Presentation Type:
Poster Presentation - Top Oral Abstract
Subject Category: Antibiotic Stewardship

Perspectives on nonprescription antibiotic use among Hispanic patients in the Houston metroplex: A qualitative study

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Background: Nonprescription antibiotic use includes taking an antibiotic without medical guidance (eg, leftover antibiotics, antibiotics from friends or relatives, or antibiotics purchased without a prescription). Nonprescription use contributes to antimicrobial resistance, adverse drug reactions, interactions, and superinfections such as *Clostridioides difficile* colitis. Qualitative studies exploring perspectives regarding nonprescription use among Hispanic patients are lacking. We used the Kilbourne Framework for Advancing Health Disparities Research to identify factors influencing Hispanic patients' nonprescription use and to organize our findings. **Methods:** Our study includes Hispanic primary-care clinic patients with different types of health coverage in the Houston metroplex who endorsed nonprescription use in a previous quantitative survey. Semistructured interviews explored the factors promoting nonprescription use in Hispanic adults. Interviews were conducted remotely, in English or Spanish, between May 2020 and October 2021. We used inductive coding and thematic analysis to identify the factors and motives for nonprescription use. **Results:** Of the 35 Hispanic participants surveyed, 69% were female and between the ages of 27 and 66. All participants had some form of healthcare coverage (eg, Medicare or private insurance, Medicaid, or the county financial assistance program). Participants reported obtaining antibiotics from their own leftover prescriptions and through trusted persons (eg, herbalists, pharmacists, friends/relatives, and others), buying them under the counter in US markets, and purchasing them without a prescription outside the United States. Thematic analysis revealed the factors contributing to nonprescription use (Fig. 1). Themes included beliefs that the 'doctor visit was unnecessary,' 'limited direct access to healthcare' in the United States (due to limited insurance coverage, high costs of the doctor's visits and medications, and long clinic wait times), 'more open indirect access to healthcare' abroad and under the counter in the United States, and communication difficulties (eg, language barriers with clinicians, perceived staff rudeness, and gaps in health literacy). Figure 2 shows representative quotes across thematic domains. Participants expressed having confidence in medical recommendations from pharmacists and trusted community members in their social networks. **Conclusions:** Antibiotic stewardship interventions that include pharmacist-driven patient education regarding appropriate antibiotic use may decrease nonprescription antibiotic use in Hispanic communities. Additionally, improving access to care while addressing communication barriers and cultural competency in clinics may improve primary care delivery and reduce potentially unsafe antibiotic use.

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① PATIENT FACTORS
Going to the Doctor is Unnecessary
- Similar symptoms
- Perceived severity of the illness

② HEALTHCARE SYSTEM FACTORS
Limited Direct Access to Healthcare
- Long clinic waits
- High healthcare costs
- Lack of insurance

Open Indirect Access to Healthcare
- Antibiotics can be purchased in pharmacies and stores abroad without a prescription
- Social networks provide non-prescription antibiotics
- Confidence in taking non-prescription antibiotics from trusted persons

③ CLINICAL ENCOUNTER FACTORS
"A Battle to Communicate" with Healthcare Providers
- Language barriers
- Perceived some clinic staff as discourteous and overwhelmed
- Patient-provider communication and gaps in health literacy

DECISION TO USE ANTIBIOTICS WITHOUT A PRESCRIPTION

Figure 1. Overview of Themes

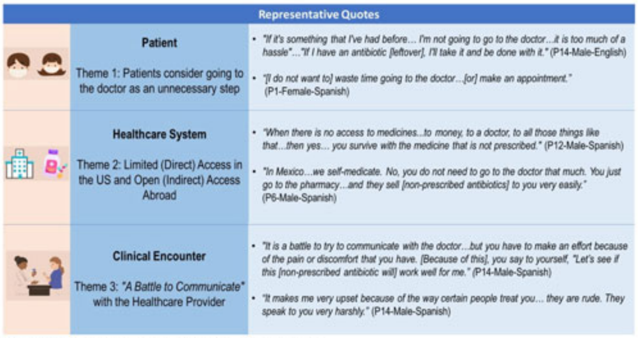
	Representative Quotes	
	Patient Theme 1: Patients consider going to the doctor as an unnecessary step	• *"If it's something that I've had before… I'm not going to go to the doctor…it is too much of a hassle"…"If I have an antibiotic [leftover], I'll take it and be done with it."* (P14-Male-English) • *"[I do not want to] waste time going to the doctor…[or] make an appointment."* (P1-Female-Spanish)
	Healthcare System Theme 2: Limited (Direct) Access in the US and Open (Indirect) Access Abroad	• *"When there is no access to medicines…to money, to a doctor, to all those things like that…then yes… you survive with the medicine that is not prescribed."* (P12-Male-Spanish) • *"In Mexico…we self-medicate. No, you do not need to go to the doctor that much. You just go to the pharmacy…and they sell [non-prescribed antibiotics] to you very easily."* (P6-Male-Spanish)
	Clinical Encounter Theme 3: *"A Battle to Communicate"* with the Healthcare Provider	• *"It is a battle to try to communicate with the doctor…but you have to make an effort because of the pain or discomfort that you have. [Because of this], you say to yourself, "Let's see if this [non-prescribed antibiotic will] work well for me."* (P14-Male-Spanish) • *"It makes me very upset because of the way certain people treat you… they are rude. They speak to you very harshly."* (P14-Male-Spanish)

Figure 2. Representative Quotes Per Theme

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Identifying nonprescription antibiotic users with screening questions in a primary care setting

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Background: Antibiotic use without a prescription (nonprescription use) leads to antibiotic overuse, with negative consequences for patient and public health. We studied whether screening patients for prior nonprescription antibiotic use in the past 12 months predicted their intentions to use them in the future. **Methods:** A survey asking respondents about prior and intended nonprescription antibiotic use was performed between January 2020 and June 2021 among patients in waiting rooms of 6 public clinics and 2 private emergency departments in economically and socially diverse urban and suburban areas. Respondents were classified as prior nonprescription users if they reported previously taking oral antibiotics without contacting a doctor, dentist, or nurse. Intended use was defined as answering "yes" or "maybe" to the question, "Would you use antibiotics without contacting a doctor, nurse, or dentist?" We calculated the sensitivity, specificity, and positive and negative predictive value (PPV and NPV) of prior nonprescription antibiotic use in the past 12 months for future intended nonprescription use. Bayes PPV and NPV were also calculated, considering the prevalence of nonprescription antibiotic use (24.8%) in our study. **Results:** Of the 564 patients surveyed, the median age was 51 years (SD, 19–92), with 72% of patients identifying as female. Most were from the public healthcare system (72.5%). Most respondents identified as Hispanic or Latino(a) (47%) or African American (33%), and 57% received Medicaid or the county financial assistance program. Prior

Table 1. Diagnostic accuracy of the screening question (reporting prior use of antibiotics without a prescription) in identifying patients with intention to use antibiotics in the future without a prescription

Screening question	Sensitivity (95% CI)	Specificity (95% CI)	PPV	NPV	Bayes PPV (95% CI)	Bayes NPV (95% CI)
Prior use of non-prescription antibiotics in the last 12 months (n=409)	75.9% (65.3-84.6)	91.4% (87.8-94.2)	69.2%	93.7%	74.5% (66.7-80.9)	92.0% (88.7-94.4)

nonprescription use was reported by 246 (43%) of 564 individuals, with 91 (16%) reporting nonprescription use within the previous 12 months. Intention to use nonprescription antibiotics was reported by 140 participants (25%). The sensitivity and specificity of prior nonprescription use in the past 12 months to predict the intention to use nonprescription antibiotics in the future were 75.9% (95% CI, 65.3–84.6) and 91.4% (95% CI, 87.8–94.2), respectively. After the Bayes' adjustment, the PPV and NPV of prior use to predict future intention were 74.5% (95% CI, 66.7–80.9) and 92.0% (95% CI, 88.7–94.4) (Table 1). **Conclusions:** These results show that prior nonprescription antibiotic use in the past 12 months predicted the intention to use nonprescription antibiotics in the future (PPV of 75%). As a stewardship effort, we suggest clinicians use a simple question about prior nonprescription antibiotic use in primary-care settings as a screening question for patients at high risk for future nonprescription antibiotic use.

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Subject Category: Molecular Epidemiology

Real-time whole-genome sequencing surveillance for outbreak detection and intervention

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Background: Detecting healthcare-associated transmission and outbreaks often relies on reactive whole-genome sequencing (WGS), which occurs after the suspected transmission has occurred. Additionally, reactive WGS frequently misidentifies transmission and misses transmission when it has occurred. We initiated weekly real-time WGS to detect bacterial transmission and direct infection prevention interventions. We describe our experience after 1 year of real-time WGS surveillance at the University of Pittsburgh Medical Center–Presbyterian Hospital, a large, tertiary-care facility. **Methods:** Weekly WGS surveillance was performed from November 1, 2021, to October 31, 2022. Cultured isolates of select bacterial pathogens from patients who were hospitalized for ≥3 days or had a recent healthcare exposure in the prior 30 days were collected and sequenced. Isolates that were ≤15 single-nucleotide polymorphisms (SNPs) were considered genetically related clusters except for *Clostridioides difficile* (≤2 SNPs). Genetically related clusters were investigated for epidemiological links and interventions to interrupt transmission were implemented at the discretion of the infection prevention team. We analyzed subsequent infections that occurred within an outbreak after an intervention was in place. **Results:** In total, 1,909 isolates were sequenced. Of 1,633 unique patient isolates clustered by sequence type, 74 clusters were identified comprising 210 (12.9%) patient isolates (Table 1). The median time from culture date to sequencing was 14 days (IQR, 5.25). The median cluster size was 2 (IQR, 1) (Table 2). Overall, 118 patient isolates (56.2%) had an epidemiological link to a prior isolate, indicating potential transmission. Of 74 clusters, 66 (89.2%) received infection prevention interventions after notification based upon epidemiological data. The infection prevention team performed 69 total interventions, which included unit education (n = 28), hand hygiene observations (n = 16), enhanced cleaning (n = 16), environmental cultures or removal of endoscope (n = 7), and enhanced microbiology surveillance (n = 2). The 59 subsequent infections after infection prevention notification included 17 (28.8%) with no clear epidemiological link, and 41 (69.5%) with an epidemiological link either to a new transmission route (n = 37) or the same route prior to infection prevention intervention (n = 4). Only 1 (1.7%) subsequent infection within a cluster occurred after an infection prevention intervention from the same potential route, which was a suspected unit-based transmission of vancomycin-resistant *Enterococcus faecium*. **Conclusions:** Real-time WGS was effective at detecting genetically related clusters, finding potential sources, and halting further transmission after interventions by the infection prevention team. Quick turnaround times from patient culture to sequencing and analysis were vital for successful WGS surveillance. Real-time WGS surveillance has the potential to substantially shift the infection prevention paradigm for outbreak detection.

Table 1. Isolates sequenced and clusters detected

Organism	Sequenced	Unique Patient	Clusters	Clustered Isolates (%)
Acinetobacter species	52	50	5	11 (22.0)
Burkholderia species	6	4		
Citrobacter species	30	29		
Clostridioides difficile	100	98	3	8 (8.2)
Enterobacter species	35	34	2	4 (11.8)
Escherichia coli	128	109	5	11 (10.1)
Klebsiella species, not *pneumoniae*	21	21		
Klebsiella pneumoniae, ESBL producing	90	67	6	23 (34.3)
Methicillin-resistant *Staphylococcus aureus*	248	221	9	21 (9.5)
Proteus species	228	189	3	6 (3.2)
Providencia species	24	23		
Pseudomonas aeruginosa	558	438	20	50 (11.4)
Pseudomonas species, not *aeruginosa*	14	14		
Serratia species	153	135	3	6 (4.4)
Stenotrophomonas maltophilia	98	85	1	2 (2.4)
Vancomycin-resistant *Enterococcus faecium*	124	116	17	68 (58.6)
TOTAL	**1909**	**1633**	**74**	**210 (12.9)**

Table 2. Cluster size and distribution by species

Organism	Number of Clusters by Cluster Size (Patients)										
	2	3	4	5	6	7	8	9	10	11	12
Acinetobacter species	4	1									
Clostridioides difficile	2		1								
Enterobacter species	2										
Escherichia coli	4	1									
Klebsiella pneumoniae, ESBL producing	4				1			1			
Methicillin-resistant *Staphylococcus aureus*	6	3									
Proteus species	3										
Pseudomonas aeruginosa	16	1	1	1	1						
Serratia species	3										
Stenotrophomonas maltophilia	1										
Vancomycin-resistant *Enterococcus faecium*	7	5	1			2		1			1

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Patient and facility characteristics of an NDM-producing *Acinetobacter baumannii* outbreak in California, 2020–2022

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Background: Carbapenem-resistant *Acinetobacter baumannii* (CRAB) are bacteria that cause healthcare-associated infections and outbreaks. Most produce carbapenemases like New Delhi metallo-β-lactamase (NDM), which are more commonly found in carbapenem-resistant Enterobacterales but rarely in CRAB. In 2018, selected laboratories began participating in a public health sentinel surveillance program by routinely submitting CRAB and other antimicrobial-resistant isolates to the AR Laboratory Network for specialized testing. In May 2020, the Antimicrobial Resistance Laboratory Network detected the first NDM-CRAB case in California, triggering an investigation. Initial whole-genome sequencing of subsequent isolates indicated high relatedness. **Methods:** We defined confirmed cases as patients with NDM detected in CRAB isolates and probable cases as NDM detected in a screening swab from a patient epidemiologically linked to a known case(s) with specimens collected during May 2020–September 2022. We defined outbreak facilities as having (1) 1 or more newly identified cases during a point-prevalence survey in response to a known case or (2) at least 2 cases identified within 4 weeks of each other that were epidemiologically linked. We analyzed demographic and specimen characteristics, as well as healthcare exposure history using R Studio version 1.3.959 software. **Results:** Of 230 total patients, 176 (77%) were confirmed and 54 (23%) were probable cases; 150 (65%) were identified