

Distribution of multi – drug resistant bacteria among hospital effluent

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Abstract:

The present study was carried out to estimate the spread of multi – drug resistant (MDR) bacterial from hospital effluent to the municipal sewage system. The total viable count of bacterial populations in hospital effluents was ranging from 10 colony forming unit(CFU)/ml for *Serratia marcescens* to 500 CFU/ml for *Echirishia. coli* in three hospitals; The percent of MDR bacteria population in all these hospitals ranged from (5%) *Serratia marcescens* to (97%) *Echirishia. coli*. Furthermore, the MDR bacteria carried simultaneous resistance for most commonly used antibiotics and obviously the spread of such MDR bacteria to the community is a matter of grave concern.

الخلاصة:

الدراسة الحالية أجريت لتقييم مدى إنتشار الجراثيم ذات المقاومة المتعددة للمضادات الحيوية في المياه الثقيلة للمستشفيات التي تصب في جهاز الصرف الصحي بدون معالجة. إن الحساب الحي للمستعمرات الجرثومية في المياه الثقيلة للمستشفيات الثلاث التي درست كان يتراوح بين 10 وحدات مكونة للمستعمرة لكل 1 مل بالنسبة لجرثومة (*Serratia marcescens*) إلى 500 وحدة مكونة للمستعمرة بالنسبة لجرثومة الإشيريشيا القولونية، بينما كانت نسبة الجراثيم متعددة المقاومة للأدوية في نفس المستشفيات تتراوح بين 5% من جرثومة (*Serratia marcescens*)، إلى 97% من جرثومة الإشيريشيا القولونية. إضافة إلى ذلك فإن الجراثيم متعددة المقاومة للمضادات حملت مقاومة متماثلة لمعظم المضادات شائعة الاستعمال، لذا فإن إنتشار الجراثيم متعددة المقاومة للمضادات الحيوية إلى المجتمع تبقى محل اهتمام كبير.

Introduction:

Bacterial resistance to antimicrobial agents has become a significant problem worldwide ^(1,2). The problem is the result of antibiotic resistant genes transferring among bacterial species, carried by plasmids, transposons or integrons ^(3,4). Goldmann⁽⁵⁾ showed that the multi-drug resistance (MDR) was through extra chromosomal autonomous genetic elements; He rightly referred to MDR as infectious drug resistance, since it could be transferred *en block* to sensitive bacteria during cell to cell contact and subsequently these plasmids have been referred to as resistance plasmids (R- plasmids). The antimicrobial selective pressure through indiscriminate use of antibiotics has played a significant role in enriching the MDR – R⁺ strain in to the hospital practice⁽⁶⁾. On the other hand, hospitalized patients become heavily colonized with R⁺ strains mainly in their gut^(7,8), so infection with MDR bacteria may be transferred to other patients in the hospital resulting in cross – infections which are referred to as hospital – borne infections. The transfer of R – plasmid has been shown to occur in extra intestinal environments like sewage system of hospitals that containing resistant strains^(9,10), thus presenting a potential risk to public health. The present study was carried out to estimate the magnitude of MDR bacteria in hospital effluent of Najaf city.

Materials and Methods:

Twelve effluent water specimens were collected from the outer most chambers of Al-sadeer Teaching Hospital, Al-Hakim, and Maternity and Children Hospitals at 12 pm before the drainage flow to the municipal sewage. Viable counts were done for all specimens by spreading 100µl of 10^{-1} to 10^{-6} dilutions of sewage prepared in a sterile saline over different culture media plates including nutrient agar, McConkey agar, SS agar and blood agar plates. The plates were incubated overnight at 37°C, and those showed 50 to 200 colonies were recorded and identified by standard cultural and biochemical methods^(11,12). For the estimation of the MDR bacteria a minimum of 50 isolates of the same species were selected and subjected to drug susceptibility test using Bauer and Kirby disk diffusion method⁽¹³⁾. For *Serratia marcescens* only 10 isolates have been selected for drug susceptibility.

Result and Discussion.

The total viable bacterial counts for hospital effluent are shown in Table (1), which reveals that the total viable counts of bacterial populations were significantly higher for Al – Sadeer hospital effluent samples than for the other two hospital.

Table* (1): The viable count of bacterial populations in the effluent specimens of three hospitals in Najaf.

Viable count CFU / ml	Source					
	Al- Sadeer H. (mean)	S.D	Al-Hakim H. (mean)	S.D	Maternity and Children H. (mean)	S.D
<i>E. coli</i>	500	10	450	5	400	2
<i>E. aerogenes</i>	300	5	200	1	200	1
<i>K. pneumonia</i>	80	2	90	2	85	0
<i>M. catarrhalis</i>	105	5	80	2	60	1
<i>P. aeruginosa</i>	300	5	200	1	200	1
<i>S. typhimurium</i>	450	5	250	0	105	5
<i>S. marcescens</i>	20	1	10	1	15	3

*Data are mean of three replicates with Standard Deviation (S.D).

Another observation was the relatively higher total bacterial count of *E. coli* and *S. typhimurium* in contrast to other species of bacteria as shown in Table-1. The percentage of MDR bacteria was significantly high in all hospitals effluent specimens , and *E. coli* showed higher rate(97%) of MDR in comparison with other species of bacteria. This could be due to the greatest usage of disinfectants and antibiotics in hospital practice^(14,15), and the possibility of conjugation happens more between strains of *E. coli*⁽¹⁶⁾.

The percentage of MDR bacteria for hospitals specimens ranged widely from 5% in *S. marscecens* to 97% in *E. coli* (Table 2). A very high percentage of MDR in most hospitals could be due to excessive use of antibiotics resulting in increased selective pressure and the resistance genes could spread, under selective antibiotic pressure, between bacterial species and in turn increase the prevalence of MDR bacteria. The single most important factor driving the emergence of resistance is the selective pressure

of antimicrobial agents.⁽¹⁷⁾ The global emergence of antimicrobial resistance has become a pre – eliminate in medicine and public health. Population genetic models suggest that resistance emerges rapidly under the selective pressure of antibiotics but decays slowly once that pressure is removed⁽¹⁸⁾.

Table (2): The percentage of MDR bacteria in different hospital effluent specimens.

The percentage of resistant isolates	Source		
	Al-Sadeer H.	Al-Hakim H.	Maternity and Children H.
<i>E. coli</i>	96	97	96
<i>E. aerugenens</i>	94	92	90
<i>K. pneumoniae</i>	90	85	88
<i>M. catarrhalis</i>	60	75	88
<i>P. aeruginosa</i>	94	92	90
<i>S. typhimurium</i>	96	90	94
<i>S. marcescens</i>	8	5	6

The pattern of MDR was shown in Table 3, Which is almost the same for diverse species (*E. coli* , *K. pneumoniae*, *M. cattaralis* , *S. marsceens* , *S. typhimurium* , and *E. aerugenens*) isolated from the effluent samples and strongly suggests prevalence of similar R – plasmids. Also, the MDR pattern seen in the bacteria isolated from hospital effluent samples included most of the antibiotics in common use. The worst fear apprehended is the transfer of such resistance to bacterial pathogens causing infection in the community, therefore most of the presently available antibiotics will be futile against the infectious organism. The origin of such MDR bacterial strains appears to be the hospital environment and the selective pressure responsible for expanding such bacterial populations in hospitals.

Table (3): Resistance patterns of MDR bacteria isolated from hospital effluent.

Antibiotic group	Antibiotic	Al-Sadeer H.	Al-Hakim H.	Maternity and Children H.
Penicillins	Ampicillin	R	R	R
	Amoxicillin	R	R	R
Cephalosporins	Ceftazidime	R	PR	R
	Cefotaxime	R	R	PR
Quinolons	Ciprofloxacin	R	R	R
Aminoglycosides	Amikacin	R	S	S
	Neomycin	S	S	S
	Gentamicin	S	R	S
Others	Erythromycin	R	R	R
	Cotrimoxazol	R	R	R
	Refampin	R	R	R
	Tetracycline	R	R	R

The present study predicts that hospital effluents can be a potential health risk by adding MDR bacteria to a city sewage pool. Similar studies need to be carried out in other cities to tackle the obnoxious problem of MDR being passed on from hospitals to the community.

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