

A Review Articles: *Pantoea agglomerans* in UTI- It is Bacteria Caused Urinary Tract Infection and Genomic Analysis related with Bacterial Resistance

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ABSTRACT

Pantoea Spp. is a plant bacteria that has been identified as an emerging pathogen in humans related with outbreaks and many clinical infections. It is referred to as a "mystery bacterium of evil and good" since it may cause both bad and good. With the proposed investigation, the researchers hope to uncover a significant risk component that is connected with reoccurring urinary tract infections (UTI). They also hope to identify bacterial reasons and antibiotic susceptibility profiles that can be used to lower the threat of reinfection and prevent complications associated with recurrent UTI. In the existence of risk variables, the likelihood of developing a UTI increases; also, a correct susceptibility pattern increases the likelihood of achieving therapeutic effectiveness and preventing illness complications. Because of its capacity to infect immunocompromised persons and produce severe illness as a consequence of its multi - drug resistance, *Pantoea agglomerans* is considered to be a dangerous opportunistic pathogen. In this paper we are going to focus on related bacteria, pathogenicity, resistance genes, classification.

Keywords- *Pantoea agglomerans*, Genes, Urinary Tract Infection.

I. INTRODUCTION

Pantoea agglomerans viewpoints for Gram-negative, rod-shaped, yellow-pigmented aerobacillus that be in the right place to the Enterobacteraceae intimate.^[1] It is a member of the Enterobacteraceae family. *Pantoea agglomerans* was in the past recognized by means of "Enterobacter agglomerans or *Erwinia herbicola*" before being given its current name.^[2] It was given a new genus and placed in a new classification. It is usual to find isolates from plants, soil, water, and food. Due to the fact that it is an opportunistic illness, it can only infect an immunocompromised host.^[3]

A new appreciation has recently been given to the therapeutic properties of *Pantoea agglomerans*, including its ability to produce antibiotics and its

function as an "immunopotentiator from *Pantoea agglomerans* 1 (IP-PA1) in the prevention and treatment of animal and human illnesses", as well as in food preservation.^[4]

Despite the fact that *Pantoea agglomerans* infections in vertebrate animals are uncommon compared to human infections, *Pantoea agglomerans* infection in humans has previously been related to different diseases. *Pantoea agglomerans* has been found in a variety of arthropods and has been shown to be harmful to plants.^[5]

II. HISTORY

Pesticide doses may be decreased thanks to the introduction of a biocontrol agent, which is good for both human health and the environment. According

to the researchers, mold infestation in pome, stone, and citrus fruits may be prevented by utilising this bacteria's formulations.^[6-9] The development of many plants, including rice and wheat, is accelerated when *Pantoea agglomerans* strains are connected to both the rhizosphere and plant tissues at the same time (as endophytes). A variety of mechanisms help plants develop, including atmospheric nitrogen fixation, phytohormone production, phytate breakd, and phosphate solubilization, which makes soil phosphorus available to plants. As a consequence, *Pantoea agglomerans* is being investigated as a bioinoculant that may be used to replace chemical fertilisers while still being ecologically friendly.^[10-13] *Pantoea* strains have been sh to digest a wide range of chemicals present in soil and water, including petroleum hydrocarbons and toxic metals. *Pantoea agglomerans* can not only produce hydrogen from trash, but they can also build a biofilm layer that prevents harmful industrial pollutants from entering deeper into the soil. As a consequence of the findings, this bacterium seems to be a valuable bioremediatory that may potentially be utilised as a low-cost energy source in certain circumstances. As a result, despite the pathologic role of *Pantoea agglomerans* in the development of allergic and immunotoxic background diseases, and occupational infections, the beneficial characteristics of this species, and related *Pantoea* genus species, are of great value for their potential application in a wide range of biotechnology fields.^[14-17] As a consequence, any restrictions on the use of these organisms and their products should be avoided if precautions are taken while dealing with *Pantoea* biopreparations.

III. HABITAT

Enterobacter spp. is bacteria that cause food poisoning is a significant source of bacteraemia, although much less so than *Klebsiella* spp., the disease-causing bacteria? *Enterobacter* may be found in soil and water, as well as human faeces and the respiratory system.^[18] Infections in the urinary tract, particularly among hospital patients, are common.

IV. CLASSIFICATION

Some of the first *Pantoea* strains were labeled *Bacillus agglomerans* and *Enterobacter agglomerans*, while others were labeled *Pantoea* sp. *Bacterium herbicola*, *Pseudomonas herbicola*, *Erwinia herbicola*, and were all synonyms subsequently confirmed.^[19-22] In 2014, Tindall published research on adverbial adverbs.

The number of new *Pantoea* species has risen dramatically since the genus *Pantoea* was founded. *Pantoea* is closely linked to the enterobacterial genera *Tatumella* and *Erwinia*, and along with these two genera, they constitute a monophyletic group that is nested inside the other enterobacterial groups. *Pantoea* is classified as an enterobacterial genus. The three bacteria constitute a monocentric group that is nested inside the other six enterobacteria, which are “*Escherichia coli*, *Salmonella*, *Citrobacter*, *Enterobacter*, *Klebsiella*, and *Cronobacter*.” It is the year 2009.^[23-26] According to the literature, *Pantoea* is thought to be made up of 20 phenotypically similar species that constitute 13 hybridization groups. For each species group, *Pantoea* type strains were acquired from a range of sources, the vast majority of which were plant-derived. We were able to construct a rooted phylogenetic tree of *Pantoea* type strains using the genes “*gyrB*, *rpoB*, and 16S rRNA”, which showed the links between the recognised species groups. “Plant pathogen isolates *P. deleyi*, *P. anthophila*, *P. allii*, *P. cyripedii*, *P. rodasii*, *P. rwandensis*, *P. conspicua*, *P. brenneri*, *P. septica*, and *P. eucrina* have all been isolated from purely plant sources, while *P. deleyi*, *P. anthophila*, *P. cyripedii*.^[27] A number of other species, including *P. citrea*, *P. punctata*, and *P. terreia*, were proposed prior to the advent of multilocus sequence analysis (MLSA) methods”; however, these were later reclassified into the genus *Tatumella*.

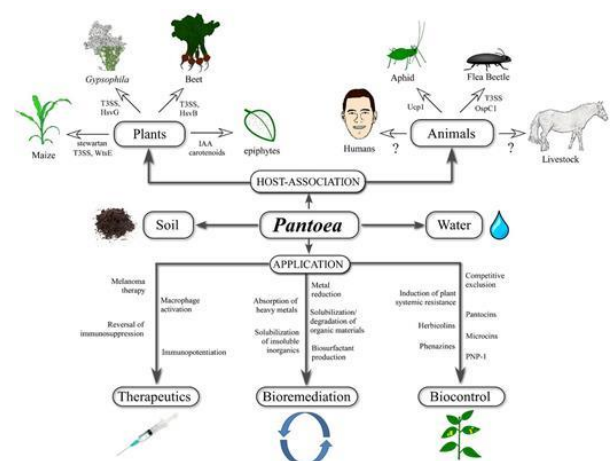


Figure 1. Classification of *Pantoea* Strains (Alyssa M. W. et al, EMS Microbiology Reviews, 2015)

The Pathosystems Resource Integration Center developed a cladogram based on common protein homologs derived from entire genomes of Enterobacteriaceae species groups and classified according to evolutionary relationships. A box represents *Pantoea*'s position in relation to the other

characters. The genomic data for Tatumella has not yet been incorporated into the Pathosystems Resource Integration Center.^[28] Therefore it is not shown. Pseudomonas was the root used (Pseudomonadaceae).

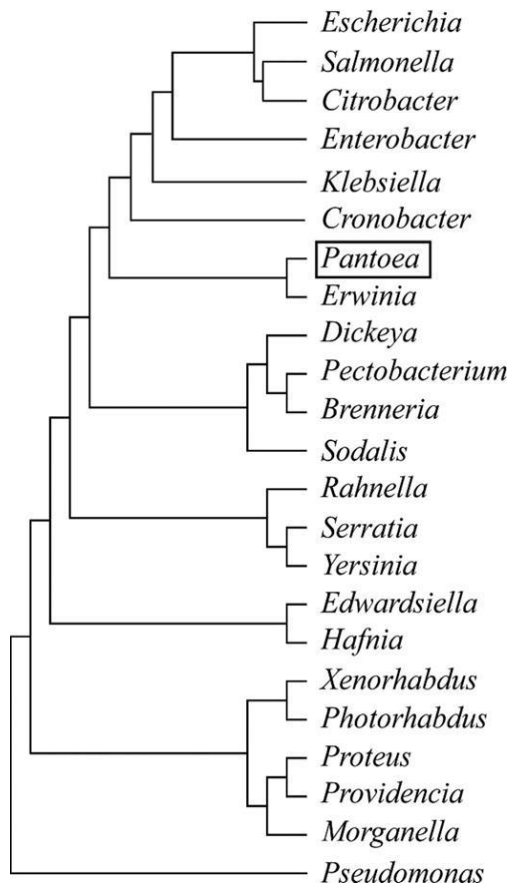


Figure 2. The Pathosystems Resource Integration Center developed a cladogram (Wang, L., et. al. (2017))

V. EPIDEMIOLOGY

The self-reported annual incidence of UTI in women is 12 percent, and 50 percent of all women report having had at least one UTI throughout their lifetimes. Women who have had an Escherichia coli UTI for the first time are at a higher risk of developing another UTI. Colis are more probable than individuals who do not have an Escherichia coli. First-time UTI sufferer Coli had a second UTI within a six-month period.^[29-35] There were around “0.70 occurrences of cystitis (lower UTI) per person-year in a study of young college women.”

A UTI will affect 50 to 70 percent of women at some point in their lives, and 20 to 30 percent of those who have one will have recurring UTIs.^[36] An increased incidence of UTI has been reported at various stages of life (childhood, honeymoon, pregnancy, and the elderly).

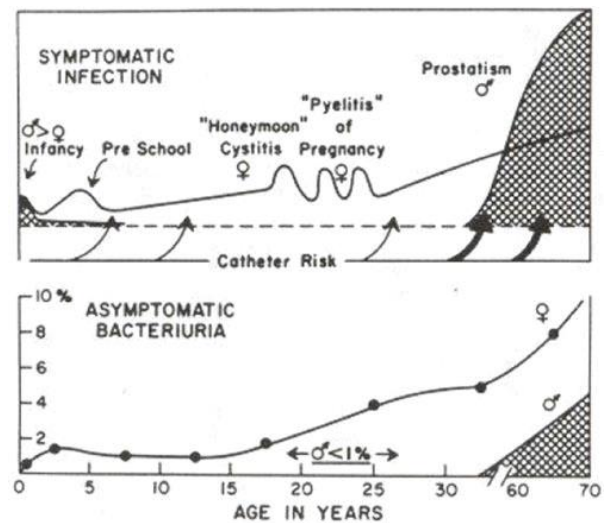


Figure 3: In both men and females, asymptomatic bacteriuria is more common than symptomatic infection (Matthew A. Mulvey et al. 2016)

Acute pyelonephritis is much less frequent than cystitis, although it is more common in young women and babies. Outpatient pyelonephritis rates in women and men were 11–12 and 3–4 cases per 10,000 patients, respectively.^[37] Urinary tract infections (UTIs) accounted for 8% of all instances of severe sepsis.

The total incidence of “symptoms consistent with chronic prostatitis/chronic pelvic pain syndrome (CP/CPPS)” is significant, at 7.3%, with prevalence ranging from 3.3 to 8.9%. According to two studies, approximately a third of men who reported prostatitis symptoms improved after a year.^[38-41]

The high prevalence of urinary tract infections (UTIs) leads in significant health-care expenditures. In the United States, a nosocomial UTI adds one extra hospital day per patient, resulting in almost 1 million more hospital days per year.^[42-45] In 1995, UTI was projected to cost \$1.7 billion a year in direct and indirect costs.

VI. CHARACTERIZATION

An API 20E test was used to analyse the biochemistry of *Pantoea agglomerans* KM1. The isolate tested positive for catalase but negative for oxidase and urease. KM1 did not decarboxylate lysine and ornithine, nor did it generate H₂S or indole. “D-glucose, D-mannitol, L-rhamnose,^[46] D-sucrose, Amygdalin, L-arabinose, and Lactose” were also fermented by the isolate. Arginine dihydrolase and tryptophan deaminase were found to be negative in the API 20E test^[47-50]. The KM1 isolate demonstrated no capacity to “ferment inositol, D-sorbitol, or D-

melibiose, but it did produce acetoin, passed the -galactosidase test, used citrate, and exhibited gelatinase activity". The isolated KM1 strain was identified as belonging to the *Pantoea agglomerans* species based on the numerical profile obtained.

VII. DETECTION BY BIOCHEMICAL TESTS AND BY MOLECULAR METHODS

Pantoea identifications may be verified by using MALDI-TOF-based molecular typing methods^[51]. Due to its conservation throughout Bacteria, the 16S ribosomal RNA (rRNA) gene is considered as a universal identification for bacteria. It provides a phylogenetic signal of about 1500 bp. *Pantoea* possesses reproducible strain typing and robust phylogenies confirmed by multi-locus sequencing analysis (MLSA technique)^[52-55]. *LeuS* has also been proposed as a single-gene barcoding method that provides consistent species identification. However, there is still no conclusive evidence that the *leuS* gene can uniquely identify and classify bacteria^[56]. This means that comparing bacterial strains across species and studies becomes considerably more difficult^[57-60]. The species resolving capability of a chaperonin with a 1650 bp long sequence has been shown. This gene is present in almost all bacteria's genomes and contains a 600-bp section that has been recognised as a species-specific marker. Also, an online database of *cpn60* sequences may be found here.

VIII. PATHOGENICITY AND CORELATED DISEASE IN HUMAN

Most of the species under the genus *Pantoea* are epiphytes, but a few species are pathogens. A number of species have been demonstrated to be oncogenic (tumor-forming). During the early 1970s, *Pantoea agglomerans* was discovered to be related to a large septicemia outbreak in the United States and Canada^[61-63]. Bacterial bloodstream infection related to intravenous fluid, parenteral nutrition, the anaesthetic medication propofol, blood products, and intravenous hydration transference tubes is associated with *Pantoea agglomerans*. People with arthritis, synovitis, or osteomyelitis have recovered from their joint fluid, if they have a chronic problem and adequate treatment. More often, thorns, wood splinters, and wooden splinters cause illness. On rare occasions, though, it is possible to develop cotton fever, which affects intravenous drug users.^[64]

To accurately identify *Pantoea* species, more specific information is needed, such as details on their evolutionary relationships and degree of genetic distinction. The study found that *Pantoea agglomerans*, *Pantoea ananatis*, and *Pantoea stewartii* were all closely linked to one another via examination of 16S rRNA^[65-68]. A single or a few strains per species were studied, and therefore, the relationships between these three Japanese strains, referred to as "*Pantoea japonica*," "*Manihot* genus " and "*Phanerochaete tuberculata*," have not been thoroughly investigated.

IX. VIRULENCE FACTORS AND GENE THAT RESPONSIBLE

The "ecp, fimH, traT, sfa/focDE, and papC genes had a higher prevalence, exceeding 50%. (98.1 percent, 86.1 percent, 77.8 percent, 74.1 percent, and 62 percent, resp.). The focG, sfaS, hlyA, cnf-1, cdt-B, cvaC, ibeA, and rfc genes had prevalences of less than 10%", whereas the "focG, sfaS, hlyA, cnf-1, cdt-B, cvaC, ibeA, and rfc genes had prevalences of less than 10%. (2.8 percent, 1.9 percent, 7.4 percent, 6.5 percent, 0.9 percent, 2.8 percent, 2.8 percent, and 0.9 percent, resp.)". The distribution of virulence genes by phylogenetic group^[69]. The majority of the virulence factors linked to phylogenetic group B2 have been discovered^[70-72]. All groups had high levels of the "ecp (A and R-B) and fimH genes (A 100 percent /78.8%, B1 100 percent /70 percent, B2 96.7 percent /91.7 percent, and D 100 percent /100 percent, respectively)^[73]. Only isolates from the B2 group had the focG, sfaS, hlyA, cnf-1, cdt-B, and cvaC genes". Only one isolate from group B1 had the rfc gene. Group B2 was favourably linked with the "hlyA, cft-1, and traT genes, whereas group A was negatively connected with the iutA and fyuA genes".

X. TREATMENTS BY ANTIBIOTICS

The Comprehensive Antibiotic Resistance Database was used to predict antibiotic resistance genes (ARGs) using the BLASTn method with a 70% identity cut-off and an E-value of 1.0 E-6 (CARD). Using the "Kirby-Bauer disc diffusion method", tests were conducted on Mueller Hinton agar (CLSI)^[74]. "Kanamycin (30 g), streptomycin (10 g), imipenem (10 g), vancomycin (10 g), ofloxacin (5 g), ampicillin (30 g), penicillin G (10 iu), rifampicin (5 g), bacitracin (10 g), fosfomycin (50 g), and chloramphenicol (30 g)"

were the antibiotic discs utilised in this research (Thermo Fisher Scientific, MA, USA).

Table 1: The ability of the cultured *Pantoea agglomerans* to respond to antibiotics

Strain, phage, cosmid or plasmid	Relevant characteristics ^a	Reference or source ^b
<i>Escherichia coli</i>		
JM109	<i>recA1 thiΔ (lac-proAB) lacZΔM15</i>	39
HB101	<i>Sm^rrecA13</i>	39
DH5β	<i>F⁻recA1 lacZΔM15 thi-1 Nal^r</i>	39
LE392	<i>hsdR514 supE44 supF58 lacY1 galK2 galT22 metB1 trpR55 λ⁻</i>	39
CC118	<i>Δ(arag-leu)7697 ΔlacX74 ΔphoA20 galE galK thi rpsE rpoB argE recA1 Sp^r</i>	32
SM10(<i>Apir</i>)	<i>thi-1 thr leu tonA lacY supE recA::RP4-2-Tc::Mu Km^rApir</i>	34
CGSC6151	<i>LamB204</i> ; resistant to lambda	M. Schwartz, <i>E. coli</i> Genetic Stock Center
<i>Erwinia amylovora</i> Ea273		
Infected apple, ATCC 49946		
<i>Pantoea agglomerans</i>		
Eh318	Rp ^r	Rundle, CUCPB 2140, from apple leaves
Eh421 (PanA ⁻)	Marker exchange mutant of Eh318, deficient in pantocin A; Km ^r	This work, CUCPB 4189
Eh439 (PanB ⁻)	Marker exchange mutant of Eh318, deficient in pantocin B; Cm ^r	This work, CUCPB 4433
Eh440 (PanAB ⁻)	Marker exchange mutant of Eh318, deficient in pantocin A and B; Km ^r Cm ^r	This work, CUCPB 4434
Eh252		Rundle, CUCPB 2050, from apple leaves
<i>Pantoea</i> sp. Eh112Y		
Billing, CUCPB 0119, from apple		
<i>P. stewartii</i> 2		
Woods (54), CUCPB 0176		

XI. RESISTANCE

It was found that there were antibiotic resistance genes (ARGs) after BLASTing against the CARD reference sequences. On the KM1 chromosome, we found 12 ARGs, and on the plasmid pKM1 3, we discovered one ARG^[75]. All of the newly discovered ARGs corresponded to well-characterized ARGs in the CARD database by more than 69.9 percent. “The resistance-nodulation-cell division (RND) antibiotic efflux pump (CRP, oqx_B, mdtA, mdtB, mdtC, acrR, acrD, and MuxB), the ATP-binding cassette (ABC) antibiotic efflux pump (msbA), and the major facilitator superfamily (MFS) antibiotic efflux pump (muxB) were the five gene families identified in KM1 (arnA)^[76]. These genes are resistant to antibiotics such as macrolides, fluoroquinolones, tetracyclines, aminoglycosides, nitroimidazoles, aminocoumarins, and peptide-based antibiotics”. Antibiotic efflux and antibiotic target modification were the main resistance mechanisms involving the anticipated multidrug resistant genes found in the KM1 genome^[77-78]. According to the Kirby-Bauer disc diffusion test, the KM1 strain is “resistant to penicillin G, vancomycin, bacitracin, fosfomycin, and rifampicin”.

XII. CONCLUSION

Large-scale molecular research on novel ExPEC strain reservoirs and pathways is needed to aid in the development of various preventive methods, such as vaccine manufacturing or treatment tactics

targeting new bacterial agents. This emphasises the need of informing farmers, traders, and sellers about new developing microbial dangers, as well as the critical role of appropriate food commerce in reducing such risks. With rising demand for chicken meat and products, food safety has become a major concern for public health. The issue of food contamination by ExPEC/UPEC strains in connection to their virulence factors is of special concern to researchers. Layers of genotyping are suggested, in which strains, plasmids, and genes are genotyped and compared to provide a more comprehensive view of this complicated issue.

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