Using Next Generation Sequencing to Understand Surgical Blade Contamination During Upper Extremity Fracture Repair - Applying New Technologies to Answer Old Questions

Bijan Dehghani[1], Ryan DeAngelis[1], Mitchell Hallman[1], Jaret Karnuta[1], Mohammed Abdullah[1], Aymen Alqazzaz[1], Derek Donegan[1], Samir Mehta[1]
[1]University of Pennsylvania, Department of Orthopedic Surgery, Philadelphia, PA

Disclosures: BD bijan.dehghani@pennmedicine.upenn.edu – (N), RD (N), MH (N), JK (N), MA (N), AA (N), DD (N), SM (N)

Introduction: Postoperative fracture site infection leads to significant patient morbidity and mortality, and further contributes to the socio-economic strain toward healthcare globally. One potential source of infection is the skin flora. Surgical dogma suggests surgical blades as a vehicle for introducing bacteria, however, the literature surrounding the prevalence of surgical blade contamination has varied significantly over the past several decades. In this study, modern high throughput DNA sequencing was used to detect bacterial DNA on surgical blades used for skin incision in patients undergoing upper extremity fracture open reduction internal fixation.

METHODS: This was a prospective, pilot study conducted at a high-volume, level 1 trauma center. All acute, closed upper extremity fractures requiring operative stabilization were consecutively enrolled in this study. The primary endpoint was defined as the presence of bacterial DNA on the surgical blade. At the time of surgery, two sterile surgical blades were opened simultaneously into the sterile field and placed on separate surgical blade handles. The control blade remained on the sterile instrument table and was not used for any part of the procedure. The test blade was used for the initial skin incision and superficial dissection. Each blade was then transferred to a sterile cup using a sterile needle driver. A separate needle driver was used for each blade. The blades were then sent for Next-Generation Sequencing (NGS) analysis following the manufacturer protocol (MicroGenDx Diagnostics, Orlando, Florida). Negative control blades were opened directly into a sterile container and sent for NGS. Positive control blades were used for skin incision through known, visible infection, and then transferred to a sterile container and sent for NGS (Figure 1)

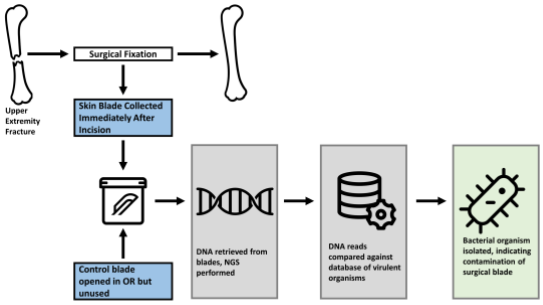

Figure 1. Workflow sequence for next generation sequencing surgical blade assessment

RESULTS: Forty patients were enrolled in this study. The median age was 33.5 years old and 30% were female; the median BMI was 26.52. Humerus fractures were the most common injury (17, 42.5%) followed by clavicle fractures (13, 32.5%), and radius/ulna fractures (10, 25.0%). NGS analysis revealed no contamination of test blades used for skin incision; however, three control blades tested positive for bacterial DNA. Median time from injury to surgery was 12.5 days, with 85% of patients treated as outpatient procedures. Negative-control blades tested negative bacterial DNA (0/2); the positive-control blades resulted in positive for bacterial DNA contamination (2/2). (Table 1)

Variable	Level	
Number of Patients		40
Age (years, median [IQR])		33.50 [26.25, 63.00]
Time to Surgery (days, median [IQR])		12.50 [10.00, 16.50]
BMI (median [IQR])		26.52 [22.70, 31.28]
Inpatient/Outpatient	Inpatient	6 (15.0)
	Outpatient	34 (85.0)
Sex (%)	Female	12 (30.0)
	Male	28 (70.0)
Insurance Type (%)	Medicaid	4 (10.0)
	Medicare	9 (22.5)
	Private	26 (65.0)
	VA	1 (2.5)
Bone (%)	Clavicle	13 (32.5)
	Forearm	10 (25.0)
	Humerus	17 (42.5)
Smoking Status (%)	Never	32 (80.0)
	Former	5 (12.5)
	Current	3 (7.5)
Next-Generation Sequencing		
Sample	**Results**	
Skin Blade	0/40 (0)	
Control Blade	3/40 (7.5)	
Negative-Control	0/2	
Positive-Control	2/2	

Table 1. Patient demographic information and next generation sequencing results

DISCUSSION: This was a prospective, observational study conducted at a high-volume, level 1 trauma center. All acute, closed upper extremity fractures requiring operative stabilization were consecutively enrolled. The primary endpoint was defined as the presence of bacterial DNA on the surgical blade used for the initial skin incision. At the time of surgery, two sterile surgical blades were opened simultaneously into the sterile field and placed on separate surgical blade handles. The control blade remained on the sterile instrument table and was not used for any part of the procedure. The test blade was used for the initial skin incision and superficial dissection. Each blade was then transferred to a sterile cup using a sterile needle driver. A separate needle driver was used for each blade. The blades were then sent for Next-Generation Sequencing (NGS) analysis following the manufacturer protocol (MicroGenDx Diagnostics, Orlando, Florida) (Figure 1). Negative-control blades were opened directly into a sterile container and sent for NGS. Positive-control blades were used for skin incision through known, grossly infected extremities, and then transferred to a sterile container and sent for NGS. Surgical blades used for skin incision in the upper extremity are not contaminated with bacteria as measured by NGS. This finding challenges established surgical dogma regarding surgical blade contamination, and, further supports that the same surgical blade can safely be used for deeper dissection.

SIGNIFICANCE/CLINICAL RELEVANCE: The results of our study challenge the historical belief that separate surgical blades must be used for superficial and deep dissection. Even though the cost of individual blades is relatively low, using the same surgical blade throughout the course of the entire dissection can help to reduce waste, increase efficiency and improve safety of operating room personnel not having to switch surgical blades and pass the knife back and forth in the field.