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Epidemiological and Bacteriological Profile of Intra-Abdominal Infections in Pediatrics

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Abstract | **Original Research Article**

Introduction: Pediatric intra-abdominal infections (IAIs) are a common surgical emergency associated with significant morbidity, particularly in developing countries. Their polymorphic clinical presentation makes diagnosis challenging, while their polymicrobial nature complicates management. Early initiation of broad-spectrum empirical antibiotic therapy is essential and should be adapted according to bacteriological findings and local microbial ecology. However, the emergence of antimicrobial resistance increasingly limits treatment effectiveness. Data on the bacteriological profile of pediatric IAIs remain scarce, hindering the development of clear guidelines. This study aims to identify the causative pathogens and evaluate their antibiotic susceptibility to optimize therapeutic strategies. ***Materials and Methods:*** A retrospective descriptive study was conducted over four years (2020–2023) in a pediatric surgery department, including children aged 1 month to 15 years treated for community-acquired intra-abdominal infections. Neonates and healthcare-associated infections were excluded. Data were collected from medical, surgical, and microbiology records. All patients underwent surgical management with systematic intraoperative sampling for bacteriological analysis. Microbiological assessment included Gram staining, aerobic and anaerobic cultures, and bacterial identification using biochemical methods or MALDI-TOF mass spectrometry. Statistical analysis was performed using descriptive methods, and associations between pathogens and resistance profiles were evaluated using Fisher's exact test, with significance set at $p < 0.05$. ***Results:*** A total of 471 patients were included, with a mean age of 8.9 years and a male predominance (66.5%). Appendicular peritonitis was the most frequent diagnosis (80.7%), followed by intra-abdominal abscesses (17.6%), with good concordance between admission and intraoperative findings. Empirical antibiotic therapy consisted predominantly of ceftriaxone, gentamicin, and metronidazole (98.5%). Microbiological analysis revealed a predominance of *Escherichia coli* (49.3%), followed by *Pseudomonas aeruginosa* (11.9%). *E. coli* showed high susceptibility rates (95.2%), whereas *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* exhibited high resistance rates (68.9% and 75%, respectively), indicating the presence of multidrug-resistant Gram-negative bacilli. Other Enterobacteriaceae also demonstrated moderate resistance rates (40–50%), while anaerobic bacteria and Gram-positive cocci remained largely susceptible. Adapted antibiotic therapy mainly relied on aminoglycosides (87.3%), third-generation cephalosporins (63.1%), and metronidazole (51.2%), with carbapenems reserved for resistant cases. Prior antibiotic therapy influenced microbiological yield, with higher rates of culture sterilization observed in alternative regimens compared to the standard protocol (85.7% vs 37.9%, p=0.015). However, these findings should be interpreted with caution due to the small sample size of alternative regimens. Overall, these results highlight a predominance of susceptible digestive flora alongside emerging resistant Gram-negative pathogens requiring targeted therapeutic adaptation.

Keywords: Pediatric intra-abdominal infections, Antibiotic susceptibility, Escherichia coli, Peritonitis, Antimicrobial resistance, Bacteriological profile.

INTRODUCTION

Intra-abdominal infections in pediatrics are a frequent surgical condition, as they rank third among digestive surgical emergencies after bowel obstruction and acute appendicitis. They pose a real diagnostic problem due to the polymorphic nature of their clinical presentation, and a true therapeutic challenge. They are associated with particularly high morbidity and mortality, especially in developing countries [1].

As soon as the diagnosis is established, a broad-spectrum empirical antibiotic therapy must be initiated, which should subsequently be adapted according to the bacteriological results of peritoneal samples. This antibiotic therapy must take into account the polymicrobial nature of intra-abdominal infections [IAIs], the local bacterial ecology of the department, as well as the patient's clinical condition [2].

The emergence of resistant bacterial strains sometimes makes the treatment of these infections difficult. Therefore, isolating and identifying the bacteria involved in complicated IAIs is essential for a rigorous monitoring of bacterial resistance profiles to antibiotics and ultimately to achieve a positive therapeutic impact in this serious condition. However, the literature concerning the pediatric population is limited and does not allow the establishment of clear guidelines.

The objective of this study is to identify the pathogens involved in these infections in order to evaluate their susceptibility to available antibiotics and to propose effective therapeutic regimens.

Materials and Methods

We conducted a retrospective descriptive study over a period of four years [2020–2023] in the pediatric surgery operating department, including children aged from 1 month to 15 years who were managed for community-acquired intra-abdominal infections. Neonates as well as healthcare-associated infections were excluded.

Data were collected from medical records, surgical reports, and microbiology laboratory reports. All patients underwent surgical management with systematic intraoperative sampling and immediate transport to the bacteriology laboratory.

The microbiological study included a direct examination after Gram staining, followed by culture on appropriate media under aerobic and anaerobic conditions, then bacterial identification using standardized biochemical galleries or MALDI-TOF mass spectrometry.

Statistical analysis was based on descriptive statistics, with qualitative variables expressed as counts and percentages, and quantitative variables as means with standard deviation; the association between isolated pathogens and resistance profiles was studied using Fisher's exact test, with a significance threshold set at $p < 0.05$.

Results

1. Epidemiological characteristics and admission diagnosis:

During the study period, 471 patients were included. The mean age of our patients was 8.94 years, with extremes ranging from 1 month to 15 years, the majority of cases involving school-aged children.

A clear male predominance was observed, with 313 boys [66.45%] compared to 158 girls [33.55%], corresponding to a male-to-female ratio of 1.9.

The admission diagnosis was dominated by appendicular peritonitis, found in 380 patients [80.68%]. Abscesses accounted for 17.62% of cases [83 cases], while peritonitis due to digestive perforation was suspected at admission in only 8 patients [1.70%].

2. Empirical antibiotic therapy initiated:

Empirical antibiotic therapy was based on the regimen Ceftriaxone + gentamicin + metronidazole in 464 patients, representing 98.51% of cases.

Other protocols [amoxicillin-clavulanate alone, amoxicillin-clavulanate + gentamicin, imipenem + amikacin] were prescribed only marginally: 0.42%, 0.85%, and 0.21% respectively.

3. Intraoperative diagnosis:

The intraoperative diagnosis confirms the predominance of appendicular peritonitis, found in 380 patients [80.68%], reflecting a good concordance between the initial clinical diagnosis and operative findings.

Abscesses were confirmed intraoperatively in 82 cases [17.41%], a figure very close to that retained at admission [83 cases].

4. Identified pathogens [overall distribution]:

Microbiological analysis of the samples shows a clear predominance of *Escherichia coli*, isolated in 232 cases, representing 49.26% of all identified pathogens. This microorganism alone accounts for nearly half of the isolates.

The second most frequently identified pathogen is *Pseudomonas aeruginosa*, present in 56 samples [11.89%].
Several other bacteria of the digestive flora were found at lower frequencies [Table 1].

5. Susceptibility and resistance profiles:

When antibiograms were performed, *E. coli* showed good overall susceptibility: 95.22% of tested strains were sensitive, compared to only 4.78% resistant.

***E. coli* had a very low probability of being resistant compared to other pathogens [$p < 0.001$].**

Conversely, *Pseudomonas aeruginosa* exhibited a much more concerning profile, with 68.89% resistant strains and only 31.11% sensitive.

Similarly, *Klebsiella pneumoniae* showed 75% resistant strains, and *Proteus mirabilis* was represented by a fully resistant strain.

Other Enterobacteriaceae such as *Enterobacter cloacae* or *Serratia marcescens* also showed non-negligible resistance rates [40–50%].

These results reflect the presence of multidrug-resistant strains among Gram-negative bacilli, likely to compromise the effectiveness of first-line antibiotic therapies [Table 1].

In contrast, several anaerobic organisms [*Bacteroides fragilis, B. ovatus, B. caccae, B. distasonis, B. vulgatus*] and some Gram-positive cocci [*Enterococcus faecalis, Enterococcus avium, Streptococcus viridans, Streptococcus constellatus*] were found to be 100% sensitive to the tested antibiotics.

Coagulase-negative staphylococci also appeared entirely sensitive in this series.

Overall, these data highlight a contrast between:

- on the one hand, classical digestive flora pathogens, mostly susceptible, and on the other hand, non-fermenting Gram-negative bacilli or certain Enterobacteriaceae [*Pseudomonas, Klebsiella, Proteus*], showing high resistance profiles, requiring targeted adaptation of treatment.

Table 1: Distribution of isolated pathogens and antibiotic susceptibility/resistance profiles

Pathogen	Antibiogram				Total Number
	resistant		Suscetible		
	Number	Percentage	Number	Percentage	Number
E.Coli	11	4,78%	219	95,22%	230
Pseudomonas aeroginosa	31	68,89%	14	31,11%	45
Streptococcus viridans	0	0,00%	7	100,00%	7
Bacteroidesfragilis	0	0,00%	6	100,00%	6
Enterobacter cloacae	2	40,00%	3	60,00%	5
Staphylococcus coagulas négative	0	0,00%	5	100,00%	5
Klebsiella pneumoniae	3	75,00%	1	25,00%	4
Bacteroidesovatus	0	0,00%	3	100,00%	3
Lactobacillus lactis	0	0,00%	3	100,00%	3
Streptococcus constellatus	0	0,00%	3	100,00%	3
Aerococcusviridans	2	100,00%	0	0,00%	2
Enterococcus avium	0	0,00%	2	100,00%	2
Enterococcus faecalis	0	0,00%	2	100,00%	2
Serratia marcescens	1	50,00%	1	50,00%	2
Sttaphylococcus aureus	1	50,00%	1	50,00%	2
Aeromonashydrophila	0	0,00%	1	100,00%	1
Bacteroidescaccae	0	0,00%	1	100,00%	1
Bacteroidesdistasonis	0	0,00%	1	100,00%	1
Bacteroidesvulgatus	0	0,00%	1	100,00%	1
Citrobacterfreundii	0	0,00%	1	100,00%	1
Enterbacteramnigenus	0	0,00%	1	100,00%	1
Enterobacter spp	0	0,00%	1	100,00%	1
Enterococcus	0	0,00%	1	100,00%	1
Entierobacteramnigenus	0	0,00%	1	100,00%	1
Fusobacteriummortiferum	0	0,00%	1	100,00%	1
Gemellamorbillorum	0	0,00%	1	100,00%	1
Lactobacillus acidophilus	0	0,00%	1	100,00%	1
Morganellamorganii	0	0,00%	1	100,00%	1
Pantoea	0	0,00%	1	100,00%	1
peptostreptococcusssp	0	0,00%	1	100,00%	1
Proteus mirabilis	1	100,00%	0	0,00%	1
Raoultellaterrigena	0	0,00%	1	100,00%	1
Staphylococcus viridans	0	0,00%	1	100,00%	1
Streptococcus	0	0,00%	1	100,00%	1

6. Adapted antibiotic therapy:

Adapted antibiotic therapy, initiated based on the results of the antibiogram, remains based on combinations providing broad coverage of digestive flora pathogens.

Gentamicin is the most commonly used antibiotic in adapted therapy, as it is prescribed in 87.26% of patients, reflecting its central role in the management of intra-abdominal infections.

Ceftriaxone is used in 63.06% of patients and metronidazole in 51.17%, confirming the frequent use of dual or triple therapy combining a third-generation cephalosporin, an aminoglycoside, and an anti-anaerobic agent.

Protected penicillins [amoxicillin–clavulanic acid] are used in 23.35% of patients, while reserve aminoglycosides [amikacin] are employed in 11.04% of cases, often as a relay or alternative therapy.

Carbapenems [imipenem in 7.86% and meropenem in 4.03%] and colistin [1.06%] are reserved for a minority of patients, probably in the presence of multidrug-resistant strains, particularly *Pseudomonas* or certain Enterobacteriaceae.

The very occasional use of fluoroquinolones [ciprofloxacin 1.06%, levofloxacin 0.21%] and agents such as tigecycline or teicoplanin [0.42% and 0.21%] indicates that they remain second-line or salvage options, depending on the resistance profile and patient context [Table 2].

Table 2: Adapted antibiotic therapy initiated according to antibiogram results

	Number	Percentage
Gentamycine	411	87,26%
Ceftriaxone	297	63,06%
Métronidazole	241	51,17%
Amoxicilline + acclav	110	23,35%
Amikacine	52	11,04%
Imipénème	37	7,86%
Méropenème	19	4,03%
Colymicine	5	1,06%
Ciprofloxacine	5	1,06%
Tigécycline	2	0,42%
Levofloxacine	1	0,21%
Teicoplanine	1	0,21%

7. Statistical analysis between pathogens and antibiogram:

The statistical analysis of antibiotic susceptibility and resistance according to the pathogen highlights highly contrasted profiles among the different isolated bacteria. *E. coli* has a very low probability of being resistant compared to other pathogens [Table 3].

Table 3: Association between pathogen type and antibiotic resistance

Germe	n total	Résistant n [%]	Sensible n [%]	OR [résistance vs autres germes]	IC95 % de l'OR	p [test exact de Fisher]
E. coli	230	11 [4,8 %]	219 [95,2 %]	**0,08**	**[0,04 – 0,18]**	**< 0,001**
Pseudomonas aeroginosa	45	31 [68,9 %]	14 [31,1 %]	**28,89**	**[12,95 – 59,38]**	**< 0,001**
Streptococcus viridans	7	0 [0,0 %]	7 [100,0 %]	0,00	[0,02 – 6,35]	0,601
Bacteroidesfragilis	6	0 [0,0 %]	6 [100,0 %]	0,00	[0,02 – 7,46]	0,596
Enterobacter cloacae	5	2 [40,0 %]	3 [60,0 %]	3,80	[0,78 – 21,03]	0,169
Staphylococcus coagulase négative	5	0 [0,0 %]	5 [100,0 %]	0,00	[0,03 – 9,01]	1,000

8. Impact of prior antibiotic administration on antibiogram results:

In the comparative analysis of empirical regimens, the standard protocol ceftriaxone + gentamicin + metronidazole [n=464] was associated with culture sterilization in 37.9% of cases [176/464]. In comparison, other regimens [n=7] showed a markedly higher proportion of sterile cultures, at 85.7% [6/7].

This difference was statistically significant [Fisher's exact test, p=0.015] and reflected a substantial increase in the likelihood of obtaining a sterile culture under "other regimens" [OR 9.82, 95% CI [1.17–82.23]].

However, this effect should be interpreted with caution because the "other regimens" group is very small, which explains the wide confidence interval [significant uncertainty around the estimate] [Table 4].

Table 4: Association between empirical antibiotic regimen and [1] culture sterilization [2] availability of an antibiogram [3] resistance

Issue [dépendante]	ceftriaxone + gentamicin + metronidazole n/N [%]	other regimens n/N [%]	OR [others vs Céftriaxone] [IC95%]	p [Fisher]
Sterile Culture	176/464 [37,9%]	6/7 [85,7%]	9,82 [1,17–82,23]	0,015
Available Antibiogram	284/464 [61,2%]	1/7 [14,3%]	0,11 [0,01–0,88]	0,017
resistance among positive cultures with an available antibiogram	47/284 [16,5%]	0/1 [0,0%]	1,67 [0,07–41,54]	1,000

Regarding the availability of the antibiogram, the standard regimen was associated with an interpretable antibiogram in 61.2% of cases [284/464], whereas this proportion dropped to 14.3% [1/7] in the "other regimens" group.

This difference was also statistically significant [p=0.017], with an OR of 0.11 [95% CI [0.01–0.88]], suggesting that "other regimens" were associated with a much lower probability of obtaining an antibiogram.

From an interpretative standpoint, this result is consistent with the idea that more frequent culture sterilization [or a lower bacteriological yield] mechanically reduces the likelihood of obtaining an antibiogram [since an antibiogram requires a positive and interpretable culture].

The detailed analysis according to the type of "other regimens" reinforces this caution. The AClav alone regimen [n=2] was associated with a sterilization rate of 50% [1/2], without a significant difference compared to the standard regimen [OR 1.63, 95% CI [0.17–15.84], p=1.000], reflecting a lack of statistical power.

Conversely, AClav + gentamicin [n=4] showed sterilization in 100% of cases [4/4], with a significant association [OR 14.71, 95% CI [0.79–274.88], p=0.021]. Despite statistical significance, the 95% CI remains extremely wide, indicating that the estimate is unstable and highly dependent on the small sample size.

Finally, imipenem + amikacin [n=1] was also associated with 100% sterilization [1/1], but without statistical significance [p=0.381] and with a very wide 95% CI [OR 4.90, 95% CI [0.20–121.03]], again due to the very small sample size [Table 5]

Table 5: Detailed analysis of culture sterilization according to the empirical antibiotic regimen [compared with the standard regimen]

empirical antibiotic therapy	N	Steril Cultur n [%]	OR Sterility vs Ceftriaxone+Genta+Métronidazol [IC95%]	p [Fisher]
aclav	2	1 [50,0%]	1,63 [0,17–15,84]†	1,000
aclav+genta	4	4 [100,0%]	14,71 [0,79–274,88]†	0,021
Imipenème+Amikacine	1	1 [100,0%]	4,90 [0,20–121,03]†	0,381

DISCUSSION

Pediatric intra-abdominal infections [IAIs] constitute a frequent medico-surgical emergency, predominantly related to appendicular complications. Our study, involving 471 patients aged from 1 month to 15 years, provides updated data on the epidemiological, microbiological, and therapeutic profile of pediatric intra-abdominal infections, and allows a relevant comparison with data from the literature and international recommendations.

Most studies show a predominance of intra-abdominal infections in school-aged children and adolescents. This distribution is explained by the high frequency of complicated appendicitis in this age group, which represents the main etiology of community-acquired pediatric IAIs [3-5].

The very low proportion of infants and young children under 2 years of age highlights both the rarity of appendicular infections at this age and their diagnostic severity when they occur. Brook [2004] and Coates *et al.,* showed that intra-abdominal infections in infants are more often related to specific etiologies [intestinal perforations, necrotizing enterocolitis], which explains their underrepresentation in series dominated by complicated appendicitis [6,7].

The observed male predominance [male-to-female ratio = 1.9] is consistent across major pediatric series, particularly those of Newman, Tartar, and Lin. Although the mechanisms remain poorly understood, this difference may be related to a higher incidence of complicated appendicitis in boys or to longer diagnostic delays [3,4,8].

According to the literature, complicated appendicular infections [appendicular peritonitis, appendicular abscess] constitute the main cause of intra-abdominal infections in pediatrics. Other etiologies

include digestive perforations, primary intra-abdominal abscesses, and, more rarely, infections secondary to inflammatory or malformative conditions [3,4].

Recommendations from scientific societies, notably the Société Française d'Anesthésie et de Réanimation [SFAR] and the Société de Réanimation de Langue Française [SRLF], emphasize that appendicular intra-abdominal infections represent the most frequent form of community-acquired IAIs in children [9].

Pediatric intra-abdominal infections are classically described as polymicrobial, involving digestive flora. Enterobacteriaceae constitute the most frequently isolated bacterial group, with *Escherichia coli* as the predominant pathogen. This observation has been consistently reported in both historical and recent pediatric microbiological studies [3,4,6,10].

Anaerobes, particularly *Bacteroides fragilis* and other species of the *Bacteroides* genus, are also well represented in our series, confirming their major role in complicated appendicular infections. Brook emphasizes the constant nature of this aerobic–anaerobic association, justifying antibiotic coverage systematically targeting both components [6].

The non-negligible frequency of *Pseudomonas aeruginosa* [11.9%] is higher than that reported in some strictly community-acquired series but remains consistent with data from the EBIIA study and Marshall et al., which show that this pathogen is more frequently isolated in severe, prolonged cases or after prior antibiotic exposure [6,11].

Escherichia coli generally retains good susceptibility to first-line antibiotics. The rates of extended-spectrum beta-lactamase [ESBL] production remain relatively low in most pediatric series [4,8].

In contrast, *Pseudomonas aeruginosa* shows a very high resistance rate in our series [nearly 70%], consistent with the observations of Marshall and the EBIIA study, which identify this pathogen as a major factor of therapeutic complexity. SFAR-SRLF recommendations emphasize that the identification of *Pseudomonas* should lead to rapid adaptation of antibiotic therapy based on antibiogram results [9,12,11].

The almost systematic use of triple therapy combining a third-generation cephalosporin, an aminoglycoside, and metronidazole in our series is consistent with SFAR-SRLF recommendations [2015] [9], One Health Trust guidelines [2025] [13], and recent recommendations reported by Cohen *et al.,* [2024] [14]. This strategy provides effective coverage of Enterobacteriaceae and anaerobes while limiting the excessive use of very broad-spectrum antibiotics.

Limitations and clinical implications:

The main limitations of our study lie in its retrospective design and the absence of detailed prognostic analysis. However, the large cohort size, the systematic use of microbiological sampling, and the comparison with a wide range of data from the literature strengthen the validity of our conclusions.

CONCLUSION

Based on a large pediatric cohort aged 1 month to 15 years, our study confirms that appendicular intra-abdominal infections represent the main cause of IAIs in pediatrics.

Their microbiology is dominated by *Escherichia coli* and anaerobes, with good adequacy of recommended empirical antibiotic regimens.

However, the high frequency of multidrug-resistant *Pseudomonas aeruginosa* highlights the need for continuous microbiological surveillance and early therapeutic adaptation based on local data.

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