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First Case in China of Recurrent Liver Abscess Complicated by Bloodstream Infection Caused by Shewanella algae After Surgery for Cholangiocarcinoma: Diagnostic Value of Metagenomic Next-Generation Sequencing

Shi Zhong
Jiangxi Provincial Maternal and Child Health Hospital

Dong Zhang
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Xinfei Chen
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Huiting Su
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Wan Huang
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Jiayu Guo
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Menglan Zhou
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Minya Lu
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Juan Du
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Qiwen Yang

Yangqiwen81@vip.163.com

Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

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Case Report

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Abstract

Background: *Shewanella algae (S. algae)* is an emerging halophilic, facultative anaerobic opportunistic pathogen, with rare reported cases of clinical infection. Here, we present a case of *S. algae* infection diagnosed with the assistance of plasma metagenomic next-generation sequencing (mNGS).

Case Presentation: An elderly man presented with recurrent fever one year after surgery for cholangiocarcinoma and had a medical history of multiple malignancies and prior infections**.** Imaging examinations revealed an enlarging liver abscess. Multiple sets of blood cultures yielded negative results, and empirical antimicrobial therapy was ineffective or associated with adverse reactions. Plasma mNGS detected *S. algae* with 231 sequence reads and a relative abundance of 14.56%. Further inquiry into the patient's history revealed seafood consumption one week before the onset of fever. Based on the mNGS findings, epidemiological characteristics, and imaging results, the patient was ultimately diagnosed with recurrent liver abscess complicated by bloodstream infection caused by *S. algae*. Following adjustment of antimicrobial therapy according to the etiological diagnosis, inflammatory markers decreased, and the liver abscess showed marked improvement. The patient was subsequently discharged in good general condition.

Conclusions: To our knowledge, this study reports the first case in China of recurrent liver abscess complicated by bloodstream infection caused by *S. algae* in a patient after surgery for cholangiocarcinoma. It is also the first time that mNGS technology has been used to assist in the diagnosis of *S. algae* infection in such patients. This case suggests that for patients with complex conditions where conventional tests fail to identify the pathogen, the possibility of infection with rare pathogens should be considered. mNGS can overcome the limitations of traditional diagnostic methods, provide evidence for accurate diagnosis, and reduce unnecessary antibiotic exposure and associated adverse reactions in clinical treatment.

Introduction

Shewanella algae (*S. algae*) is a motile, flagellated, Gram-negative bacillus with a facultatively aerobic metabolism (1). Currently, the genus *Shewanella* comprises more than sixty recognized species. Previous studies have demonstrated that only four *Shewanella* species are known to cause human infections, namely *Shewanella putrefaciens, Shewanella algae, Shewanella haliotis and Shewanella xiamenensis* (2, 3). Among clinical cases, *S. algae* and *Shewanella putrefaciens* are the two most frequently encountered pathogens (4). Owing to their striking phenotypic similarities, these two species are prone to being misidentified by conventional biochemical assays or automated identification systems (5). Furthermore, false-negative results in microbial cultures are common following empirical antimicrobial administration, which often leads to missed diagnoses. Infections caused by *S. algae* are predominantly associated with seawater exposure or the consumption of seafood (1, 6). With the increasing global availability of seafood products, the incidence of *S. algae* infections has exhibited a corresponding upward trend (7). Therefore, there is an urgent clinical need for accurate diagnosis and

differentiation of *S. algae* infections, which remains a challenging task in practice. Traditional diagnostic approaches primarily include microbial culture, polymerase chain reaction (PCR) and serological testing. However, these techniques are often constrained by prolonged turnaround times, low diagnostic sensitivity and the lack of commercially available reagents, resulting in delayed or missed diagnosis.

Metagenomic next-generation sequencing (mNGS) is an untargeted, high-throughput sequencing-based assay that enables the direct identification of a broad spectrum of pathogens including bacteria, fungi, viruses and parasites from clinical specimens, thereby overcoming the inherent limitations of conventional culture and PCR-based methods (8). Its key advantage lies in the unbiased sequencing of all nucleic acids present in a sample, independent of prior microbial culture or targeted amplification, which renders it particularly valuable for the diagnosis of fastidious or rare infections (9). Accumulating evidence has indicated that mNGS plays an important auxiliary role in the diagnosis of rare or polymicrobial infections that cannot be confirmed by traditional diagnostic modalities (10). Here, we report the first case in China of recurrent pyogenic liver abscess complicated by bloodstream infection caused by *S. algae*, which was identified with the assistance of mNGS. This case highlights the diagnostic value of mNGS in complex infectious diseases and expands the known clinical spectrum of *S. algae* infections. Our findings also suggest that *S. algae*, as an opportunistic pathogen, warrants clinical vigilance for its potential to cause infections not only in coastal regions but also in inland areas, and at non-classical infection sites.

Case Presentation

The patient was an 85-year-old man with a medical history of cholangiocarcinoma, prostate cancer, colon cancer, hepatitis B, duodenal ulcer, and gastrointestinal bleeding. There were multiple cases of malignant tumors in his family. The patient underwent surgical resection for cholangiocarcinoma at a renowned tertiary (Level A) hospital in Beijing. Postoperatively, he experienced recurrent fever complicated by infections at multiple sites and received several courses of antimicrobial therapy.

In late 2024, the patient developed high-grade fever accompanied by chills following cold exposure. Abdominal imaging revealed a patchy hypodense lesion in the right hepatic hilum, suggestive of a liver abscess. *Aeromonas caviae* was isolated from blood cultures and was resistant to ceftazidime but susceptible to levofloxacin and meropenem. As the lesion was adjacent to the hepatic hilum, percutaneous drainage was not feasible. Conservative treatment with meropenem and levofloxacin was therefore initiated, resulting in gradual reduction of the lesion with a favourable clinical response.

On 29 April 2025, the patient was admitted to our hospital with a history of recurrent fever for more than one year after surgery for cholangiocarcinoma and renewed fever for three days. Four days prior to admission, the patient developed fatigue without identifiable predisposing factors. Two days later, he experienced recurrent fever with a maximum temperature of 38.6 °C, presenting with one daily fever spike accompanied by chills, but without rigors, cough, abdominal pain or other associated symptoms.

On admission, the patient was in good general condition with stable vital signs, and no other abnormal findings were noted on physical examination.

Abdominal ultrasound performed on admission indicated the presence of a liver abscess (Figure 1B), which was larger than the lesion identified at the initial onset of infection (Figure 1A). A follow-up examination conducted approximately two weeks after treatment initiation demonstrated a reduction in lesion size compared with the initial admission imaging (Figure 1C). Dynamic changes in the patient's body temperature and inflammatory markers during hospitalization are shown in Figure 2. Coagulation function gradually recovered from a hypercoagulable state to normal ranges. Two sets of blood cultures were collected on the day of admission and on the third day post-admission, respectively; all cultures yielded negative results after three days of incubation, and other laboratory parameters were unremarkable.

The patient was given a definitive diagnosis of liver abscess; however, the causative pathogen initially remained unidentified. On 4 May, plasma samples were submitted for mNGS testing, which identified *Shewanella algae* (244 sequence reads, relative abundance of 26.13%). Given the rarity of this pathogen in clinical settings, the laboratory repeated the assay on 6 May, with *S. algae* still detected (231 sequences, relative abundance of 14.56%). Further retrospective inquiry into the patient's medical history revealed a history of seafood consumption prior to the onset of symptoms. Based on the patient's clinical manifestations and epidemiological characteristics, *S. algae* was considered the suspected aetiological agent.

After admission, the patient received empirical treatment with meropenem at a dosage of 1 g twice daily for two days; however, the therapeutic response was suboptimal. On 1 May, linezolid was added to the regimen as combination therapy at a dosage of 0.6 g twice daily for six days. During this period, the patient developed suspected drug-related adverse reactions, including hearing loss and black tongue. On 7 May, based on the plasma mNGS results and epidemiological information, the clinical team suspected *Shewanella algae* infection and adjusted the antimicrobial regimen to ceftazidime at a dosage of 1 g three times daily for seven days. The patient was discharged after improvement in all clinical parameters. At a follow-up visit approximately two weeks later, the patient remained in good general condition.

Discussion

Shewanella algae (*S. algae*) is an opportunistic pathogen ubiquitously distributed in marine environments. Emerging evidence suggests that global warming may facilitate the cross-regional dissemination of this pathogen by expanding its habitat range and enhancing its transmission capacity (11). Cases of *S. algae* infection have been documented across Asia, Europe and the Americas, indicating its broad geographical distribution and potential for trans-regional spread (6). In addition to community-acquired infections, hospital reports have documented *S. algae* as a nosocomial pathogen responsible for healthcare-associated infections (12). Clinically reported cases typically occur in coastal

cities during summer (6). However, the present case manifested in Beijing, an inland region, in spring. *S. algae* infections predominantly affect the elderly, immunocompromised individuals, patients with malignancies, hepatobiliary diseases or a history of surgery (1,13). The patient in this case was an elderly individual with a medical history of multiple tumours and compromised immunity, placing him in the high-risk group for *S. algae* infection. Regarding the transmission route, retrospective inquiry revealed a history of seafood consumption one week prior to symptom onset, suggesting oral ingestion as the likely route of infection. Post-cholangiocarcinoma surgery anatomical alterations and biliary composition imbalance may have facilitated the intrahepatic colonisation and recurrent infection of *S. algae* in the biliary tract. The pathogenesis of this case is highly consistent with the hepatobiliary system-specific susceptibility reported in existing literature (14).

S. algae pathogenicity is associated with multiple virulence factors, including haemolysins, proteases, siderophore systems, type VI secretion systems and biofilm formation (6). Among these, the cyclic di-guanosine monophosphate (c-di-GMP) signalling pathway and the *BarA–UvrY* two-component system can promote biofilm and extracellular polysaccharide (EPS) synthesis, enhancing bacterial adhesion and resistance to bile salts and oxidative stress (15). Whole-genome sequencing of bile-isolated *S. algae* strain (ACC) has identified genes such as *exbBD*, *wecA* and *galU*, which are closely associated with adhesion and colonisation of biliary epithelial cells (16), further supporting the potential of *S. algae* to survive in the biliary environment in this case. The presence of multiple virulence factors enables *S. algae* to cause not only common superficial skin and soft tissue infections (17) but also invasive infections involving the lungs, bone marrow and intervertebral discs (14,18,19), highlighting its strong virulence and propensity for invasive infection. This study reports liver and bloodstream infections caused by *S. algae*, which not only corroborates the high virulence of this pathogen but also expands the known spectrum of *S. algae* infections, providing new insights for clinical practice.

In terms of treatment, *S. algae* is generally susceptible to third- and fourth-generation cephalosporins, fluoroquinolones, and carbapenems, but resistant to penicillins and first-generation cephalosporins (7). Comparative genomic and phylogenetic analyses have revealed that carriage of the *sul1* and *dfrA12* genes mediates sulfonamide resistance (20), while the *bla*$_{OXA\text{-}55\text{-}like}$ gene is associated with carbapenem resistance (16,21). In addition, the *GyrA S83V* mutation has been identified as a mechanism underlying quinolone resistance (22). These studies suggest that *S. algae* possesses the potential to develop antimicrobial resistance through both horizontal gene transfer and point mutations (6,20,22). In the present case, *Aeromonas caviae* (resistant to ceftazidime but susceptible to levofloxacin and meropenem) was isolated from a previous liver abscess culture. Accordingly, meropenem monotherapy was initiated upon admission. However, the clinical response was suboptimal, prompting the addition of linezolid to broaden antimicrobial coverage. Suspected drug-related adverse reactions (hearing loss and tongue discoloration) subsequently developed. The limited response to meropenem monotherapy and improved outcomes with combination therapy suggest potential contributing factors, including potentially unstable carbapenem susceptibility in *S. algae* (21), insufficient duration of antimicrobial therapy, polymicrobial infection or inadequate tissue penetration of the antimicrobial agents. Ultimately, based on mNGS results, the treatment regimen was adjusted from broad-spectrum antibiotics to the

more targeted ceftazidime, resulting in significant clinical improvement, avoidance of unnecessary carbapenem exposure and prevention of drug-related adverse reactions.

Currently, clinical detection of *S. algae* primarily relies on conventional microbial culture, automated identification systems, matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF MS) and 16S rRNA gene sequencing (1,11,23,24). Conventional identification systems, such as VITEK 2 or API 20 NE, are prone to misidentifying *S. algae* as *Shewanella putrefaciens* due to database limitations, leading to suboptimal accuracy (1). MALDI-TOF MS enables rapid bacterial identification but may exhibit cross-reactivity with the closely related *Shewanella abalonis* (23). The currently recommended detection strategy involves bacterial culture combined with MALDI-TOF MS for initial screening and 16S rRNA gene sequencing for confirmation. However, the detection rate of bacterial culture remains limited, and the clinical application of 16S rRNA gene sequencing in patients with complex infections is not widespread. As a result, the advent of mNGS has partially addressed these limitations, particularly demonstrating advantages in culture-negative and complex infections by directly detecting pathogens from blood or bile samples and providing aetiological evidence (9,25). In the present case, multiple sets of blood cultures yielded negative results. As percutaneous drainage was not feasible because of the lesion's proximity to the hepatic hilum, plasma samples were submitted for mNGS. Consistent detection of *Shewanella algae* in both the initial and repeat mNGS assays indicates good reproducibility and reliability of the test results. Several potential explanations may account for the discordance between negative blood culture results and positive plasma mNGS findings in this case. First, antimicrobial interference: the administration of antimicrobial agents prior to blood sampling may have inhibited bacterial growth; however, free bacterial nucleic acids can persist in plasma and thus remain detectable by mNGS. Second, limitations of culture conditions: *S. algae* is a halophilic, microaerophilic bacterium, and standard blood culture systems may not provide optimal growth conditions, thereby increasing the likelihood of false-negative results. Third, release of cfDNA from infectious foci: bacterial lysis within infectious lesions, such as liver abscesses, may release cell-free DNA (cfDNA) into the bloodstream, resulting in positive mNGS findings despite negative culture results. Fourth, intermittent or low-level bacteraemia: *S. algae* may be present in the bloodstream only transiently or at low levels; insufficient blood sampling volume or collection outside the peak bacteraemic period may therefore lead to negative culture results. In summary, the use of mNGS as an adjunctive diagnostic tool for *S. algae* infection highlights its unique value in identifying rare pathogens in plasma when conventional diagnostic methods fail to establish the aetiological agent.

This case report has certain limitations: direct tracing of *S. algae* in the seafood consumed by the patient was not performed, and no phylogenetic analysis was conducted between the seafood-derived and liver abscess-derived *S. algae* strains. Furthermore, failure to isolate the pathogen precluded in vitro antimicrobial susceptibility testing to clarify the resistance profile of the infecting strain.

Conclusion

This study reports the first case in China of recurrent liver abscess complicated by bloodstream infection caused by *S. algae* in a patient after surgery for cholangiocarcinoma. This case expands the currently recognized clinical spectrum of *S. algae* infections and highlights the considerable environmental adaptability of this pathogen, suggesting that *S. algae* may represent an important opportunistic pathogen in immunocompromised populations. The successful use of mNGS as an adjunctive diagnostic tool in this patient indicates that, in immunocompromised individuals in whom conventional diagnostic tests fail to identify the aetiological agent, the possibility of infection with rare pathogens should be considered. In such cases, molecular diagnostic technologies such as mNGS should be applied judiciously to achieve rapid and accurate aetiological diagnosis, thereby guiding individualized anti-infective therapy.

Abbreviations

mNGS: metagenomic next-generation sequencing; MALDI-TOF MS: matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry

Declarations

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Authors'contributions

SZ and JD made the conception and design of the work; MLZ and XFC guided the methods; XFC, HTS, JYG and MYL collected the clinical data; XFC and DZ interpreted the data; SZ drafted the manuscript; JD reviewed the manuscript; QWY supervised the study; DZ administrated the project; QWY and SZ acquired the fund of the study.

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Data Availability

All data generated or analyzed during this study are included in this published article.

Ethics approval and consent to participate

Not applicable.

Competing interests

The authors declared that they have no competing interests.

Consent for publication

Written informed consent for patient information to be published was provided by the patient.

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Figures

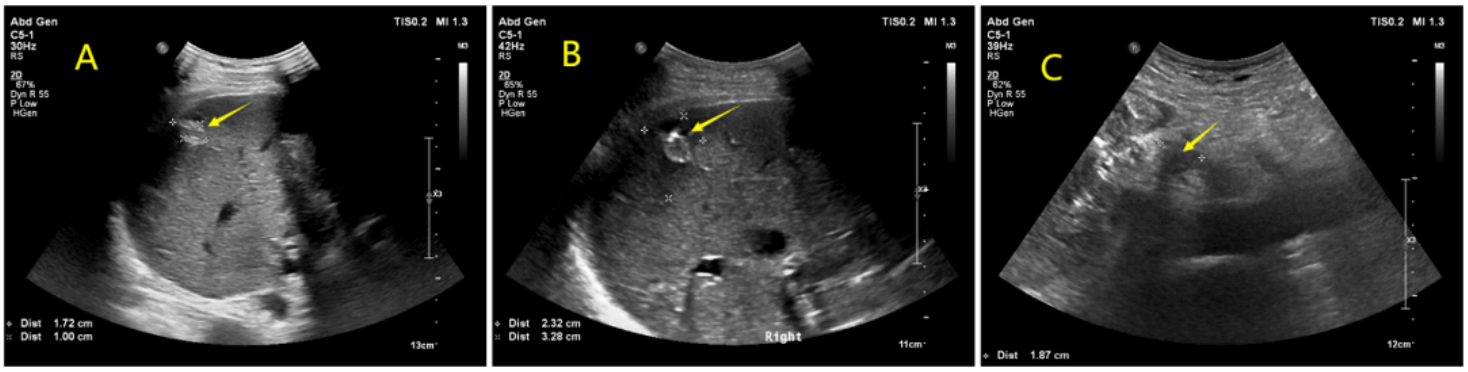


Figure 1

Serial changes in liver abscess on abdominal ultrasonography

(A) 14 April 2025: A mixed echoic lesion measuring 1.7 × 1.0 cm in the right hepatic lobe adjacent to the diaphragmatic dome. (B) 29 April 2025: A mixed echoic lesion measuring 2.2 × 3.3 cm in the right hepatic lobe adjacent to the diaphragmatic dome. (C) 12 May 2025: A mixed echoic lesion measuring 1.8 × 1.4 cm in the right hepatic lobe adjacent to the diaphragmatic dome.

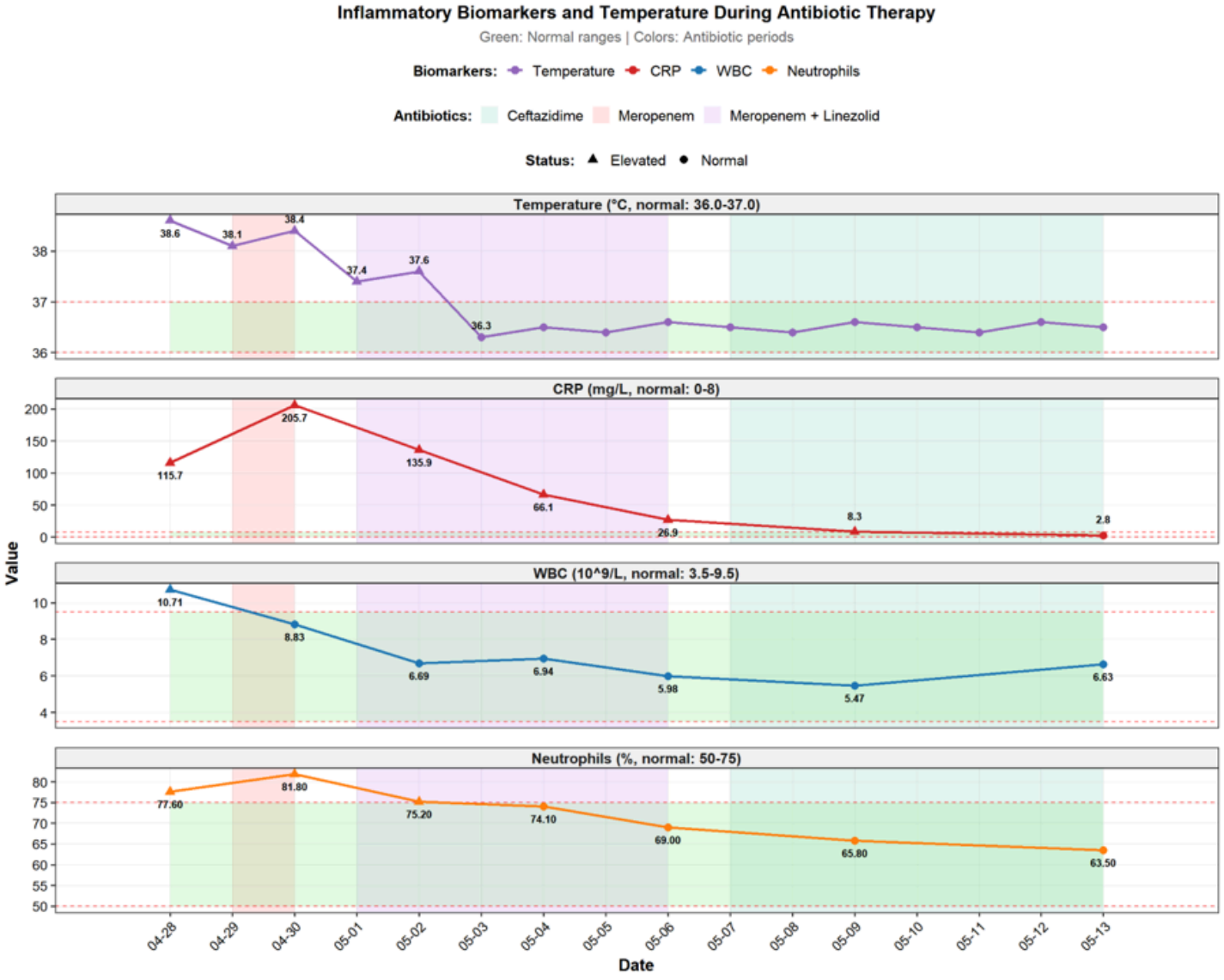


Figure 2

Dynamic trends in antimicrobial administration, axillary temperature, C-reactive protein levels, total white blood cell counts and neutrophil percentages during the patient's hospitalisation