Getting a Knack for the GPACs & GNACs:
The Basics, and some more...

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Disclosures:

• Currently (11/2019) involved in ongoing compensated research projects with Attostar LLC
Objectives:

• 1: Describe the important organisms in the GPAC and GNAC categories

• 2: Familiarize oneself with the emerging disease associations of clinical relevance

• 3: Understand the importance of the microbiology laboratory identification of these organisms, and the underlying purpose behind identifying them

Guidepost:

• 1. Anaerobes, in general
• 2. Focusing on cocci:
  – GPAC
  – GNAC
• 3. Laboratory Considerations
• 4. Current issues of interest
When invoke anaerobes?

• Reasonable suspicion:
  – Gram stain discordant with culture
  – Infections of the gut, or mucus membrane
    • Trauma, penetrations, procedures, or plastics that cross between these zones
  – Gas production
  – Stinky
Understanding the microbiome of diabetic foot osteomyelitis: insights from molecular and microscopic approaches.

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Abstract
OBJECTIVES: Rigorous visual evidence on whether or not biofilms are involved in diabetic foot osteomyelitis (DFO) is lacking. We employed a suite of molecular and microscopic approaches to investigate the microbiome, and phenotypic state of microorganisms involved in DFO.

METHODS: In 20 consecutive subjects with suspected DFO, we collected intraoperative bone specimens. To explore the microbial diversity present in infected bone we performed next generation DNA sequencing. We used scanning electron microscopy (SEM) and peptide nucleic acid fluorescent in situ hybridization (PNA-FISH) with confocal microscopy to visualize and confirm the presence of biofilms.

RESULTS: In 19 of 20 (95%) studied patients presenting with DFO, it was associated with an infected diabetic foot ulcer. By DNA sequencing of infected bone, Corynebacterium sp. was the most commonly identified microorganism, followed by Finegobia sp., Staphylococcus sp., Streplococcus sp., Porphyromonas sp. and Anaerococcus sp. Six of 26 bone samples (30%) contained only one or two pathogens, while the remaining 14 (70%) had polymicrobial communities. Using a combination of SEM and PNA-FISH, we identified microbial aggregates in biofilms in 16 (60%) bone specimens and found that they were typically coccolid or rod-shaped aggregates.

CONCLUSIONS: The presence of biofilms in DFO may explain why non-surgical treatment of DFO, relying on systemic antibiotic therapy, may not resolve some chronic infections caused by biofilm-producing strains.
Clinical and microbiological features of bacteremia with Gram-positive anaerobic cocci: a population-based retrospective study

Abstract

Objective

Gram-positive, anaerobic cocci (GPC) can cause infections in humans. Only a few cases of bacteremia with GPC have been reported. We describe the clinical and microbiological characteristics of GPC bacteremia.

Methods

A retrospective population-based study of GPC bacteremia 2016–2016 in southern Sweden was performed. GPC were identified using matrix-associated laser desorption ionization time-of-flight mass spectrometry or 16S rRNA gene sequencing. Efforts were made to determine antibiotic susceptibility. Data on patient and infection characteristics, treatment, and outcome were collected from the medical records.

Results

A total of 463 isolates of GPC bacteremia in adults were studied; this corresponds to an annual incidence of 3.4 cases per 100,000 persons per year. The bacteria identified were Anaerococcus spp. (n = 49), Atopobium spp. (n = 5), Eubacterium spp. (n = 8), Pseudobutyrivibrio spp. (n = 1), Peptostreptococcus spp. (n = 5), and Veillonella spp. (n = 1). Resistance to ciprofloxacin and clindamycin was not identified, whereas resistance among the 230 isolates to penicillin was detected in five, to metronidazole in six, and to clindamycin in 10 isolates. The median age of patients was 71 years (20, 97). AEP, SAE, were made and complications were common. Fifty-one percent of infections were polymicrobial. In 85% of cases a focus of infection was identified. Forty percent of patients had either organ dysfunction or shock. The 30-day mortality was 11%, and nosocomial infections were over-represented among the deceased.

Conclusions

GPC bacteremia is much more common than previously reported. GPC bacteremia is a condition with significant mortality and mainly affecting elderly persons with comorbidities.

Gram Stain Rules All:
Two Groups to Discuss:

• Gram Positive Anaerobic Cocci (GPACs)
  – The vast majority of organisms of clinical consequence today

• Gram Negative Anaerobic Cocci (GNACs)
  – Occasional players in select circumstances

Isolation of oxidase-positive Gram-negative cocci not belonging to the genus *Neisseria* from the urogenital tract

D. J. PLATT AND J. J. S. SNELL

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SYNOPSIS In a 12-month period, oxidase-positive, Gram-negative cocci showing similar characteristics in biochemical tests have been isolated from the urogenital tract of 39 male and female patients. Although these organisms superficially resemble *Neisseria gonorrhoeae*, biochemical characterization and the results of DNA base composition analysis indicate that they do not belong to the genus *Neisseria*. The relationship of these organisms to the genera *Neisseria*, *Achromobacter*, and *Pseudomonas* is discussed.

The isolation of *Neisseria* spp other than *Neisseria gonorrhoeae* from the urogenital tract has been reported (Wilkinson, 1952). More recently, Jephcott and Morton (1972) have reported the isolation of *N. lactaminus* from a genital site, and *N. meningitidis* rectum were inoculated on to a modified Thayer Martin medium (Riddell and Buck, 1970) and incubated in candle extinction jars at 37°C for 48 hours.
Groups: GPAC

- **GPAC** (Gram Positive Anaerobic Cocci):
  - *Peptostreptococcus*
  - Peptococcus
  - **Finegoldia**
  - Parvimonas
  - Peptinophilus
  - Atopobium
  - Anaerococcus
GPACs: The History

- Variably called collectively “Peptostreptococci,” peptococci, etc
- 25-33% of all anaerobes isolated from humans
- Usually polymicrobial (abscess)
- May stain poorly
- Metronidazole disks

Frequent players in clinical infections

- Surgical infections (Meleney Gangrene)
- Fairly tolerant to specimen mishandling

Anaerococcus

- Multiple species (9+)
- Commonly Anaerococcus prevotii
- Considered normal human flora
- ? Body odor (axillae)

- Multiple disease associations
- Polymicrobial abscess(es)
- ? Increasing resistance in diabetic foot wounds

Antibiotic resistance

In general, GPAC have variable resistance to penicillins (7-10%), clindamycin (7-20%), and metronidazole (5-10%), whereas these bacteria are more susceptible to β-lactam/β-lactamase inhibitors, cephalosporins, carbapenems, and chloramphenicol (Hecht, 2006). Also, resistance to tetracycline and erythromycin has been reported (Brazier et al., 2003; Boyanova et al., 2004). Data describing differences in antimicrobial susceptibility between various species of GPAC are increasing (Bowker et al., 1996; Brazier et al., 2003, 2008; Koeth et al., 2004; Roberts et al., 2006; Könönen et al., 2007) and are described in more detail for the major groups below.

Regarding the continuous rise in antibiotic resistance amongst GPAC and anaerobes in general, more surveillance testing will be needed. Moreover, due to differences in antibiotic susceptibility between GPAC species, it is important to identify isolates in clinical specimens for susceptibility testing to adapt the correct antibacterial therapy.
Case report

Septic arthritis in a native joint due to *Anaerococcus prevotii*

S Jain, Y Bu, C Spencer, L Yee

Abstract

A 37-year-old injecting drug user presented with signs and symptoms of septic arthritis. *Staphylococcus aureus* was grown from his blood cultures. Despite treatment with flucloxacillin and fusidic acid his condition continued to deteriorate. Echocardiography showed no signs of endocarditis. Culture of his knee aspirate grew *Anaerococcus prevotii* after 5 days of incubation. Metronidazole was added to his treatment regime. A collection of pus (800 ml) was drained from the right thigh and *A. prevotii* was isolated. His condition improved gradually and he was subsequently transferred to a drug rehabilitation unit after completing his antibiotic course. The importance of anaerobic streptococci in septic arthritis, as a very rare cause, is highlighted.

A newly discovered *Anaerococcus* strain responsible for axillary odor and a new axillary odor inhibitor, pentagalloyl glucose.

Fukui T, Shinozaki J, Kajita T, Iwaseki K, Fudou R.

Author information

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Abstract

Skin surface bacteria contribute to body odor, especially axillary odor. We aimed to investigate anaerobic bacteria that had not been previously studied for axillary odor formation. A new anaerobic *Anaerococcus* sp. A20, that releases 3-hydroxy-3-methyl-hexanoic acid (HMHA, main component of axillary odor) from its glutaryl conjugate, was discovered from axillary isolates. This strain showed strong resistance to the antimicrobial agents, triclosan and 4-isopropyl-3-methylphenol; therefore, we screened plant extracts that inhibit the A20 strain. We discovered that pentagalloyl glucose (PGG) extracted from the Chinese gall plant exhibited both antibacterial and inhibitory activities against HMHA release by the A20 strain. As the excellent antibacterial activity and inhibitory effect of PGG against HMHA release were seen in vitro, we conducted an open study to evaluate the deodorant effects of PGG on axillary odor. The sensory tests on odor strength showed that application of the PGG solution could reduce axillary odors in vivo. Although there was a small change in axillary microbiota, the microbial count of A20 significantly reduced. These results strongly indicate PGG as a new innovative deodorant material that only affects odor-releasing bacteria in the axillary microbiota.

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Keywords: 3-hydroxy-3-methyl-hexanoic acid; *Anaerococcus*; axillary odor; pentagalloyl glucose; skin microbiota

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Age old microbiology: if it smells, there's anaerobes!
Atopobium "strange living thing"
• Rods, or elliptical cocci (occasionally chains)
• Bacterial Vaginosis
  – Some consider it a commensal?
  • Implicated in biofilm (therefore, in persistence)

Fig. 1 Atopobium vaginæ culture, Gram stain, magnification 100 x
(courtesy of M. Vaneechoutte, Belgium)

Rare disease
CASE REPORT

Infective endocarditis due to Atopobium vaginæ: a rare association
between genital infection and endocarditis of the tricuspid valve

Josephine Mansell¹, Yannis Gourtsoyannis², Nehal Drar³, Ruairidh Buchanan⁴

Author affiliations →

Summary

Atopobium vaginæ is an anaerobic gram-positive organism associated with genitourinary infections. Bacteraemia is rare, with only
two cases reported in the literature. This case describes an 18-year-old type 1 diabetic, presenting with sepsis and haemoptysis, on
a background of poor dental hygiene and recurrent hospital admissions. Blood cultures grew A. vaginæ and echocardiogram
revealed a large tricuspid valve lesion. Despite medical therapy, symptoms of pulmonary embolus continued and she therefore
underwent surgical resection of the lesion. Histopathological findings were of a vegetation; culture of the lesion was negative but
16S ribosomal PCR was positive, detecting 16S rRNA of A. vaginæ. The patient was treated with 4 weeks of vancomycin and made
a good recovery. To our knowledge, this represents the first report of infective endocarditis due to this organism. We also provide a
review of the literature, including comparing published drug susceptibility data with consensus breakpoints for antimicrobial
agents.
Peptococcus

• Lonely *Peptococcus niger*
  – Others reclassified elsewhere

*The phylogenetic position of Peptococcus niger based on 16S rRNA sequence studies.*

Ludwig W¹, Weisenzapper M, Dorn S, Andreason J, Schleifer KH.

1. Lehrstuhl für Mikrobiologie, Technische Universität München, F.R.G.

Abstract

A 1330 base-pair fragment of a 16S rRNA gene has been amplified, cloned and sequenced. Comparison to other 16S rRNA sequences of eubacteria showed that *P. niger* represents a deep branch within the subdivision “Gram-positive with Gram-negative cell walls”. It is not related to peptostreptococci, representatives of this genus studied so far are more closely related to clostridia.

FWID: 1703504 DOI: 10.1111/j.1574-6968.1990.tb03612.x

Indexed for MEDLINE
Peptostreptococcus (genus)

• Several representatives:
  – Peptostreptococcus anaerobius

Antimicrobial Susceptibilities of Peptostreptococcus anaerobius and the Newly Described Peptostreptococcus stomatis
Isolated from Various Human Sources

Fija Könönen, Anne Bock, Päivi Niemi, and Arja Kaukonen-Nordström

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Peptostreptococcus anaerobius was recently reclassified into several groups:

– Peptostreptococcus
– Finegoldia
– Parvimonas
– Peptoniphilus

Several representatives:

– Peptostreptococcus anaerobius
– Peptostreptococcus stomatis
– Peptoniphilis asaccharolyticus
– Peptoniphilis harei

Peptostreptococcus anaerobius is a Gram-positive, anaerobic bacterium that is commonly found in the human oral cavity. It is known to be more resistant than other gram-positive anaerobic cocci. Antimicrobial susceptibility testing of Peptostreptococcus isolates is important to guide appropriate treatment.
Primary sternal osteomyelitis due to Peptostreptococcus anaerobius.

Chen YL, Tsai SH, Hsu KC, Chen CS, Hsu CW.

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1 Department of Emergency Medicine, National Defense Medical Center, Taipei, Taiwan.

Abstract
Primary sternal osteomyelitis (PSO) is a rare syndrome. In adults, it usually occurs with underlying predisposing factors, such as immunodeficiency, or intravenous (IV) drug abuse. The infecting organism in these patients is usually Staphylococcus aureus or Pseudomonas aeruginosa. Peptostreptococcus species are Gram-positive anaerobic cocci and are part of the normal flora of human mucocutaneous surfaces. Peptostreptococcal infection can occur in all body sites, including the central nervous system, head, neck, chest, abdomen, pelvis, skin, bone, joint, and soft tissue. Here, we report on a 32-year-old previously healthy Chinese man who was diagnosed with PSO and P. anaerobius was yielded in the bacterial culture. He was treated empirically with antibiotics, but these failed. After additional limited surgical intervention with debridement, the PSO was cured.
Parvimonas micra
• Most common GPAC from the skin
• Also found in the mouth (tonsillar "core")
– Important role in dental plaque, or infections following dental procedures/manipulations
• Adherence and virulence factors are well studied
– Implicated in Periodontal Disease
• Implant‐associated failures (implantitis)
• Small colonies on solid media, with a milky halo (smooth or rough variants)
An Unusual Presentation of *Parvimonas micra* Infective Endocarditis

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Disclosures can be found in Additional Information at the end of the article

**Abstract**

*Parvimonas micra* has been identified as a prominent oral pathogen. This organism has been implicated in periodontal, soft tissue and bone infections. It causes a subacute presentation with high morbidity. We present a case of severe infective endocarditis caused by *Parvimonas micra* requiring valvular surgery despite appropriate antibiotics. To our knowledge, this is the second case report of *Parvimonas micra* infective endocarditis since its reclassification in 2006.
Infections following device emplacement, instrumentation, and procedures will continue to be evolving issues (and drive a multi-billion dollar industry in the direction of disposal devices (e.g. endoscopes)

**Peptoniphilus**

- Increasing player in chronic wounds
- ? Sinus disease
  - Fluoroquinolone resistance

**Bloodstream infections due to Peptoniphilus spp.: report of 15 cases**

K. Brown⁴, D. Church⁴, T. Lynch⁴ and D. Gregson⁴

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**Abstract**

Peptoniphilus asaccharolyticus is a commonly isolated Gram-positive anaerobic coccus (GPAC) (7). However, the type strain, ATCC 14963, is not representative of the species. Hax et al. (4) described the DNA-DNA homology between the type strain and clinical isolates as being <25%.

Mistaken Identity of *Peptoniphilus asaccharolyticus*³

Peptoniphilus asaccharolyticus is a commonly isolated Gram-positive anaerobic coccus (GPAC) (7). However, the type strain, ATCC 14963, is not representative of the species. Hax et al. (4) described the DNA-DNA homology between the type strain and clinical isolates as being <25%.

Each other phenotypically, Holdenman-Moore et al. (3) commented in 1986 that one should be cautious in reporting on isolation and incidence of *P. asaccharolyticus*. In our opinion, this caution still stands. The fact that the type strain of *P. asaccharolyticus*, ATCC 14963, is atypical of clinical isolates (Y07839), Peptoniphilus is a rare but important cause of BSI.
**Finegoldia magna**

- Formerly *Peptostreptococcus magnus (et al)*
- Increasingly becoming the “big player” in the who’s-who of anaerobes
  - Most common GPAC of consequence from skin, soft tissue, bone, and subcutaneous specimens
  - Implicated in a wide variety of disease states
    - Frustrated by slow growth, commingling, and sample bias
- Multiple virulence factors
  - May be the “*Staphylococcus aureus*” of the GPACs
Abstract

This review focuses on the virulence arsenal of the most pathogenic species among Gram positive anaerobic cocci, *Finegoldia magna* according to recently published data from 2012 to 2016. Virulence factors like sortase dependent pili and *F. magna* adhesion factor (FAF) facilitate the start of the infection. Albumin binding protein (PAB) enhances *F. magna* survival. FAF, subtilisin-like extracellular serine protease (SuFA) and superantigenic protein L protect the bacteria from factors of innate defense system. SuFA, capsule and tissue-destroying enzymes provide a deep penetration or spread of the infections and the protein L is associated with infection severity. Biofilm production results in infection chronification and complicated treatment as well as to persistence of multi-species biofilms. Resistance rates to quinolones (13.0–70%) and clindamycin (0–40.0%) are important, and resistance to penicillins (<4%), chloramphenicol (7.0%) and metronidazole (<7%) has been reported. *F. magna* should not be overlooked when present in monoinfections or mixed infections in humans.
Finegoldia magna Isolated from Orthopedic Joint Implant-Associated Infections

Bo Söderquist, a,b Sanna Björklund, a Bengt Hellmark, a,b Anders Jensen, a Holger Brüggemann a

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ABSTRACT The anaerobic Gram-positive coccus Finegoldia magna is a rare cause of infections of bone and joints. The aim of this study was to describe the microbiological and clinical characteristics of orthopedic implant-associated infections caused by F. magna. We retrospectively analyzed samples consisting of anaerobic Gram-positive cocci and samples already identified as F. magna from patients with orthopedic infections. The isolates found were determined to the species level using matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS). The antibiotic susceptibility pattern was determined by Etest. Whole-genome sequencing (WGS) was performed. Clinical data were extracted from each patient's journal. In nine patients, orthopedic joint implant-associated infections were identified as being caused by F. magna. The isolates were susceptible to most of the antibiotics tested, with the exception of rifampin and moxifloxacin in a few cases. Five of the nine infections were nonmetabolical. The most common antibiotic used to treat the infection was penicillin V, but five of the nine patients received a combination of antibiotics. Eight patients underwent surgical treatment, with extrac...
Finegoldia magna (formerly Peptostreptococcus magnus): an overlooked etiology for toxic shock syndrome?

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Abstract

Finegoldia magna is an anaerobic Gram-positive coccus, previously classified as Peptostreptococcus magnus. It is normal flora of the gastrointestinal and genitourinary tract, and can be isolated from skin and the oral cavity and is often regarded as a contaminant in cultures. As the most frequently isolated anaerobic coccus, it is implicated in a range of mono- and polymicrobial infections, including skin and skin structure, bone and joint (native and prosthetic joints), infective endocarditis (native and prosthetic valves), necrotizing pneumonia, mediastinitis and meningitis. Recently, whole genome sequencing furthered the understanding of the pathogenicity of this organism by elucidating both chromosomally encoded and mobile plasmid-mediated virulence factors. Although no cases of toxic shock syndrome have been attributed to *F. magna*, we present a case of a fatal monomicrobial *F. magna* bacteremia and hypothesize that superantigen activity, mediated via Protein L binding the variable domain of the κ light chains of IgG, resulted in the syndrome observed in our patient. Additionally, we suspect the overall significance of this pathogen is underestimated and with more sensitive detection methods, this organism will be identified more frequently in clinical cultures and associated with true infection.

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Most likely, the incidence of *F. magna* is highly underestimated due to problems of obtaining good quality anaerobic clinical specimens. For instance, detection of *F. magna* in blood cultures was found to be dependent on the blood culture system used (Bassetti et al., 2003). In this case of prosthetic valve endocarditis caused by *F. magna*, several blood cultures incubated in BacT/ALERT (BioMérieux) and BACTEC 9240 (Becton Dickinson) systems were negative despite growth of *F. magna* from biopsies of the aortic wall of the patient (Bassetti et al., 2003). Additional tests demonstrated that the isolated strain did grow in other blood culture systems like SEPTI-CHEK BHI-S (Becton-Dickinson) and ISOLATOR (Du Pont Co.) or in thioglycolate medium and on blood agar (Bassetti et al., 2003). This is consistent with other reports on prosthetic valve endocarditis caused by *F. magna*, where the bacterium could only be detected in cultures from the infected valve (Pouëdras et al., 1992; van der Vorm et al., 2000). Thus, the relevance of *F. magna* as the infectious agent in patients with apparent culture-negative endocarditis has to be considered. Inter-
Finegoldia magna

• Antibiotic resistance:
  – An emerging, worsening problem

<table>
<thead>
<tr>
<th>Antimicrobial agent*</th>
<th>No. of isolates with MIC (μg/ml):</th>
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<td>FG</td>
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<td>AC</td>
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*FG, benzylpenicillin; AC, amoxicillin; CM, clindamycin; MZ, metronidazole; LZ, linezolid; RI, rifampin; VA, vancomycin; MIF, moxifloxacin.

Bonus GPAC: Fastidiosipila sanguinis

First Human Case of Fastidiosipila sanguinis Infection

Clémence Bourruelle,* Mervé Le Bars,* Laurence Pougnet,* Ludovic Leneçq,* Philippe Buisson,* Geneviève Méry-Amaud**

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Fastidiosipila sanguinis is a Gram-positive anaerobic coccus. We report the first case of osteitis implicating this species. The strain was accurately identified by 16S rRNA sequence analysis, matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) identification having failed. The reservoir remained unclear; an endogenous origin is suspected.
**Groups: GNAC**

- **GNAC** (Gram Negative Anaerobic Cocci):
  - *Veillonella*
  - *Acidaminococcus*
  - *Megasphaera*
  - *Anaeroglobus*
  - *Negativicoccus*

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**Veillonella**

- GNAC
- Normal flora of GI / GU tract
  - High quantities in *saliva, and on tongue*
- Generally sensitive to antimicrobials:
  - Penicillin G
  - Clindamycin
  - Metronidazole
    - Can be confused with *Dialister (nim!)*
Veillonella

- A Real Case:
  - 47 YO transgender female with AIDS (CD4 ~22), off HAART, undomiciled, admitted for dysphagia, dysphonia, and ? Hemoptysis
  - Erosive esophagitis on EGD, ?? Candida
  - Tissue from esophagus grew:
    - Lactobacillus spp x 1 specimen, scant
    - Veillonella (multiple spp) x 3 specimens, heavy
  - Improved dramatically with Augmentin

Megasphaera

- Probably belongs with the Clostridia
- Many species
  - Megasphaera micronuciformis
- Implicated in Bacterial Vaginosis
  - ? Relapsing/recurrent BV in WSW?
A Few Words on BV:

• A hot topic in microbiology, microbiomics, and in the wake of rising STD rates worldwide:
  – By definition, a “dysbiosis”
    • Lactobacillus (H2O2), pH, stability of the ecosystem
    • Switch to anaerobiosis = problems
  – Increases risk for infections (HIV, STDs, PID)
  – Negative implications in Obstetrics
  – Recalcitrant problem in some women
GPAC/GNAC Specimens:

• Proper specimen is imperative!
  – Vary in their aerotolerance
  – Vary in their proportion in mixed infections
  – Clinicians may need to be reminded that anaerobes exist, cause disease, grow “differently”, and have special considerations for sensitivity testing and identification on the back end.
Perhaps blood cultures are not the ideal means for identifying GPACs/GNACs, though in all cases the proper specimens (transport, storage, etc) assure a higher probability of correctly isolating the organisms.

MALDI-TOF’s usefulness is generally in proportion to the degree of curation of the databases used...

...but that won’t be the end of anaerobic identification in the modern era (much now being done with metagenomics, shotgun sequencing, and microbiomics approaches).
Anaerobic Sensitivities?

• **Generally a good idea if:**
  – Agent selection is critical for disease control
  – Long-term antibiotics are anticipated
  – Anaerobe(s) found in a **sterile site**
  – Usual regimen has failed
  – Strict anaerobiosis is presumed (i.e. no aerobes)
    • Microaerophile GPACs problematic
  – Honorable mention:
    • **When a good reason exists to do them**
      – Eye, Brain, valve, endograft, prosthetic, transplant, ? PJI
Final Words:

• GPACs/GNACs will continue to play an evolving role in Infectious Disease

• The medical laboratorian will need to stay abreast of changes in taxonomy, diagnostics, drug sensitivity, and impact on clinical cases

Thank you!

Inquiries?

also sent to my email; will reply in a few days, or so...