The increasing use of colistin in the clinic has led to the emergence and spread of colistin resistance. According to the literature, antibiotic resistance can have a metabolic cost, resulting in poor adaptation and survival, i.e. reduced bacterial fitness. The aim of this study was to investigate molecular mechanisms underlying resistance to colistin and their effect on the bacterial fitness of carbapenem-resistant (carba-R) strains of K. pneumoniae isolated from the patients of Moscow hospitals in 2012–2017. Of 159 analyzed carba-R isolates, 71 (45%) were resistant to colistin (minimum inhibitory concentration over 2 mg/L). By conducting Sanger sequencing, we were able to identify the mechanisms underlying colistin resistance in 26 (37%) isolates. Growth curves were constructed by measuring optical density at 600 nm wavelength for 15 hours. The competitive growth of colistin-resistant (col-R) K. pneumoniae isolates was assessed relative to the colistin-susceptible (col-S) isolate. Col-R and col-S cultures harvested in the exponential phase were combined at the ratio of 1:1, incubated in the Luria-Bertani medium and plated onto Luria-Bertani agar plates with 10 mg/L colistin and without it. The competition index was calculated as the ratio of grown col-R and col-S colonies.

Resistance to colistin did not fit the growth kinetics of K. pneumoniae, but did reduce the competitive ability of the bacteria as compared to the col-S isolates. However, some col-R isolates were more competitive than the col-S strains of the same sequence type. Further research is needed to elucidate the effects of colistin resistance on bacterial fitness.

Keywords: Klebsiella pneumoniae, bacterial fitness, colistin resistance, mgrB, sequence type

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Compliance with ethical standards: the study was carried out following the safety guidelines on the manipulations with pathogens of hazard groups III and IV.

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УСТОЙЧИВОСТЬ КАРБАПЕНЕМРЕЗИСТЕНТНЫХ ШТАММОВ KLEBSIELLA PNEUMONIAE К КОЛИСТИНУ: МОЛЕКУЛЯРНЫЕ МЕХАНИЗМЫ И БАКТЕРИАЛЬНЫЙ ФИТНЕС

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В последние годы широкое использование колистина в лечении инфекционных заболеваний привело к появлению и распространению колистинрезистентности. По данным литературы, формирование устойчивости может приводить к затратам внутренних биологических ресурсов и снижению уровня жизнедеятельности (бактериального фитнеса). Целью исследования было изучить молекулярные механизмы резистентности к колистину и их влияние на бактериальный фитнес карбапенемрезистентных (карба-Р) штаммов K. pneumoniae, выделенных у пациентов в г. Москве в 2012–2017 гг. Из 159 карба-Р-изолятов 71 изолят (45%) обладал резистентностью к колистину (минимум подавляющая концентрация больше 2 мг/л); секвенирование по методу Сенгера позволило обнаружить механизмы устойчивости у 26 (37%) изолятов. Кривые роста были построены путем измерения оптической плотности при длине волны 600 нм в течение 15 ч. Конкурентный рост карбапенемрезистентных (карба-Р) изолятов K. pneumoniae оценивали относительно колистинчувствительного (кол-Ч) изолата. Кол-Р- и кол-Ч-изолят в экспериментальной фазе роста смешивали в пропорции 1:1, инкубировали в среде Лурций-Бертани и затем наносили на агар Лурций-Бертани, содержащий 10 мг/л колистина, и без него. Интеграл роста рассчитывали как отношение высоких кол-Р- и кол-Ч-колоний. Резистентность к колистину не влияла на кинетику роста K. pneumoniae, но снижала конкурентоспособность относительно кол-Ч-изолата. Тем не менее были обнаружены кол-Ч-изолаты с высоким уровнем конкурентоспособности по сравнению с кол-Ч-изолатами такого же сиквенс-типа. Таким образом, необходимы дальнейшие исследования влияния резистентности на карбапенемрезистентных штаммов K. pneumoniae.

Ключевые слова: Klebsiella pneumoniae, бактериальный фитнес, колистинрезистентность, mgrB, сиквенс-тип

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Соблюдение этических стандартов: исследование проведено в соответствии с существующими нормативами исследования в области биомедицины.

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Klebsiella pneumoniae is a common cause of infections that require medical attention [1]. The emergence and global spread of high-risk multidrug-resistant (MDR) K. pneumoniae sequence types is a worrying trend [2, 3]. Carbapenem-resistant (carba-R) K. pneumoniae are an especially serious concern because resistance to carbapenems often co-occurs with resistance to other antimicrobial drugs, which dramatically narrows the range of therapeutic options for K. pneumoniae infection. As revealed by multilocus sequence typing (MLST), the majority of carba-R isolates are represented by a small group of sequence types that universally dominate nosocomial populations [4, 5]. At present, the following sequence types are classed as globally disseminated: ST14/15, ST17/20, ST43, ST147, ST258, ST395 [5, 6], and ST307, which only recently has been recognized as clinically relevant [7].

The polycationic antibiotic colistin, also known as polymyxin E, retains activity against carba-R gram-negative microorganisms. However, its wide use in the clinic in the backdrop of rampant resistance to carbapenems has driven the emergence of colistin resistance [4, 8], which can significantly reduce the efficacy of antimicrobial therapy and result in increased mortality in patients infected with colistin-resistant (col-R) K. pneumoniae [9].

Resistance to colistin arises from the structural modification of bacterial lipopolysaccharides (LPS) that prevents the antibiotic from binding to the bacterial cell wall [10]. This modification is associated with alterations in the two-component PhoPQ/ phosphoreceptor Mediator system and its regulator MgrB caused by mutations in the mcrB gene, as well as with plasmid-borne mcr genes [8, 10].

Naturally, being able to thrive in the presence of an antibiotic, resistant strains have an advantage over susceptible strains; however, there is a biological cost to pay: resistant strains grow at a slower rate and are less competitive in the absence of selective pressure exerted by antibiotics, i.e. have lower bacterial fitness [11, 12] than their susceptible counterparts [13, 14]. Considering that resistance to colistin is linked to LPS modifications, which is the key component of the bacterial cell wall, colistin resistance might be associated with reduced bacterial fitness.

The aim of this study was to characterize the genotype of carba-R K. pneumoniae isolated from the inpatients of Surgery and Intensive Care Units of Moscow hospitals, describe molecular mechanisms underlying resistance to colistin and investigate the effect of colistin resistance on the growth kinetics and the competitive ability of this bacterial population.

METHODS

We analyzed 159 carba-R K. pneumoniae isolates (the minimum inhibitory concentrations (MIC) of meropenem and imipenem were > 8 mg/L and > 4 mg/L, respectively, as defined by EUCAST criteria) [15] with and without resistance to colistin that had been collected from the patients of Surgery and Intensive Care Units of Moscow hospitals in 2012 through 2017. Only one K. pneumoniae isolate per patient was included in the collection. Biological samples had been taken from normally sterile sites (blood, urine, cerebrospinal fluid), the respiratory tract (aspirates, sputum), the oropharyngeal cavity, stomas, wounds, and the anus.

MIC of meropenem, imipenem and tigecycline were determined by performing Etests (BioMerieux; France) on Mueller-Hinton agar plates (Bio Rad; France). Susceptibility to aminoglycosides (gentamicin, netilmicin, amikacin), ciprofloxacin, fosfomycin, ceftazidime, cefepime, and ceftazidime was evaluated using an automated VITEK 2 Compact instrument for bacterial identification and susceptibility testing (BioMerieux; France). Colistin MIC were measured by broth microdilution as recommended in the National Standards of the Russian Federation (GOST R ISO 20776-1-2010); colistin used in the experiments was a powder formulation. The ATCC 25922 strain of Escherichia coli served as a control. According to EUCAST, colistin susceptibility and resistance breakpoints for K. pneumoniae are ≤ 2 mg/L and > 2 mg/L, respectively [15]. Detection and/or Sanger sequencing of the mcr-1, mcrB, pmrA, pmrB, phoP, and phoQ genes and the analysis of amino acid sequences of the PmrA, PmrB, PhoP, and PhoQ proteins were carried out following the previously described protocols [16]. An mcr-1-positive strain of E. coli provided by the Research Institute of Antimicrobial Chemotherapy (Smolensk State Medical University, Russia) was used as a control for mcr-1 detection. K. pneumoniae strains were genotyped by means of multilocus sequence typing (MLST) [17]. Insertions were identified using the ISfinder database [18].

Bacterial fitness was studied in a subset of colistin-susceptible (col-S) and colistin-resistant (col-R) K. pneumoniae isolates with disrupted and wild-type mcrB. The cultures were grown on Luria–Bertani agar (HiMedia Laboratories Pvt. Limited; India) for 24 h. Protocols for assessing bacterial fitness were previously described in [14]. One bacterial colony was suspended in LB and incubated in an orbital shaker incubator ES-20 (BioSan; Latvia) at 37 °C for 3 h at constant stirring at 250 rpm. Bacterial concentrations were measured using a Novocyt flow cytometer (ACEA Biosciences; USA).

To construct and compare growth curves for col-R and col-S strains, the obtained suspension was diluted to a concentration of 5 × 10^6 bacterial cells per 1 ml. The resulting suspension (250 µl) was plated on flat-bottom 96-well plates containing 0, 1, 2, 4, 8, 16, or 64 mg/L colistin, and growth was measured in a microplate reader (Tecan; Austria) at 37 °C for 15 h. Growth was recorded in Magellan 6.6 software (Tecan; Austria). The area under the growth curve (AUGC) was an indicator of bacterial growth; it was calculated using 6.6 software (Tecan; Austria). The area under the growth curve (AUGC) was an indicator of bacterial growth; it was calculated using the 6.6 software (Tecan; Austria).

To evaluate the competitive ability of col-R and col-S K. pneumoniae isolates, the competition index (CI) was calculated. Briefly, the suspensions of col-R and col-S isolates were mixed in equal concentrations, and optical density at OD_{600} was monitored in time (Fig. 1). AUGC was expressed as OD_{600} per hour.

!![Image](Image 345x131 to 527x285)

**Fig. 1.** Typical growth curves for K. pneumoniae isolates in the colistin-free culture medium. The shaded region on the graph represents an area under the growth curve (AUGC). The growth curve for col-S isolates is shown in red; the growth curve for col-R isolates is shown in green.
adjusted to 1.5 × 10^9 cells per 1 ml and combined at a 1 : 1 ratio (1.5 × 10^9 CFU per 1 ml for each strain). The mixture of col-R and col-S isolates and suspensions of unmixed col-S and col-R strains were grown in LB at 37 °C at 180 rpm for 16–18 h. Upon incubation, the suspensions were diluted 10^5-fold and plated on Petri dishes containing LB agar supplemented with 10 mg/L colistin or LB agar without colistin; plating was performed using an easySpiral automated spiral plater (Interscience; France). The cells were incubated at 37 °C for 16–18 h. CFU were counted using an automated Scan 500 colony counter (Interscience; France). CI was calculated as a ratio of col-R CFU in the LB dish with colistin to col-S CFU in the dish without colistin. CI < 1 was interpreted as reduced competitive ability of the resistant isolate, as compared to the susceptible isolate. The experiments were conducted in 3 replicates.

Statistical analysis was carried out in IBM SPSS Statistics 20.0 (IBM SPSS Inc; USA). Below, AUGC values and the number of colonies are presented as a median (P_{25}; P_{75}). CI is presented as a mean and a standard deviation. Differences in CI were evaluated using the Kruskal–Wallis test; pairwise comparisons were done using the Mann–Whitney U test. The differences were considered significant at р < 0.05.

RESULTS

Characterization of carba-R isolates of K. pneumoniae

All 159 carba-R K. pneumoniae isolates had an MDR-phenotype, i.e. were resistant to at least 3 classes of antimicrobial drugs. All studied strains were resistant to the third and fourth-generation cephalosporins and were highly resistant to ciprofloxacin (93%), fosfomycin (90%), netilmicin (82%), gentamicin (84%), amikacin (50%), and colistin (45%). The majority of carba-R K. pneumoniae isolates were susceptible to tigecycline; only 7% were resistant to this drug.

As revealed by MLST, the studied carba-R isolates were represented by 18 sequence types, of which only 5 dominated the collection, occurring in 86% of cases. Those included ST307 (n = 46, 29%), ST395 (n = 40, 25%), ST377 (n = 17, 10%), ST48 (n = 17, 10%), and ST23 (n = 16, 10%).

Mechanisms of colistin resistance

Resistance to colistin was observed in 71 (45%) carba-R K. pneumoniae isolates; for those isolates, colistin MIC varied from 4 to 1024 mg/L or was even higher. Investigation of

| Isolate ID | ST | Colistin MIC, mg/L | mgrB status a |
|------------|----|-------------------|---------------|
| 69–77      | 23 | 128               | ISF1, family IS-1 (+127/+128) |
| 56-1790    | 307| 64                | ISF1, family IS-1 (+36/+37) |
| 68-66-1    | 48 | 16                | ISKpn14, family IS-1 (+141/+142) |
| 58-2876    | 48 | 128               | ISKpn14, family IS-1 (+141/+142) |
| 58-3431    | 48 | 128               | ISKpn14, family IS-1 (+141/+142) |
| 58-2966    | 48 | 512               | ISKpn14, family IS-1 (+141/+142) |
| 56-1678    | 48 | ≥ 1024            | ISKpn14, family IS-1 (+141/+142) |
| 56-1053    | 48 | ≥ 1024            | ISKpn14, family IS-1 (+141/+142) |
| 71-1375    | 307| 512               | ISKpn14, family IS-1 (+141/+142) |
| 76-2089    | 377| 512               | ISKpn14, family IS-1 (+141/+142) |
| 64-574     | 307| 256               | ISKpn26, family IS-5 (+74/+75) |
| 4469       | 395| 128               | ISKpn26, family IS-5 (+74/+75) |
| 52-1659    | 307| 256               | ISKpn26, family IS-5 (+74/+75) |
| 58-1363    | 307| 16                | MITEKpn1, family IS-5 (+74/+75) |
| 55-148     | 307| 64                | MITEKpn1, family IS-5 (+74/+75) |
| 58-566     | 307| 128               | MITEKpn1, family IS-5 (+74/+75) |
| 58-1286    | 307| 128               | MITEKpn1, family IS-5 (+74/+75) |
| 56-613     | 307| 512               | MITEKpn1, family IS-5 (+74/+75) |
| 48-1594    | 307| ≥ 1024            | MITEKpn1, family IS-5 (+74/+75) |
| 78-296     | 37 | 16                | Δ mgrB locus |
| 37262      | 147| 64                | Δ mgrB locus |
| 29423      | 70 | 128               | Δ mgrB locus |
| 36-2246    | 395| 128               | Δ mgrB locus |
| 48-1574    | 307| 128               | Wild type b |
| 48-2246    | 395| ≥ 1024            | Wild type a |
| 56-410     | 48 | 128               | Wild type c |

Note: ST — sequence type; MIC — minimum inhibitory concentration; a — the position of the insertion sequence is specified in brackets; b — PmrB alteration (T157P); c — PmrA (A141T) and PmrB (L213M, G256R) alterations; d — PmrB alteration (deletion at 27–30 (CL3S)).
molecular mechanisms underlying resistance to colistin was started with a search for the plasmid-borne gene mcr-1, which, according to the literature, is the most common cause of resistance [19]. We found that none of 71 col-R K. pneumoniae isolates carried the mcr-1 gene.

Then, we went on to analyze the sequence integrity of the mcrB gene whose disruption might be associated with colistin resistance. Mutations in the mcrB gene were observed in 23 (32%) col-R isolates (Table 1). Deletion of the entire mcrB locus was detected in 4 (17%) isolates. In 13 (56%) isolates, there were insertions of 4 different types (IS1A, IS1R, ISKpn14, and ISKpn26), which occurred at different positions and represented the IS-1 and IS-5 families (Table 1). In 6 (26%) col-R isolates, the mcrB gene harbored a new mobile element (MITEKpn1) described in our previous publication [16].

Summing up, the mcrB gene was wild-type in only 48 of 71 (68%) col-R K. pneumoniae isolates. Therefore, we had to continue looking for other mechanisms underlying colistin resistance. We analyzed the amino acid sequences of the proteins PmrA, PmrB, PhoP, and PhoQ in all 48 isolates. These proteins participate in LPS modification. Alterations in their sequences can cause resistance to colistin [10]. Significant alterations in PmrA and/or PmrB sequences were detected in 3 isolates from 3 different sequence types (ST307, ST395, ST48), with colistin MIC ranging from 128 to 1024 mg/L or being even higher (Table 1).

**Effects of colistin resistance on bacterial fitness**

In the absence of colistin, the growth kinetics of col-R and col-S K. pneumoniae did not differ significantly. Median AUGC values were 4.2 (3.9; 4.3) and 4.05 (3.9; 4.6) OD600 per 1 h, respectively (p = 0.842; Table 2). Addition of 1 mg/L colistin to the culture of col-S isolates caused AUGC to drop abruptly to 1.9 (0.95; 4.13) OD600/1h per 1 h (p = 0.065), whereas higher concentrations of colistin completely inhibited the growth of col-R K. pneumoniae isolates.

**Table 2. Effects of colistin resistance on the bacterial fitness (growth kinetics and competition index) of carba-R K. pneumoniae isolates**

| Isolates                  | Colistin MIC, mg/L; Me (P25; P75) | AUC (OD600 per 1 H), Me (P25; P75) | CI, mean (SD) |
|--------------------------|------------------------------------|-----------------------------------|---------------|
|                          |                                    | Colistin concentration, mg/L      |                |
|                          |                                    | 0      | 1      | 4      | 16     | 64     |
| Col-S (n = 6)            | < 1 (< 1; < 1)                     | 4.05 (3.9; 4.6)                   | 1.9 (0.95; 4.13) | 0 (0; 4.03) | 0 (0; 0) | 0 (0; 0) | n/a |
| Col-R (n = 32)           | 256 (126; 512)                     | 4.2 (3.9; 4.3)                    | 4.1 (3.7; 4.2) | 3.9 (3.2; 4.15) | 3.3 (2.2; 3.45) | 0.9 (0; 3) | 0.15 (0.21) |
| Of them:                 |                                    |                                    |                |               |                |            |              |
| mcrB disrupted (n = 15)  | 256 (126; 512)                     | 4.1 (3.9; 4.2)                    | 4 (3.9; 4.2)   | 3.9 (3.1; 4.1) | 3.4 (0.9; 3.7) | 1.1 (0; 3.3) | 0.1 (0.1) |
| mcrB, wild type (n = 17) | 256 (96; 512)                      | 4.3 (3.85; 4.4)                   | 4.2 (3.53; 4.25) | 3.8 (3.18; 4.25) | 3.25 (2.75; 3.43) | 0.9 (0; 3) | 0.19 (0.26) |

Note: MIC — minimum inhibitory concentration; AUGC — area under growth curve; Me — median; P25 and P75 — the 25th and 75th percentiles; CI — competition index; SD — standard deviation; col-S — colistin-susceptible isolates; col-R — colistin-resistant isolates; n/a — not applicable; * — p = 0.842 for comparison with col-S AUGC; ** — p = 0.19 for comparison with col-R AUGC at 0 mg/L colistin; *** — p = 0.016 for comparison with col-R AUGC at 0 mg/L colistin; **** — p < 0.001 for comparison with col-R AUGC at 0 mg/L colistin; ***** — p = 0.05 for comparison with col-R AUGC at 0 mg/L colistin; ****** — p = 0.05 for comparison with col-R AUGC at 0 mg/L colistin; ******* — p = 0.001 for comparison with col-R AUGC at 0 mg/L colistin; ******** — p = 0.016 for comparison with col-R AUGC at 0 mg/L colistin; ********* — p = 0.05 for comparison with col-R AUGC at 0 mg/L colistin; ********** — p = 0.283 for comparison with CI of the isolates with disrupted mcrB.
Table 3. The competition index of col-R and col-S isolates of carba-R K. pneumoniae representing the same sequence types

| Col-R isolates | Mechanism of colistin resistance | CFU count (SD) | CI (SD) |
|----------------|----------------------------------|----------------|--------|
|                |                                  | Col-R (LB agar + colistin, 10 mg/L) | Col-S + col-R (LB agar) |
|                |                                  | 80             | 141    | 1.3   |
| ST23           | 37261                            | 39             | 168    | 0.3   |
| 69–77          | Mutant mgrB                      | 25             | 112    | 0.29  |
| 37243          | Unknown                          | 5              | 114    | 0.05  |
| 37224          | Unknown                          | 37 (32)        | 134 (26) | 0.48 (0.56) |
| Total ST23:    |                                  | 88             | 135    | 1.87  |
| ST395          | 52–1659                          | 3              | 138    | 0.02  |
| 78–1127        | Unknown                          | 38             | 282    | 0.16  |
| 59–397         | Unknown                          | 79             | 232    | 0.52  |
| 4469           | Mutant mgrB                      | 55 (53)        | 142 (8) | 1.1 (1.24) |
| Total ST395:   |                                  | 90             | 335    | 0.37  |
| ST377          | 76–1648                          | 38             | 282    | 0.16  |
| 76–2053        | Unknown                          | 38             | 282    | 0.16  |
| 76–2089        | Mutant mgrB                      | 79             | 232    | 0.52  |
| Total ST377:   |                                  | 69 (27)        | 263 (52) | 0.35 (0.18) |
| ST307          | 64–574                           | 33             | 287    | 0.13  |
| 56–566         | Mutant mgrB                      | 68             | 210    | 0.48  |
| 71–1375        | Mutant mgrB                      | 63             | 196    | 0.47  |
| Total ST307:   |                                  | 55 (19)        | 231 (49) | 0.36 (0.2) |
| ST147          | 37–262                           | 3              | 201    | 0.02  |
| ST48           | 58–2966                          | 8              | 152    | 0.06  |

Note: CI — competition index; SD — standard deviation.

DISCUSSION

The majority of carba-R isolates of K. pneumoniae in our collection were represented by 5 major sequence types; of them, types ST307 and ST395 made up 54% of the entire sample. A while ago, ST307 was not recognized as a dominant sequence type in Russia [20, 21], but at present, it is becoming one of the leading high-risk international sequence types [7], which is consistent with our findings.

Of all carba-R isolates analyzed in this paper, 45% were resistant to colistin. The multicenter study MARAPHON [2, 3] showed that the prevalence of col-R isolates in the large sample of nosocomial K. pneumoniae isolates was generally low, in spite of an increase from 4.5% in 2012 to 7.9% in 2014. Our data might reflect the global trend of growing antibiotic resistance, including resistance to colistin. According to a 15-year retrospective study conducted at a large hospital in Athens, the proportion of col-R K. pneumoniae isolates from blood cultures surged from 0% in 2002 to 26.9% in 2016 [22]. On the other hand, the high prevalence of col-R strains in our collection might be explained by the fact that our sample was dominated by nosocomial strains recovered from intensive care units, where, as reported by Fereezakis et al. [23], the proportion of col-R K. pneumoniae isolates from blood cultures surged from 0% in 2002 to 26.9% in 2016 [22]. On the other hand, the high prevalence of col-R strains in our collection might be explained by the fact that our sample was dominated by nosocomial strains recovered from intensive care units, where, as reported by Fereezakis et al. [23], the proportion of col-R K. pneumoniae isolates from blood cultures surged from 0% in 2002 to 26.9% in 2016 [22].

Colistin resistance did not affect the kinetics of bacterial growth in the absence of this antibiotic and did not depend on the mgrB status.

The effects of colistin resistance on bacterial fitness were additionally investigated in carba-R/col-S and carba-R/col-R pairs of K. pneumoniae of the same sequence types. We selected isolates of 5 most common ST (ST23, ST48, ST307, ST377 and ST395) and one rare ST (ST147); at least one isolate in this subset was colistin-sensitive (Table 3). The competitive ability of all col-R isolates belonging to types ST48, ST147, ST307 and ST377 was diminished compared to the col-S isolates of the same sequence types (CI < 1). However, the situation was different for the isolates represented by sequence types ST23 and ST395. One col-R isolate of type ST23 (CI = 1.3) and 2 col-R isolates of type ST395 (CI = 1.87 and CI = 2.5, respectively) were more fit than col-S isolates (Table 3).
undermines the dynamics of bacterial growth [13, 25], which might explain the relatively high prevalence of enterobacteria possessing chromosomal resistance to colistin in comparison with col-R A. baumannii and P. aeruginosa.

At the same time, the majority of col-R isolates were less competitive than col-S isolates of K. pneumoniae; this is also typically seen in other bacteria, such as A. baumannii [13] and P. aeruginosa [25]. There are reports of reduced bacterial fitness in col-R K. pneumoniae that carry the mcr-1 gene [26].

Another interesting finding came from the experiments comparing bacterial fitness between col-R and col-S K. pneumoniae isolates of one sequence type, i.e. bacteria with very similar genotypes but very different susceptibility to colistin. Six different sequence types were analyzed. The majority of col-R isolates had low CI. At the same time, 2 col-R isolates of type ST395 and 1 col-R isolate of type ST23 were more competitive than col-S isolates of the same sequence type. This finding can be explained by the presence of compensatory mutations in the bacterial genome, as was the case with resistance to fluoroquinolones and colistin in Escherichia coli [27] and A. baumannii [28]. Unlike mutations that confer resistance, compensatory mutations boost bacterial fitness and thus promote resistance even in the absence of selective pressure exerted by an antibiotic [27, 28].

We conclude that resistance to colistin is common in the population of carba-R K. pneumoniae isolated from Moscow patients. This alarming trend requires close monitoring.

CONCLUSION

Our collection of carba-R K. pneumoniae isolates was dominated by sequence types ST307 and ST395; disruption of the mcrB gene by a variety of insertion sequences was the leading mechanism of colistin resistance.

Resistance to colistin did not affect the kinetics of bacterial growth in col-R K. pneumoniae in the absence of the antibiotic and did not depend on the status of the mcrB gene; the overwhelming majority of col-R K. pneumoniae isolates were less competitive than col-S strains; but within one sequence-type, there could be col-R isolates with increased competitive ability. Further research into bacterial fitness might elucidate the causes underlying the spread of colistin resistance among enterobacteria.

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