Clinical management of resistance evolution in a bacterial infection
A case study

Robert J. Woods*1 and Andrew F. Read2,3

1Division of Infectious Diseases, Department of Internal Medicine, University of Michigan, Ann Arbor, MI 48109, USA;
2Department of Biology, Center for Infectious Disease Dynamics, Pennsylvania State University, University Park PA 16802, USA and 3Department of Entomology, Center for Infectious Disease Dynamics, Pennsylvania State University, University Park PA 16802, USA
*Corresponding author. 5510C MSRB I, SPC 5680 1150 W. Medical Center Dr. Ann Arbor, MI 48109-5680. Tel: 734-763-2674; Fax: 734-615-2156; E-mail: robertwo@med.umich.edu
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ABSTRACT
We report the case of a patient with a chronic bacterial infection that could not be cured. Drug treatment became progressively less effective due to antibiotic resistance, and the patient died, in effect from overwhelming evolution. Even though the evolution of drug resistance was recognized as a major threat, and the fundamentals of drug resistance evolution are well understood, it was impossible to make evidence-based decisions about the evolutionary risks associated with the various treatment options. We present this case to illustrate the urgent need for translational research in the evolutionary medicine of antibiotic resistance.

KEYWORDS: antibiotic resistance; resistance management; evolutionary risk; clinical decisions; Enterobacter; MRSA

INTRODUCTION
Antibiotic therapy represents one of greatest achievements of modern medicine, but this achievement is threatened by the growing challenge of antibiotic resistance. A case is described of a patient with a chronic, open bacterial infection for which definitive source control could not be obtained. The patient eventually died because her infection evolved resistance to available antibiotics. This patient’s presentation is characteristic of a broad array of cases where the primary determinant of the quality and quantity of life is the rate of resistance evolution. Such patients may also be a source of resistant ‘superbugs’ in health care settings. Our goal is to describe the nature of the clinical choices that had to be made and the knowledge deficits that prevented the application of evolutionary principles in this clinical setting. By more clearly defining the problem we hope to encourage the search for solutions.

CASE PRESENTATION
The patient was a 56-year-old female with a medical history of type 2 diabetes, hyperlipidemia,
pulmonary embolism and nonischemic cardiomyopathy diagnosed 15 years prior. The cardiomyopathy was complicated by secondary pulmonary hypertension and paroxysmal atrial fibrillation. An implantable cardioverter-defibrillator was placed for primary prophylaxis of sudden cardiac death. She underwent Heartware\textsuperscript{®} Left Ventricular Assist Device (LVAD) placement 2 years prior to presentation. She was not a candidate for heart transplant. She presented with a small amount of brown-colored discharged from around the LVAD driveline, which connects the LVAD to the external power source (Fig. 1). She had no fevers, chills, night sweats or weight loss. Her dyspnea was stable, and she had no chest pain and no pain along the driveline. On exam, she was an obese female who was in no acute distress. She was afebrile, with regular heart rate and baseline blood pressure. Inspection of the driveline entry site showed a scant amount of bloody drainage. Laboratory values were notable for a normal white blood cell count and creatinine. The drainage from the driveline was cultured and grew methicillin resistant \textit{Staphylococcus aureus} (MRSA), which was resistant to tetracycline but sensitive to trimethoprim/sulfamethoxazole (Bactrim), erythromycin, clindamycin and vancomycin. An ultrasound was performed that showed no fluid pocket along the driveline. Treatment with vancomycin was initiated via a peripherally inserted central catheter (or PICC line), and she was discharged from the hospital.

**CASE MANAGEMENT AND OUTCOME**

The timing of subsequent hospital visits, antibiotic treatments and the resistance profiles of bacteria isolated from the patient are summarized in Figure 2. The patient had monthly scheduled appointments at an infectious disease outpatient clinic. Throughout, resistance phenotypes were defined as sensitive, intermediate or resistant based on Clinical and Laboratory Standards Institute (CLSI) breakpoints with minimal inhibitory concentrations (MIC) measured by Vitek or e-test.

The patient was seen in clinic 4 weeks after the original presentation. She continued to be without significant symptoms other than persistent drainage around the driveline, indicating ongoing infection. Culture of the drainage again grew MRSA, with the same resistance pattern. Vancomycin was continued. When she returned to clinic at 8 weeks, the drainage was persistent. The PICC line was removed to limit the risk of a PICC line-associated infection, and the patient started clindamycin orally. She remained on clindamycin for about 4 months, when she presented to the hospital with fevers, elevated white blood cell count and left-sided abdominal pain. She was found to have bacteremia with MRSA that now was resistant to clindamycin. Ultrasound of the driveline showed no fluid accumulation amenable to surgical drainage. Vancomycin was restarted, and she left the hospital.

She returned to the hospital 1 month later with confusion and increasing abdominal pain around the driveline. One of two blood cultures grew a coagulase negative \textit{Staphylococcus} (considered to be a contaminant). Urine culture grew vancomycin resistant \textit{Enterococcus} (VRE). She was discharged from the hospital on daptomycin via a PICC line, to cover the MRSA and the VRE. Persistent drainage from the driveline was noted. She presented again 2 months later with fever, leukocytosis and acute renal injury. Blood cultures were negative. Ultrasound of the driveline showed no pocket of fluid accumulation. A urine culture grew an extended spectrum beta-lactamase (ESBL) producing \textit{Escherichia coli}. Broad-spectrum antibiotics were used throughout the hospitalization (daptomycin

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**Figure 1.** Schematic of a left ventricular assist device (LVAD) \textit{in situ}, with driveline to external power source. CT scans of the patient revealed evidence of bacterial build up around the efferent limb of the LVAD and the anastamosis to the ascending aorta. The presumed route of invasion was the drive line. Reproduced from http://www.heartware.com/media-resources with permission.
and cefepime, and briefly vancomycin) and she was discharged on daptomycin alone.

One month later she presented to the hospital with fever. Computed Tomography (CT) scan of the chest revealed gas bubbles around the LVAD and the anastomosis to the ascending aorta (Fig. 1). Incision and drainage of the abscess pocket was performed and the wound was left open to allow daily dressing changes. Blood cultures grew *Enterobacter cloacae*, and cultures from the abscess grew *Enterobacter* and MRSA. The MRSA had a daptomycin MIC of four (resistant). Daptomycin was discontinued, and vancomycin was restarted. The patient was discharged on cefepime and vancomycin.

Two months later she was admitted with fatigue, fever and elevated white blood cell count. Blood and wound cultures again grew *Enterobacter*, but the cefepime MIC had increased from 1 and 2 (sensitive) to 8 (intermediate resistance). Cefepime was stopped and meropenem was started. CT imaging was stable, and did not reveal a drainable abscess. She was seen again in clinic after 6 weeks of meropenem and vancomycin. The wound was still open, and was being packed daily, but appeared to be improving. The PICC line was removed, and she was started on moxifloxacin (to cover both infections). Twelve days after switching to moxifloxacin she was admitted with fatigue and abdominal pain. Blood cultures grew *Enterobacter*. The patient was switched back to meropenem, requiring a PICC. No coverage for the MRSA was used at that time.

The patient was seen in clinic 6 weeks later, nearly 1 year from her initial presentation, at which point the PICC line was removed and the patient started high dose ciprofloxacin, to cover both MRSA and *Enterobacter*. The patient was admitted three days later (Fig. 2, asterisk) with fevers, chills and shortness of breath. Blood cultures were again positive for *Enterobacter*, now resistant to ciprofloxacin. Meropenem was restarted. The patient was discharged on meropenem for the *Enterobacter* and Bactrim for the MRSA.

The patient remained on Bactrim and meropenem for 4 months when she was admitted to the hospital with fatigue, subjective fevers, ‘shakiness’ and elevated white blood cell count. One out of two blood cultures on admission were positive for *Corynebacterium* that was believed to be a contaminant. The Bactrim was discontinued and vancomycin started. She was discharged after a week when her energy subjectively improved, although her leukocyte count remained elevated. The patient was readmitted to the hospital 3 weeks later with fatigue, and she was discharged the subsequent day on the same medications. Blood cultures were negative.

Three weeks later, she presented again with progressive lethargy. Blood culture grew *Enterobacter* with a meropenem MIC of 4 (sensitive), and the meropenem was continued, but 3 days into the hospitalization the blood cultures grew *Enterobacter* with a meropenem MIC of $>$16 (resistant). The

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**Figure 2.** The patient’s course from initial signs of LVAD driveline infection through death. Bars in blue show administration of drug, vertical pink lines the timing and duration of hospital visits and the symbols show levels of resistance to the various antibiotics of MRSA (squares) and *Enterobacter* (circles) isolates taken at various time points, where green is defined as susceptible, yellow is intermediate susceptibilities, and red is resistance. MIC were measured with Vitek or E-test and cutoffs were standard CLSI break points. Drug names in bold can only be given intravenously for this infection. Asterisk shows the timing of the clinical decision discussed in the main text.
antibiotic was switched to a combination of cefepime and vancomycin (this Enterobacter had a cefepime MIC of ≤1, sensitive). However the patient became increasingly obtunded, the white blood cell count continued to rise. The patient’s family decided to withdraw care. She succumbed to the infection.

DISCUSSION

Infection involving prosthetic material, such as an LVAD, is virtually impossible to eradicate without removal of the device, which could not be done in this case. While this patient’s initial infection was susceptible to multiple antibiotics, successive antibiotic choices were met with increasing antibiotic resistance (Fig. 2). The evolution of antibiotic resistance became the key threat to the clinical outcomes that mattered most: the duration and quality of her remaining life. However, clinically relevant data to guide treatment choices to minimize resistance evolution are remarkably limited.

The time to clinical failure of a treatment regimen due to resistance evolution is determined by the duration of two phases [1]. The first phase is the time taken for a resistant organism to first appear in the infection. Resistance arises by mutation, horizontal gene transfer (HGT) or immigration of already resistant bacteria. The second phase is the time taken for resistant organisms to replicate and spread to life-threatening densities. A fundamental dilemma is that many treatment choices have contrasting impacts on the duration of these two phases [2].

Clinical Decision-Making

The goal of treatment was to identify a regimen that gave an immediate improvement in the patient’s health and at the same time maximally delayed the emergence of resistance. Decisions had to be made concerning choice of drug(s), dose, infusion time and dosing frequency and about whether to maintain a regimen until it failed and then switch to another, or whether to change treatment after some fixed interval, perhaps rotating treatments.

To illustrate the issues involved, we focus only on the choice of drug(s) and consider the options available for the treatment of the Enterobacter infection when the patient was admitted to the hospital 1 year into the infection (Fig. 2, asterisk). At that point, it was felt that antibiotic treatment could not be stopped because doing so would result in the infection rapidly overwhelming the patient.

Based on the resistance profiles of the Enterobacter isolated from blood and wound cultures, the drug options were (i) continuing a carbapenem such as meropenem, (ii) switching back to cefepime, a fourth generation cephalosporin, to which the Enterobacter was not fully resistant, (iii) combination therapy with meropenem and cefepime, which is not typically considered an option clinically due to lack of data, (iv) combining one of those antibiotics with another agent for which there was resistance, such as a fluoroquinolone like levofloxacin and/or (v) treatment for a short duration with an antibiotic with significant side effects that would limit prolonged use such as an aminoglycoside (e.g. gentamicin) or colistin.

None of these treatment options is clearly superior based on immediate health outcomes in the treatment of Enterobacter. A small case series with 12 Enterobacter infections shows that 3 failing cefepime therapy were successfully treated with a carbapenem [3]. However, in a series of 51 patients with Enterobacter cloacae bacteremia, cefepime and meropenem therapy had similar outcomes [4]. In a propensity-matched cohort study, 32 patients treated with cefepime had outcomes similar to 32 patients treated with meropenem for bacteremia, pulmonary infection or intra-abdominal infections [5]. These studies are of tenuous relevance to situation of a chronic LVAD infection in which source control cannot be obtained.

Moreover, those studies say little about evolution, a key issue in this case. A major question was whether sequential monotherapy, e.g. meropenem until failure then cefepime or vice versa (options 1 and 2 above), would select for cross-resistance more or less rapidly than would combination therapy with two drugs (option 3). Answering that question involves estimating the impact of sequential and combination therapy on both the origin and the spread of meropenem resistance, cefepime resistance and meropenem–cefepime cross resistance. Combination therapy can reduce the probability of resistance mutations arising because the probability of multiple resistance mechanisms arising de novo in the same bacterium can be vanishingly small, so long as the chosen drugs have independent mechanisms of resistance [1]. However, both antibiotics are beta-lactams. There are resistance mechanisms unique to each drug and mechanisms that confer
resistance to both. Alternatively, meropenem could be combined with one of the earlier-used drugs, like ciprofloxacin against which resistance had already arisen (option 4), in the hope that the cost of resistance to ciprofloxacin would, in the presence of meropenem, favor ciprofloxacin-sensitive bugs [1, 6, 7]. However, combination therapy may also lead to more rapid emergence of a fully resistant organism by way of acquisition of multi-drug resistance genes such as those encoding efflux pumps, or by acquisition of mobile genetic elements that carry resistance genes to multiple classes of antibiotics. It is not clear if adding an additional drug for brief periods to either mono- or combination therapy (option 5) would help retard resistance evolution.

A large literature on these drugs and Enterobacter and related bacteria shows that each of the possible routes of resistance evolution can occur (chromosomal mutations, cross resistance, plasmids, immigration of resistant bacteria). For example, a common step in de novo resistance evolution for both cefepime and meropenem is often derepression of the chromosomally encoded ampC beta-lactamase [8, 9] but this derepression by itself is unlikely to yield clinical resistance to either drug [10, 11]. Cefepime resistance may also require mutations in ampC that improve catalytic activity [12, 13], which have also been observed in other members of this bacterial genus and family [14, 15]. For meropenem, ampC mutations plus outer membrane mutations proteins (ompF) may be required for clinical resistance in Enterobacter [16] and Serratia [17]. The evolution of carbapenem resistance in vivo has been seen to involve both ampC induction and mutations that reduce permeability [18], or may occur in the absence detectable beta-lactamase activity [19]. The risk of acquiring antibiotic resistance through horizontal gene transfer introduces even more uncertainty. Plasmid-borne beta-lactamases often, but not always, confer resistance to the multiple betalactams (reviewed by [20]), and frequently carry resistance to other classes of antibiotics [21, 22]. Furthermore, antibiotic use and indwelling catheter, as was used in this patient, are risk factors for colonization and infection with carbapenem-resistant organisms [23, 24].

Thus, each of the possible routes of resistance evolution can occur, but knowing that something can occur says very little about the likelihood that it will, and the likelihoods are what matter. It should be possible to estimate those probabilities. For instance, what were the chances that this patient’s Enterobacter infection would acquire plasmids conferring cross-resistance? That depends on the likelihood such plasmids exist in her microbiota, her home environment, the hospital, the local region—and whether bacteria bearing such plasmids will contact her Enterobacter. Likewise, if chromosomal mutations are the primary source of resistance, how likely were mutations conferring cross-resistance? If the probability of acquiring plasmids or mutations which confer cross-resistance is low, successive monotherapy (meropenem then cefepime) will likely fail faster than combination therapy (both together). What was the probability of new resistant pathogens invading? Even targeted treatment can create resistance elsewhere in a patient’s microbiome. What was the probability that off-target evolution in non-pathogenic species would be a significant source of resistance for the Enterobacter infection or of new resistant bacteria species?

The general topic of combination therapy against bacteria has a long, and somewhat controversial history in clinical medicine [25–29]. Combination therapy to prevent resistance emergence was shown in early head-to-head trials in tuberculosis [30, 31]. This logic cannot be directly extended to our case. Large meta-analyses of Gram negative bacteremia have not found general support for improved outcomes with combination therapy [27, 28]. A separate meta-analysis specifically looking at the evolution of resistance similarly saw no difference between use of a beta-lactam compared to a beta-lactam plus an aminoglycoside [32]. A large meta-analysis with 173 drug trials, which looked at a broad collection of bacterial infections and antibiotics, did not show a significant difference in resistance emergence between combination therapy and monotherapy, with the exception of penicillin and aminoglycoside monotherapy which has a slightly higher rate [33]. While patients in such trials are not directly analogous to the chronic LVAD infection presented here, they caution against extrapolating from TB.

Clinicians at a patient’s bedside must weigh treatment options with respect to ultimate outcomes. Despite a comprehensive search of the literature, we concluded that it was impossible to make even crude estimates of the evolutionary risks associated with the different treatment options. Consequently, we decided on a treatment plan that avoided potential toxicity, and administered the drug in a manner that was easiest for the patient. Thus meropenem,
the strongest single drug against Enterobacter, was used as monotherapy. Dosing was 1 g every 8 h, easier than the alternative 500 mg every 6 hours. The drug choice was based on the earlier hints of lowered susceptibility to cefepime and to keep a drug available should meropenem fail. After meropenem resistance arose, the patient rapidly succumbed to infection, despite being switched to cefepime.

Future Research Needs
In Box 1, we list specific questions that, had we been able to answer them, would have led to better clinical...
Conclusions. They can all be addressed with currently available technologies. For example, post hoc whole-genome studies of longitudinal isolates taken from patients can directly address how resistance evolved following a given set of choices. Microbiome approaches can define the community dynamics and the potential donor pool of resistance genes. The likelihood of acquiring cross-resistance by HGT could be estimated by examining local and regional isolate collections for cross-resistance. Eventually trials could be done to test which antibiotic choices improve evolutionary outcomes. It remains to be determined whether general rules of thumb can be guided to guide decision making (e.g. start with combination therapy from the beginning, or always use the least amount of the narrowest spectrum drug), or whether each situation will require a different approach (personalized medicine). There is the very interesting possibility that experimental evolution done in real time with bacteria taken from a patient could inform clinical decisions and lead to improved patient outcomes (diagnostic experimental evolution). How does evolutionary risk depend on the pathogen, the patient, the infection and the care setting?

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