A Pain in the Neck: Cervical Pyomyositis, a Rare Case of Extraintestinal Nontyphoidal Salmonellosis Further Characterized by Whole-Genome Sequencing

Pishoy Haroun, MD[1], Shangxin Yang, PhD[1], Paul C. Adamson, MD MPH[1], Ashlyn N. Sakona, MD DTM&H[1]
[1]*University of California, Los Angeles*

Background

- Nontyphoidal salmonellosis (NTS) is the second-most common foodborne illness in the US.
- Extraintestinal manifestations are rare.
- We describe a case of sternocleidomastoid (SCM) pyomyositis, a rare entity, caused by *Salmonella enterica,* further delineated by whole-genome sequencing (WGS).

Case

A 55 year old male with liver cirrhosis and uncontrolled type-II diabetes mellitus presented with a six-day history of an enlarging left-sided neck mass. He had no fevers, chills, night sweats, nausea, vomiting or diarrhea. He had recently returned from Saudia Arabia with exposures to camels, bats and lemurs. He did not consume raw foods or dairy products.

Physical exam revealed normal vital signs and a large firm neck mass. Labs were notable for leukocytosis and hyperglycemia. Neck computed tomography revealed a 6 cm heterogeneous mass inseparable from the left SCM. He required repeated drainage procedures; histopathology revealed skeletal muscle with inflammation, but no malignancy. Blood and procedural cultures grew Salmonella group B. He was treated with ceftriaxone then trimethoprim-sulfamethoxazole. Follow-up 4 weeks after presentation revealed only residual induration.

Methods

- WGS was performed using Illumina MiSeq.
- Genotype and antimicrobial resistance markers were identified using MLST, KmerFinder and ResFinder on Center of Genomic Epidemiology.
- Virulence factors were identified using VFanalyzer.

Results

- The bacteria was identified as *Salmonella enterica subspecies enterica* serovar Typhimurium, typed as ST19, the major phylogroup of Typhimurium globally.

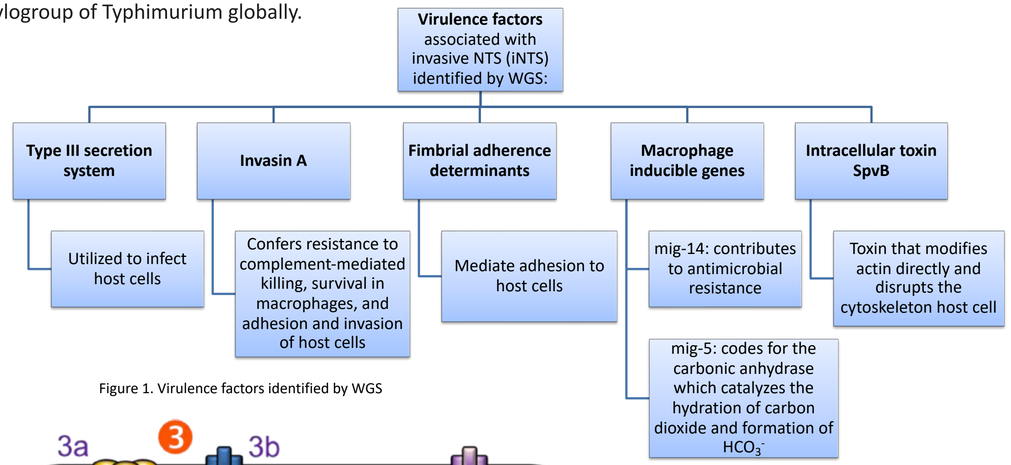

Figure 1. Virulence factors identified by WGS

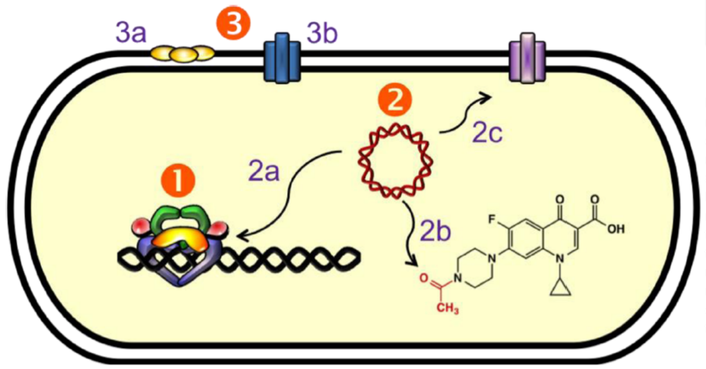

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Figure 2. Mechanisms of quinolone resistance. (1) Target-mediated resistance. Mutations in gyrase and topoisomerase IV weaken quinolone–enzyme interactions. (2) Plasmid-mediated resistance. (2a) Qnr proteins (yellow) decrease topoisomerase–DNA binding and protect enzyme–DNA complexes from quinolones. (2b) Aac(6′)-Ib-cr is an aminoglycoside acetyltransferase that acetylates the free nitrogen on the C7 ring of ciprofloxacin and norfloxacin, decreasing their effectiveness. (2c) Plasmid-encoded efflux pumps decrease the concentration of quinolones in the cell. (3) Chromosome-mediated resistance. (3a) Underexpression of porins in Gram-negative species decreases drug uptake. (3b) Overexpression of chromosome-encoded efflux pumps decreases drug retention in the cell

Drug	Class	Predicted Susceptibility	Gene	Resistance Mechanism
Amikacin	Aminoglycoside	Resistant	*aac(6')-Iaa*	Antibiotic modification
Tobramycin	Aminoglycoside	Resistant	*aac(6')-Iaa*	Antibiotic modification
Ciprofloxacin	Quinolone	Resistant	*qnrB19*	Antibiotic target protection

Table 1. Antibiotic resistance as predicted by WGS

Discussion

- Patient comorbidities, such as type-II diabetes mellitus and liver cirrhosis, likely contributed to this case of invasive NTS.
- WGS identified organism-specific factors, such as serovar and sequence type, as well as multiple virulence factors that likely contributed to invasive NTS, such as Invasin A and intracellular toxin SpvB,.
- WGS also identified multiple antimicrobial resistance genes, including one conferring resistance to fluoroquinolones.
- Two of the main mechanisms that result in fluroquinolone resistance include mutations in topoisomerase genes (*gyrA, gyrB, parC, parE*), and presence of plasmid-mediated quinolone resistance (PMQR) genes, which typically confer low-level resistance.
  - Mutations in topoisomerase genes affect the ability of the drug to bind to topoisomerase enzyme targets
  - Presence of PMQR genes may lead to protective proteins, efflux pumps and/or drug modification.
- PMQR gene qnrB19 was identified; however, no mutations in *gyrA, gyrB, parC, or parE* were identified.
- Phenotypic antibiotic susceptibility testing revealed “intermediate” susceptibility to Ciprofloxacin.

Key Points

- Host factors (immunocompromising conditions (ie AIDS, diabetes, chronic liver disease)) and organism-specific factors (serovar, virulence factors) contribute to invasive disease and morbidity in NTS.
- Fluoroquinolone resistance is a rising concern, and may be mediated by multiple mechanisms.
- WGS can identify antimicrobial resistance and its mechanism, as well as organism characteristics that may influence morbidity.