Comparison of Routine Microbiology Results at Definitive Closure and Wound Infection in Type III Tibia Fractures

The Major Extremity Trauma Research Consortium (METRC)

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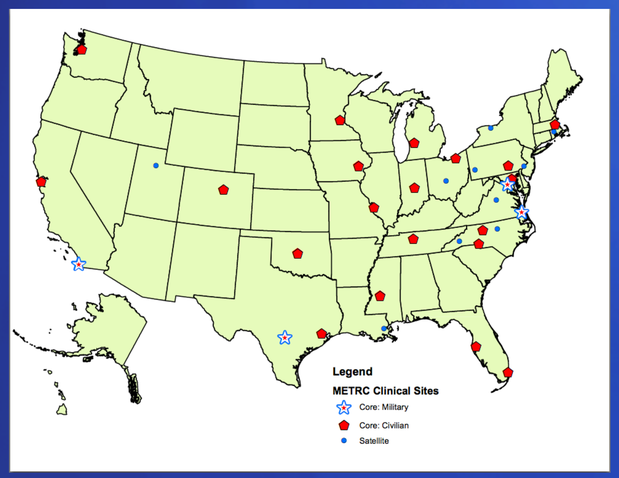
PURPOSE

Infection is a common and significant complication following high-energy fractures. Relating the patient's initial wound bioburden profile to a subsequent deep infection as well as early antibiotic treatment to the later infecting pathogen remains a significant clinical challenge. This analysis examines the correlation between routine microbiology results at the time of soft tissue coverage with subsequent wound infection in Type III tibia fractures and transtibial amputations.

METHODS

447 patients with Type III tibia fractures/traumatic amputation were recruited across 38 trauma centers (see Figure 1) and followed for 6 months after definitive soft tissue coverage. Debrided tissues and swabs collected at the time of final soft tissue coverage and at subsequent infection were sent for routine microbiology at a central laboratory. Bivariate analyses & multivariate regression examined the relationship between routine microbiology results at baseline and subsequent infection.

FIGURE 1



RESULTS

Figure 2 shows this cohort to be moderately to severely injured on the whole based on the OTA Open Fracture Classification. The overall infection rate was 15%. Among 338 participants with negative microbiology results at baseline, the 6-month infection rate was 11%. Among 109 patients with positive routine microbiology results at baseline, the infection rate was 26%. After adjusting for confounders, participants with positive baseline results were twice as likely to develop an infection (OR 2.72; p=0.001). Figure 3 displays complications by the level of initial contamination. The presence of surface and embedded wound contamination at initial debridement were also predictive of infection (OR 2.42 & 3.11, respectively; p<0.05 for both).

Overall, the percent of positive baseline routine microbiology species matching the species identified at the subsequent infection was 65% (see Figure 4). The 3 most common species identified at soft tissue coverage were *Enterobacter cloacae*, *Enterococcus*, and *Serratia marcescens*. Of those with these species present at baseline, 8/10, 3/6 and 3/6 developed subsequent infection with these bacteria. Among patients with positive baseline cultures who later developed infection, Enterobacter and Serratia marcescens were the most common infecting organisms (39% & 22%). In the entire cohort of 43 participants with an infection, the most common organism (18 of 43, or 42%) detected was *Staphylococcus aureus*, (11 of these 18 were *MSSA*). *Staphylococcus aureus,* however, was only observed in 3 baseline results.

FIGURE 4

Positive at Baseline and Follow Up

65% correlation of initial culture to later infection

	Baseline	Follow Up		Baseline	Follow Up
1	staphylococcus	mssa	13	serratia marcescens	mssa
2	serratia marcescens pseudomonas aeruginosa	mrsa pseudomonas aeruginosa	14	enterobacter cloacae	enterobacter cloacae burkholderia
3	enterococcus	enterococcus	15	aeromonas providencia alcalifaciens	serratia marcescens staphylococcus diphtheroids
4	enterobacter cloacae	enterobacter cloacae	16	stenotrophomonas maltophilia	pseudomonas aeruginosa
5	enterobacter cloacae	enterobacter cloacae	17	enterobacter cloacae	enterobacter cloacae
6	serratia marcescens	serratia marcescens	18	staphylococcus	propionibacterium acnes
7	serratia marcescens	serratia marcescens	19	enterococcus	enterococcus
8	fusarium	mssa serratia marcescens	20	serratia marcescens enterococcus enterobacter cloacae	serratia marcescens enterobacter cloacae enterococcus hafnia alvei
9	enterococcus	diphtheroids	21	enterobacter cloacae	enterobacter cloacae
10	enterobacter cloacae	enterobacter cloacae	22	citrobacter amalonaticus klebsiella pneumoniae	citrobacter amalonaticus klebsiella pneumoniae
11	enterobacter cloacae; acinetobacter calcoaceticus-baumannii complex klebsiella oxytoca streptococcus	enterobacter cloacae; acinetobacter calcoaceticus-baumannii complex klebsiella oxytoca streptococcus	23	serratia marcescens pseudomonas putida stenotrophomonas maltophilia fusarium	enterobacter cancerogenus enterobacter cloacae
12	enterococcus	enterococcus			

FIGURE 2

OTA OFC Classification

OFC Domain	Lowest Severity	Middle Severity	Highest Severity
Bone Loss	94 (21%)	183 (41%)	127 (28%)
Muscle	87 (19%)	227 (51%)	90 (20%)
Skin	133 (30%)	162 (36%)	109 (24%)
Arterial	303 (68%)	73 (16%)	28 (6%)
Contamination	101 (23%)	174 (39%)	129 (29%)

FIGURE 3

Complications by Level of Initial Contamination

Complication	No grossly visible contamination n=101	Surface contamination visible n=174	Contamination embedded in bone n=129
None	49 (49%)	67 (39%)	45 (35%)
Deep Infection	7 (7%)	29 (17%)	24 (19%)
Amputation	0 (0%)	3 (2%)	3 (2%)
Flap Failure	2 (2%)	5 (3%)	3 (2%)
Nonunion	15 (15%)	19 (11%)	18 (14%)
Other Bone Graft	0 (0%)	15 (9%)	9 (7%)
All Other Complications	28 (28%)	36 (21%)	27 (21%)

CONCLUSIONS

We document a correlation between bioburden (measured by routine microbiology) at the time of soft tissue coverage and subsequent infection. Wound characteristics – surface contamination and embedded debris were strong predictors of infection. *Enterobacter cloacae* was the most common species among patients with positive baseline results. *S. aureus*, however, (primarily *MSSA*) was the most prominent among all patients presenting with infection. The low detection of *S. aureus* at baseline could be related to antibiotic coverage at that time. These data suggest that we might need to know and treat wound bioburden at the time of coverage to lower our infection rates. A cephalosporin might not be the appropriate antibiotic and short prophylactic doses might be inadequate. There appear to be limitations in routine microbiology and the use of enhanced techniques for baseline microbial identification might be critical in new strategies for the prevention of infection.

Improving outcomes through collaborative research…

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