green area is good quality sequence data.

b. Data Assembly:

The assembly of good quality reads were performed through spades (Bankevich et al., 2012). there was total 21 contigs, with total genome size of 3878839 base pair having GC content of 51.03%. The L50 count is 3 (which is consider to be the count of smallest number of contigs sum of length produce half of genome). The N50 length is 682621bp (which is consider to be the shortest contig that cover half of genome size. The details of genome assembly are shown in table no 9.

Table 9 Detail of assemble Genome containing number of contigs, genome size, GC

# contigs	21
Largest contig	814006
Total length	3878839
GC (%)	51.03
N50	682621
N90	215167
auN	572067.9
L50	3
L90	7
# N's per 100 kbp	0.00

content.

c. Genome Annotation:

Genome was annotated by using prokka (Seemann, 2014). This genome has 3,857 protein coding sequences (CDS), 73 transfer RNA (tRNA) genes, and 5 ribosomal RNA (rRNA) genes. The annotated features are summarized in Table 10.

Table 10 Detailed summary of identified *Morganella morganii* genome including (CDS/Coding sequences, tRNA, rRNA of).

Annotated genome features	
CDS	3,591
tRNA	64
rRNA	9
Partial CDS	0
Miscellaneous RNA	0
Repeat Regions	0

Circos plot contracted by prokka shows all genes distributed across the genome *of Morganella morganii*. From outer to inner rings, it comprises coding sequences on forward strand and coding sequences on reverse strand, Coding sequencing virulence factors, CDS with homology to known antimicrobial resistance genes, RNA genes, GC content and GC skew. The subsystem to which these genes belong is shown by the colors of the Coding sequences on the forward and backward strands. (Subsystems mentioned below) shown in figure 8.

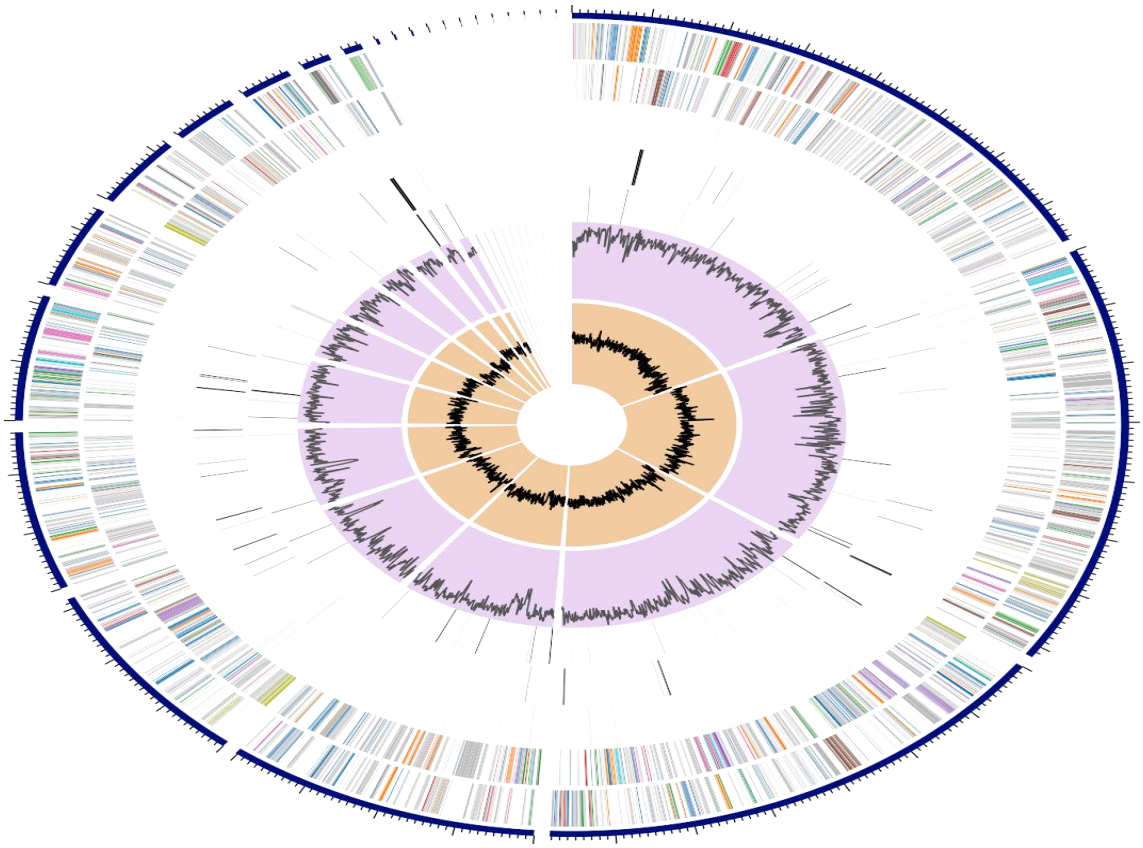


Figure 8 Circos plot that showing gene distribution across the genome of *Morganella morganii* from outer to inner rings, it comprises coding sequences on forward strand and coding sequences on reverse strand, Coding sequencing virulence factors, CDS with homology to known antimicrobial resistance genes, RNA genes, GC content and GC skew.

d. Subsystem Examination:

A subsystem is a collection of proteins that work together to carry out a particular biological process or structural complex. An examination of the subsystems that are particular to each genome is part of the PATRIC annotation process. Detailed information on this genome's subsystems provided in figure 9.

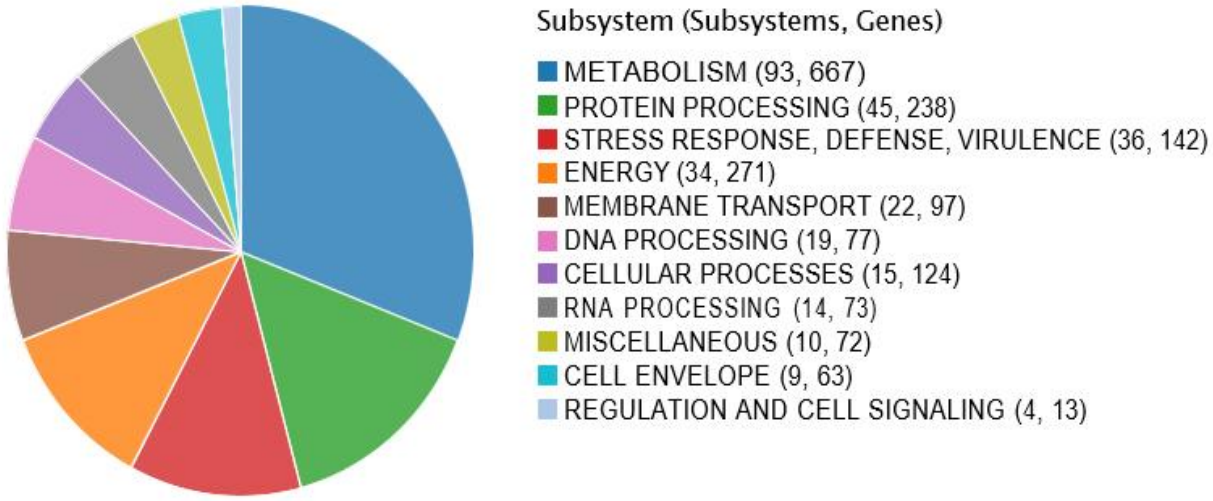


Figure 9 Graphical representation of all the genes mentioned through different colors responsible for different functions such as metabolism, protein processing, defense, virulence, RNA processing, regulation and cell signaling

3. 5 Important Functional Genes:

Several of the annotated genes are homologous to drugs targets, virulence factors, and genes that are resistant to antibiotics and drugs. The quantity of genes and the particular source database that showed homology were found as shown in table 11.

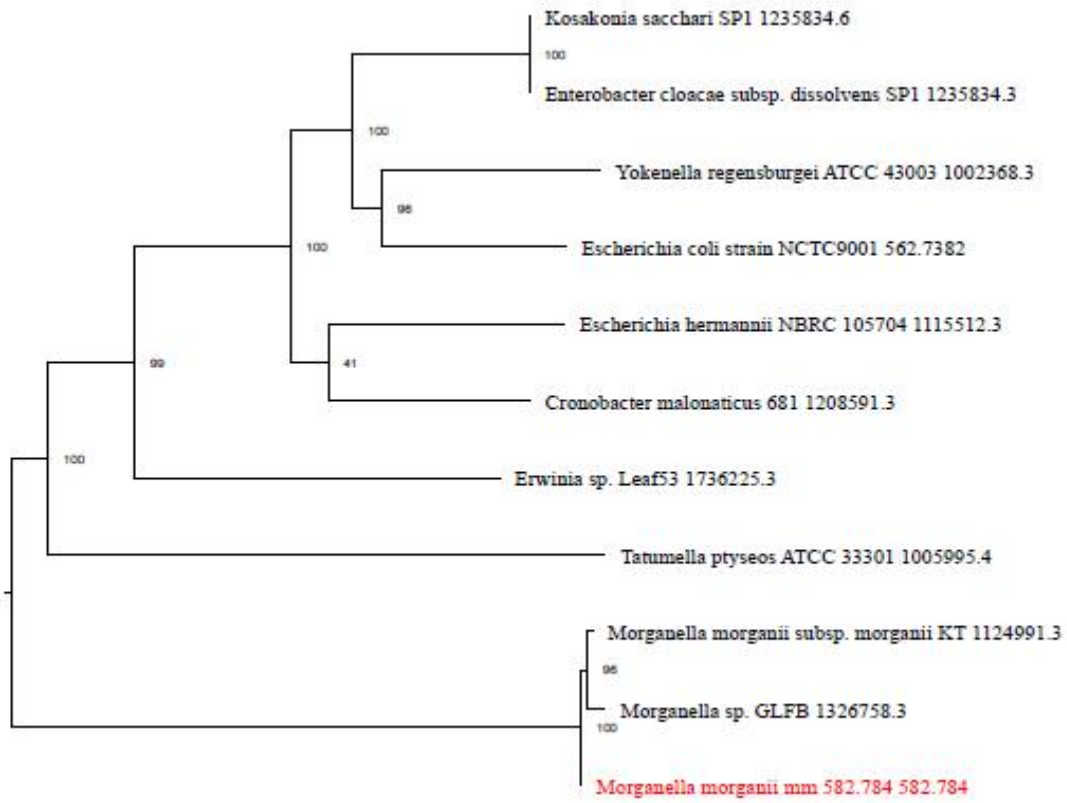
Specialty Genes

	Source	Genes
	Victors	2
Antibiotic Resistance	CARD	10
Antibiotic Resistance	NDARO	2
Antibiotic Resistance	PATRIC	45
Drug Target	DrugBank	96
Drug Target	TTD	13
Transporter	TCDB	90
Virulence Factor	PATRIC_VF	38
Virulence Factor	VFDB	3
Virulence Factor	Victors	52

Table 11 List of genes responsible for AMR, Drug target, Transporter, virulence factor and their source of database such as Card, NDARO, Drug Bank, VFDB

3.6 Phylogenetic Analysis:

Phylogenetic Analysis of identified genome was done in PATRIC (Olson et al., 2023). Phylogenetic analysis in PATRIC provides Representative and Reference genomes. Mash/mi Hash identify closest Representative genome and Reference genome. Phylogenetic location of these genomes was determined by Patric global proteins families (Pfams) that are selected from the genomes. Muscle was used to aligned the protein families and nucleotides sequences were mapped for protein alignment. Data matrix was created from joined nucleotide and amino acid alignments, Matrix was analyzed by RaxML, support values in the phylogenetic tree was created with



bootstrapping as shown in figure 10.

Figure 10 Phylogenetic tree of different strains of *Morganella morganii* and the identified genome (mentioned in red color) is closely resembled to the *Morganella morganii* Kt 1124991.3 and Morganella sp. GLFB 1326758.3 strains

3.7 AMR Gene Identification:

Finally, the antibiotics resistance genes were identified by CARD (McArthur, n.d.) was used for Antibiotic resistance genes detection as show in table no 12 and figure no 11. Ten important antibiotic resistance genes were identified in the genome of *Morganella morganii* isolate which are shown in table no. The major and more prevalent resistant gene that were found in the isolate of *Morganella morganii* **DHA-27** that belongs to DHA beta-lactamase gene family. That gene makes the bacteria resistant to beta lactam drug class which mainly includes cephalosporin, ampicillin, cephamycin and amoxicillin.
The second most important resistant gene was **kpnH** which belongs to major facilitator superfamily (MFS) antibiotic efflux pump gene family. That gene makes the bacteria resistant to multiple class of drugs such as macrolide antibiotic, fluoroquinolone antibiotic, aminoglycoside antibiotic, carbapenem, cephalosporin, penams, peptide antibiotic.
The one of important antibiotic resistance gene **rsmA** gene and **CRP** gene which is responsible for resistance nodulation cell division (RND) antibiotic efflux pump. The RND efflux pump is mediated by local repressor gene mutations, global regulatory gene mutations that contribute intrinsic multidrug resistance in *Morganella morganii*. Thes genes are responsible for resistance to fluoroquinolone antibiotic, diaminopyrimidine antibiotic, phenicol antibiotic, macrolide antibiotic, fluoroquinolone antibiotic, penam.
Another gene is **PBP3** gene that are responsible for Penicillin-binding protein mutations conferring resistance to beta-lactam antibiotics such as penam, cephalosporin and cephamycin. The fluroquinolone class antibiotic family resistant gene was also identified in the isolate of *Morganella morganii* which is **gryB** gene.
The peptide inhibitor antibiotic resistance gene were also identified in the genome of *Morganella morganii* that is **ArnT** resistance gene. The small multidrug resistance (SMR) antibiotic efflux pump family **qacG** resistance gene was also found in *Morganella morganii* that makes the bacteria resistant to disinfecting agent and antiseptics. Fosfomycin thiol transferase family **fosA8** resistance gene were also identified that confer resistance to phosphonic acid antibiotic.

Table 12 Responsible AMR genes, their family and Antibiotics to which these AMR gene are Resistant

Gene	Gene family	Antibiotics
DHA-27	DHA beta-lactamase	cephalosporin, ampicillin, cephamycin and amoxicillin.
kpnH	major facilitator superfamily (MFS) antibiotic efflux pump	macrolide antibiotic, fluoroquinolone antibiotic, aminoglycoside antibiotic, carbapenem, cephalosporin, penams, peptide antibiotic
gyrB	fluroquinolone class antibiotic family	Fluroquinolone
rsmA, CRP	RND Resistance nodulation cell division efflux pump	fluoroquinolone antibiotic, diaminopyrimidine antibiotic, phenicol antibiotic, macrolide antibiotic, fluoroquinolone antibiotic, penam
PBP3	Penicillin-binding protein mutations conferring resistance to beta-lactam	penam, cephalosporin and cephamycin
qacG	small multidrug resistance (SMR) antibiotic efflux pump family	disinfecting agent and antiseptics
ArnT	(Pmr) phosphoethanolamine transferase	Peptide inhibitors
FosA8	Fosfomycin thiol transferase	Phosphoric acid antibiotics

Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	elfamycin resistant EF-Tu	elfamycin antibiotic

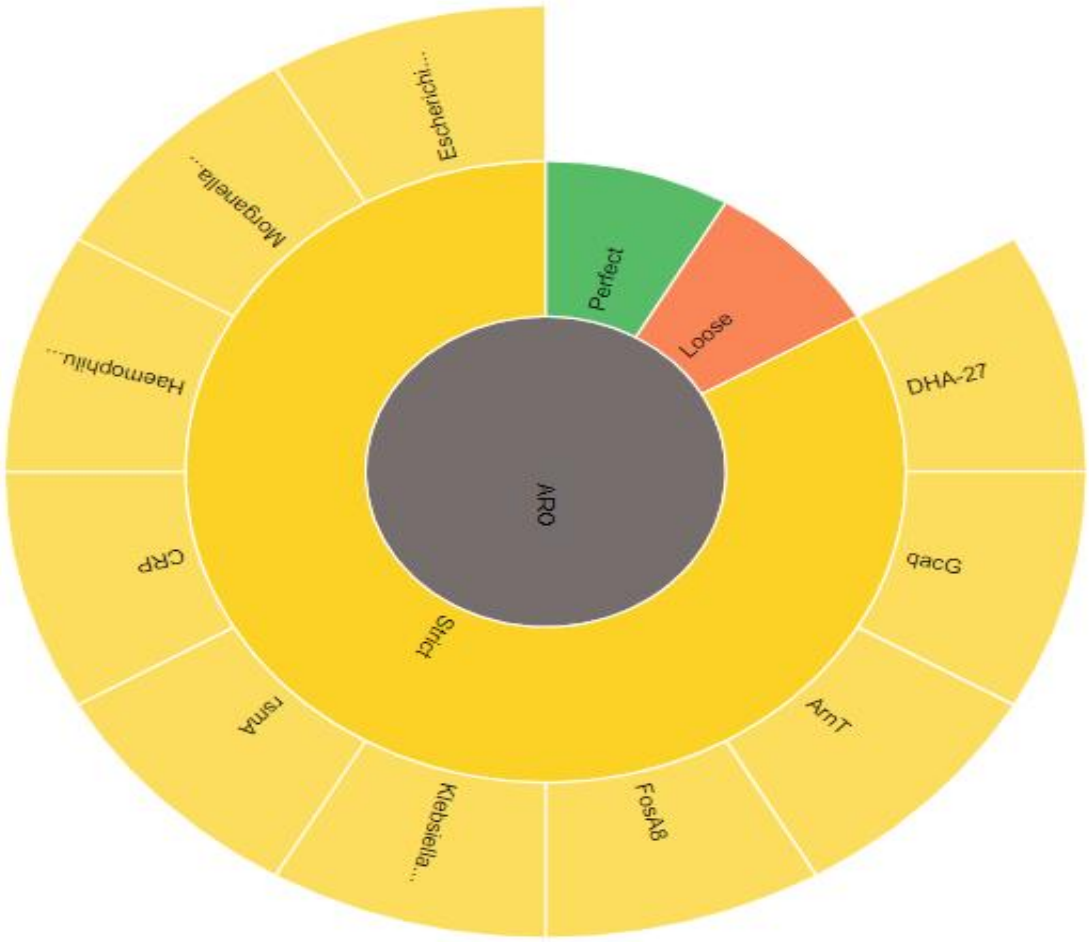


Figure 11 DHA-27, qacG, Arnt, FosA8, KpnH, rsmA, CRP, EF-Tu, gyrB are identified AMR genes in the genome of *Morganella morganii*

3.8 Phylogenetic Analysis of Important Identified AMR genes:

Upon phylogenetic analysis of important Antibiotic resistance such as (DHA-27) which are closely resemblance or 100 % similar with MH067965 *Escherichia coli* strain 1644443 having origin from Taiwan shown in figure 12.

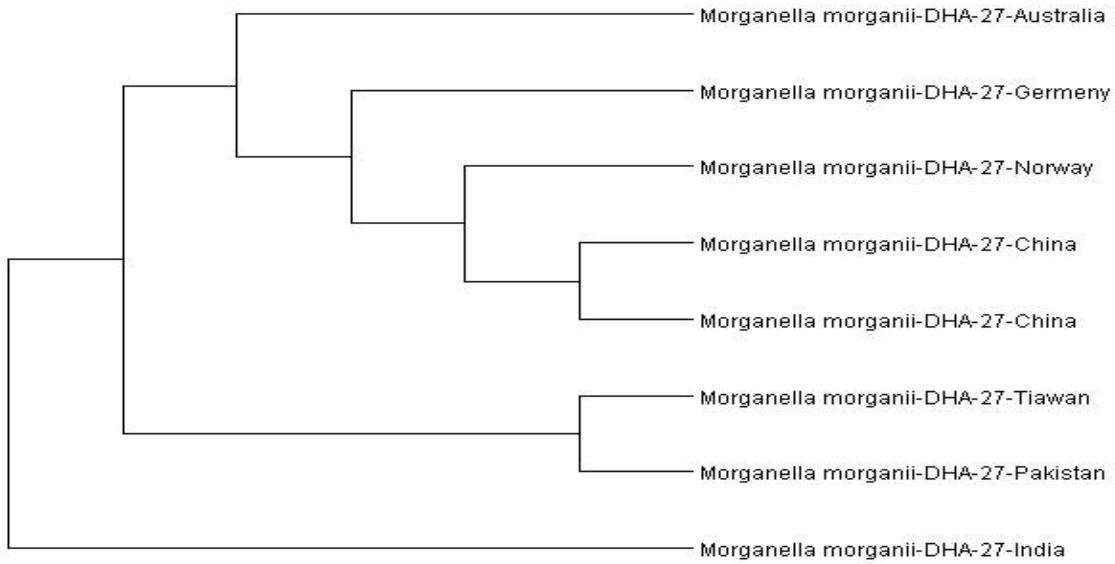


Figure 12 Phylogenetic Tree of identified antibiotic resistance genes (DHA-27)

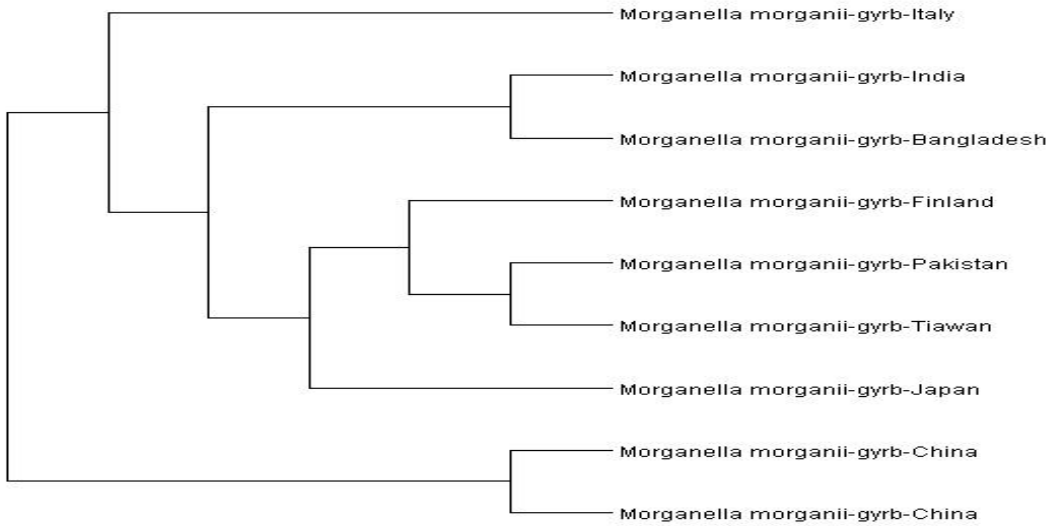


Figure 13 gyrB gene in identified *Morganella morganii* have similarity with *Morganella morganii* subsp. morganii MM20190808-1-1 having origin of Taiwan.

DISCUSSION

Most commonly microbial culture is used to monitor the microbiota. However, this has some significant drawbacks, most notably the inability to fully characterize the drug-resistance profile of the contaminating microbiota and the lengthy time period needed to collect the data. The implementation of environmental surveillance systems utilizing more efficient techniques is therefore urgently needed. Molecular methods, such as next-generation sequencing and PCR assays, shotgun metagenomic may be practical and efficient instruments to track microbial contamination, particularly the expanding AMR (Cason et al., 2022).

In current study shotgun genome sequencing of single MDR strain reveals different kind of antibiotics resistance genes that includes DHA-27, KpnH, fosA8, gyrB, ArNT, CRP, rsmA, PBP3, qacG and EF-Tu that are acquired from other bacteria. Upon phylogenetic analysis of some of identified genes show similarity with genes identified in tiawani populations. The selected MDR stain were subjected to multiple 1^{sts}, 2^{nd}, 3^{rd} and 4^{th} generation of antibiotics. And show resistance to 13 antibiotics in all 16 applied antibiotics which include the 4^{th} generation antibiotics. The resistance conferred by that single MDR Morganella morganii in Kp Pakistan is striking feature. Most of bacteria have horizontal gene transfer that acquired the genes from other bacterial species. To find out the bacterial mechanism of transformation of such acquired resistance gene inside *Morganella morganii* isolates we need further study needed in order to stop the transmission of such MDR strains of *Morganella morganii.* A study conducted by (Xiang et al, 2021) reported that 300 isolates of *Morganella morganii* were identified in urine samples. In these isolates most of isolates of *Morganella morganii* were identified in female patient one of main reason of that high prevalence of Morganella morganii in female patient were due to hospital acquired catheterization. In the current study total 20 isolated of *Morganella morganii* were identified in which 14 isolates were detected in females and their history shows no hospital acquire catheter associated infection so there should be may another reason of high prevalence of Morganella morganii in females.

Comparative genome analysis based on SNP of different strains of *Morganella morganii* from different samples such as stool, urine, rectal swab, blood, sputum, pleural fluid of different host (human, animal and environment) and the species of *Morganella morganii* from different countries China, USA, UK, Japan, Brazil, Russia, south Africa, Malaysia, South Korea, Canda, Switzerland, India reported by (Guo et al., 2019). And concluded

that the genome of *Morganella morganii* distributed widely antibiotics resistance genes from different isolate of *Morganella morganii* of different countries. Among these isolates of *Morganella morganii* form different host and from different sites have common beta lactamases antibiotics resistance gene blaDHA. Furthermore, no replication of plasmid was identified among most of *Morganella morganii* isolates. In his study blaNDM5 positive first *Morganella morganii* specie was identified and complete genome was sequenced. The antibiotic resistance gene blaNDM5 was present on INcX3 transmissible plasmid that are transmitted to other species of Enterobacterales including *Morganella morganii*. So IncX3 plasmid must be addressed and further research should need to stop the transmission of blaNDM encoding plasmid IncX3.

According to (Bandy, 2020) due increase antibiotic resistant of *Morganella morganii* have significant effect and become new superbug. The unproper utilization of antibiotics have led to evolution of antibiotics resistance gene inside the bacteria and producing Extensively drug resistant (XDR) and multi drug resistant (MDR) and pan drug resistant variants in the public sector. Furthermore, due to the transfer of resistant gene for species-to-species paly major role in antibiotics resistance and complicating this problem more and more. According to (Bandy et, al) *Morganella morganii* have natural resistant to 1st, 2nd and 3rd generation antibiotics such as macrolides, lincosamides and cephalosporins. Mostly acquired resistance of *Morganella morganii* is due to mobile extra genetics elements. According to (Bandy, 2020) globally XDR and MDR cases of *Morganella morganii* increases. According to surveillance report *Morganella morganii* is 42% resistant to carbapenems (imipenem). In south western Nigeria clinically treated wound infected individuals *Morganella morganii* has negative effect with resistance of Ceftazidime, cloxacillin, ampicillin, amoxicillin clavulanate. In a study reported that Egypt have increase prevalence of antibiotics resistance to carbapenem. *Morganella morganii*. Another study reported in Ethiopia also reported the prevalence of *Morganella morganii* antibiotics resistance to carbapenem. One of study in literature review revealed that horizontal transfer of plasmid and sequence are responsible for the resistance of carbapenem.

In the current total 20 isolates of *Morganella morganii* were tested against these antibiotics among these all isolates of *Morganella morganii* were at least resistant to one of 16 antibiotics which were tested as shown in table no 9. The most frequently antibiotics to which *M. morganii* were resistant includes Co-amoxiclav (COA) (100%), followed by Cefepime (FEP) (95%), Ceftazidime (CAZ) (95%), Co-trimoxazole (COT) (90%), Ampicillin (AMP) (75%), Aztreonam (ATM) (70%), Tigecycline (TIG) (15%). Isolate of

Morganella morganii were more susceptible to Amikacin (AMK) (95%), Ciprofloxacin (95%), Sulbactam (95%), Pipracillin+tazobactum (95%), Gentamicin (GIN) (90%), Tigecycline (TIG) (90%) as shown in table no 9. Among these 20 isolates of *Morganella morganii* no isolate was resistant to Meropenem and Imipenem. Furthermore, among these 20 isolates of *Morganella morganii* 1 isolate were found to be MDR that show resistant to all antibiotics except Meropenem and Imipenem.

According to (Al-Muhanna et al., 2016) *Morganella morganii* is capable of developing tolerance to broad-spectrum cephalosporins due to chromosomally encoded AmpC beta-lactamases. The blaCTXM, blaSHV, blaTEM, blaOXA, and blaCMY genes for -lactamase resistance, as well as the blaSIM, blaSPM, blaGIM, blaVIM, blaKPC, and blaNDM carbapenemases, were found using PCR, and sequencing was carried out using consensus primers and amplification conditions that *M. morganii* tested positive for the genes blaVIM, blaCTXM, and blaSHV but negative for other genes encoding -lactamases and carbapenemases (Al-Muhanna et al., 2016). However, because PCR-based techniques are focused on particular microbes and genes, they are unable to characterize the entire microbiome and/or resistome. In order to enable timely monitoring of any potential changes in microbial populations and in their AMR, an effective monitoring system should give a deep characterization of the environmental bioburden, delivering rapid and detailed information on the microbial population (Cason et al., 2022),In the current study shotgun sequencing of single MDR strain of *Morganella morganii* also revealed multiple antibiotics resistance genes which is not detected by any culture or simple PCR technique so shotgun sequence is one of good approach in detecting antibiotic resistance genes.

CONCLUSION

In the current study prevalence of *Morganella morganii* were identified in kp region. The prevalence of *Morganella morganii* is lower as compared to other uropathogen because our result indicates 20 positive cases (10%) of *Morganella morganii* out of 200 urine samples. Moreover, shotgun genome sequencing of *Morganella morganii* revealed presence of different antibiotics resistant genes in single MDR strain. This study is conducted in one region and emergence of such MDR strain of *Morganella morganii* is an important health issue. Therefore, further studies are required to prevent the spread of AMR genes in *Morganella morganii*.

References

1. Afgan, E., Baker, D., Batut, B., Van Den Beek, M., Bouvier, D., Ech, M., Chilton, J., Clements, D., Coraor, N., Grüning, B. A., Guerler, A., Hillman-Jackson, J., Hiltemann, S., Jalili, V., Rasche, H., Soranzo, N., Goecks, J., Taylor, J., Nekrutenko, A., & Blankenberg, D. (2018). The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Research*, *46*(W1), W537–W544. https://doi.org/10.1093/nar/gky379
2. Afroz, S., Habib, Z. H., Billah, S. M. B., Akhter, H., Jahan, H., & Parveen, R. (2020). Spectrum and Antibiotic Resistance Pattern of Bacteria Causing Urinary Tract Infections (UTI) in a Tertiary Care Hospital. *Journal of Surgical Sciences*, *23*(1), 13–18. https://doi.org/10.3329/jss.v23i1.44239
3. Al-Muhanna, A. S., Al-Muhanna, S., & Alzuhairi, M. A. (2016). Molecular investigation of extended-spectrum beta-lactamase genes and potential drug resistance in clinical isolates of Morganella morganii. *Annals of Saudi Medicine*, *36*(3), 223–228. https://doi.org/10.5144/0256-4947.2016.223
4. Alcock, B. P., Raphenya, A. R., Lau, T. T. Y., Tsang, K. K., Bouchard, M.,

Edalatmand, A., Huynh, W., Nguyen, A. L. V., Cheng, A. A., Liu, S., Min, S. Y., Miroshnichenko, A., Tran, H. K., Werfalli, R. E., Nasir, J. A., Oloni, M., Speicher, D. J., Florescu, A., Singh, B., … McArthur, A. G. (2020). CARD 2020: Antibiotic resistome surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Research*, *48*(D1), D517–D525. https://doi.org/10.1093/nar/gkz935

5. Alsaadi, A., Alghamdi, A. A., Akkielah, L., Alanazi, M., Alghamdi, S., Abanamy, H., Aljehani, S., Aldibasi, O. S., & Bosaeed, M. (2023). Epidemiology and Clinical Characteristics of Morganella morganii infections: A Multicenter Retrospective Study. *Journal of Infection and Public Health*, *17*(3), 430–434. https://doi.org/10.1016/j.jiph.2023.12.013
6. Anjum, M. F., Zankari, E., & Hasman, H. (2017). Molecular Methods for Detection of Antimicrobial Resistance. *Microbiology Spectrum*, *5*(6), 1–17. https://doi.org/10.1128/microbiolspec.arba-0011-2017
7. Bandy, A. (2020). Ringing bells: Morganella morganii fights for recognition. *Public Health*, *182*, 45–50. https://doi.org/10.1016/j.puhe.2020.01.016
8. Bankevich, A., Nurk, S., Antipov, D., Gurevich, A. A., Dvorkin, M., Kulikov, A. S., Lesin, V. M., Nikolenko, S. I., Pham, S., Prjibelski, A. D., Pyshkin, A. V., Sirotkin, A. V., Vyahhi, N., Tesler, G., Alekseyev, M. A., & Pevzner, P. A. (2012). SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing. *Journal of Computational Biology*, *19*(5), 455–477. https://doi.org/10.1089/cmb.2012.0021
9. Bilal, H., Khan, M. N., Rehman, T., Hameed, M. F., & Yang, X. (2021). Antibiotic resistance in Pakistan: a systematic review of past decade. *BMC Infectious Diseases*, *21*(1), 1–19. https://doi.org/10.1186/s12879-021-05906-1
10. Biondo, C. (2023). Bacterial Antibiotic Resistance: The Most Critical Pathogens. *Pathogens*, *12*(1), 0–1. https://doi.org/10.3390/pathogens12010116
11. Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: A flexible trimmer

for Illumina sequence data. *Bioinformatics*, *30*(15), 2114–2120. https://doi.org/10.1093/bioinformatics/btu170

12. Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., … Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9
13. Brito, O. A. de, Santos, F. A. dos, Al Yafawi, T. T., Saraiva, C. R. N., Macedo da Silva, R. O., Leandro, L. M. G., De Aquino, P. E. A., De Sousa Júnior, D. L., & Silva Leandro, M. K. do N. (2022). Comparing protocols of DNA extraction from Escherichia coli: Analysis of purity and concentration by gel electrophoresis. *Baghdad Journal of Biochemistry and Applied Biological Sciences*, *3*(02), 133–144. https://doi.org/10.47419/bjbabs.v3i02.123
14. Cabello-Aguilar, S., Vendrell, J. A., & Solassol, J. (2023). A Bioinformatics Toolkit for Next-Generation Sequencing in Clinical Oncology. *Current Issues in Molecular Biology*, *45*(12), 9737–9752. https://doi.org/10.3390/cimb45120608
15. Cason, C., D'Accolti, M., Soffritti, I., Mazzacane, S., Comar, M., & Caselli, E. (2022). Next-generation sequencing and PCR technologies in monitoring the hospital microbiome and its drug resistance. *Frontiers in Microbiology*, *13*(July), 1–10. https://doi.org/10.3389/fmicb.2022.969863
16. Chen, Y. T., Peng, H. L., Shia, W. C., Hsu, F. R., Ken, C. F., Tsao, Y. M., Chen, C. H., Liu, C. E., Hsieh, M. F., Chen, H. C., Tang, C. Y., & Ku, T. H. (2012). Whole-genome sequencing and identification of Morganella morganii KT pathogenicity-related genes. *BMC Genomics*, *13 Suppl 7*(Suppl 7). https://doi.org/10.1186/1471-2164-13-s7-s4
17. Divala et al. (2022). Public Health Action Campaign. *Public Health Action*, *12*(1), Syzdykova, A., Zolfo, M., Malta, A., Diro, E., O.

http://dx.doi.org/10.5588/pha.16.0125%0ASetting:

18. Edrees, W. H., Al-Ofairi, B. A., Alrahabi, L. M., Al-Munkari, I. M., Alawi, A. S., Al-Mashdali, A.-H. T., Samin, G. B., Naseer, Y. A., Bamousa, Z. A., & Al-Shehari, W. A. (2022). Seroprevalence of the Viral Markers of Hepatitis B, Hepatitis C, and Hiv Among Medical Waste Handlers in Some Hospitals in Sana'a City- Yemen. *Universal Journal of Pharmaceutical Research*, *July*. https://doi.org/10.22270/ujpr.v7i3.774
19. Guo, X., Rao, Y., Guo, L., Xu, H., Lv, T., Yu, X., Chen, Y., Liu, N., Han, H., & Zheng, B. (2019). Detection and genomic characterization of a morganella morganiiisolate from China that produces NDM-5. *Frontiers in Microbiology*, *10*(MAY), 1–9. https://doi.org/10.3389/fmicb.2019.01156
20. Hosseinpour, M., Pezeshgi, A., Mahdiabadi, M. Z., Sabzghabaei, F., Hajishah, H., & Mahdavynia, S. (2023). Prevalence and risk factors of urinary tract infection in kidney recipients: a meta-analysis study. *BMC Nephrology*, *24*(1), 1–13. https://doi.org/10.1186/s12882-023-03338-4
21. Hussain, T., Moqadasi, M., Malik, S., Salman Zahid, A., Nazary, K., Khosa, S. M., Arshad, M. M., Joyce, J., Khan, R., Puvvada, S., Walizada, K., & Khan, A. R. (2021). Uropathogens Antimicrobial Sensitivity and Resistance Pattern From Outpatients in Balochistan, Pakistan. *Cureus*, *13*(8). https://doi.org/10.7759/cureus.17527
22. Iqbal, Z., Sheikh, A. S., Basheer, A., Hafsa, H. tul, Ahmed, M., Sabri, A. N., & Shahid, S. (2023). Antibiotic Drug Resistance Pattern of Uropathogens in Pediatric Patients in Pakistani Population. *Antibiotics*, *12*(2). https://doi.org/10.3390/antibiotics12020395
23. Janda, J. M., Abbott, S. L., Khashe, S., & Robin, T. (1996). Biochemical investigations of biogroups and subspecies of Morganella morganii. *Journal of Clinical Microbiology*, *34*(1), 108–113. https://doi.org/10.1128/jcm.34.1.108-113.1996

24. John, A. S., Mboto, C. I., & Agbo, B. (2016). *A review on the prevalence and predisposing factors responsible for urinary tract infection among adults*. *6*(4), 7–11.
25. Kaur, R., & Kaur, R. (2021). Symptoms, risk factors, diagnosis and treatment of urinary tract infections. *Postgraduate Medical Journal*, *97*(1154), 803–812. https://doi.org/10.1136/postgradmedj-2020-139090
26. Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Meintjes, P., & Drummond, A. (2012). Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, *28*(12), 1647–1649. https://doi.org/10.1093/bioinformatics/bts199
27. Khan, A. (2023). Prevalence of urinary tract infections and antibiotic effectiveness against uropathogens among females of different ages in Dera Ismail Khan, Khyber Pakhtunkhwa-Pakistan. *Pure and Applied Biology*, *12*(2), 1286–1294. https://doi.org/10.19045/bspab.2023.120131
28. Liu, H., Zhu, J., Hu, Q., & Rao, X. (2016). Morganella morganii, a non-negligent opportunistic pathogen. *International Journal of Infectious Diseases*, *50*, 10–17. https://doi.org/10.1016/j.ijid.2016.07.006
29. Maraki, S., Mantadakis, E., Spernovasilis, N., Mathioudaki, A., Peristeris, G., Alexakis, K., Kofteridis, D., & Samonis, G. (2022). Morganella morganii Infections in a Greek University Hospital. *Infectious Diseases in Clinical Practice*, *30*(2), 1–5. https://doi.org/10.1097/ipc.0000000000001110
30. McArthur, A. G. (n.d.). *The Comprehensive Antibiotic Resistance Database*. Retrieved February 14, 2024, from https://card.mcmaster.ca/about
31. Medina, M., & Castillo-Pino, E. (2019). An introduction to the epidemiology and burden of urinary tract infections. *Therapeutic Advances in Urology*, *11*, 3–7. https://doi.org/10.1177/1756287219832172

32. Olson, R. D., Assaf, R., Brettin, T., Conrad, N., Cucinell, C., Davis, J. J., Dempsey, D. M., Dickerman, A., Dietrich, E. M., Kenyon, R. W., Kuscuoglu, M., Lefkowitz, E. J., Lu, J., Machi, D., Macken, C., Mao, C., Niewiadomska, A., Nguyen, M., Olsen, G. J., … Stevens, R. L. (2023). Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. *Nucleic Acids Research*, *51*(1 D), D678–D689. https://doi.org/10.1093/nar/gkac1003
33. Öztürk, R., & Murt, A. (2020). Epidemiology of urological infections: a global burden. *World Journal of Urology*, *38*(11), 2669–2679. https://doi.org/10.1007/s00345-019-03071-4
34. Purushothaman, S., Meola, M., & Egli, A. (2022). Combination of Whole Genome Sequencing and Metagenomics for Microbiological Diagnostics. *International Journal of Molecular Sciences*, *23*(17). https://doi.org/10.3390/ijms23179834
35. Rosen, D. A., Hooton, T. M., Stamm, W. E., Humphrey, P. A., & Hultgren, S. J. (2007). Detection of intracellular bacterial communities in human urinary tract infection. *PLoS Medicine*, *4*(12), 1949–1958. https://doi.org/10.1371/journal.pmed.0040329
36. Seemann, T. (2014). Prokka: Rapid prokaryotic genome annotation. *Bioinformatics*, *30*(14), 2068–2069. https://doi.org/10.1093/bioinformatics/btu153
37. Sharpton, T. J. (2014). An introduction to the analysis of shotgun metagenomic data. *Frontiers in Plant Science*, *5*(JUN), 1–14. https://doi.org/10.3389/fpls.2014.00209
38. Talebi Bezmin Abadi, A., Rizvanov, A. A., Haertlé, T., & Blatt, N. L. (2019). Who,2019. *BioNanoScience*, *9*(4), 778–788.
39. Tan, C. W., & Chlebicki, M. P. (2016). Urinary tract infections in adults. *Singapore Medical Journal*, *57*(9), 485–490.

https://doi.org/10.11622/smedj.2016153

40. Xiang, G., Lan, K., Cai, Y., Liao, K., Zhao, M., Tao, J., Ma, Y., Zeng, J., Zhang, W., Wu, Z., Yu, X., Liu, Y., Lu, Y., Xu, C., Chen, L., Tang, Y. W., Chen, C., Jia, W., & Huang, B. (2021). Clinical Molecular and Genomic Epidemiology of Morganella morganii in China. *Frontiers in Microbiology*, *12*(September), 1–11. https://doi.org/10.3389/fmicb.2021.744291
41. Yang, J. H., Sheng, W. H., & Hsueh, P. R. (2020). Antimicrobial susceptibility and distribution of extended-spectrum β-lactamases, AmpC β-lactamases and carbapenemases among Proteus, Providencia and Morganella isolated from global hospitalised patients with intra-abdominal and urinary tract infections: R. *Journal of Global Antimicrobial Resistance*, *22*, 398–407. https://doi.org/10.1016/j.jgar.2020.04.011
42. Yang, X., Chen, H., Zheng, Y., Qu, S., Wang, H., & Yi, F. (2022). Disease burden and long-term trends of urinary tract infections: A worldwide report. *Frontiers in Public Health*, *10*. https://doi.org/10.3389/fpubh.2022.888205
43. Zaric, R. Z., Jankovic, S., Zaric, M., Milosavljevic, M., Stojadinovic, M., & Pejcic, A. (2021). Antimicrobial treatment of Morganella morganii invasive infections: Systematic review. *Indian Journal of Medical Microbiology*, *39*(4), 404–412. https://doi.org/10.1016/j.ijmmb.2021.06.005