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Antimicrobial Resistance in More than 100,000 *Escherichia coli* Isolates According to Culture Site and Patient Age, Gender, and Location▽†

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Escherichia coli **and the antimicrobial pressure exerted on this microorganism can be modulated by factors dependent on the host. In this paper, we describe the distribution of antimicrobial resistance to amikacin, tobramycin, ampicillin, amoxicillin clavulanate, cefuroxime, cefoxitin, cefotaxime, imipenem, ciprofloxacin, fosfomycin, nitrofurantoin, and trimetoprim-sulfametoxazole in more than 100,000** ***E. coli*** **isolates according to culture site and patient age, gender, and location. Bayesian inference was planned in all statistical analysis, and Markov chain Monte Carlo simulation was employed to estimate the model parameters. Our findings show the existence of a marked difference in the susceptibility to several antimicrobial agents depending on from where** ***E. coli*** **was isolated, with higher levels of resistance in isolates from medical devices, the respiratory system, and the skin and soft tissues; a higher resistance percentage in men than in women; and the existence of a clear difference in antimicrobial resistance with an age influence that cannot be explained merely by means of an increase of resistance after exposure to antimicrobials. Both men and women show increases in resistance with age, but while women show constant levels of resistance or slight increases during childbearing age and greater increases in the premenopausal age, men show a marked increase in resistance in the pubertal age. In conclusion, an overwhelming amount of data reveals the great adaptation capacity of** ***E. coli*** **and its close interaction with the host. Sex, age, and the origin of infection are determining factors with the ability to modulate antimicrobial resistances.**

Escherichia coli is a commensal microorganism in humans and in many different animal species (23, 32). Structural factors such as the presence of fimbriae and adhesins confer the bacteria adherence ability to epithelial cells and allow its persistence in the colonized areas, mainly in the gastrointestinal tract (2, 36). In addition, these factors are adapted to different habitats or species (8, 10, 32). The wide biochemical flexibility that *E. coli* exhibits in its use of different carbon sources as nutrients is another evidence of its successful adaptability. This nutritional and adaptive flexibility has enabled it to acclimatize to new environments and to colonize countless niches (32, 36).

For all these reasons, this organism is one of the main pathogens isolated in samples of various kinds, from urinary tract infections to meningitis (7). This variety illustrates the different relationships between *E. coli* and its host and also the different physiological profiles and virulence factors it has developed, including antimicrobial resistance (20, 31, 38).

Under the hypothesis that both *E. coli* and the antimicrobial pressure exerted on this microorganism can be modulated by factors dependent on the host, the aim of this paper is to describe the distribution of antimicrobial resistance of *E. coli* isolated in our region according to culture site and patient age, gender, and location, i.e., samples originating from hospital-admitted patients versus samples from the community, and to study the possible relationships observed.

MATERIALS AND METHODS

This is a retrospective study of antimicrobial resistance in *E. coli* from patients from the Comunitat Valenciana, a state in Spain with a surface equal to 23,255 km^2 and a population of 5,029,601. Samples were obtained from January 2007 to October 2009. Data were retrieved from the Comunitat Valenciana Microbiological Surveillance Network (RedMIVA), which daily compiles and analyzes information from 25 microbiology laboratories that manage more than 90% of the total population (13, 24, 25).

Studied antimicrobials included amikacin (AMK), tobramycin (TOB), ampicillin (AMP), amoxicillin clavulanate (AMC), cefuroxime (CXM), cefoxitin (FOX), cefotaxime (CTX), imipenem (IPM), ciprofloxacin (CIP), fosfomycin (FOF), nitrofurantoin (NIT), and trimetoprim-sulfametoxazole (STX).

Microbial identification and antimicrobial susceptibility testing were performed according to laboratory standard procedures conforming to CLSI antimicrobial susceptibility breakpoints, either by regular biochemical reactions and agar diffusion susceptibility tests or automated methods. Susceptible and intermediate isolates were grouped together for statistical analysis.

Samples were classified in the following groups: abscesses, digestive system, urine, genitourinary system, medical devices, bones and deep tissues, prostatic fluid, respiratory system, blood, and skin and soft tissues.

For the study of the distribution of resistance according to sex and age, groups were established every 5 years, except for the first group, which included patients less than 1 year old, and the last group, which included all patients aged 85 years or more.

E. coli isolates were considered of nosocomial origin when the sample was obtained from a hospitalized patient.

Statistical analysis. For each available covariate, a logistic regression model was performed for antimicrobial resistance. The relationship with age as a continuous variate was expressed in the following model: $Y_i \sim \text{binomial}(p_i; n_i)$, $\text{logit}(p_i) = \alpha_0 + \alpha_1 \times x_i$, where Y_i is the number of resistant isolates in the age group, n_i is the total number of observations in this group, p_i is the probability that an isolate is resistant for the age group, α_0 and α_1 are the regression parameters being estimated, and x_i is the covariate.

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TABLE 1. Antimicrobial resistance in community patients versus hospital-admitted patients

Antimicrobial	% (no.) of samples from community vs hospital-admitted patients with antimicrobial resistance	DIC[a]	
		Different probabilities	Equal probabilities
Amikacin	0.3 (98,052) vs 0.5 (30,390)	**18.33**	32.31
Amoxicillin clavulanate	6.1 (107,962) vs 9.2 (33,621)	**24.44**	396.27
Ampicillin	64.8 (91,603) vs 71.4 (26,939)	**26.24**	433.85
Cefotaxime	8.6 (81,603) vs 12.7 (26,252)	**24.51**	391.37
Cefoxitin	3.1 (89,307) vs 5.9 (29,172)	**22.83**	433.15
Cefuroxime	11.2 (107,835) vs 17.2 (33,680)	**25.32**	822.20
Ciprofloxacin	31.6 (107,142) vs 37.0 (33,481)	**26.85**	359.22
Fosfomycin	2.4 (94,526) vs 1.8 (20,473)	**21.26**	48.28
Imipenem	0.1 (98,177) vs 0.2 (30,888)	16.39	15.00
Nitrofurantoin	1.8 (94,297) vs 1.8 (20,619)	21.04	19.02
Tobramycin	6.2 (103,535) vs 7.8 (32,174)	**23.91**	120.71
Cotrimoxazole	33.7 (100,875) vs 37.5 (28,705)	**26.67**	162.75

[a] DIC values obtained for models with different and equal probabilities between both groups. Boldface type indicates the models with substantial differences. Different probabilities, significant differences between groups; equal probabilities, no significant differences between groups.

To analyze the differences between several categories for the remaining factors, the logistic regression was expressed as $Y_i \sim \text{Binomial}(p_i; n_i)$, $\text{logit}(p_i) = \mu + \alpha_i$, subject to the restriction $\sum\alpha_i = 0$, where μ is the global value and α_i is the effect of the category i.

Additionally, a complete multivariate model incorporating all the covariates was also analyzed and compared with partial models to assess the relevance of each factor.

Bayesian inference was planned in all situations. Markov chain Monte Carlo (MCMC) simulation was employed to estimate the model parameters (12). We ran all these models in WinBUGS version 1.43 (34). To compare the adjustment of the different models, we used the deviance information criterion (DIC). DIC is a measure of model fit penalized by the complexity of the model, and its value is calculated by adding the effective number of parameters to the posterior mean deviance of the model. The "best fit" model is the one with the smallest DIC value (33). Differences of less than 3 indicate that the two models are indistinguishable, greater differences indicate that the poorer model has considerably less support, and differences of more than 10 indicate that the poorer model has essentially no support (6).

In order to fully manage the statistical modeling, prior distributions were established for the parameters. Noninformative prior knowledge was considered with normal distributions with large variances for covariate parameters.

RESULTS

The numbers of isolates varied according to the antimicrobial tested, between 141,583 for AMC and 107,855 for CTX. Urine samples comprised the group with the greater amount of isolates and comprised 80% of all isolates from women. This group presented two crests of incidence in the number of isolates, one at the reproductive age and the other after menopause. In men, urine samples represented 60% of all isolates, showing a continuous increase in the number of isolates through age. The number of isolates from community patients was higher than that from hospital-admitted patients.

Resistance according to patient location: hospital-admitted versus community patients. The comparison of percentages of resistance between hospitalized and community patient samples revealed a greater proportion of resistant organisms in the hospitalized group for all antimicrobials studied except for FOF, which shows the greatest resistance in the community population, and for NIT and IPM, for which differences are almost nonexistent (Table 1).

However, there was a group of samples in which the resis-

TABLE 2. Antimicrobial resistance distribution according to sample type in women

Antimicrobial	% (no.) of samples from women with antimicrobial resistance by sample type[b]							DIC[a]	
	ABS	DIS	GUS	MED	URI	BDT	RES	BLO	SST	Different probabilities	Equal probabilities
AMK	0 (551)	0.3 (953)	0.3 (1,901)	0.6 (315)	0.3 (77,357)	0.5 (3,692)	0.6 (680)	0.3 (3,433)	0.2 (1,200)	47.3	**43**
AMC	9.5 (576)	8.9 (1,084)	3.7 (1,913)	9.6 (333)	5.4 (85,777)	12.0 (4,087)	15.1 (755)	8.6 (3,917)	9.0 (1,219)	**80.2**	525.4
AMP	71.6 (443)	67.4 (947)	55.8 (1,701)	77.9 (299)	62.3 (72,238)	75.5 (3,269)	82.6 (643)	69.8 (3,316)	75.3 (1,041)	**87.1**	658.8
CTX	13.3 (511)	16.9 (828)	4.8 (1,567)	17.7 (266)	7.6 (64,556)	13.8 (3,295)	15.3 (561)	9.5 (3,254)	14.4 (936)	**80.5**	421
FOX	5.3 (563)	7.1 (1,055)	1.8 (1,833)	8.6 (327)	2.6 (69,144)	7.3 (3,962)	10.2 (713)	4.4 (3,740)	6.4 (1,195)	**75.6**	507.1
CXM	16.5 (576)	19.6 (1,094)	5.8 (1,959)	22.5 (338)	10.0 (85,564)	19.2 (4,152)	22.0 (771)	13.7 (3,889)	18.5 (1,229)	**84.4**	748.2
CIP	32.2 (577)	29.0 (1,081)	11.7 (1,916)	52.8 (337)	28.7 (85,060)	39.9 (4,096)	45.4 (760)	32.1 (3,916)	48.9 (1,222)	**88.8**	1,026.5
FOF	0.7 (150)	1.9 (156)	1.5 (261)	3.0 (167)	2.2 (82,917)	2.5 (1,027)	3.8 (131)	2.0 (759)	2.6 (231)	55.4	**45.3**
IPM	0 (531)	0 (1,038)	0.1 (1,870)	0 (327)	0.1 (76,785)	0.2 (3,915)	0 (725)	0.1 (3,762)	0 (1,099)	**24.7**	28.7
NIT	1.2 (171)	3.6 (167)	0.8 (261)	0 (168)	1.6 (82,789)	2.3 (946)	3.9 (127)	2.4 (696)	3.1 (322)	**51.1**	58.7
TOB	5.6 (570)	6.0 (1,061)	2.8 (1,906)	9.5 (336)	5.4 (81,510)	9.1 (4,013)	11.7 (683)	6.1 (3,828)	10.8 (1,225)	**78.3**	276.8
STX	34.8 (379)	34.8 (876)	26.6 (1,152)	42.4 (311)	32.6 (81,280)	39.7 (3,312)	44.9 (602)	36.7 (3,125)	43.3 (954)	**87.2**	279

[a] DIC values obtained for models with different and equal probabilities between both groups. Boldface type indicates the models with substantial differences. Different probabilities, significant differences between groups; equal probabilities, no significant differences between groups.

[b] ABS, abscesses; DIS, digestive system; GUS, genitourinary system; MED, medical devices; URI, urine; BDT, bones and deep tissues; RES, respiratory system; BLO, blood; SST, skin and soft tissues.

TABLE 3. Antimicrobial resistance distribution according to sample type in men

Antimicrobial	% (no.) of samples from men with antimicrobial resistance by sample type										DIC[a]	
	ABS	DIS	GUS	MED	URI	BDT	PRO[b]	RES	BLO	SST	Different probabilities	Equal probabilities
AMK	0.1 (907)	0.7 (1,382)	0 (208)	1.5 (329)	0.4 (22,987)	0.7 (4,102)	0.8 (589)	0.5 (1,675)	0.7 (3,297)	0.6 (994)	**55.5**	59.2
AMC	7.8 (931)	9.5 (1,618)	7.5 (213)	13.2 (340)	7.2 (25,037)	13.6 (4,576)	5.4 (610)	15.7 (1,831)	12.8 (3,793)	12.2 (1,028)	**87.2**	452.8
AMP	73.7 (693)	69.4 (1,400)	66.5 (203)	84.8 (297)	72.2 (20,806)	78.6 (3,519)	67.0 (466)	83.2 (1,467)	74.8 (3,239)	78.0 (836)	**92.6**	279
CTX	10.5 (842)	14.0 (1,246)	9.5 (179)	20.2 (267)	11.6 (18,292)	15.5 (3,679)	9.0 (489)	17.5 (1,443)	15.1 (3,154)	18.7 (754)	**88**	202.1
FOX	3.9 (900)	6.3 (1,585)	1.5 (200)	8.2 (340)	4.3 (19,600)	7.5 (4,461)	4.3 (586)	10.3 (1,761)	7.4 (3,600)	8.2 (995)	**81.4**	276.6
CXM	14.1 (930)	17.1 (1,643)	9.7 (216)	25.2 (353)	15.4 (24,974)	20.6 (4,619)	11.3 (619)	24.5 (1,856)	21.3 (3,759)	22.5 (1,031)	**91.9**	334.7
CIP	28.2 (928)	26.1 (1,620)	26.3 (213)	52.8 (358)	42.1 (24,762)	41.9 (4,575)	34.4 (607)	50.4 (1,866)	42.1 (3,795)	45.9 (1,026)	**96.9**	441.2
FOF	0.4 (242)	1.6 (250)	0 (33)	2.7 (147)	3.0 (24,143)	1.9 (1,271)	0.5 (195)	1.8 (390)	1.7 (722)	3.4 (233)	**53.8**	69.6
IPM	0 (872)	0.1 (1,552)	0 (202)	0.3 (340)	0.1 (22,849)	0.2 (4,447)	0.2 (562)	0.2 (1,800)	0.2 (3,605)	0.1 (929)	41.5	**32.7**
NIT	0.7 (288)	0.4 (277)	0 (23)	3.8 (159)	2.3 (24,191)	2.3 (1,158)	2.0 (196)	3.1 (422)	4.2 (662)	4.0 (302)	**57**	67.9
TOB	6.4 (918)	6.3 (1,584)	5.9 (203)	12.7 (354)	8.6 (24,040)	9.6 (4,520)	4.7 (600)	10.7 (1,704)	8.6 (3,697)	11.2 (1,028)	**85.3**	130.4
STX	34.0 (579)	33.5 (1,291)	39.7 (136)	42.3 (324)	37.8 (23,965)	40.6 (3,713)	34.1 (446)	42.4 (1,484)	38.9 (2,989)	45.4 (801)	**94.5**	137.9

[a] DIC values obtained for models with different and equal probabilities between both groups. Boldface type indicates the models with substantial differences. Different probabilities, significant differences between groups; equal probabilities, no significant differences between groups.
[b] PRO, prostatic fluid.

tance was against the general trend and was higher in community samples than in hospital samples, including AMC in abscesses (12.7% [n = 393 samples] versus 7.2% [n = 1,125 samples]), CIP in medical devices (63.4% [n = 161 samples] versus 49.3% [n = 538 samples]), and TOB in bone and deep tissue samples (10.4% [n = 3,760 samples] versus 8.5% [n = 4,915 samples]), with lower DIC values for the two-group model.

Resistance according to patient sex and culture site. In the comparison of antibiotic resistance according to culture site and patient sex, respiratory and medical device samples from both men and women and skin and soft tissue samples from men had the highest percentages of resistance. Genitourinary samples from both sexes as well as urine samples from women presented the lowest percentages (Tables 2 and 3).

The differences observed between the different types of samples in each sex presented lower DIC values, except for IPM in men and for AMK and FOF in women.

The resistance range observed for each antibiotic was very variable, and less resistance was frequently found in samples from women, while greater resistance was frequently found in samples from men. Figure 1 illustrates these differences in CIP and CXM.

Resistance according to sex and age. In terms of the distribution of resistance according to age and sex, the various antimicrobials exhibited different patterns in men and women, except for IPM, with a higher percentage of resistance in men (see the tables in the supplemental material). These differences are the most evident in those antimicrobials with higher resistances.

A poor fit was obtained through the use of data adjustment using linear regression (Fig. 2), while a logistic regression was better adapted, justifying different models for men and women according to the calculated DIC (Table 4), except for IPM.

The patterns observed for the different antimicrobials are very similar in women, with constant levels of resistance or slight increases during childbearing age and higher levels in the premenopausal age. In men, although various patterns were observed, they are all very similar, with a marked increase in resistance in the pubertal age that is better appreciated in antimicrobials with higher resistance percentages, such as ciprofloxacin, cotrimoxazole, or cephalosporins (Fig. 2).

Multivariate analysis. Four different statistical models were created for each antimicrobial in order to explain which variates were relevant to antimicrobial resistance. All of them contemplated age as a continuous variate. The first model

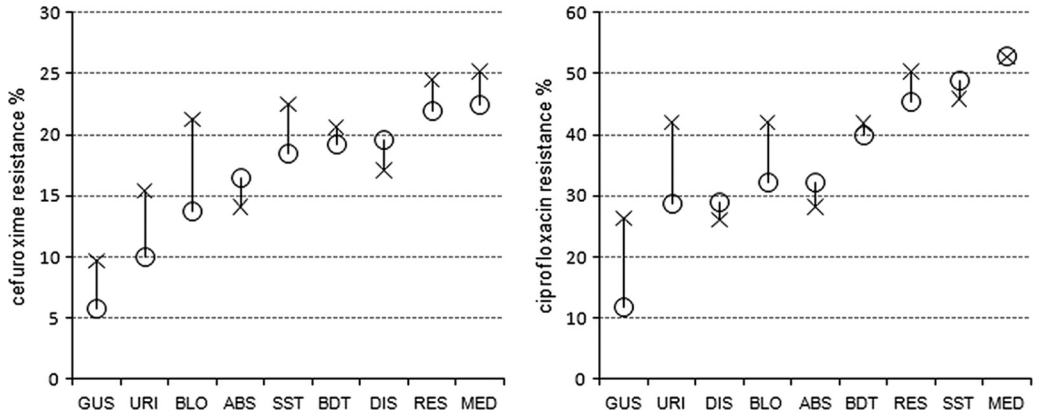

FIG. 1. Cefuroxime and ciprofloxacin resistance in women and men according to culture site. X, men; O, women; ABS, abscesses; DIS, digestive system; URI, urine; GUS, genitourinary system; MED, medical devices; BDT, bones and deep tissues; RES, respiratory system; BLO, blood; SST, skin and soft tissues.

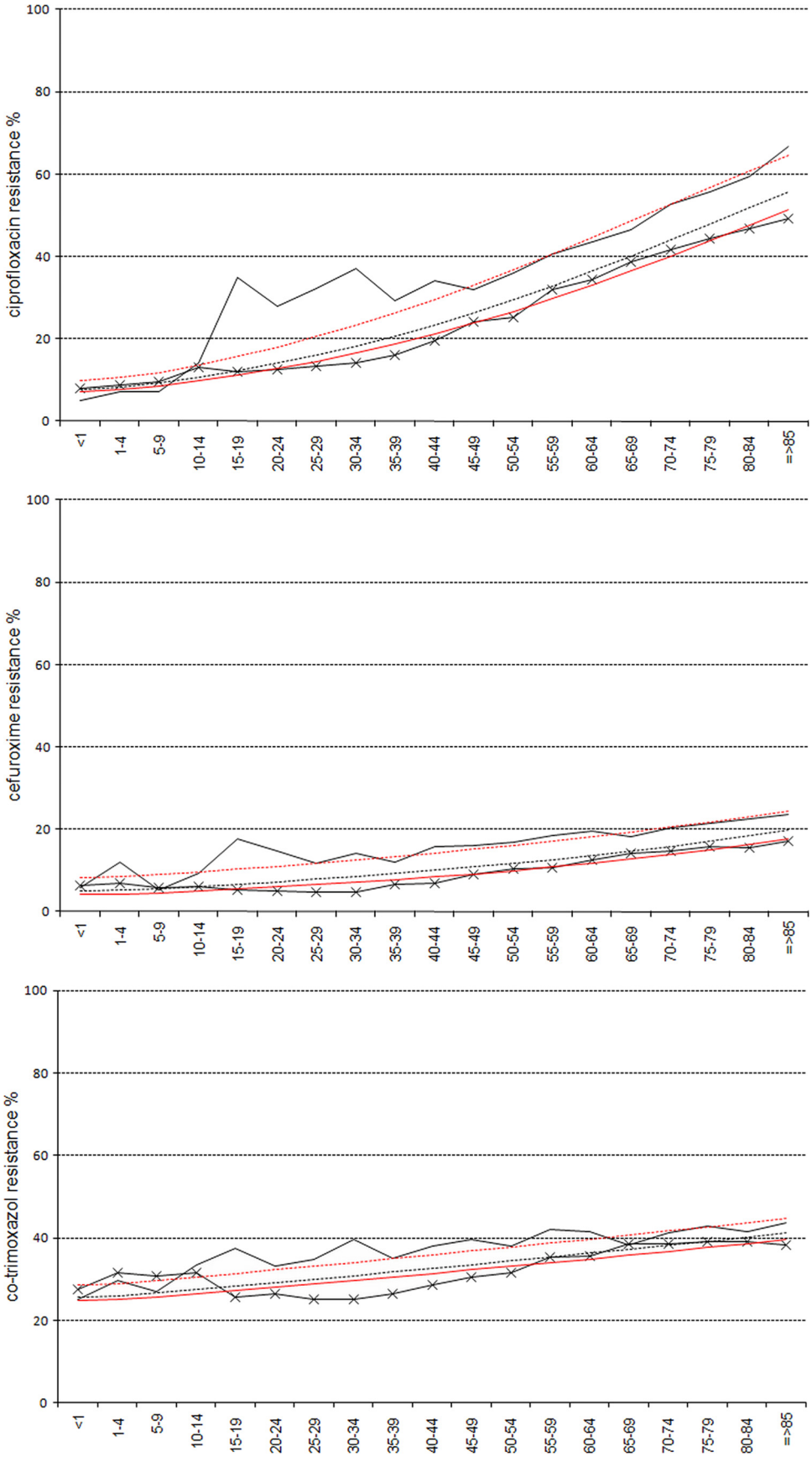

FIG. 2. Antimicrobial resistance according to age and gender. Men, black line; women, black line with exes; man model, red dotted line; woman model, red line; joint model, black dotted line.

TABLE 4. DIC for antimicrobial resistance distribution throughout life according to sex

Antimicrobial	DIC[a]	
	Separate models	Joint model
Amikacin	**207.6**	227.5
Amoxicillin clavulanate	**396.2**	762.6
Ampicillin	**641.1**	1,652.3
Cefotaxime	**467.3**	890.3
Cefoxitin	**360.4**	668.6
Cefuroxime	**609.9**	1,468.4
Ciprofloxacin	**858.8**	2,181.5
Fosfomycin	**327.9**	360.2
Imipenem	151.0	148.6
Nitrofurantoin	**308.4**	340.9
Cotrimoxazole	**700.5**	920.2
Tobramycin	**399.5**	696.1

[a] Separate models (different age curves for men and women) are contrasted with a joint model (both sexes share the same age curve). Boldface type indicates the models with substantial differences. Separate models, significant differences between groups; joint model, no significant differences between groups.

included all the covariates, i.e., sex, hospitalization, and culture site, while the other three lacked one of them. The analysis demonstrated that every factor was needed to correctly represent antimicrobial resistance, except with FOF, for which the addition of culture site to the model did not provide any significant improvement, and IPM, for which no significant differences were observed between models (Table 5).

DISCUSSION

The main findings of this study are (i) the existence of a marked difference in the susceptibility to several antimicrobial agents depending on what part of the body the *E. coli* was isolated from, (ii) low percentages of resistance to fosfomycin, nitrofurantoin, amikacin, and imipenem, (iii) the existence of a clear difference in antimicrobial resistance between isolates from men and women with an age influence that cannot be explained merely by means of an increase of resistance after exposure to antimicrobials, and (iv) a higher resistance percentage in men than in women.

This study highlights the differences in susceptibility to antimicrobial agents depending on where the *E. coli* is isolated from and therefore reinforces previous studies in which an association between several *E. coli* phylogroups and infection sites, or antimicrobial resistance, was found (5, 18, 27). Despite the large amount of data provided, our study is entirely retrospective. Thus, factors such as whether the observed differences depend solely on the existence of distinct subpopulations or phylogroups in different sites, on the antimicrobial concentration to which *E. coli* is exposed in the site, on the activation of various genes influenced by the environment, or on the antimicrobial exposure itself are left unsolved (3, 15, 17, 19, 22, 37). Some situations where we have found high rates of resistance, such as the colonization of medical devices, where formation of biofilms is frequent, or colonization of the skin and respiratory tract, determine circumstances of exposure to low concentrations of antimicrobials and changes in terms of growth rate or nutrient intake (11, 17, 35) that can select subpopulations. On the other hand, the colonization of these niches requires the initial presence of certain physiological and phenotypical characteristics (20, 27, 38) so that some phylogroups may be favored over others.

As described in other studies (4, 29), levels of antimicrobial resistance were higher among hospitalized patients' isolates than among community isolates, illustrating the higher antimicrobial pressure that enhances the selection for resistant strains and the transmission of resistance mechanisms (23, 32, 39). Just the opposite occurs with FOF, because it is a widely and empirically used drug for the treatment of urinary tract infections in outpatients due to its ease and convenience of use (9).

Cases in which greater levels of resistance were found in community samples for both AMC and CIP may illustrate the abusive use of these drugs for outpatients in our region (26), while further studies are necessary to find possible causes for this difference for TOB.

Four drugs, FOF, NIT, AMK, and IPM, maintain very low resistance regardless of the colonization site or patient sex or age. For FOF and NIT, the explanation lies in the decreased fitness of *E. coli* after acquiring a mutation that confers resistance to these drugs (1, 30), which, as the antimicrobial pressure disappears, allows the strains without the mutation to grow faster and displace the resistant ones. The explanation for AMK and IPM is probably the fact that these are very powerful

TABLE 5. DIC values for the different multivariate analyses

Antimicrobial	DIC[a]			
	Complete model	Model without hospitalization	Model without sex	Model without culture site
Amikacin	**6,715.73**	6,721.76	6,729.28	6,730.02
Amoxicillin clavulanate	**72,341.6**	72,364.1	72,493	72,822.2
Ampicillin	**155,360**	155,397	156,062	155,862
Cefotaxime	**68,709.6**	68,764.7	68,941	68,895.7
Cefoxitin	**38,314.3**	38,355.3	38,435.6	38,657.4
Cefuroxime	**107,189**	107,345	107,670	107,514
Ciprofloxacin	**167,795**	167,809	169,140	168,398
Cotrimoxazole	**167,041**	167,057	167,229	167,155
Fosfomycin	**26,495.2**	26,527.4	26,539.9	**26,494.1**
Imipenem	2,667.9	2,667.9	2,667.1	2,667.62
Nitrofurantoin	**19,953.1**	19,957.9	19,986.2	19,966.2
Tobramycin	**67,017.7**	67,025	67,277.8	67,130.2

[a] Boldface type indicates the models with substantial differences.

drugs used only in a hospital setting and not as first-line therapy and, therefore, have lower selective pressure due to their restricted use.

Finally, the biggest surprise of this study was to find different patterns for men and women in the acquisition of resistance throughout life. These patterns rule out a model that can be understood only as an increase of resistance with age due to a greater exposure to antimicrobials. In contrast, we observed how puberty is a key point in which a sharp increase in resistance—in all antimicrobials but AMK and IPM—is produced among men, who end up being the group with the highest percentage of resistance, whereas there seems to be a slowing down of resistance in women that is accelerated at premenopausal age. The most striking case is that of CIP, which shows a large increase of resistance in previously unexposed young men, since this antimicrobial is not used in children because it alters growth. Livermore et al. (21) found that the prevalence of CIP resistance was strongly associated with men with bacteremia and, to a lesser extent, age, with a peak of resistance in the 15- to 44-year age group for men, which perfectly fits with our own observations.

Gordon et al. found differences in *E. coli* populations in humans depending on age and sex from hospitalized patients' fecal samples, without observing differences in antimicrobial susceptibility (14). But while this study was based on 266 isolates, ours included over 100,000 isolates. The fact that such changes have been found in two periods when important hormonal and physiological changes occur certainly deserves more specific studies and could have significant implications in the decision of which antimicrobial therapy to use.

A possible sample bias in our study is that a large amount of isolates came from urine samples and that simpler cases might be treated empirically; therefore, there is a risk that resistant cases are selected. Interestingly, both the Spanish Society of Infectious Diseases and Clinical Microbiology and the guidelines issued by the Comunitat Valenciana local government recommend bacterial cultures to be carried out in all cases except with nonhospitalized healthy young women presenting uncomplicated cystitis. Thus, if a sample bias occurs, differences between community and hospitalized patients, and men and women, would be greater than observed. Another significant limitation to our study lies in the origin of infection classification; since the times from admission or hospital discharge until infection were not available, isolates were categorized depending on the patient's location at the time the sample was obtained. Thus, community urinary tract infections taking place during the first 2 days after admission could be classified as hospital infections. But again, since community infections present lower levels of resistance, differences between community versus hospitalized patients would be greater than those observed.

To date, we do not know of any other study that describes this same behavior associated with age and sex in so many antimicrobials. Thus, discovering whether *E. coli* is directly affected by host hormones as suggested by other authors (16, 28) or if it simply gets adapted to the new and changing niche conditions caused by physiological changes represents an exciting task.

In conclusion, an overwhelming amount of data reveals the great adaptation capacity of *E. coli* to its location and its close interaction with the host. Sex, age, hospitalization, and the origin of infection are determining factors with the ability to modulate antimicrobial resistances, as confirmed by multivariate analysis.

Additionally, this work could not have been done without RedMIVA, which highlights the usefulness of being able to rely on large databases of microbiological information.

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