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Poster Session VI
Miscellaneous

CLINICAL SIGNIFICANCE, BACTERIAL IDENTIFICATION AND ANTIMICROBIAL SUSCEPTIBILITY OF THE EMERGING PATHOGEN HELCOCOCCUS KUNZII

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***Objectives*:** The genus *Helcococcus* comprises catalase-negative, facultatively anaerobic, Gram-positive cocci. To date, three species have been described: *H. kunzii* (1993), *H. ovis* (1999) and *H. sueciensis* (2004). As part of the human skin flora, *H. kunzii* is mainly isolated from infected wounds of lower extremities, particularly in diabetic patients. However, only few case reports have described the role of this emerging pathogen. The aim of the study was then to determine clinical significance, methods of identification and antimicrobial susceptibility of *H. kunzii* clinical isolates.

***Methods*:** From 2008 to 2013, 40 clinical isolates of *H. kunzii* collected in four institutions (3 in France and 1 in Switzerland) were included. Clinical data were obtained for each patient (age, gender, predisposing conditions, site of isolation and clinical presentation). Identification was carried out by MALDI-TOF mass spectrometry and confirmed by sequencing of the *sodA* gene. MIC values of 19 antibiotics were determined by the microdilution method in Mueller-Hinton broth with lysed horse blood (5%) and β-NAD (20 mg/L). Screening for the following resistance genes was performed by PCR: *erm*(A), *erm*(TR), *erm*(B), *erm*(C), *msr*(A), *tet*(L), *tet*(M) and *tet*(O).

***Results*:** All the strains were recovered from wounds of lower limbs, except one that was isolated from blood. The mean age of patients was 62 years (range 21-91 years), with a sex ratio M/F at 4. Underlying comorbidities were present in all patients: diabetes mellitus (48%), cardiac pathology (30%), vascular pathology (55%), obesity (8%) and cancer (10%). The different types of clinical presentation were leg ulcer, osteitis and gangrene, with a vast majority (95%) of mixed cultures (i.e. staphylococci, streptococci). Both MALDI-TOF and *sodA* sequencing accurately identified all isolates to the species level. All isolates were susceptible to b-lactams, glycopeptides, linezolid and daptomycin (Table 1). Some strains presented acquired resistance to macrolides and related compounds (n = 10, 25%) due to the presence of the *erm*(TR) gene [subclass of *erm*(A)], while another (2.5%) was resistant to tetracycline by production of Tet(M).

***Conclusion*:** This is the largest case series of infections caused by *H. kunzii*, an emerging pathogen that should be detected in wound infections, especially in patients suffering from diabetes mellitus.

Table 1. Antimicrobial susceptibility of the 40 *H. kunzii* clinical isolates.

Antibiotic	MIC (mg/L)		
	MIC_{50}	MIC_{90}	Range
Penicillin G	0.03	0.06	0.01-0.12
Amoxicillin	0.06	0.12	0.01-0.25
Cefotaxime	0.25	0.5	0.01-1
Imipenem	0.01	0.03	0.01-0.03
Levofloxacin	1	2	0.25-32
Ciprofloxacin	2	4	1-32
Erythromycin	1	>256	0.25->256
Clindamycin	0.25	>256	0.03->256
Quinupristin-Dalfopristin	0.5	1	0.12-2
Gentamicin	2	4	0.5-64
Daptomycin	0.5	0.5	0.25-1
Linezolid	2	2	1-2
Rifampicin	0.03	0.12	0.01-2
Vancomycin	0.5	0.5	0.25-1
Teicoplanin	0.12	0.25	0.03-0.25
Tetracycline	0.12	0.25	0.06-16
Tigecycline	<0.01	<0.01	<0.01
Cotrimoxazole	0.5	1	0.12-8
Colistin	>256	>256	>256