



***Klebsiella pneumoniae*: Morphological characteristics, Growth, cultural characters, Antigenic Structures, Virulence Factors and Vaccines Strategies**

Hend Abdalla El-sayed Moustafa¹, Amal Maher Ibrahim Hussein^{1*}, Lamiaa Gaber Zaki², Gehan Ahmed El-shennawy¹

¹Medical Microbiology and Immunology Department, Faculty of Medicine, Zagazig University, Egypt.

² Chest diseases Department, Faculty of Medicine, Zagazig University, Egypt.

Abstract

Members of the genus *Klebsiella* have rapidly evolved within the past decade, generating organisms that simultaneously exhibit both multidrug resistance and hypervirulence (MDR-hv) phenotypes; such organisms are associated with severe hospital- and community-acquired infections. Carbapenem-resistant infections with unknown optimal treatment regime were of particular concern among the MDR-hv *Klebsiella* strains. Recent studies have revealed the molecular features and the mobile resistance elements they harbour, allowing identification of genetic loci responsible for transmission, stable inheritance, and expression of mobile resistance or virulence-encoding elements that confer the new phenotypic characteristics of MDR-hv *Klebsiella* spp.

Keywords: *Klebsiella*, MDR, virulence.

Review article

*Corresponding Author, e-mail: amalkasem21@gmail.com

1. Introduction

The *Klebsiella* genus comprises a wide diversity of species, including the *Klebsiella pneumoniae* species complex (KpSC) and several more genetically distant species [1]. Strains of this genus were first isolated in the late 19th century and named by Trevisan (1885) to honor the German microbiologist Edwin Klebs [2]. *Klebsiella* is classified under the Enterobacteriaceae family which contained a large array of biochemically distinct genus, including the model organism *Escherichia coli* and the notorious human pathogens *Salmonella*, *Yersinia*, *Serratia*, *Enterobacter*, *Citrobacter*, *Kluyvera*, *Leclercia*, *Raoultella*, *Cronobacter*, etc [1]. The *Klebsiella* genus currently comprises a wide diversity of species, including species belonging to the *K. pneumoniae* species complex (KpSC) and other *Klebsiella* species (*K. indica*, *K. terrigena*, *K. spallanzanii*, *K. huaxiensis*, *K. oxytoca*, *K. grimontii*, *K. pasteurii* and *K. michiganensis*) that share an average of only 90% nucleotide identity with KpSC [1]. Seven phylogroups that belong to KpSC have been classified, including *K. pneumoniae* (Kp1), *K. quasipneumoniae* subspecies *quasipneumoniae* (Kp2), *K. variicola* subsp. *variicola* (Kp3), *K. quasipneumoniae* subsp. *similipneumoniae* (Kp4), *K. variicola* subsp. *tropica* (Kp5), *K. quasivariicola* (Kp6) and *K. africana* (Kp7) [3]. Two subspecies of *K. pneumoniae*,

namely *K. pneumoniae* subsp. *ozaenae* and *K. pneumoniae* subsp. *rhinoscleromatis*, which are associated with a specific disease syndrome (atrophic rhinitis and rhinoscleroma, respectively), have been reported [4].

2. Morphological characteristics:

Klebsiella spp. is non-motile, straight rod shape, 0.3-1µm in diameter and 0.6-6µm in length, when these bacteria are stained with a Gram stain, they give pink color (negative bacteria) with a prominent polysaccharide capsule. This capsule encases the entire cell surface and provides resistance against many host defense mechanisms [5].

3. Habitat:

Klebsiella pneumoniae has a strong association with human as resident flora and colonises almost every part of the human body with most preferential in the respiratory, gastrointestinal and urinary tract. The other predominant habitats include soil, plants, surface water, sewage and industrial effluent [6]. Despite the source of origin, clinical isolates cause nosocomial and community-acquired infections. This leads to the serious therapeutic threats given the increase in drug resistant phenotypes and decrease in effective antibiotics [7].

4. Growth and cultural characters:

Based on the presence or absence of capsular (K) somatic(O) and slime(M) antigens ,the Klebsiella strains have been divided into 4 smooth and 4 rough forms

Smooth forms	Rough forms
1. MKO	MKR mucoid capsulated
2. KO	KR non mucoid capsulated
3.	MO MR mucoid non capsulated
	OR non mucoid non capsulated [8].

When kept at room temperature, cultures remain viable for weeks or months. They are facultative anaerobic bacteria. There is no haemolysis of horse or sheep red cells. Lactose fermenting large moist glistening colonies due to polysaccharide capsule (K-antigen) in MacConkey agar. The optimum temperature for growth is 37° the limits are 12° and 43° [9]. When much capsular material is produced, the growth on agar is luxuriant, greyish white, mucoid and almost diffluent .This is due to high proportion of water(92%)in the capsular material [10]. Moist heat at 55° kill The organisms in 30 min. They are survive drying for months [11].

5. Biochemical activities:

The key biochemical tests used to differentiate Klebsiella species are listed in table (1).

6. Antigenic structures and virulence factors (Fig.2):

All K.pneumoniae isolates carry a set of core genes responsible for their pathogenicity and required to establish opportunistic infections in humans and other hosts [13].

A) K-Antigens :

The surface of Klebsiella species is shielded by a thick layer of capsular polysaccharide, historically known as K-antigen, that protects the bacteria from phagocytosis and prevents killing of the bacteria by bactericidal serum factors [14]. Hyper virulent K.pneumoniae (Hv-Kp) strains are known to produce a hypercapsule, resulting in a hypermucoviscous phenotype which further contribute to increased resistance to complement-mediated or phagocyte-mediated killing [15]. Traditionally, 77 K-antigens have been identified among Klebsiella spp. based on the diversity in their sugar composition, type of glycosidic linkages, and the nature of enantiomeric and epimeric forms [16]. Recently, additional K-types have been reported based on the arrangement of the capsule polysaccharide synthesis (cps) locus or K locus (KL), known as the KL series [17]. Among the different K-antigens, K1, K2, K5, K16, K23, K27, K28, K54, K62 and K64 are some of the most commonly isolated serotypes globally [18]. K1 and K2 strains are generally more virulent than strains of other serotypes based on the most frequently isolated serotypes collected from patients and results from mouse experiments. In addition, K2 strains are the most prevalent type of K.pneumoniae strain isolated clinically, followed by K1 strains,and they are more resistant to phagocytosis and intracellular killing by alveolar macrophages and neutrophils than other strains, and this phenotype is independent of whether they are hypercapsule producers [19]. Plasmid located virulence gene(regulator of mucoid phenotype A (rmpA)) is responsible for Synthesis of capsular polysaccharides; highmucus phenotype of

(hvKP),while, rmpA2 is responsible for capsule upregulation [20].

B) Lipopolysaccharide(Endotoxin) :

Polysaccharide represents an important and essential factor in bacterial pathogenicity, especially *K. pneumoniae*, as it is one of the superficial compositions of bacteria that helps it to resist phagocytosis and participates in protecting bacteria against the host's complement system.(Fig.1) [21]. LPS is both a benefit and a hindrance for *K. pneumoniae* during infection, as it is an important virulence factor that protects against humoral defenses but also can be a strong immune activator [22]. LPS consists of three parts: O-antigen, a core polysaccharide, and lipid A antigen which are encoded by genes in the wb, waa, and lpx gene clusters, respectively [23].

i. O-Antigens:

The O-antigen moiety of the LPS has a limited range of structures, resulting from different sugar composition, glycosidic linkages and epimeric or enantiomeric forms of the sugars [24]. The most recent classification includes 11 O-serotypes: O1, O2a, O2ac, O2afg, O2aeh (previously known as O9), O3 (divided in subserotypes O3, O3a and O3b), O4, O5, O7, O8 and O12 [17]. Among clinical *K. pneumoniae* isolates O1 is the most common serotype [25].

ii. Lipid A :

Lipid A is formed in the cytoplasm by conserved constituent enzymes and transmitted by the ATP-binding cassette(ABC) transporter MsbA and is concentrated in the outer membrane [26]. Lipid A, is a potent ligand of Toll like receptor-4 (TLR4) which stimulation leads to the production of cytokines and chemokines that help recruit and activate cellular responses, including neutrophils and macrophages, which combate *K. pneumoniae* infection and control spread to other tissues [22]. *K. pneumoniae* may use another method to prevent recognition by the immune response which is modification of the LPS to a form that is no longer recognizable by certain immune receptors [27]. The lipid A portion of *K. pneumoniae* LPS plays a beneficial role in virulence as both in vitro and in vivo experiments have shown that lipid A protects against some cationic antimicrobial peptides [19].

iii. Core polysaccharide :

Two types of core polysaccharide (Type I and Type II) have been identified to be produced by these bacteria,they are encoded by two different groups of wa gene cluster [28].

C) Fimbriae

Fimbriae are organelles appointed to facilitate attachment and adherence to eukaryotic cells, but also involved in other functions, such as interaction with macrophages, biofilm formation, intestinal persistence, and bacterial aggregation [29]. Most clinical *K. pneumoniae* isolates express two types of fimbrial adhesins, type 1 fimbriae and type 3 fimbriae [30]. Besides type 1 and type 3 fimbriae, a third type named *K. pneumoniae* complex (KPC) fimbria was identified and its heterologous expression in *E. coli* demonstrated an active role of this protein in biofilm formation [13]. Several genes encoding Fimbriae in *K. pneumoniae* have been described such as fimH, mrkD and cf29A that encode type 1 fimbriae, type 3 fimbriae and non-fimbrial adhesion factor ,respectively [31].

Table 1: Differentiation of Klebsiella species.

Properties	<i>K.pneumoniae</i>	<i>K. ozaenae</i>	<i>K.rhinoscleromatis</i>	<i>K. oxytoca</i>
Indole	-	-	-	+
Vogesproskauer	+	-	-	+
Urea hydrolysis	+	-	-	+
Lysine decarboxylase	+	V	-	+
ONPG	+	+	-	+
Growth at 4°C	-	-	-	-
Growth at 10°C	-	-	-	+
Growth at 44°C	+	V	UK	+

+ most strains positive; - most strains negative; V some strains positive, others negative; UK unknown; ONPG (O -nitrophenyl-B - galactopyranoside test) [12]

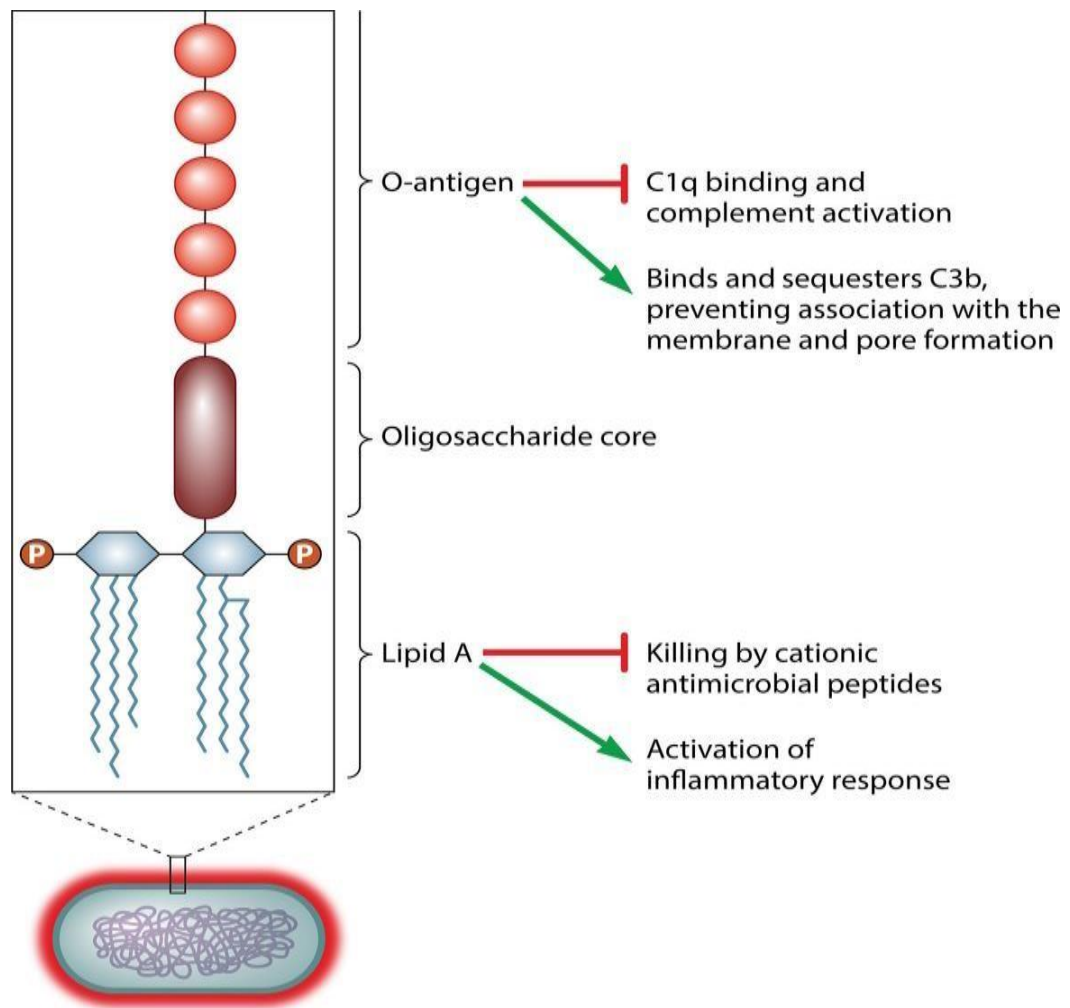


Figure 1: Role of lipopolysaccharide in *K. pneumoniae* virulence, [19].

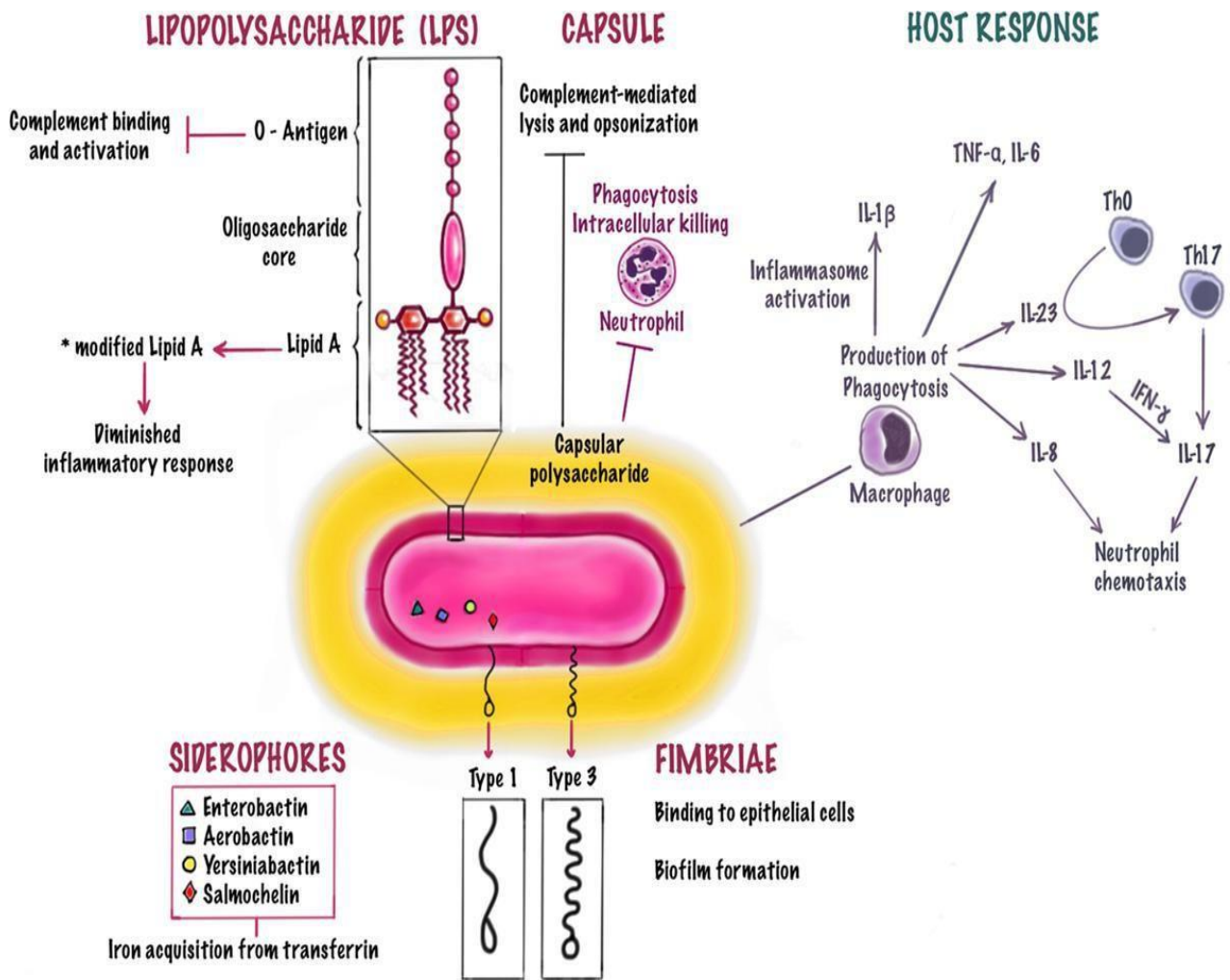


Figure 2: Schematic presentation of *K. pneumoniae* virulence factors and host innate immune response, [6].

Another *K. pneumoniae* fimbrial antigen named KPF-28 has been reported to be expressed by several *K. pneumoniae* circulating strains and its role in colonization has been demonstrated by using KPF-28 antisera to inhibit bacterial adhesion to intestinal cells. However, besides a correlation of the expression of this adhesin with an antibiotic resistance phenotype, no further information has been collected about KPF-28 over the last two decades [13]. Type 1 fimbriae are made by a polymer of the major building element FimA. FimH, together with the minor subunits FimF and FimG, forms a flexible tip fibrillum that is connected to the distal end of the pilus rod and that is responsible for the adhesion to the host [32]. Type 1 fimbriae were described to be phase-variable with a different role in lungs and urinary or intestinal tract infections. Indeed, fimbrial expression was found to be highly upregulated in the bacterial population in urine and infected bladders and downregulated in the lungs. In this organ, expression of type 1 fimbriae may be a disadvantage for the bacteria because of their ability to adhere to phagocytic cells in the lungs and therefore to be rapidly eliminated [33]. Type 3 fimbriae have been extensively proven to mediate binding to extracellular matrix (ECM) proteins such as collagen molecules and to strongly promote biofilm formation [34].

D) Siderophores :

Siderophores are secreted small molecules that can bind the iron present externally and re-enter to the bacterial cells through specific receptors [35]. Since iron is essential for the survival of bacteria, it is also necessary to obtain iron source through siderophores during the colonization stage of *K. pneumoniae*. Nearly all bacteria, including all opportunistic pathogens of the airway, require an iron source to survive [36]. *K. pneumoniae* production of siderophores such as enterobactin, yersiniabactin, salmochelin and aerobactin has been shown to strongly correlate with in vivo virulence and differentiate Hv-Kp from classical *K. pneumoniae* strains. For this reason, siderophores have been suggested as potential biomarkers to be further implemented in screening laboratory tests [37]. Each of these molecules presents a specific receptor on the bacterial surface able to bind the siderophore and to mediate the iron uptake, which is essential for the pathogen survival [38]. Salmochelin is associated with invasive diseases, and is common in highly virulent *K. pneumoniae* strains that cause severe community related infections, such as liver abscess and pneumonia [39].

7. Pathogenic strains and infections caused by *K. pneumoniae*:

Historically, *K. pneumoniae* infections have been caused by "classic" *K. pneumoniae* (cKp) strains which were found widely in hospital environs in Asia, causing infections in immunocompromised patients with debilitating conditions. On the other hand, Hypervirulent *K. pneumoniae* (Hv-Kp) variant strains first isolated in the Asian Pacific Rim [40]. The HvKp strains cause life threatening community-acquired metastatic and invasive infections such as liver abscess, meningitis, endophthalmitis and septic arthritis in immunocompetent individuals [41]. HvKp infection requires minimal number of bacteria to occur. As studies in mice showed that an inoculum dose of as little as 50 bacteria was lethal compared to the inoculum size of 107 needed for classical *K. pneumoniae* (cKp) strains [42]. The recent emergence and widespread dissemination of the new cKp strains of multidrug-resistant (MDR) *K. pneumoniae* and the global spread of hvKp strains put *K. pneumoniae* on the WHO and the US centers for disease control list of priority MDR pathogens [43]. With the acquisition of an extended-spectrum beta-lactamase, many strains have additional resistance to amoxicillin, ceftazidime, ceftriaxone, and carbenicillin [6]. In 2009, a novel gene called New Delhi metallo-beta-lactamase (NDM-1) was reported in strains of *K. pneumoniae* in India and Pakistan and gives *K. pneumoniae* resistance even to intravenous antibiotic carbapenem. To treat these infections, Physicians have resorted to use older previously discarded antibiotics which include colistin and tigecycline with few novel antibiotics under development [6]. Recent reports have indicated the presence of colistin-resistant strains of KP in ICUs. Consequently, superbugs with pan resistance to all known classes of antibiotics, including the polymyxins, have emerged [6]. *K. pneumoniae* is the causative agent of a range of infections, including:

A) Respiratory infections:

K. pneumoniae pneumonias can be split into two broad categories:

- 1) Hospital-acquired pneumonias (HAPs).
- 2) Community-acquired pneumonias (CAPs).

1) Hospital -acquired pneumonias (HAPs):

K. pneumoniae HAPs are far more prevalent than *K. pneumoniae* CAPs. HAP is generally defined as pneumonia that presents at least 48 h after admission to a hospital in individuals with no symptoms of pneumonia prior to admission and about 11.8% of HAPs are caused by *K. pneumoniae* [44]. HAPs occur in both ventilated and nonventilated patients, and *K. pneumoniae* is the causative agent in 8 to 12% and 7% of these cases, respectively [45].

There is a significantly higher risk of *K. pneumoniae* being multidrug resistant in nosocomial infections than in community-acquired infections because many patients have been treated with antibiotics and are carrying antibiotic-resistant flora [46].

2) Community-acquired pneumonias (CAPs):

CAPs are potentially serious infections that can progress rapidly and lead to hospitalization, intensive care

unit (ICU) stays and high rates of morbidity and mortality [47]. Both classical and HV strains can cause CAPs, the increased prevalence of *K. pneumoniae* as the etiological agent of CAPs in Asia and Africa is likely due to the increased prevalence of hypervirulent strains in these areas [19]. Reports estimate that *K. pneumoniae* CAPs comprise 22 to 32% of cases requiring admission to the ICU, with mortality rates in these ICU patients ranging from 45 to 72% [19-48]. Cases usually present with cough, fever, leukocytosis and chest pain which are similar to symptoms typical of acute pneumonias and can also display the trademark *K. pneumoniae* characteristic of "currant jelly sputum" which is the production of thick blood-tinged mucous resulting from high levels of inflammation and necrosis in the lungs [49].

B) Urinary tract infections:

K. pneumoniae strains are the second or third most frequent cause of UTIs behind *Escherichia coli*, which causes the vast majority of UTIs [50]. *K. pneumoniae* accounts for 2 to 6% of nosocomial UTIs and 4.3 to 7% of community-acquired UTIs [51]. *K. pneumoniae* UTIs resulting from seeding of *K. pneumoniae* from the GI tract [52]. The symptoms include dysuria, increased frequency, urgency of voiding and hematuria [53]. C) Bacteremia: *K. pneumoniae* is second only to *E. coli* among gram-negative pathogens as the causative agent of both community-associated and nosocomial bacteremias [54]. Mortality rates following *K. pneumoniae* bacteremia ranged from 27.4 to 37% [55]. The increase in antibiotic resistance makes treatment of lung and bladder *K. pneumoniae* infections more difficult and prolongs time that patients carry *K. pneumoniae* at these sites, allowing *K. pneumoniae* to spread to the bloodstream and brain [56].

D) Gastrointestinal tract infections:

HV strains cause primary liver abscesses in patient populations that do not appear to have any underlying liver disease but are likely initiated from a breach in host defenses in the GI tract that permits intestinal microbiota to seed tissue sites unlike other pyogenic liver abscesses caused by polymicrobial sources [57]. The intestinal flora has an effect on *K. pneumoniae* colonization. For instance, a healthy gut microbiome provides an extra layer of defense and helps eliminate exogenous bacteria. However, changes in intestinal flora after antibacterial treatment lead to increase the level of available monosaccharides in the intestinal tract and promote the growth of pathogenic or opportunistic bacteria *K. pneumoniae* [58].

E) Central nervous system infections:

In Taiwan, several epidemiologic studies of adult bacterial meningitis (ABM) have also revealed that *K. pneumoniae* is the most commonly implicated pathogen of community-acquired infection. Presence of DM and liver disease especially cirrhosis are the most common underlying medical conditions of this specific group of CNS infection [59].

Brain abscess, which may occur alone or in combination with ABM, is the most common form of

intracranial focal suppuration of *K. pneumoniae* infection [59].

F) Other infections:

HV *K. pneumoniae* infections can also lead to severe skin and soft tissue infections (e.g., cellulitis, necrotizing fasciitis, and myositis), endophthalmitis and abscesses in a number of other tissues (e.g., neck, lungs and kidneys) [60]. *K. pneumoniae* has been implicated in the development of ankylosing spondylitis because of the high incidence of Klebsiella in the bowel flora of patients whose disease is in an active state [61].

8. Vaccines and Monoclonal Antibodies (mAb) Strategies

With little hope of new drugs and an increase in antimicrobial-resistant and virulent strains, vaccines offer the best solution against the rapidly increasing global threat of *K. pneumoniae* infections, as recognized by the WHO [62]. No vaccines are currently licensed against *K. pneumoniae*, but several vaccine targets have been described in the past few decades. Moreover, a therapeutic approach based on the use of monoclonal antibodies (mAbs) against antimicrobial resistant (AMR) pathogens has been taking place over the last years [63].

A) K-Antigen Based Approaches

Bacterial capsule polysaccharides have been used historically as vaccine target antigens and several formulations have been developed against different pathogens [64]. The ideal capsule-based vaccine should be multivalent in order to cover the majority of all bacteraemic isolates. Subsequently tested a polyvalent Klebsiella vaccine, composed of six K-serotypes (K2, K3, K10, K21, K30, and K55), which resulted to be safe and immunogenic in humans. This study raised the awareness that a Kp vaccine able to cover around 70% of clinically relevant *K. pneumoniae* strains should include at least 25 capsular polysaccharides [65]. An interesting study was performed in 2019 by Feldman et al. [42] who tested for the first time a bioconjugate vaccine encompassing capsules from the K1 and K2 serotypes, causing around 70% of all Hv-Kp infections worldwide.

B) O-Antigen Based Approaches

K. pneumoniae O-antigens are alternative targets for the vaccine development, due to their limited range of structures. Indeed, four serotypes (O1, O2, O3 and O5) were predicted to cover over 80% of clinically relevant Kp strains [18]. Immunization with purified O1 LPS vaccine could protect mice against K2:O1 challenges. Additionally, it was reported that O1 LPS, incorporated either into liposomes or sodium alginate microparticles, could protect rodents against lobar pneumonia and resulted to be less toxic than free LPS in mice [66]. Hegerle et al. [67] reported the development of combined *K. pneumoniae* and *Pseudomonas aeruginosa* glycoconjugate vaccine comprising O1, O2, O3, O5 Kp O-serotypes, chemically linked to the two *Pseudomonas* flagellin types (FlaA, FlaB). The quadrivalent conjugate vaccine generated antibody titers to the four *K. pneumoniae* O-antigens and both Fla antigens in rabbits. Innovative strategies have been recently proposed for the generation of

O2a glycoconjugate vaccines including a semi-synthetic approach and a bioconjugation approach [68]. Anti *K. pneumoniae* O-antigen mAbs also proved to be able to reduce bacterial burden, enhance survival, and show synergy with current standard of care therapy [69]. Serotype specific anti-O1 (KPE33) and anti-O2 (KPN42) human mAbs are able to protect mice against *K. pneumoniae* infection via opsonophagocytic killing [70]. Anti-O3 mAb 2F8 able to cross-react with all three O3 sub-serogroups (O3, O3a and O3b) [71].

C) Protein Based Approaches

Protein virulence factors have also been proposed as targets for the development of vaccines and therapeutic mAb against *K. pneumoniae*. These antigens are characterized by low variability, especially when compared to the K-antigens and O-antigens polysaccharides. In particular, type 3 fimbriae structural protein MrkA has gained a strong interest as a putative target for a vaccine as, besides being expressed by most of *K. pneumoniae* strains, including Hv-Kp, it shows a structural position on the pilus filament that may ensure easy access to antibodies. There are already data showing that immunization with purified fimbriae was able to protect mice against a lethal challenge in a model of acute pneumonia [72]. Type 1 and 3 fimbriae were used as carrier proteins conjugated to E. coli core oligosaccharide, proving to be immunogenic also in rabbits [73]. Recently, using bioinformatic prediction tools, Zargaran et al., [74] found four B cell epitopes (each for one Fim antigen) that were proposed as suitable vaccine candidates for *K. pneumoniae* as these epitopes may be recognized by the B cell receptor, triggering humoral responses. Indeed, in silico analysis suggested that these epitopes are immunogenic and antigenic, not similar to human peptides, not allergenic and not toxic. However, these results still need to be supported by in vitro and in vivo testing. A reverse vaccinology approach is applied on a total of 222 available complete genomes of *K. pneumoniae* and four outer membrane proteins were shortlisted for vaccine designing: the outer membrane protein OmpA, the copper/silver efflux RND transporter, the phosphoprotein PhoE and the peptidoglycan-associated lipoprotein Pal. Of these antigens, a total of four epitopes were joined together using flexible linkers resulting in a potential multi-epitope vaccine against *K. pneumoniae* [75]. Another virulence factor recently investigated as a potential vaccine target is the highly conserved YidR, an ATP/GTP-binding protein that mediates the hyperadherence phenotype and is involved in biofilm formation. Recombinant YidR has been proven to protect mice from challenge with a low dose of *K. pneumoniae* [76].

9. Conclusions

The molecular features and the mobile resistance elements they harbour, allowing identification of genetic loci responsible for transmission, stable inheritance, and expression of mobile resistance or virulence-encoding elements that confer the new phenotypic characteristics of MDR-hv Klebsiella spp.

References

- [1] K.L. Wyres, M.M. Lam, K.E. Holt. (2020). Population genomics of *Klebsiella pneumoniae*. *Nature Reviews Microbiology*. 18(6): 344-359.
- [2] S. Brisse, F. Grimont, P.A. Grimont. (2006). The genus *klebsiella*. *The prokaryotes*. 159-196.
- [3] M.M. Lam, R.R. Wick, S.C. Watts, L.T. Cerdeira, K.L. Wyres, K.E. Holt. (2021). A genomic surveillance framework and genotyping tool for *Klebsiella pneumoniae* and its related species complex. *Nature communications*. 12(1): 4188.
- [4] S. Brisse, C. Fevre, V. Passet, S. Issenhuth-Jeanjean, R. Tournebize, L. Diancourt, P. Grimont. (2009). Virulent clones of *Klebsiella pneumoniae*: identification and evolutionary scenario based on genomic and phenotypic characterization. *PLoS one*. 4(3): e4982.
- [5] S.A. Jasim. *Klebsiella* spp. PATHOGENIC BACTERIA. 6: 76.
- [6] E.-T. Piperaki, G.A. Syrogiannopoulos, L.S. Tzouveleki, G.L. Daikos. (2017). *Klebsiella pneumoniae*: virulence, biofilm and antimicrobial resistance. *The Pediatric infectious disease journal*. 36(10): 1002-1005.
- [7] D. Van Duin, D.L. Paterson. (2016). Multidrug-resistant bacteria in the community: trends and lessons learned. *Infectious disease clinics*. 30(2): 377-390.
- [8] A.H. Al-Charrakh, S.Y. Yousif, H.S. Al-Janabi. (2011). Occurrence and detection of extended-spectrum β -lactamases in *Klebsiella* isolates in Hilla, Iraq. *African Journal of Biotechnology*. 10(4): 657-665.
- [9] R. Bonnet. (2004). Growing group of extended-spectrum β -lactamases: the CTX-M enzymes. *Antimicrobial agents and chemotherapy*. 48(1): 1-14.
- [10] S.M. Deshmukhe, G. Karande, S.B.K. Sharma, S. Patil, R. Shinde, S. Pawar, H. Patil, P. Mane. Prevalence of ESBL in *Klebsiella* Sp. and Its Antibiotic Resistance Pattern from Various Clinical Samples in a Tertiary Care Hospital.
- [11] A.M. Ali, S.A. Abbasi, M. Ahmed. (2009). Frequency of Extended Spectrum Beta-Lactamases (ESBL) Producing Nosocomial Isolates in a Tertiary Care Hospital in Rawalpindi. *Pakistan Armed Forces Medical Journal*. 59(2): 154-8.
- [12] J. Farmer, M. Farmer, B. Holmes. (2010). The Enterobacteriaceae: general characteristics. *Topley & Wilson's Microbiology and Microbial Infections*. 2: 1317-1359.
- [13] V. Arato, M.M. Raso, G. Gasperini, F. Berlanda Scorza, F. Micoli. (2021). Prophylaxis and treatment against *Klebsiella pneumoniae*: current insights on this emerging anti-microbial resistant global threat. *International journal of molecular sciences*. 22(8): 4042.
- [14] M. Sathya. Detection of multidrug resistance in *klebsiella* species by phenotypic and genotypic methods in a tertiary care hospital. *Madras Medical College, Chennai*, 2018.
- [15] D. Pomakova, C. Hsiao, J. Beanan, R. Olson, U. MacDonald, Y. Keynan, T. Russo. (2012). Clinical and phenotypic differences between classic and hypervirulent *Klebsiella pneumoniae*: an emerging and under-recognized pathogenic variant. *European journal of clinical microbiology & infectious diseases*. 31: 981-989.
- [16] L.P.P. Patro, T. Rathinavelan. (2019). Targeting the sugary armor of *Klebsiella* species. *Frontiers in Cellular and Infection Microbiology*. 9: 367.
- [17] L.P.P. Patro, K.U. Sudhakar, T. Rathinavelan. (2020). K-PAM: a unified platform to distinguish *Klebsiella* species K-and O-antigen types, model antigen structures and identify hypervirulent strains. *Scientific reports*. 10(1): 16732.
- [18] R. Follador, E. Heinz, K.L. Wyres, M.J. Ellington, M. Kowarik, K.E. Holt, N.R. Thomson. (2016). The diversity of *Klebsiella pneumoniae* surface polysaccharides. *Microbial genomics*. 2(8): e000073.
- [19] M.K. Paczosa, J. Mecsas. (2016). *Klebsiella pneumoniae*: going on the offense with a strong defense. *Microbiology and molecular biology reviews*. 80(3): 629-661.
- [20] J. Turton, F. Davies, J. Turton, C. Perry, Z. Payne, R. Pike. (2019). Hybrid resistance and virulence plasmids in "high-risk" clones of *Klebsiella pneumoniae*, including those carrying bla NDM-5. *Microorganisms*. 7(9): 326.
- [21] R. Podschun, U. Ullmann. (1998). *Klebsiella* spp. as nosocomial pathogens: epidemiology, taxonomy, typing methods, and pathogenicity factors. *Clinical microbiology reviews*. 11(4): 589-603.
- [22] L.R. Standiford, T.J. Standiford, M.J. Newstead, X. Zeng, M.N. Ballinger, M.A. Kovach, A.K. Reka, U. Bhan. (2012). TLR4-dependent GM-CSF protects against lung injury in Gram-negative bacterial pneumonia. *American Journal of Physiology-Lung Cellular and Molecular Physiology*. 302(5): L447-L454.
- [23] T.S. Jensen, K.V. Opstrup, G. Christiansen, P.V. Rasmussen, M.E. Thomsen, D.L. Justesen, H.C. Schönheyder, M. Lausen, S. Birkelund. (2020). Complement mediated *Klebsiella pneumoniae* capsule changes. *Microbes and infection*. 22(1): 19-30.
- [24] B.R. Clarke, O.G. Ovchinnikova, S.D. Kelly, M.L. Williamson, J.E. Butler, B. Liu, L. Wang, X. Gou, R. Follador, T.L. Lowary. (2018). Molecular basis for the structural diversity in serogroup O2-antigen polysaccharides in *Klebsiella pneumoniae*. *Journal of Biological Chemistry*. 293(13): 4666-4679.
- [25] M. Choi, N. Hegerle, J. Nkeze, S. Sen, S. Jamindar, S. Nasrin, S. Sen, J. Permal-Booth, J. Sinclair, M.D. Tapia. (2020). The diversity of lipopolysaccharide (O) and capsular polysaccharide (K) antigens of invasive *Klebsiella pneumoniae* in a multi-country collection. *Frontiers in microbiology*. 11: 1249.
- [26] C.R. Raetz, C.M. Reynolds, M.S. Trent, R.E. Bishop. (2007). Lipid A modification systems in

- gram-negative bacteria. *Annu. Rev. Biochem.* 76(1): 295-329.
- [27] E. Llobet, V. Martínez-Moliner, D. Moranta, K.M. Dahlström, V. Regueiro, A. Tomás, V. Cano, C. Pérez-Gutiérrez, C.G. Frank, H. Fernández-Carrasco. (2015). Deciphering tissue-induced *Klebsiella pneumoniae* lipid A structure. *Proceedings of the National Academy of Sciences.* 112(46): E6369-E6378.
- [28] S. Fresno, N. Jiménez, R.o. Canals, S. Merino, M.M. Corsaro, R. Lanzetta, M. Parrilli, G. Pieretti, M. Regué, J.M. Tomás. (2007). A second galacturonic acid transferase is required for core lipopolysaccharide biosynthesis and complete capsule association with the cell surface in *Klebsiella pneumoniae*. *Journal of bacteriology.* 189(3): 1128-1137.
- [29] J.G. Johnson, C.N. Murphy, J. Sippy, T.J. Johnson, S. Clegg. (2011). Type 3 fimbriae and biofilm formation are regulated by the transcriptional regulators MrkHI in *Klebsiella pneumoniae*. *Journal of bacteriology.* 193(14): 3453-3460.
- [30] B. Morrissey, A.C. Leney, A.T. Reˆgo, G. Phan, W.J. Allen, D. Verger, G. Waksman, A.E. Ashcroft, S.E. Radford. (2012). The role of chaperone-subunit usher domain interactions in the mechanism of bacterial pilus biogenesis revealed by ESI-MS. *Molecular & Cellular Proteomics.* 11(7): M111. 015289-1-M111. 015289-11.
- [31] M. Ali, A. Zahab. (2011). Extended Spectrum β -Lactamases in *Escherichia coli* and *Klebsiella pneumoniae*, their molecular characterization and associated risk factors. *Egyptian Journal of Medical Microbiology.* 20(3): 35-45.
- [32] J. Lillington, S. Geibel, G. Waksman. (2014). Biogenesis and adhesion of type 1 and P pili. *Biochimica et Biophysica Acta (BBA)-General Subjects.* 1840(9): 2783-2793.
- [33] C. Struve, M. Bojer, K.A. Krogfelt. (2008). Characterization of *Klebsiella pneumoniae* type 1 fimbriae by detection of phase variation during colonization and infection and impact on virulence. *Infection and immunity.* 76(9): 4055-4065.
- [34] C. Schroll, K.B. Barken, K.A. Krogfelt, C. Struve. (2010). Role of type 1 and type 3 fimbriae in *Klebsiella pneumoniae* biofilm formation. *BMC microbiology.* 10: 1-10.
- [35] M. Miethke, M.A. Marahiel. (2007). Siderophore-based iron acquisition and pathogen control. *Microbiology and molecular biology reviews.* 71(3): 413-451.
- [36] S.J. Siegel, J.N. Weiser. (2015). Mechanisms of bacterial colonization of the respiratory tract. *Annual review of microbiology.* 69(1): 425-444.
- [37] T.A. Russo, R. Olson, C.-T. Fang, N. Stoesser, M. Miller, U. MacDonald, A. Hutson, J.H. Barker, R.M. La Hoz, J.R. Johnson. (2018). Identification of biomarkers for differentiation of hypervirulent *Klebsiella pneumoniae* from classical *K. pneumoniae*. *Journal of clinical microbiology.* 56(9): 10.1128/jcm. 00776-18.
- [38] T.A. Russo, C.M. Marr. (2019). Hypervirulent *Klebsiella pneumoniae*. *Clinical microbiology reviews.* 32(3): 10.1128/cmr. 00001-19.
- [39] M.M. Lam, R.R. Wick, K.L. Wyres, C.L. Gorrie, L.M. Judd, A.W. Jenney, S. Brisse, K.E. Holt. (2018). Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICE Kp in *Klebsiella pneumoniae* populations. *Microbial genomics.* 4(9): e000196.
- [40] M. Ye, J. Tu, J. Jiang, Y. Bi, W. You, Y. Zhang, J. Ren, T. Zhu, Z. Cao, Z. Yu. (2016). Clinical and genomic analysis of liver abscess-causing *Klebsiella pneumoniae* identifies new liver abscess-associated virulence genes. *Frontiers in Cellular and Infection Microbiology.* 6: 165.
- [41] R.M. Martin, M.A. Bachman. (2018). Colonization, infection, and the accessory genome of *Klebsiella pneumoniae*. *Frontiers in Cellular and Infection Microbiology.* 8: 4.
- [42] M.F. Feldman, A.E. Mayer Bridwell, N.E. Scott, E. Vinogradov, S.R. McKee, S.M. Chavez, J. Twentyman, C.L. Stallings, D.A. Rosen, C.M. Harding. (2019). A promising bioconjugate vaccine against hypervirulent *Klebsiella pneumoniae*. *Proceedings of the National Academy of Sciences.* 116(37): 18655-18663.
- [43] M. Ciccozzi, E. Cella, A. Lai, L. De Florio, F. Antonelli, M. Fogolari, F.M. Di Matteo, M. Pizzicannella, B. Colombo, G. Dicuonzo. (2019). Phylogenetic analysis of multi-drug resistant *Klebsiella pneumoniae* strains from duodenoscope biofilm: microbiological surveillance and reprocessing improvements for infection prevention. *Frontiers in public health.* 7: 219.
- [44] H.S. Ghafour. Detection of biofilm formation in carbapenamase resistance *Klebsiella* spp. *Sakarya Üniversitesi,* 2021.
- [45] M.S. Vallecocchia, C. Dominedò, S.L. Cutuli, I. Martin-Loeches, A. Torres, G. De Pascale. (2020). Is ventilated hospital-acquired pneumonia a worse entity than ventilator-associated pneumonia? *European Respiratory Review.* 29(157).
- [46] J. Choby, J. Howard-Anderson, D. Weiss. (2020). Hypervirulent *Klebsiella pneumoniae*—clinical and molecular perspectives. *Journal of internal medicine.* 287(3): 283-300.
- [47] R.N. Jones. (2010). Microbial etiologies of hospital-acquired bacterial pneumonia and ventilator-associated bacterial pneumonia. *Clinical Infectious Diseases.* 51(Supplement_1): S81-S87.
- [48] C. Cillóniz, C. Dominedò, A. Torres. (2019). Multidrug resistant gram-negative bacteria in community-acquired pneumonia. *Annual Update in Intensive Care and Emergency Medicine* 2019. 459-475.
- [49] D.E. Blue, B.H. Schmitt. (2016). Microbiology for the surgical pathologist. *Essentials of anatomic pathology.* 349-442.
- [50] N. Agyepong, U. Govinden, A. Owusu-Ofori, S.Y. Essack. (2018). Multidrug-resistant gram-negative bacterial infections in a teaching hospital in Ghana. *Antimicrobial Resistance & Infection Control.* 7: 1-8.

- [51] I. Linhares, T. Raposo, A. Rodrigues, A. Almeida. (2013). Frequency and antimicrobial resistance patterns of bacteria implicated in community urinary tract infections: a ten-year surveillance study (2000–2009). *BMC infectious diseases*. 13: 1-14.
- [52] S. Clegg, C.N. Murphy. (2017). Epidemiology and virulence of *Klebsiella pneumoniae*. *Urinary Tract Infections: Molecular Pathogenesis and Clinical Management*. 435-457.
- [53] Y.-H. Wu, P.-L. Chen, Y.-P. Hung, W.-C. Ko. (2014). Risk factors and clinical impact of levofloxacin or cefazolin nonsusceptibility or ESBL production among uropathogens in adults with community-onset urinary tract infections. *Journal of microbiology, immunology and infection*. 47(3): 197-203.
- [54] R. Matta, S. Hallit, R. Hallit, W. Bawab, A.-M. Rogues, P. Salameh. (2018). Epidemiology and microbiological profile comparison between community and hospital acquired infections: a multicenter retrospective study in Lebanon. *Journal of infection and public health*. 11(3): 405-411.
- [55] S.C. Zammit, N. Azzopardi, J. Sant. (2014). Mortality risk score for *Klebsiella pneumoniae* bacteraemia. *European journal of internal medicine*. 25(6): 571-576.
- [56] J. Biliński, P. Grzesiowski, J. Muszyński, M. Wróblewska, K. Mądry, K. Robak, T. Dzieciatkowski, W. Wiktor-Jedrzejczak, G.W. Basak. (2016). Fecal microbiota transplantation inhibits multidrug-resistant gut pathogens: preliminary report performed in an immunocompromised host. *Archivum immunologiae et therapiae experimentalis*. 64: 255-258.
- [57] B. Rossi, M.L. Gasperini, V. Leflon-Guibout, A. Gioanni, V. de Lastours, G. Rossi, S. Dokmak, M. Ronot, O. Roux, M.-H. Nicolas-Chanoine. (2018). Hypervirulent *Klebsiella pneumoniae* in cryptogenic liver abscesses, Paris, France. *Emerging infectious diseases*. 24(2): 221.
- [58] K.M. Ng, J.A. Ferreyra, S.K. Higginbottom, J.B. Lynch, P.C. Kashyap, S. Gopinath, N. Naidu, B. Choudhury, B.C. Weimer, D.M. Monack. (2013). Microbiota-liberated host sugars facilitate post-antibiotic expansion of enteric pathogens. *Nature*. 502(7469): 96-99.
- [59] W.-N. Chang, C.-R. Huang, C.-H. Lu, C.-C. Chien. (2012). Adult *Klebsiella pneumoniae* meningitis in Taiwan: an overview. *Acta Neurol Taiwan*. 21(2): 87-96.
- [60] N.-C. Cheng, H.-C. Tai, S.-C. Chang, C.-H. Chang, H.-S. Lai. (2015). Necrotizing fasciitis in patients with diabetes mellitus: clinical characteristics and risk factors for mortality. *BMC infectious diseases*. 15: 1-9.
- [61] M.C. Hwang, L. Ridley, J.D. Reveille. (2021). Ankylosing spondylitis risk factors: a systematic literature review. *Clinical rheumatology*. 40: 3079-3093.
- [62] B. Tornimbene, S. Eremin, M. Escher, J. Griskeviciene, S. Manglani, C.L. Pessoa-Silva. (2018). WHO global antimicrobial resistance surveillance system early implementation 2016–17. *The Lancet infectious diseases*. 18(3): 241-242.
- [63] D.V. Zurawski, M.K. McLendon. (2020). Monoclonal antibodies as an antibacterial approach against bacterial pathogens. *Antibiotics*. 9(4): 155.
- [64] F. Micoli, P. Costantino, R. Adamo. (2018). Potential targets for next generation antimicrobial glycoconjugate vaccines. *FEMS microbiology reviews*. 42(3): 388-423.
- [65] S. Cryz Jr, P. Mortimer, A. Cross, E. Fürer, R. Germanier. (1986). Safety and immunogenicity of a polyvalent *Klebsiella* capsular polysaccharide vaccine in humans. *Vaccine*. 4(1): 15-20.
- [66] A. Clements, A.W. Jenney, J.L. Farn, L.E. Brown, G. Deliyannis, E.L. Hartland, M.J. Pearse, M.B. Maloney, S.L. Wesselingh, O.L. Wijburg. (2008). Targeting subcapsular antigens for prevention of *Klebsiella pneumoniae* infections. *Vaccine*. 26(44): 5649-5653.
- [67] N. Hegerle, M. Choi, J. Sinclair, M.N. Amin, M. Ollivault-Shiflett, B. Curtis, R.S. Laufer, S. Shridhar, J. Brammer, F.R. Toapanta. (2018). Development of a broad spectrum glycoconjugate vaccine to prevent wound and disseminated infections with *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. *PloS one*. 13(9): e0203143.
- [68] Z. Zhang, R. Qin, Y. Lu, J. Shen, S. Zhang, C. Wang, Y. Yang, F. Hu, P. He. (2020). Capsular polysaccharide and lipopolysaccharide O type analysis of *Klebsiella pneumoniae* isolates by genotype in China. *Epidemiology & Infection*. 148: e191.
- [69] T.S. Cohen, M. Pelletier, L. Cheng, M.E. Pennini, J. Bonnell, R. Cvitkovic, C.-s. Chang, X. Xiao, E. Cameroni, D. Corti. (2017). Anti-LPS antibodies protect against *Klebsiella pneumoniae* by empowering neutrophil-mediated clearance without neutralizing TLR4. *JCI insight*. 2(9).
- [70] M.E. Pennini, A. De Marco, M. Pelletier, J. Bonnell, R. Cvitkovic, M. Beltramello, E. Cameroni, S. Bianchi, F. Zatta, W. Zhao. (2017). Immune stealth-driven O2 serotype prevalence and potential for therapeutic antibodies against multidrug resistant *Klebsiella pneumoniae*. *Nature communications*. 8(1): 1991.
- [71] L.M. Guachalla, K. Stojkovic, K. Hartl, M. Kaszowska, Y. Kumar, B. Wahl, T. Paprotka, E. Nagy, J. Lukasiewicz, G. Nagy. (2017). Discovery of monoclonal antibodies cross-reactive to novel subserotypes of *K. pneumoniae* O3. *Scientific reports*. 7(1): 6635.
- [72] Q. Wang, C.-s. Chang, M. Pennini, M. Pelletier, S. Rajan, J. Zha, Y. Chen, R. Cvitkovic, A. Sadowska, J. Heidbrink Thompson. (2016). Target-agnostic identification of functional monoclonal antibodies against *Klebsiella pneumoniae* multimeric MrkA fimbrial subunit. *The Journal of infectious diseases*. 213(11): 1800-1808.
- [73] D. Witkowska, M. Mieszala, A. Gamian, M. Staniszewska, A. Czarny, A. Przondo-Mordarska, M. Jaquinod, E. Forest. (2005). Major structural

- proteins of type 1 and type 3 *Klebsiella* fimbriae are effective protein carriers and immunogens in conjugates as revealed from their immunochemical characterization. *FEMS Immunology & Medical Microbiology*. 45(2): 221-230.
- [74] F.N. Zargarani, A. Akya, S. Rezaeian, K. Ghadiri, R.C. Lorestani, H. Madanchi, S. Safaei, M. Rostamian. (2021). B cell epitopes of four fimbriae antigens of *Klebsiella pneumoniae*: a comprehensive in silico study for vaccine development. *International journal of peptide research and therapeutics*. 27: 875-886.
- [75] H.A. Dar, T. Zaheer, M. Shehroz, N. Ullah, K. Naz, S.A. Muhammad, T. Zhang, A. Ali. (2019). Immunoinformatics-aided design and evaluation of a potential multi-epitope vaccine against *Klebsiella pneumoniae*. *Vaccines*. 7(3): 88.
- [76] M.X. Rodrigues, Y. Yang, E.B. de Souza Meira Jr, J. do Carmo Silva, R.C. Bicalho. (2020). Development and evaluation of a new recombinant protein vaccine (YidR) against *Klebsiella pneumoniae* infection. *Vaccine*. 38(29): 4640-4648.