

第6回医療環境委員会主催 オンラインセミナー  
医療環境中の上水について考える  
水に関連する医療関連感染 <各論>  
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# 医療環境の水と一般細菌

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# 上水

- 施設に供給される**上水**(当院は都水)は**その質が担保されている**
- 施設内に供給された上水は、**貯水槽**や**貯湯槽**で貯留され、その後、長い**配管**で分配、**吐水口**から排出される
- 施設によって、上水に井戸水を使用しているため自施設で濾過・消毒を実施している

# 上水の汚染

- 処理前の水は汚染されている
- 処理後の貯水槽内の水は病原微生物の存在は稀  
微生物伝播の原因を貯水槽内に求めるのは他の原因が  
否定されてから
- ただし、貯水槽から各フロアに分配される配管と吐水口で微生物汚染のリスクが増加

# Check List for Water Hygiene

- 感染管理の専門知識を有する責任者がいるか
- 水の調達は、公共施設からか、自施設（井戸水 etc.）か
- 自施設の調達では適切な処置をしているか
- 給湯は**配管全て**の箇所で50-60度か
- 給水は**配管全て**の箇所で25度以下か
- 温度管理以外に、塩素消毒など化学的消毒は可能か
- 全ての**蛇口**や**シャワー**は、週1回、数分間放水しているか
- 全ての**蛇口**や**シャワー**は、定期的に清掃しているか
- **配管内**のどこかに、停滞する箇所はないか
- **配管内**のどこかに、目に見える汚れ、ヌメリ、堆積物はないか

# 吐水口から出た水の汚染

- 貯水槽／貯湯槽から分配された
  - 長く複雑な配管
  - 多数に及ぶ吐水口、シャワー
- 吐水口から出た水が汚染されるリスクは予想以上

# Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections

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Although the source of drinking water (DW) used in hospitals is commonly disinfected, biofilms forming on water pipelines are a refuge for bacteria, including possible pathogens that survive different disinfection strategies. These biofilm communities are only beginning to be explored by culture-independent techniques that circumvent the limitations of conventional monitoring efforts. Hence, theories regarding the frequency of opportunistic pathogens in DW biofilms and how biofilm members withstand high doses of disinfectants and/or chlorine residuals in the water supply remain speculative. The aim of this study was to characterize the composition of microbial communities growing on five hospital shower hoses using both 16S rRNA gene sequencing of bacterial isolates and whole-genome shotgun metagenome sequencing. The resulting data revealed a *Mycobacterium*-like population, closely related to *Mycobacterium rhodesiae* and *Mycobacterium tusciae*, to be the predominant taxon in all five samples, and its nearly complete draft genome sequence was recovered. In contrast, the fraction recovered by culture was mostly affiliated with *Proteobacteria*, including members of the genera *Sphingomonas*, *Blastomonas*, and *Porphyrobacter*. The biofilm community harbored genes related to disinfectant tolerance (2.34% of the total annotated proteins) and a lower abundance of virulence determinants related to colonization and evasion of the host immune system. Additionally, genes potentially conferring resistance to  $\beta$ -lactam, aminoglycoside, amphenicol, and quinolone antibiotics were detected. Collectively, our results underscore the need to understand the microbiome of DW biofilms using metagenomic approaches. This information might lead to more robust management practices that minimize the risks associated with exposure to opportunistic pathogens in hospitals.

## Letter to the editor

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## Peritonitis caused by *Blastomonas natatoria* in a patient submitted to peritoneal dialysis

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## 腹膜透析患者の腹膜炎

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Sir,

Peritoneal dialysis is a method of renal replacement therapy for renal disease patients. Peritonitis is a major complication of peritoneal dialysis and increasing morbidity and mortality of patients. Peritoneal dialysis-related peritonitis can be caused by different microorganisms. *Staphylococcus* spp., *Enterococcus* spp. and *Enterobacteriaceae* are the main pathogenic producers of peritoneal dialysis-related peritonitis. Here we describe the first case of an infection caused by *Blastomonas natatoria* which is a microorganism that has been found as a frequent contaminant of medical devices.

We report the case of a 65-year-old man on automated peritoneal dialysis (APD) who presented an episode of peritonitis caused by an exceptional microorganism. The patient, a native of Morocco, had been diagnosed with of mellitus diabetes type 2 more than twenty-five years ago, with retinopathy and nephropathy. He also had a medical history of arterial hypertension, dyslipidemia, and recurrent thrombosis of peripheral and main vessels, needing anticoagulation. He started renal replacement therapy by hemodialysis in October 2011. In March 2014 he received a kidney transplant, which failed, so the patient remained dependent on hemodialysis. In March 2014 he presented superior cave vein syndrome with extended thrombotic occlusion of the superior cave vein, innominate trunks and central region of both subclavian veins. In October 2014 he showed thrombosis of the inferior cave vein and the iliac common vein. After this event, it was not possible for him to continue in hemodialysis because of the lack of vascular accesses, so the only renal replacement therapy possible for him was the peritoneal dialysis.

In September 2016, after a trip to Morocco, the patient

presented an episode of abdominal pain with diarrhea. Physical examination revealed diffuse abdominal pain, with peritonism. His blood pressure, heart rate and temperature were 162/79 mmHg, 90 beats per minute and 36.2°C, respectively. In blood analysis, he presented a leukocytosis of 12,800/mm<sup>3</sup> (84.6 of neutrophils). The dialysis effluent shown in figure 1, was cloudy, with a white blood cell (WBC) count of 38,300/mm<sup>3</sup>, with 92% neutrophils. The appearance and the characteristics of the effluent are shown in table 1 and figure 1. Ambulatory intraperitoneal empiric antibiotic treatment with vancomycin, tobramycin and ampicillin intraperitoneal at home was started. Blood cultures were not taken but a sample of peritoneal fluid was aseptically collected and sent to the microbiology laboratory for culture purposes. Direct Microscopic observation of the sample was performed after Gram staining, and it revealed abundant polymorphonuclear cells as well as Gram-negative rods. Vancomycin and ampicillin were stopped and intraperitoneal cefotaxime was added to the treatment. The dosage regimen consisted of two doses of tobramycin, the first dose of 100 mg at the beginning of treatment and a second dose of 50 mg. Cefotaxime (500 mg four times a day) was added to the infusion bag of peritoneal dialysis fluid (2000 cc).

The sample was plated onto 5% sheep blood Columbia agar medium incubated at 36°C under aerobic and anaerobic conditions, onto Chocolate agar incubated at 37°C in a 5% CO<sub>2</sub> atmosphere, and onto Schaedler agar + 5% sheep blood, Pheniletanol blood agar and Schaedler Neomycin plus Vancomycin agar + 5% sheep blood incubated at 36°C under anaerobic conditions (all media were from bioMérieux, Marcy l'Étoile, France). Additionally, 1 ml of the suspensions was injected into a pair of aerobic and anaerobic culture bottles (BACTEC Plus Aerobic/F and Plus Anaerobic/F) and incubated for 7 days in a BACTEC 9240 Blood Culture System (Becton Dickinson Microbiology Systems, Sparks MD, USA). After 3 days of incubation, yellow colonies were observed on aerobic and microaerophilic incubation plates. Furthermore, broth aerobic medium yielded positive growth on the 4th day. The microorganism was doubly

## 脳梗塞症治療中に発症した *Paenibacillus polymyxa* 菌血症の 1 例

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Key words: *Paenibacillus polymyxa*, bacteremia

### 序 文

*Paenibacillus polymyxa* は従来 *Bacillus* 属に分類されていた。通性嫌気性グラム陽性の有芽胞桿菌で広く自然界に分布している土壌細菌である。平素はヒトや家畜に対して無害とされ、臨床的意義は不明である。*P. polymyxa* (Prazmowski 1880) は 1994 年, Ash らによって報告され<sup>1)</sup>同義語として *Clostridium polymyxa*<sup>2)</sup> (Prazmowski 1880), “*Granulobacter polymyxa*” (Prazmowski 1880) Beijerinck 1893 年, そして *Aerobacillus polymyxa*<sup>3)</sup> (Prazmowski 1880) Donker 1926 年, と変更されており, 近年では Validation List 2000 の記載<sup>4)</sup>で *Paenibacillus* 属は 16 菌種に分類されている。

今回, 我々は本邦で報告例のない脳梗塞症治療中に発熱で発症した *P. polymyxa* による菌血症の 1 例を経験したので細菌学的特徴と若干の文献的考察を加えて報告する。

### 症 例

患者: 93 歳, 女性。

主訴: 右片麻痺。

家族歴: ペット, 家畜, 家禽などは飼育していない。

既往歴: 心房細動, 慢性心不全にて通院加療中。

現病歴: 2002 年 6 月 17 日朝, 家人が声をかけると頭を持ち上げる程度, 右片麻痺で口が曲がっており起き上がれない状態で発見され救急外来を受診した。

入院時現症: 意識障害 JCS3・3・9 方式 20~30, 脈拍 72/min・不整, 体温 36.7°C, 血圧 170/90 mmHg, 左口角下垂, 右片麻痺あり, 頭部 CT 検査にて脳梗塞症疑いで同日入院となった。

入院時検査所見 (Table 1): 血液学的検査では白血球数 13,200/μl と白血球増多を認め, 生化学検査では LDH 448 IU/l, ALP 419 IU/l と高値, また, 尿中蛋白陽性であった。他の検査は, CRP を含め異常は認められなかった。また, 広範囲な脳梗塞に反応して白血球数は高値となった。

臨床経過 (Fig. 1): 入院後, MRI 検査, 臨床症状により脳梗塞症, うっ血性心不全悪化と診断した。6 月 20 日, 25 日と 2 度, 38°C 以上の発熱を認め, いずれも静脈血培養を施行した。20 日発熱時に *P. polymyxa* が検出され, 抗菌薬を使用せず経過観察をした。25 日では尿培養と共に *Escherichia coli* が検出された。6 月 25 日静脈血培養施行後より, meropenem (MEPM) 0.5g×2/day の抗菌薬投与を開始し解熱, 入院時より尿道留置カテーテルを挿入していたが尿路感染も改善した。その後, 右片麻痺のリハビリテーションを行い, 順調に機能回復。以後入院経過中の発熱は認めなかった。

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## Persistent *Legionella* contamination of water faucets in a tertiary hospital in Japan



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### ABSTRACT

**Objective:** The feasibility of the decontamination procedure for *Legionella pneumophila* of water systems in healthcare facilities varies by water purification and disinfection methods in each country. We evaluated the efficacy of feasible decontamination strategies in Japan.

**Methods:** This study was conducted at Tokyo Medical University Hospital (1015 beds) between 2015 and 2018. Samples from the water system and cooling tower were cultured periodically. Hyper-chlorination of cool tap water (>0.2 ppm), increases in the temperature of hot water (>55 °C), and flushing were used as decontamination strategies. The case of healthcare-associated legionellosis was surveyed. Environmental and clinical isolates were genotyped.

**Results:** 1439 environmental samples were collected; 19 (1.3%) samples tested positive for *L. pneumophila* from water faucets of patient rooms, toilets, waste rooms, and water sourced from wells. Genotyping of 12 isolates confirmed that the same strains were present in eight environmental isolates and two isolates from patients over three years. Although the environmental contamination of the water system was persistent, the number of positive locations of hospital environments gradually decreased; eight in 2015, four in 2016, three in 2017, and four in 2018, respectively.

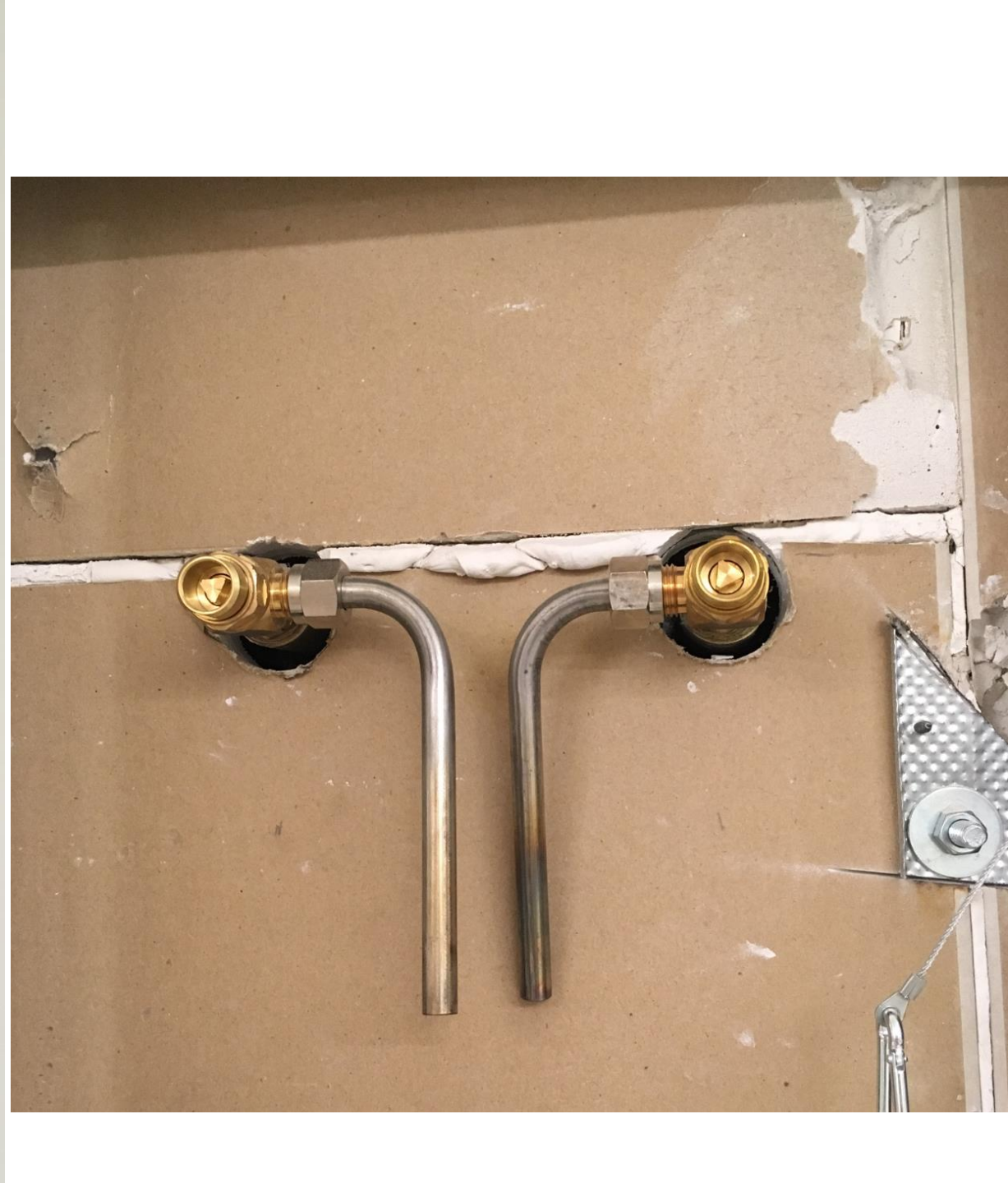
**Conclusions:** Monitoring contamination, hyper-chlorination, controlling temperature, and flushing were effective as a *Legionella* decontamination strategy.

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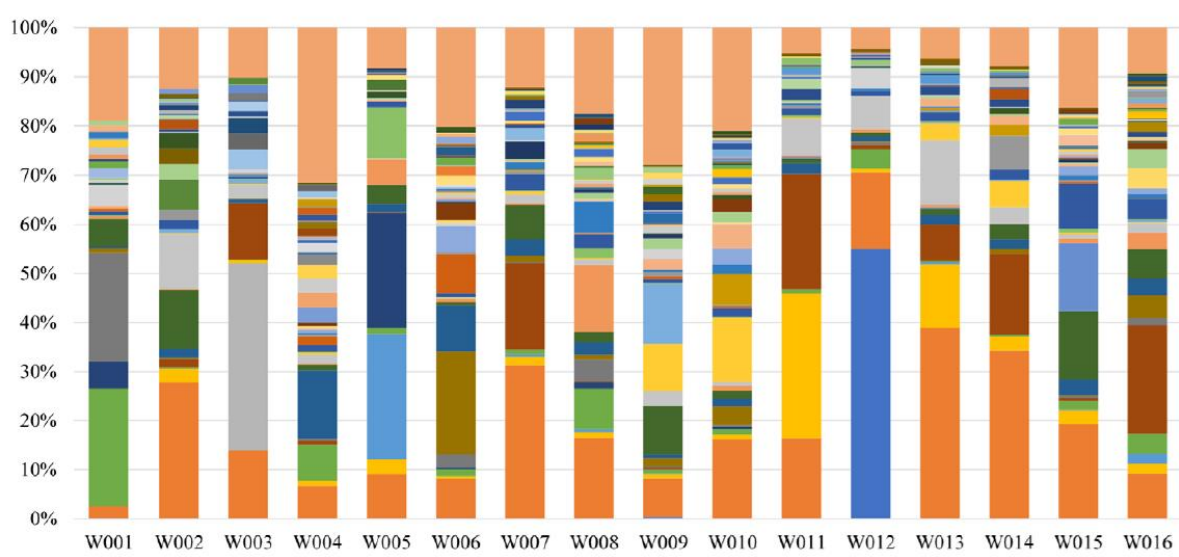
- 病室の水回りの背面

Dr. Hubert L. Holz  
MKM Marienhaus Klinikum Mainz





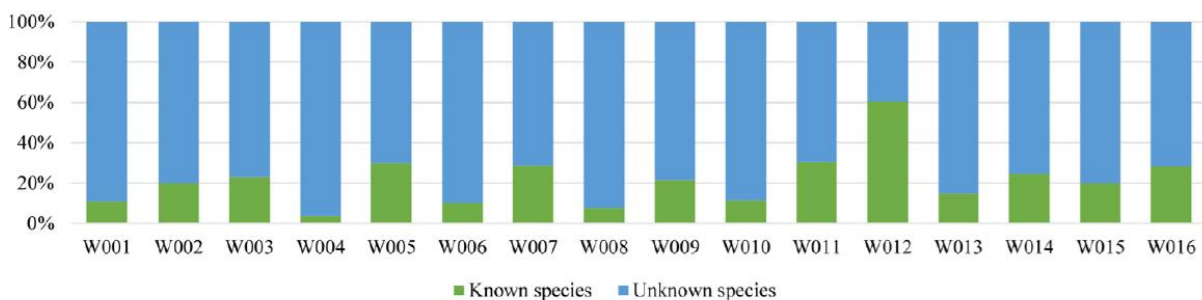
A



C

Profiled species	Prevalence
<i>Sphingomonas</i> spp.	100%
<i>Sphingopyxis</i> spp.	100%
<i>Novosphingobium</i> spp.	100%
<i>Sphingobium</i> spp.	100%
<i>Bradyrhizobium</i> spp.	100%
<i>Pseudomonas</i> spp.	100%
<i>Erythrobacter</i> spp.	94%
<i>Blastomonas</i> spp.	94%
<i>Mesorhizobium</i> spp.	94%
<i>Sphingorhabdus</i> spp.	88%
<i>Mycolicobacterium</i> spp.	88%
<i>Rhizobium</i> spp.	88%
<i>Paraburkholderia</i> spp.	88%
<i>Sphingomonas ursincola</i>	81%
<i>Phenylbacterium</i> spp.	81%
<i>Blastomonas fulva</i>	81%
<i>Aquabacterium</i> spp.	81%
<i>Burkholderia</i> spp.	81%
<i>Mycobacterium</i> spp.	75%
<i>Methylobacterium</i> spp.	75%
<i>Nitrospira</i> spp.	75%
<i>Hephaestia</i> spp.	75%
<i>Massilia</i> spp.	75%
<i>Streptomyces</i> spp.	75%
<i>Afipia</i> spp.	69%
<i>Aquisediminimonas</i> spp.	69%
<i>Qipengyuania</i> spp.	69%
<i>Brevundimonas</i> spp.	69%
<i>Acidovorax</i> spp.	69%
<i>Legionella</i> spp.	69%
<i>Croceicoccus</i> spp.	69%
<i>Azospirillum</i> spp.	69%
<i>Tsuneonella</i> spp.	63%
<i>Pseudaxanthomonas</i> spp.	63%
<i>Stakelama</i> spp.	63%
<i>Caulobacter</i> spp.	63%
<i>Polymorphobacter</i> spp.	56%
<i>Blastomonas natatoria</i>	56%
<i>Reyranela</i> spp.	56%
<i>Erythrobacter colymbi</i>	56%
<i>Rhodopseudomonas</i> spp.	56%
<i>Roseomonas</i> spp.	56%
<i>Cupriavidus</i> spp.	56%
<i>Nitrosomonas</i> spp.	50%
<i>Bosea</i> spp.	50%
<i>Sediminibacterium</i> spp.	50%
<i>Novosphingobium subterraneum</i>	50%
<i>Aromatoleum</i> spp.	50%
<i>Paracoccus</i> spp.	50%
<i>Paenibacillus</i> spp.	50%

B



**Fig. 1.** Microbial composition of 16 drinking water samples collected from different locations of the Parma District and delivered by the city water supply system.

Panel A displays a histogram with the relative abundance of each microbial species identified in the analysed samples. From left to right, the colour-coding order of the legend reflects average abundances from largest to smallest, i.e. 55% *Acidovorax delafieldii* in sample W012, 38.9% *Sphingomonas* spp. in sample W013, and so on.

Panel B shows the percentage of unknown and known bacterial species profiled, while Panel C depicts the prevalent bacterial taxa identified among all processed samples.

Tap water as a natural vehicle for microorganisms shaping the human gut microbiome  
 Environ Microbiol. 2022; 24: 3912–3923.

PMID:35355372

# 上水に含まれうる一般細菌

- *Pseudomonas aeruginosa*
- *Pseudomonas* spp.
- *Stenotorophomonas maltophilia*
- ブドウ糖非発酵グラム陰性桿菌
  
- *Serratia* spp., *Enterobacter* spp.等の腸内細菌目細菌
- *Staphylococcus* spp.等のグラム陽性球菌
  
- *Legionella* spp.
- *Mycobacterium* spp.

# 上水に含まれうる一般細菌の特徴

- 病原性が弱いものが検出されやすい  
 栄養要求度との関連  
 一般的な微生物検査室では検出れても同定できないことも
- 病原性が高いものは頻度は低いが検出され得る  
 特に大切なのは *Pseudomonas aeruginosa*
- 水設備にバイオフィルム形成が起こると定着が促進される

# Take Home Message

- 貯水槽／貯湯槽よりも上流の上水が汚染されていることは稀
- 配管と吐水口で汚染が発生しえる
- 基本的には病原性の低い微生物が多いが、時に緑膿菌等の病原性が高いものに汚染されている